**Studies on** **Genetic Variability and Divergence Analysis in Blackgram [*Vigna* mungo (L.) Hepper] using Mahalanobis D2 statistic**

**Abstract**

The current research used 29 distinct genotypes of blackgram and was carried out during the 2021 zaid season at the Crop Research Centre of Sardar Vallabhbhai Patel University of Agriculture and Technology in Meerut, Uttar Pradesh. Many traits were noted, such as the number of days until 50% flowering, the number of days until maturity, the height of the plant, the number of branches per plant, the number of pods per plant, the length of the pods, the number of seeds per pod, the biological yield per plant, the test weight, the harvest index, the weight of all the pods per plant (g), and the seed yield per plant. Using analysis of variance, it was discovered that each of the twelve variables had a substantial degree of variability. Using analysis of variance, it was discovered that each of the twelve variables had a substantial degree of variability. In contrast, biological yield per plant, pod length, days to 50% flowering, number of seeds per pod, grain yield per plant, harvest index, and days to maturity showed moderate (10–20%) and test weight showed low (<10%) characteristics. Plant height, number of pods per plant, weight of total pods/plant (g), and number of primary branches per plant showed high PCV & GCV. Furthermore, the importance of the environment in character expression was shown by the fact that the PCV estimate was greater than the matching GCV for each character. High heritability and substantial genetic progress were found for plant height alone, indicating that additive gene activity is the source of the heritability. The twenty-nine Blackgram genotypes were split into five groups based on their D2 scores. Cluster I included nine genotypes and was the largest of the five clusters. Clusters II and V each contained four genotypes, but clusters III and IV each had six. Cluster III had the greatest intra-cluster distance, followed by clusters II, I, and V. Cluster IV had the least distance (1.987).

**Keywords**-Genetic variability, heritability, genetic advance, GCV, PCV, D2 values

**INTRODUCTION**

The tropical legume known as urdbean, or Blackgram [Vigna mungo (L.) Hepper], with chromosomal number 2n=22, belongs to the fabaceae and sub-family papilionaceae. It is grown for its dried seeds, which are a substantial source of protein, and is self-pollinating. With high levels of protein (25g/100g), potassium (983 mg/100g), calcium (138 mg/100g), iron (7.57 mg/100g), niacin (1.447 mg/100g), thiamine (0.273 mg/100g), and riboflavin (0.254 mg/100g), blackgram is one of the most nutrient-dense pulses. (USDA, 2021–2022, National Nutrient Database). Its genome is about 1.56 pg/IC (574 Mbp) in size. Blackgram, another staple in India, provides the essential amino acids present in most cereals. The biological value of wheat or rice and pulses like blackgram is enhanced because of the complementary interactions between essential amino acids like as arginine, leucine, lysine, isoleucine, valine, and phenylalanine, among others (Goyal et al., 2010). For milch cattle, its green feed is nutrient-dense and very advantageous. As green manure, it may also be used. It may restore soil fertility and fix nitrogen from the atmosphere since it is a leguminous plant (Goyal et al., 2010). It is grown in a variety of soil types, ranging from sandy soils to heavy black cotton soils. It thrives on soil that is rather heavy. The ideal soil would be a loam with a pH of 6.0 to 7.5 that drains nicely. After pigeon pea, it is the second most important pulse crop in India in terms of both production and acreage. This is one of the most important grain legumes in Asian agriculture, particularly in South Asia. India is the world's largest producer and consumer of urdbeans, accounting for about 90% of global production. In India, it is grown on more than 4.6 million hectares and produces 24.5 lakh tons of urd year (Anonymous 2021b). The states that produce the most blackgram in India are Madhya Pradesh, Uttar Pradesh, Andhra Pradesh, Maharashtra, and Tamil Nadu. It accounts for over 19% of the country's total area under pulse crops and ranks fourth in terms of both area and production, after mungbean, chickpea, and pigeon pea. With a total area of 5.64 lakh hectares, Uttar Pradesh produces 3.03 lakh tons and has a productivity of 537 kg/ha (IIPR, Kanpur 2020-21). Although India produces around 70% of the world's blackgram, its productivity is very low in comparison to the potential yields in many other countries. In addition to India, Bangladesh, Myanmar, Pakistan, and Afghanistan are important blackgram-growing countries. Pulses' genotypes are more vulnerable to poor management, which limits productivity even if they could have superior genetic potential than cereals. This is due to the fact that pulses are consistently grown on marginal soils that are under moisture stress and poor in fertility. Other names for blackgram (Vigna mungo (L. Hepper)) are urad, mash, and kalai. With genetic diversity concentrated in India, blackgram has a primary origin in India and a secondary origin in Central Asia.

An essential first step in every research endeavor aiming at boosting crop yield is evaluating the genetic diversity of pulses. The lack of stable, high-yielding cultivars is one of the primary barriers to its production, therefore high-yielding genotypes selected from germplasm may perform better in a range of agro-ecological conditions. Instability and the weak genetic base of existing cultivars are the primary obstacles to this crop's wider adaptation. Ayyadurai et al. (2024) found that improved crop management is practically essential for raising blackgram yields. Their study, carried out in Tamil Nadu, showed that the use of Good Agricultural Practices (GAPs), including optimal planting, balanced fertilization, and suitable spacing, resulted in significant increases in output. This demonstrates how crop management techniques may significantly affect how a genotype displays its potential in the field, even if genetic improvement is still vital. Their findings provide useful perspective for evaluating the efficacy of different genotypes and breeding lines in real-world field situations. Breeders place special emphasis on the genotypic and phenotypic coefficient of a metric character, which indicates how effectively a genotype can be recognized by its phenotypic manifestation. This coefficient gauges the degree of resemblance between the parents and the offspring. The required selection pressure is also exerted by genetic advancement. Genetic progress and heritability are given as a proportion of variation and mean. Selecting parents with significant genetic difference should result in superior and desirable segregants after crossing (Bhatt, 1973). It is also known that certain advantageous genes present in germplasm collections provide resistance to a range of illnesses; hence, assessing and describing such local germplasm provides useful information for breeding attractive cultivars. Genetic variation is thus one of the considerations for parent selection in the hybridization scheme. The availability of diverse segregants in a plant breeding endeavor is determined by the diversity of the parents.

**MATERIALS AND METHODS**

The present investigation was carried out during *zaid* 2021 at Crop Research Centre of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut (U.P.), situated at an elevation of about 297 meters above mean sea level with 29.01 º’N latitude and 77.75 º’E longitudes, representing the North western plain zone. The experimental material consisted of 29 blackgram genotypes obtained from IIPR, Kanpur. The experiment used a randomized block design with three replications. Three rows were planted in each 5.0 m long plot, with a 30 cm space between rows and a 10 cm space between plants. This spacing was maintained with appropriate thinning. To document the findings on the following twelve traits, five competitive plants from each genotype in each replication were selected at random and tagged. The average values of each replication's twenty-nine genotypes were utilized for statistical analysis. The environmental coefficient of variation (ECV), phenotypic coefficient of variation (PCV), and genotypic coefficient of variation (GCV) were computed using Burton and Devane's (1952) methodology. Heritability in the broadest sense, or h2 (b), was calculated as the ratio of genotypic to phenotypic variance (Allard, 1960). Following Rao (1952), genetic divergence in thirty-eight genotypes was measured using Mahalanobis D2 statistic (1936), and genetic advancement as a percentage of mean for each character was calculated in line with Johnson et al. (1955).

**Results and Discussion**

A successful plant breeding program requires a high degree of genetic variety because it allows breeders to choose superior individuals from a genetically diverse base population. Since many economically important qualities are greatly influenced by environmental conditions, the amount that a crop may be enhanced mostly depends on the kind, degree, and size of genotypic variety present in a population. A large range of variability among the genotypes that must be assessed for all the attributes is also necessary in order to find significantly superior genotypes.

The average performance of 29 blackgram line genotypes is shown in Table 1. Analysis of variance revealed highly significant genotype differences for all the traits: days to 50% flowering, days to maturity, plant height, number of pods per plant, number of branches per plant, number of seeds per pod, weight of total pods per plant, length of pod, biological yield per plant, test weight, harvest index, and seed yield per plant. This suggests that the experimental material had significant genetic variability. These results were in line with those of Priyanka et al. (2016), Rolaniya et al. (2017), Nagi and Lal et al. (2017), Kumar et al. (2015), and Balachandran et al. (2010).

Estimates of the genotypic and phenotypic coefficients of variation (GCV and PCV) for different characteristics are shown in Table 2. The results of the current study indicate that the GCV and PCV were moderate (10–20%) for the number of pods per plant, harvest index, number of seeds per plant, biological yield per plant, number of seeds per pod, test weight, days to 50% flowering, and pod length; they were low (<10%) for the days to maturity. The GCV and PCV were higher (>20%) for the weight of all the pods per plant, the number of branches per plant, and the height of the plant. The study's findings also demonstrated that the PCV estimates were much higher than the corresponding GCV for each of the characteristics that were looked at. This suggests that environmental factors had the least effect on the phenotypic expression of the genotypes, and that simple selection procedures could provide the intended improvement. In line with these findings were the findings of the following studies: Sharma et al. (2006), Konda et al. (2009), Senapati and Mishra (2010), Kodanda Rami Reddy et al. (2011), Meshram et al. (2013), Deepshikha et al. (2014), Patel et al. (2014), Ramya et al. (2014), Kumar et al. (2015), Patel et al. (2015), Gowsalya et al. (2016), and Patidar et al. (2018). The genetic parameters analyzed revealed that the weight of all the pods on a plant, the number of branches on a plant, and the height of the plant had significant phenotypic and genotypic coefficients of variation, suggesting that there is sufficient genetic diversity for these features in the population. As a result, it provides the basis for selecting favorable genotypes from the diverse population to boost blackgram production. The present research found that plant height, number of branches per plant, and weight of total pods per plant all increased genetic variability. This implies that the hybridization program may use parent selection based on these traits' performance to produce desired transgressive segregants.

A high heritability estimate indicates the effectiveness of selection based on phenotypic performance rather than necessarily indicating a significant genetic gain for that particular trait. Heritability estimates for the various features in the present investigation are given in Table 2. Harvest index, biological yield per plant, number of pods per plant, days to 50% flowering, days to maturity, test weight, plant height, number of branches per plant, weight of total pods per plant, number of seeds per pod, and length of pod were all found to have high magnitude heritability. This suggested that these traits were least affected by environmental factors. In other words, it may be concluded that the phenotypic expression of these traits correctly represented their genotype. Such high heritability estimates have been reported by Priyanka et al. (2016), Patidar et al. (2018), Neelavathi and Govindarasu (2010), Panigrahi et al. (2014), and Balachandran et al. (2010). Strong heritability and high genetic progress for the weight of all pods per plant, according to the research's results, suggested that additive gene action was the source of the heritability and that these traits might be improved by straightforward selection. Similar results were obtained by Balachandran et al. (2010), Konda et al. (2009), and Sharma et al. (2006).

Examining the variance in Blackgram genotypes was the goal of the present investigation. The twenty-nine genotypes were grouped into five groups. The clustering pattern showed that there was sufficient divergence for the formation of separate groups. Each cluster contains treatments with a variety of genesis and origins from many research sites. As the clustering pattern indicates, geographic diversity is not a good measure of genetic variability. Therefore, Mahalanobis D2 analysis is a helpful technique for evaluating genetic difference, even when using material from the same geographic location. Table 3 shows that the number of seeds per pod, days to maturity, days to 50% flowering, number of pods per plant, length of pods, weight of total pods per plant, biological yield per plant, number of branches per plant, height of plant, seed yield per plant, test weight, and harvest index were the current factors that contributed most to genetic divergence. This perspective has been supported by research by Shanthi et al. (2006), Umadevi and Ganesan (2007), Niranjan and Rama Chandra (2009), Neelavathi and Govindarasu (2010), Geethanjali et al. (2015), and Hadimani et al. (2016).

**Grouping of twenty-nine genotypes of blackgram [(*Vigna mungo* L.) Hepper] in five clusters**

Twenty-nine blackgram genotypes [(Vigna mungo L.) Hepper] were divided into five groups, as shown in table 4. Cluster I was the largest of the five clusters, including nine genotypes. While clusters II and V each contained four genotypes, clusters III and IV each had six. The results of the research suggest that there were parallels between genetic and geographic diversity. These findings are somewhat in line with those of Shanthi et al. (2006), Nandlal and Mishra (2006), Umadevi and Ganesan (2007), Konda et al. (2007), Chauhan et al. (2008), Elangaimannan et al. (2008), Niranjan and Rama Chandra (2009), Neelavathi and Govindarasu (2010), Singh et al. (2012), Jayamani and Sathya (2013), Geethanjali et al. (2015), Hadimani et al. (2016), Veni et al. (2016), and others. Table 5 displays the average D2 values for each of the 29 genotypes of blackgram [(Vigna mungo L.) Hepper] within and within five clusters. The largest inter-cluster distance (5.093) was found between Clusters IV and V. The genotypes present in these clusters exhibit a broad range of genetic diversity, which may be exploited in a blackgram crossing strategy to boost grain yield. Cluster I and IV, on the other hand, had the least inter-cluster distance (2.735), indicating that the genotypes in these clusters may not be used in the hybridization process due to their near proximity. Out of all the clusters, cluster IV had the least intra-cluster distance (1.987) and cluster III the largest (2.498). The greatest intra-cluster distance was caused by the significant genetic diversity of its genotypes. It is very unlikely that genotypes from the same cluster with low intra-cluster distance values would cross to produce appropriate segregants. As a result, it would be worthwhile to experiment with crosses between the genotypes of clusters that are further apart. The restricted variety and selection of parents within clusters with higher means for a certain feature may be advantageous for the future creation of high-yielding blackgram cultivars.

**Table 1 Analysis of variance (ANOVA) for twelve characters of twenty-nine genotypes in blackgram [(*Vigna mungo* L.) Hepper]**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Source of variation** | DF | Days to 50% flowering | Days to maturity | Plant height (cm) | No. of pods per plant | No. of branches per plant | No of seeds/pod | Weight Of total pods/plant(g) | Pod length(cm) | Biological yield/plant(g) | Test weight(g) | Harvest index(%) | Seed yield/plant(g) |
| Replication | 2 | 2.62 | 0.36 | 7.61 | 14.66 | 0.02 | 0.09 | 26.79 | 0.003 | 0.86 | 0.04 | 10.68 | 0.79 |
| Treatment | 28 | 144.37\*\* | 124.06\*\* | 210.90\*\* | 103.66\*\* | 1.96\*\* | 1.44\*\* | 152.18\*\* | 0.762\*\* | 63.09\*\* | 3.33\*\* | 77.41\*\* | 7.51\*\* |
| Error | 56 | 3.55 | 3.27 | 1.38 | 2.05 | 0.02 | 0.06 | 1.90 | 0.025 | 1.03 | 0.02 | 1.17 | 0.02 |
| Total | 86 | 49.38 | 42.53 | 69.74 | 35.43 | 0.65 | 0.51 | 51.41 | 0.264 | 21.23 | 1.10 | 26.21 | 2.48 |

**Table 2 Estimates of general mean, range, GCV, PCV, heritability *h*2 % (BS), genetic advance and genetic advance as percent of mean for 12 characters in blackgram [(*Vigna mungo* L.) Hepper]**

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Genotypes | Mean | Min | Max | var (g) | var (p) | Heritability (%) | GA | GA% mean | GCV (%) | PCV (%) | ECV)%) | % cont |
| Days to 50% flowering | 63.38 | 47.33 | 76.67 | 46.94 | 50.49 | 92.97 | 13.61 | 21.47 | 10.81 | 11.21 | 2.97 | 9.66 |
| Days to maturity | 79.20 | 70.33 | 91.00 | 40.26 | 43.54 | 92.48 | 12.57 | 15.87 | 8.01 | 8.33 | 2.28 | 10.79 |
| Plant height (cm) | 33.34 | 22.60 | 53.22 | 69.84 | 71.22 | 98.06 | 17.05 | 51.13 | 25.07 | 25.31 | 3.53 | 7.40 |
| No. of pods per plant | 36.92 | 27.67 | 51.00 | 33.87 | 35.92 | 94.28 | 11.64 | 31.53 | 15.76 | 16.23 | 3.88 | 9.46 |
| No. of branches per plant | 3.02 | 1.97 | 4.10 | 0.65 | 0.67 | 96.81 | 1.63 | 54.02 | 26.65 | 27.09 | 4.84 | 7.85 |
| No of seeds/pod | 5.09 | 3.93 | 7.03 | 0.46 | 0.52 | 87.95 | 1.31 | 25.73 | 13.32 | 14.20 | 4.93 | 10.99 |
| Weight Of total pods/plant(g) | 21.56 | 13.08 | 38.27 | 50.09 | 52.00 | 96.34 | 14.31 | 66.37 | 32.83 | 33.44 | 6.40 | 8.55 |
| Pod length(cm) | 4.63 | 4.05 | 6.37 | 0.25 | 0.27 | 90.73 | 0.97 | 21.01 | 10.71 | 11.24 | 3.42 | 9.12 |
| Biological yield/plant(g) | 29.00 | 20.98 | 41.93 | 20.69 | 21.72 | 95.26 | 9.14 | 31.53 | 15.68 | 16.07 | 3.50 | 8.22 |
| Test weight(g) | 8.09 | 5.84 | 10.03 | 1.11 | 1.12 | 98.66 | 2.15 | 26.59 | 13.00 | 13.08 | 1.52 | 5.95 |
| Harvest index(%) | 30.00 | 20.33 | 41.15 | 25.41 | 26.58 | 95.60 | 10.15 | 33.84 | 16.80 | 17.19 | 3.61 | 5.73 |
| Seed yield/plant(g) | 8.61 | 6.28 | 12.80 | 2.50 | 2.52 | 99.12 | 3.24 | 37.63 | 18.35 | 18.43 | 0.00 | 6.26 |

**Table 3. Cluster mean values for 12 characters of twenty-nine genotypes in blackgram [(*Vigna mungo* L.) Hepper]**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Clusters |  | Days to 50% flowering | Days to maturity | Plant height (cm) | No. of pods per plant | No. of branches per plant | No of seeds/pod | Weight Of total pods/plant(g) | Pod length(cm) | Biological yield/plant(g) | Test weight(g) | Harvest index(%) | Seed yield/plant(g) |
| **I** | **Mean** | 61.48 | 75.41 | 27.97 | 33.35 | 2.78 | 4.61 | 18.36 | 4.52 | 28.23 | 7.29 | 27.33 | 7.61 |
|  | **± SE** | 3.26 | 3.62 | 2.90 | 2.92 | 0.68 | 0.50 | 3.95 | 0.35 | 5.42 | 1.07 | 2.80 | 0.84 |
| **II** | **Mean** | 64.83 | 80.00 | 39.78 | 38.00 | 3.79 | 6.26 | 18.80 | 5.56 | 30.50 | 8.08 | 25.80 | 7.71 |
|  | **± SE** | 5.51 | 5.48 | 7.09 | 4.70 | 0.51 | 0.52 | 4.51 | 0.56 | 4.47 | 0.81 | 4.66 | 0.47 |
| **III** | **Mean** | 62.28 | 79.33 | 29.82 | 44.69 | 2.67 | 4.81 | 31.02 | 4.41 | 30.49 | 8.82 | 35.85 | 10.76 |
|  | **± SE** | 4.71 | 5.33 | 3.69 | 5.28 | 0.81 | 0.29 | 6.90 | 0.20 | 4.91 | 0.62 | 5.04 | 1.21 |
| **IV** | **Mean** | 72.50 | 88.06 | 29.93 | 32.89 | 2.53 | 4.97 | 17.63 | 4.52 | 27.25 | 7.93 | 29.52 | 7.97 |
|  | **± SE** | 3.07 | 3.01 | 2.75 | 4.00 | 0.53 | 0.04 | 2.18 | 0.32 | 4.31 | 0.88 | 3.99 | 1.24 |
| **V** | **Mean** | 54.17 | 73.42 | 49.37 | 38.25 | 4.03 | 5.62 | 23.22 | 4.41 | 29.63 | 9.06 | 32.17 | 9.49 |
|  | **± SE** | 6.50 | 3.59 | 3.95 | 3.01 | 0.00 | 0.59 | 8.35 | 0.33 | 3.30 | 0.65 | 3.07 | 1.01 |

**Table 4. Grouping of twenty-nine genotypes of blackgram [(*Vigna mungo* L.) Hepper] in five clusters**

|  |  |  |
| --- | --- | --- |
| **Clusters** | **No of genotypes** | **Genotypes** |
| **I** | **9** | **4,5,6,8,11,22,23,25,29** |
| **II** | **4** | **1,10,14,16,** |
| **III** | **6** | **9,12,13,17,20,24** |
| **IV** | **6** | **2,3,15,19,21,28** |
| **V** | **4** | **7,18,26,27** |

**Table 5. Average inter and intra cluster (D2 values) among five clusters of twenty-nine genotypes in blackgram [(*Vigna mungo* L.) Hepper]**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Clusters** | **I** | **II** | **III** | **IV** | **V** |
| **I** | **2.299** |  |  |  |  |
| **II** | **3.965** | **2.415** |  |  |  |
| **III** | **4.077** | **5.042** | **2.498** |  |  |
| **IV** | **2.735** | **4.022** | **4.195** | **1.987** |  |
| **V** | **4.320** | **3.868** | **3.937** | **5.093** | **2.099** |

**Conclusion**

Research on genetic characteristics utilizing these genotypes was valuable, and variance analysis revealed a significant degree of genetic variability in the existing breeding material collection. Plant height, days to 50% flowering, days to maturity, number of pods per plant, number of branches per plant, number of seeds per pod, weight of total pods per plant, length of pod, biological yield per plant, test weight, harvest index, and seed yield per plant are all effective traits in response to direct selection. The traits that had the highest estimates of heritability were grain yield per plant, test weight, plant height, number of branches per plant, weight of total pods per plant, harvest index, biological yield per plant, number of pods per plant, days to 50% flowering, days to maturity, pod length, and number of seeds per pod. In order to improve the blackgram harvest, direct selection based on these attributes may be beneficial, since this showed how additive gene activity affects the expression of these traits. The research indicated that the weight of all pods per plant had high genetic progress and strong heritability. This suggests that heredity is caused by additive gene action and that these traits might be improved by simple selection. Crosses between clusters IV and V's genetically varied genotypes are expected to exhibit strong heterosis and probably provide novel combinations with desired traits to produce desirable segregates with greater yield for creating superior blackgram cultivars. This is because the D2 study showed that the inter-cluster distance was largest between clusters IV and V.

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1.

2.

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**References**

1. Allard R.W. (1960). *Principles of Plant Breeding*. John Wiley and Sons, Inc., New York.
2. Ayyadurai P., Kathiravan M., Senthilkumar P., Sasikumar K., Thukkaiyannan P., Govindan K., Senthilkumar M., Paramasivan M., & Deivamani M. (2024). Enhancing blackgram (*Vigna mungo* L.) productivity through good agricultural practices in Tamil Nadu, India. *Journal of Scientific Research and Reports*, 30(11), 636–645.
3. Balachandran D.L., Mullainathan S., Velu, and Thilagavathi C. (2010). Study of genetic variability, heritability and genetic advance in blackgram. *African Journal of Biotechnology*, 9(19): 2731–2735.
4. Bhatt G.M. (1973). Significance of path coefficient analysis in determining the nature of character association. *Euphytica*, 22: 338–343.
5. Burton G.W. and Devane R.W. (1953).Estimating heritability in tall fescue (Festuca arundinacea) from replicated clonal material. *Agronomy Journal*, 45: 478–481.
6. Chauhan M.P., Mishra A.C. and Ashok K.S. (2008). Genetic divergence studies in urdbean (Vigna mungo (L.) Hepper). *Legume Research*, 31(1): 63–67.
7. Deepshikha, Lavanya R.G. and Kumar S. (2014). Assessment of genetic variability for yield and its contributing traits in blackgram. *Trends in Biosciences*, 7(18): 2835–2838.
8. Elangaimannan R., Anbuselvam Y. and Karthikeyan P. (2008). Genetic diversity in blackgram. *Legume Research*, 31(1): 57–59.
9. Geethanjali, Anuradha C. and Suman. (2015). Genetic diversity for yield and its components in blackgram (Vigna mungo L.). *International Journal*, 4(8): 2277–8179.
10. Goyal A.K., Middha S.K. and Sen A. (2010). Evaluation of the DPPH radical scavenging activity, total phenols and antioxidant activities in Indian wild *Bambusa vulgaris* vittata methanolic leaf extract. *Journal of Natural Pharmaceutics*, **1**: 40–45.
11. Hadimani A., Konda C.R., Nidagundi J.M. and Patil R. (2016). Genetic diversity analysis in blackgram (Vigna mungo (L.) Hepper) based on quantitative traits. *Green Farming*, 3: 598–601.
12. Jayamani P. and Sathya M. (2013). Genetic diversity in pod characters of blackgram (Vigna mungo (L.) Hepper). *Legume Research*, 36(3): 220–223.
13. Johanson H.W., Robinson H.F. and Comstock R.E. (1955). Estimates of genetic and environmental variability in soybean. *Journal of Agronomy*, 47: 314–318.
14. Kodanda Rami Reddy D., Venkateshwarlu O., Siva Jyothi G.L. and Obaiah M.C. (2011). Genetic parameters and inter-relationship analysis in blackgram (Vigna mungo (L.) Hepper). *Legume Research*, 34: 149–152.
15. Konda C.R., Salimath P.M. and Mishra M.N. (2007). Genetic diversity estimation in blackgram. *Legume Research*, 30(3): 212–214.
16. Konda C.R., Salimath P.M. and Mishra M.N. (2009). Genetic variability studies for productivity and its components in blackgram (Vigna mungo (L.) Hepper). *Legume Research*, 32(1): 59–61.
17. Kumar G.V., Vanaja M., Lakshmi N.J. and Maheshwari M. (2015). Studies of variability, heritability and genetic advance for quantitative traits in blackgram (Vigna mungo (L.) Hepper). *Agricultural Research Journal*, 52(4): 28–31.
18. Mahalanobis P.C. (1936). On the generalized distance in statistics. *Proceedings of the National Academy of Sciences, India*, 2: 49–55.
19. Meshram M.P., Ali R.I., Patil A.N. and Sunita M. (2013). Variability studies in M3 generation in blackgram (Vigna mungo (L.) Hepper). *The Bioscan*, 8(4): 1357–1361.
20. Nagi P. and Lal G.M. (2017). Estimates of genetic variability and heritability for yield and yield component traits in blackgram (Vigna mungo (L.)). *International Journal of Agricultural Sciences*, 9(36): 4550–4552.
21. Neelavathi S. and Govindarasu R. (2009). Analysis of variability, correlation and diversity in rice fallow blackgram (Vigna mungo L. Hepper). *Legume Research*, 33(3): 206–210.
22. Neelavathi S. and Govindarasu R. (2010). Estimation of genotypic variability in blackgram. *Legume Research*, 33(3): 206–210.
23. Niranjan S. and Rama Chandra M. (2009). Genetic divergence and selection indices among the micro mutant lines in blackgram (Vigna mungo (L.) Hepper). *Journal of Crop Science and Biotechnology*, 12(2): 69–72.
24. Panigrahi K.K., Mohanty A. and Baisakh B. (2014). Genetic divergence, variability and character association in landraces of blackgram from Odisha (Vigna mungo (L.) Hepper). *Journal of Crop and Weed*, 10(2): 155–165.
25. Patel R.V., Patil S.S., Patel S.R. and Jadhav B.D. (2014). Genetic variability and character association in blackgram (Vigna mungo (L.) Hepper). *Trends in Biosciences*, 7(23): 3795–3798.
26. Patel R.V., Patil S.S., Patel S.R. and Jadhav B.D. (2015). Genetic variability and character association in blackgram (Vigna mungo (L.)). *Indian Journals*, 7(23): 3795–3798.
27. Patidar M., Sharma H. and Haritwal S. (2018). Genetic variability studies in blackgram (Vigna mungo (L.) Hepper). *International Journal of Chemical Studies*, 6(2): 1501–1503.
28. Priyanka S., Rangaiah S. and Showkath Babu B.M. (2016). Genetic variability estimates of quantitative and qualitative traits in blackgram. *International Journal of Agricultural Sciences*, 8(40): 1821–1824.
29. Ramya B., Nallathambi G. and Ram S.G. (2014). Genetic variability, heritability and genetic advance in induced mutagenesis blackgram (Vigna mungo (L.) Hepper). *Plant Archives*, 14(1): 139–141.
30. Rao C. R. (1952). *Advanced statistical methods in biometrical research* (1st ed.). John Wiley & Sons
31. Rolaniya D.K., Jinjwadiya M.K., Meghawal D.R. and Lal G.M. (2017). Studies on genetic variability in blackgram (Vigna mungo (L.) Hepper) germplasm. *Journal of Pharmacognosy and Phytochemistry*, 6(4): 1506–1508.
32. Senapati N. and Mishra R.C. (2010). Genetic divergence and variability studies among micro mutants in blackgram (Vigna mungo (L.) Hepper). *Legume Research*, 33(2): 108–113.
33. Shanthi P., Jebaraj S. and Manivannan N. (2006). Genetic diversity in urdbean (Vigna mungo L. Hepper). *Legume Research*, 29(3): 181–185.
34. Sharma D.K., Billore M. and Kataria V.P. (2006). Breeding criteria for selection of blackgram (Vigna mungo L.) genotypes for hill agro-ecology of Jhabua district in western Madhya Pradesh. *International Journal of Agricultural Sciences*, 2(1): 201–204.
35. Singh M., Swarup I., Billore M. and Chaudhari P.R. (2012). Genetic diversity for yield and its components in blackgram (Vigna mungo L.). *Research Journal of Recent Sciences*, 2.
36. USDA National Nutrient Database. (2021–2022). Blackgram (Vigna mungo L.) raw, mature seeds, and nutritive value per 100 g.
37. Veni K., Murugan E., Mini M.L., Vanniarajan C. and Radhamani T. (2016). Genetic relationship between yield and battering quality in blackgram (Vigna mungo L.). *Legume Research*, 39(3): 355–358.
38. Umadevi M. and Ganesan N.M. (2007). D² analysis for yield and quality characters in blackgram (Vigna mungo (L.) Hepper). *Legume Research*, 30(3): 197–200.