***Original Research Article***

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

**Abstract**

The present investigation was carried out with 29 diverse genotypes of Black gram at Crop Research Centre of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, U.P during the zaid season of 2021.Observations were recorded on various characters viz. days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, biological yield per plant, test weight, harvest index, and seed yield per plant. Analysis of variance revealed substantial amount of variability for all eleven characters. Analysis of variance revealed substantial amount of variability for all eleven characters. High PCV & GCV were observed for plant height, number of pods per plant and number of primary branches per plant, moderate (10-20%) for 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 and low (<10%) for test weight. Further, the estimate of PCV was higher in magnitude than the respective GCV for all the characters indicating the important role of environment in the expression of characters. High heritability coupled with high genetic advance observed for plant height only indicating that the heritability is due to additive gene action.The twenty-nine genotypes of black gram were grouped into five clusters based on D2 values. Among the five clusters, cluster I was largest including nine genotypes, followed by cluster III and IV having six genotypes each and cluster II and V both having four genotypes in it. The maximum intra-cluster distance was found for cluster III, followed by cluster II, cluster I, cluster V and lowest intra cluster distance for cluster IV (1.987).

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

**INTRODUCTION**

Blackgram [*Vigna mungo* (L.) Hepper] chromosome number 2n=22 also known as urdbean, is a tropical legume and belongs to family fabaceae and sub-family papilionaceae, mode of pollination is self-pollinated grown for its dry seeds, which are important source of proteins. Among the pulses, Black gram is very nutritious as it contains 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). (USDA, National Nutrient data base 2021-2022). It has genome size is approximately 1.56 pg/IC (574 Mbp). Blackgram complements the essential amino acids provided in most cereals and plays an important role in the diets of the Indian people. The biological value improves when wheat or rice is combined with pulse like blackgram because of the complementary relationship of the essential amino acids such as arginine, leucine, lysine, isoleucine, valine and phenylalanine etc. (Goyal *et al.*, 2010). In addition, its green fodder is of very nutritive and useful for milch cattle. It is also used as green manure. Being a leguminous plant it has the capacity to fix atmospheric nitrogen and restore soil fertility (Goyal *et al.*, 2010). It is grown on a variety of soils ranging from a sandy soil to heavy black cotton soils. It thrives well in relatively heavier soil. The most ideal soil would be a well-drained loam with a pH range from 6.0 to 7.5. It is the second important pulse crop of India in terms of area and production next to pigeon pea. It is one of the most important grain legumes in Asian agriculture, particularly in South Asia. Almost 90% of the world’s urdbean comes from Asia and India is the world’s largest producer of urdbean and consumer of urdbean. It is grown in about 4.6 (Anonymous 2021b) million hectares in India that produces 24.5 lakh tonnes of urd annually. In India, major blackgram producing states are Madhya Pradesh, Uttar Pradesh, Andhra Pradesh, Maharashtra and Tamil Nadu. It occupies about 19% of the total area under pulse crops in the country and ranks fourth in area and production after chickpea, pigeon pea and mungbean. Uttar Pradesh constitutes about 5.64 lakh ha, of the area with production of 3.03 lakh tones and productivity of 537 kg/ha (IIPR, Kanpur 2020-21). About 70 per cent of world’s blackgram production comes from India, but the productivity is very low compared with its potential yields obtained in many other countries. Apart from India, other major black gram growing countries are Pakistan, Afghanistan, Bangladesh and Myanmar. Pulses are being ceaselessly grown under marginal lands of low fertility and moisture stress conditions hence genotypes are more adoptable to poor management which registers limited yield, this does not reflect low genetic potential but they may have higher genetic potential than cereals. Blackgram (*Vigna mungo (L*). Hepper) is commonly known as urad, mash or kalai. India is primary centre of origin of Black gram and Central Asia is a secondary centre of origin with centre of genetic diversity in India.

An assessment of the genetic diversity of pulses is an important first step in a research programme to improve crop yield. Since, lack of stable and high yielding cultivars is one of the major constraints in its production, high yielding genotypes selected from germplasm could prove their superiority under various agro-ecological conditions. Low genetic base of existing cultivars and instability are the most limiting factors for wider adaptation of this crop. Heritability and genetic advance as percentage of mean and variance, genotypic and phenotypic coefficient of a metric character is a parameter of particular significance to the breeder as it measures the degree of resemblance between the parents and the offsprings and its magnitude indicates the efficacy with which a genotype can be identified by its phenotypic expression, while genetic advance aids in exercising the necessary selection pressure.The selection of highly genetically divergent parents is expected to throw superior and desirable segregants following crossing (Bhatt, 1973). It is also known that germplasm collections have some valuable genes which provide tolerance to various diseases, hence characterization and evaluation of such local germplasm provides useful material for breeding good varieties .Therefore, genetic diversity is one of the criteria for parent selection in the hybridization programme. The availability of diverse segregant in any plant breeding program depends upon the diversity between the parents involved.

**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 twenty-nine genotypes of black gram obtained from IIPR, Kanpur. The experiment was conducted in a randomized block design with three replications. Each plot consisted of a three row of 5.0 m length with a spacing of 30 cm between rows and 10 cm between plants was maintained by proper thinning. Observations were recorded by selecting five randomly competitive plants from each genotype in each replication were tagged for recording the observations on the following twelve characters. The mean values of forty genotypes in each replication were used for statistical analysis . The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) were computed following **Burton and Devane, (1952)** method. Heritability in broad sense h² (b) was calculated as a ratio of genotypic variance to phenotypic variance **(Allard, 1960)**. Genetic advance as percent of mean for each character was calculated as suggested by **Johnson *et al.,* (1955)** and the genetic divergence in thirty eight genotypes was estimated using **Mahalanobis D2 statistic, (1936)** following **Rao, (1952).**

**Results and Discussion**

A broad-spectrum of genetic variability is fundamental requisite for success of a plant breeding programme since it provides opportunity to breeders to make selection for desirable superior individuals from genetically diverse base population. Since, many characters of economic importance are highly influenced by environmental conditions; the improvement of a crop mainly depends upon the amount, nature and magnitude of genotypic variability present in the population. Wide range of variability existing among the genotypes to be tested for all the characters is also necessary to isolate significantly superior genotypes.

The mean performance of twenty nine genotypes of black gram lines are presented in Table 1 .Analysis of variance revealed highly significant differences among the genotypes for all the traits viz; 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, pod length, biological yield per plant, test weight, harvest index and seed yield per plant indicating the presence of considerable genetic variability in the experimental material. These results were in agreement with the findings of **Balachandran *et al* (2010), Kumar *et al* (2015), Priyanka *et al* (2016), Rolaniya *et al* (2017), Nagmi and lal *et al* (2017)** .

The estimates of genotypic co-efficient of variance (GCV), and phenotypic co-efficient of variance (PCV) for different characters are presented in Table2. Results from the present study indicates that the GCV and PCV were higher (>20%) observed for weight of total pods per plant, number of branches per plant and plant height, moderate (10-20%) for seed yield per plant, harvest index, number of pods per plant, biological yield per plant, number of seeds per pod, test weight, days to 50% flowering and pod length and low (<10%) for days to maturity. Further the present findings exhibited that the estimates of PCV were magnitudinally higher than their corresponding GCV for all the traits studied. This suggests that phenotypic expression of the genotypes was least influenced by environmental factors and desirable improvement can be achieved through simple selection procedures. These results were in consonance with the findings of **Sharma *et al.* (2006), Konda *et al.* (2009), Senapati and Mishra (2010), Kodanda Rami Reddy *et al.* (2011), Meshram *et at.* (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 perusal of the genetic parameters revealed that weight of total pods per plant, number of branches per plant and plant height exhibited high phenotypic and genotypic coefficient of variation suggesting that the existence of sufficient genetic variability for these traits in the population. Thus, it provides the basis for selection of desirable genotypes from the diverse population for enhancement of black gram production. The present study indicated higher contribution of weight of total pods per plant, number of branches per plant and plant height towards genetic variability and thereby suggesting that parent selection on the performance of these characters may be utilized in the hybridization programme for getting desirable transgressive segregants.

High heritability estimate indicates the effectiveness of selection based on phenotypic performance, but does not necessarily mean of high genetic gain for that particular trait. In the present investigation, heritability estimates for various characters is given in table 3. It was found that heritability for 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 were of high magnitude. This suggested that these traits were least influenced by environmental factors. In other words, it could be concluded that the phenotypic expression for these traits were true representative of its genotype. Such high heritability estimates has been reported by **Balachandran *et al.* (2010), Neelavathi and Govindarasu (2010), Patidar *et al.* (2018), Priyanka *et al.* (2016), Patel *et al.* (2015), Panigrahi *et al.* (2014).** Results obtain from the study revealed that high heritability coupled with high genetic advance for weight of total pods per plant indicating that the heritability is due to additive gene action and simple selection for such traits could be practiced for improving them. Similar results were obtained by **Sharma *et al.* (2006), Konda *et al.* (2009), Balachandran *et al.* (2010).**

The present investigation which was undertaken with a view to studied the diversity among genotypes of black gram. Twenty-nine genotypes were grouped into five clusters. From the clustering pattern it concluded that sufficient divergence was present to enable the formation of individual clusters. All clusters are of heterogeneous origin and included those treatments originations from different research stations. The clustering pattern is suggestive of the fact that the geographic diversity is not efficient index of genetic diversity. Therefore, Mahalanobis D2 analysis is a powerful tool to estimate genetic divergence among the material selected even from the same geographic region. The present contribution of number of seeds per pod, days to maturity, days to 50% flowering, number of pods per plant, pod length, weight of total pods per plant, biological yield per plant, number of branches per plant, plant height, seed yield per plant, test weight and harvest index contributed most towards genetic divergence as given in table 4. This view has been supported by the work of **Shanthi *et al.* (2006), Umadevi and Ganesan (2007), Niranjan and Rama Chandra (2009), Neelavathi and Govindarasu (2010), Geethanjali *et al.* (2015), Hadimani *et al.* (2016).**

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

Grouping of twenty-nine genotypes of black-gram [(*Vigna mungo* L.) Hepper] in five clusters as shown in table 5 Among the five clusters, cluster I was the largest including nine genotypes followed by cluster III and IV having six genotypes each and cluster II and V both having four genotypes in it. Based on the results obtained from study it can be concluded that, there was parallelism between genetic and geographic diversity. These results are somewhat in accordance with the findings 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).** Table 6shows average inter and intra cluster (D2 values) among five clusters of twenty-nine genotypes in black-gram [(*Vigna mungo* L.) Hepper]. The highest inter cluster distance was revealed between cluster IV and V (5.093). It clearly indicates that the genotypes included in these clusters are having broad spectrum of genetic diversity and could very well be used in crossing programme of black gram for improving the grain yield. In other hand, the least inter cluster distance was observed between cluster I and IV (2.735) which indicates that the genotypes belong to these cluster may not be used in hybridization programme due to close relationship among the genotypes. The intra cluster distance among various clusters exhibited maximum intra cluster distance for cluster III (2.498) and lowest intra cluster distance for cluster IV (1.987). The maximum intra cluster distance was because of wide genetic diversity among its genotypes. The chance of developing good segregants by crossing the genotypes of the same cluster showing low value for intra cluster distance are very low. Therefore, it could be logical to attempt crosses between the genotypes of clusters separated by larger inter cluster distance. The little diversity and selection of parents within the clusters having higher mean for a particular character may also be useful for further developing high yielding black gram varieties**.**

**Table 1 Analysis of variance (ANOVA) for twelve characters of twenty-nine genotypes in Black-gram [(*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 | Wht. Of total pods/plant(gm) | Pod length(cm) | Biological yield/plant(g) | 1000 seed weight | Harvest index(%) | Seed yield/plant(gm) |
| 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 black-gram [(*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 |
| Wht. Of total pods/plant(gm) | 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 |
| 1000 seed weight | 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(gm) | 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 black-gram [(*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 | Wht. Of total pods/plant(gm) | Pod length(cm) | Biological yield/plant(g) | 1000 seed weight | Harvest index(%) | Seed yield/plant(gm) |
| **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 black-gram [(*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 black-gram [(*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**

Variance analysis revealed sufficient amount of genetic variability among the present set of breeding material and study for genetic parameters, with these genotypes, was worth for valuable findings. All the traits viz., 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, pod length, biological yield per plant, test weight, harvest index and seed yield per plant to respond to direct selection is effective. The estimates of heritability was high for all the traits under study viz., grain yield per plant, followed by 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. This indicated the influence of additive gene action for expression of these characters and hence direct selection based on these traits may be useful for effective improvement in black gram crop.

Results obtain from the study revealed that high heritability coupled with high genetic advance for weight of total pods per plant indicating that the heritability is due to additive gene action and simple selection for such traits could be practiced for improving them. From D2 analysis the highest inter cluster distance was found between cluster IV and V, thus the crosses between the genetically diverse genotypes of clusters IV and cluster V are expected to exhibit high heterosis and are also likely to produce new combinations with desired characters to get desirable segregates with higher yield for developing superior varieties of black gram.

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