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GENETIC VARIABILITY FOR GROWTH, YIELD, AND YIELD-RELATED TRAITS IN BLACKGRAM (*VIGNA MUNGO* (L.) HEPPE) GENOTYPES

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ABSTRACT

Blackgram (*Vigna mungo* (L.) Hepper) is an important legume crop extensively grown in Asia. It is one of the most abundant sources of protein, minerals, and vitamins. Studying genetic variability is an important task for genetic improvement of this crop. Ten blackgram genotypes were experimented on a randomized complete block design with three replications at Sundarbazar, Lamjung during July- October of 2019 to analyze their genetic variability. Plant height at maturity, days to 50% flowering, number of primary branches, branch length, number of pods bearing peduncles, the longest peduncle length, pod length, number of seeds per pod, 1000 seed weight, and grain yield per plant were significantly different between genotypes. BLG0076-2 had produced the highest grain yield per plant (6.19 g), followed by BLG0066-1-1 (5.42 g). The number of pods per plant had the highest genotypic coefficient of variation (GCV) (37.30 %) and phenotypic coefficient of variation (PCV) (46.44 %), followed by the number of pods bearing peduncles (GCV: 34.47, PCV: 46.44). Heritability values for branch length (0.94) are the greatest, followed by seeds per pod (0.92). Genetic advance (GA) was the highest in branch length (20.68), followed by the number of pods per plant (19.79). Similarly, the number of pod bearing peduncles had the highest genetic advance as a percent of the mean (GAM) (66.10), followed by branch length (63.59). Cluster analysis revealed that cluster 2 and cluster 3 had the greatest distance between cluster centroids (24.99), indicating genetic dissimilarity. This study suggests that blackgram genotypes, namely BLG0076-2 and BLG0066-1-1 were potential germplasm for varietal improvement programs.

KEY WORDS

Black gram, cluster analysis, grain yield, heritability, genetic variability.

Blackgram (*Vigna mungo* L.) Hepper, also known as mash or urd bean, is a widely cultivated grain legume belonging to the Fabaceae family, order Fabales, and class dicotyledon. Blackgram is one of the most abundant sources of vegetable protein, as well as certain important minerals and vitamins for the human body. Grain is composed of 56 % carbohydrates, 25% protein, 2% fat, 4% mineral, and 0.4% vitamins (Panigrahi et al., 2014). When supplied with most cereals (rice or wheat), blackgram complements the essential amino acids (arginine, leucine, lysine, isoleucine, valine, and phenylalanine) and serves a crucial dietary role (Paul, 2016). Pulses are consumed in Nepal at a rate of 24 grams per capita per day, compared to the 80 grams recommended by the World Health Organization (Shrestha et al., 2011). Blackgram can fix atmospheric nitrogen in a symbiotic relationship with nodule-producing bacteria, which aids in soil improvement (Pokhrel et al., 2019). It fixes roughly 50-55 kg of nitrogen per hectare. Blackgram contributes 5.21% of the country's pulse production (MoALD, 2019). It is grown on 23,492 hectares in Nepal, with a production of 19928 metric tons and productivity of 848 kg per hectare, respectively (MoALD, 2019). Many species of food legumes may be cultivated in Nepal's various climates and environments,



and blackgram is grown as a mixed, cash, and sequence crop in a variety of cropping systems. It is also produced as a solo crop under residual moisture conditions after rice harvest and as a relay crop before rice harvest (Parveen et al., 2011). Despite their importance in Nepalese farming systems, pulses are just a minor component of total agricultural systems due to the greater importance given to cereals as main food crops (Pandey et al., 2000). Blackgram is still grown in marginal areas in rainfed environments with terminal drought, which has a significant impact on its production (Patidar and Sharma, 2017). As a result, pulses have lower production stability and larger storage losses than cereals (Pandey et al., 2000). The lack of a suitable ideotype for varied cropping systems, low harvest indices, and sensitivity to diseases are all major obstacles to generating higher yields and stability in blackgram (Rana et al., 2019). Many attempts have been made to determine the degree of variability in black gram productivity and its component traits. However, research on this plant has lagged behind cereals and other legumes in some ways. The lack of adequate varieties and genotypes that are adapted to local environments is one of the issues that influence production and farmer preferences (Paul, 2016). In the face of disease epidemics and fluctuating environmental conditions, genetic variability is essential for improving yields and maintaining output. As a result, using available genetic diversity to improve this crop is required (Pyngrope et al., 2015).

Any breeding program's success is primarily determined by how well existing variability in the base material is used, as well as the extent of variability in the targeted traits. Furthermore, crop improvement programs require the measurement of genetic diversity for both quantitative and qualitative features of economic value. As a result, collecting, evaluating, and utilizing available genetic diversity to meet specific ecosystem demands is desirable and should be encouraged to develop new varieties (Pokhrel et al., 2019). Similarly, phenotypic and genotypic coefficients of variation, genetic advance, and heritability all play a role in identifying superior genotypes, assisting in effective selection and improving existing cultivars (Reni et al., 2013). Evaluation of genetic diversity would aid in the efficient use of genetic variations in breeding programs. The current study was conducted to assess the growth, yield and yield-related performance of black gram genotypes and analyze their variation, heritability and genetic advance in the hopes of developing superior varieties.

MATERIALS AND METHODS OF RESEARCH

Experimental location. This experiment was conducted in the research field of the Institute of Agriculture and Animal Science (IAAS), Lamjung Campus, Sundarbazar, Lamjung, Nepal from July to October 2019. The study site is located at 28.12°N latitude, 84.41°E longitude, and 620 m elevation. The experimental area's soil type was sandy loam. Table 1 shows the climatic data collected during the experiment.

Table 1 – Meteorological data of the experimental location in 2019

Months	Maximum Temperature (°C)	Minimum Temperature (°C)	Rainfall (mm)
July	21	14	658.7
August	22	14	367.2
September	19	13	435.8
October	17	8	45.3

Table 2 – List of blackgram genotypes used in this study

SN	Genotypes	Source	SN	Genotypes	Source
1	BLG0061-2-2	NGLRP	6	BLG0035-1	NGLRP
2	BLG0066-1-1	NGLRP	7	BLG0041-1	NGLRP
3	BLG0092-1	NGLRP	8	BLG0076-2	NGLRP
4	BLG0069-1	NGLRP	9	Shekhar-1 (Check)	NGLRP
5	BLG0036-1	NGLRP	10	Khajura mash (Check)	NGLRP

NGLRP: National Grain Legumes Research Program (NGLRP), Khajura, Banke, Nepal.



Experimental materials. Ten genotypes of blackgram were used for the experiment. The source of these genotypes was National Grain Legumes Research Program (NGLRP), Khajura, Banke (Table 2).

Experimental details and cultural practices. This experiment was conducted in a randomized complete block design (RCBD) with three replications and ten blackgram genotypes. Field preparation was performed on July 8, 2019, and seeding was completed on July 15, 2019, at a pace of two seeds per hill. Each 4m² (2m × 2m) experimental plot included 100 plants with a crop geometry of 40cm x10cm (RR×PP), correspondingly. Inorganic fertilizer was applied at a rate of 20:40:20 NPK kg ha⁻¹. At the time of planting, a full dose of nitrogen, phosphorus (P₂O₅), and potassium (K₂O) was applied as the basal dose. The fertilizers were Urea, DAP (Diammonium Phosphate) and MOP (Muriate of Potash). In all plots, the entire agronomical package of procedures as recommended by NGLRP, Khajura was implemented uniformly.

Data Collection and analysis. The data was collected from ten plants chosen at random and left with two border rows on each side. After harvesting and drying at the optimum moisture level, yield and yield component traits such as pod length, no. of pods per plant, no. of seeds per pod, 1000 seed weight, and grain yield were measured. Data was collected independently for each genotype in each replication. The various genetic parameters, such as phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), were computed using the formula given by Burton (1952), while heritability and GA as percent mean were determined using the formula adopted by Johnson et al. (1955). The average linkage clustering method was used for cluster analysis, and the Euclidian method was used to compute inter-cluster distance.

Statistical analysis. MS-Excel 2016 was used to enter the data. R Studio was used to analyze the data. A randomized complete block design (RCBD) with one-way ANOVA was used to evaluate the data. At 5% level of significance, the least significant difference (LSD) was employed to compare the treatment means (Gomez, Gomez, 1984).

RESULTS AND DISCUSSION

Agro-morphological performance of genotypes. Tables 3a and 3b show the agro-morphological variability among blackgram genotypes. Plant height at maturity, days to 50% flowering, number of primary branches, branch length, number of pods bearing peduncle, longest peduncle length, pod length, number of seeds per pod, 1000 seed weight, and grain yield were all substantially different between genotypes, except for the number of pods per plant. BLG0036-1 had the longest flowering days (29.3 days) and BLG0092-1 had the shortest flowering days (26 days). The number of primary branches ranged from 10.46 (Khajura mash) to 8.36 (BLG0069-1). The branch length was found to be the maximum in BLG0041-1(43.73cm), followed by check variety Shekhar-1 and the minimum in BLG0092-1(23.06cm). The number of pods bearing peduncles varied from 21.267 (Khajura mash-1; check variety) to 11.33 (BLG0092-1). The peduncle length varied from 10.62 (BLG0069-1) to 7.45 (Khajura mash-1; check variety). The longest days to 50% maturity was found in Shekhar-1 (56 days). Early maturing varieties were found to be BLG0036-1, BLG0092-1, BLG0069-1 and Khajura mash-1. The pod length ranged from 5.046 cm (Shekhar-1) to 4.26 cm (BLG0092-1). The value of no. of pods per plant ranged from 49.4 (BLG0069-1) to 25.26 (BLG0092-1). The maximum number of seeds per pod was found in Shekhar-1 (7.16), while the minimum was found in BLG0092-1 (5.50). The mean value for 1000 seed weight ranged from 47.78 g (BLG0069-1) to 40.96 g (BLG0041-1). Plant height varied from 50.86cm to 34.33cm. The highest grain yield per plant was found in genotype BLG0076-2 (6.19 g) and the lowest in Shekhar-1 (3.49 g). These findings were similar to findings found by Kumar et al. (2015), Thirumalai and Murugan (2020) and Patidar et al., (2018) who observed variability among the evaluated genotypes in their experiments.

Phenotypic and genotypic coefficients of variation. Table 4 shows that the number of pods per plant (143.09 and 221.85) had the highest genotypic and phenotypic variation, followed by branch length (106.6 and 112.75). For all of the characters, phenotypic variance



was higher than genotypic variance, showing that environmental factors had an impact on these traits. Konda et al. (2009), Senthamizhselvi et al. (2019), Sabesan et al. (2018) and Reddy et al. (2018) all found similar results. According to Sivasubramanian and Menon (1973), phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were classified as low (less than 10%), moderate (10-20%), and high (more than 20%). PCV values varied from 46.44 for no. of pods per plant to 7.402 for days to 50 percent mature pods, while GCV values ranged from 37.297 for number of pods per plant to 7.049 for days to 50% mature pods. Except for no. of pods per plant, the difference between GCV and PCV was small for all traits studied, indicating that traits other than no. of pods per plant are more genetically controlled and less influenced by environmental factors.

Table 3a – Mean values of various growth and yield traits of ten genotypes of blackgram at Lamjung in 2019

Genotypes	Plant height at maturity (cm)	Days to 50% flowering	Number of primary branches	Branch length (cm)	Number of pods bearing peduncle	Longest peduncle length (cm)	Days to 50% matured pod
BLG0061-2-2	45.87ab	28.67ab	8.80cd	35.27bc	15.97bcd	8.84bc	53.33bc
BLG0066-1-1	45.20abc	26.67bc	8.90cd	30.70cd	12.37de	8.28cd	54.00ab
BLG0092-1	34.33e	26.00c	9.27bcd	23.07e	11.33e	8.84bc	50.67d
BLG0069-1	37.23de	27.67abc	8.37d	25.93e	13.73cde	10.62a	50.67d
BLG0036-1	43.07bcd	29.3337a	8.53cd	33.00bc	17.33bc	9.80ab	49.67d
BLG0035-1	42.87bcd	28.00abc	8.53cd	36.37b	13.73cde	8.39cd	54.67ab
BLG0041-1	50.87a	28.00abc	9.60abc	43.73a	14.93bcde	8.63bcd	53.00bc
BLG0076-2	37.93de	27.33abc	10.00ab	27.43de	10.00ab	7.93cd	51.33cd
Shekhar-1	39.63cde	29.33a	8.73cd	36.40b	12.83de	8.09cd	56.00a
Khajura mash-1	39.07de	26.00c	10.47a	33.33bc	21.27a	7.46d	50.00d
Grand Mean	41.6	27.7	9.12	32.52	15.21	8.69	52.33
F test	***	**	**	***	***	***	***
LSD(5%)	5.54	1.83	0.98	4.25	3.52	1.13	1.39
CV%	7.77	3.86	6.29	7.62	13.49	7.62	2.26

Note: **=significant at $P < 0.01$. ***=significant at $P < 0.001$. Different letters represent significant differences based on LSD test at $p < 0.05$. CV: Coefficient of variation, LSD: Least significant difference.

Table 3b – Mean values of various growth and yield traits of ten genotypes of blackgram at Lamjung in 2019

Genotypes	Pod length (cm)	Number of pods per plant	Number of seeds per pod	1000 seed weight (g)	Yield per plant (g)
BLG0061-2-2	4.34cd	36.6	6.13de	45.21b	4.50def
BLG0066-1-1	4.63bc	26.33	6.80ab	45.04b	5.42b
BLG0092-1	4.26d	25.27	5.50f	44.30bc	5.32bc
BLG0069-1	4.33cd	49.4	5.87ef	47.79a	4.40ef
BLG0036-1	4.67b	25.53	6.43bcd	45.33b	5.26bc
BLG0035-1	4.53bcd	29.33	6.27cde	43.79bcd	3.92fg
BLG0041-1	4.69b	31.5	6.33cd	40.96e	5.19bcd
BLG0076-2	4.40bcd	38.43	6.00de	42.52cde	6.19a
Shekhar-1	5.05a	29.4	7.17a	45.41b	3.494g
Khajura mash-1	4.48bcd	28.93	6.60bc	41.89de	4.66cde
Grand Mean	4.54	32.07	6.3	44.22	4.84
F test	***	NS	***	***	***
LSD(5%)	0.27	17.93	0.41	2.05	0.66
CV%	3.49	27.67	3.81	2.70	7.91

Note: Ns=Not significant. ***=significant at $P < 0.001$. Different letters represent significant differences based on LSD test at $p < 0.05$. CV: Coefficient of variation, LSD: Least significant difference.

The PCV and GCV of no. of pods per plant, branch length, number of pods bearing peduncle, and yield per plant were all found to be high. PCV and GCV were found to be moderate in the number of primary branches, peduncle length, and seeds per pod, indicating that direct selection via phenotype observation is effective. Plant height was shown to have a high value of PCV when the GCV was moderate, whereas days to 50% flowering, days to 50% mature pods, pod length, and thousand seed weight were found to have low GCV and PCV, indicating that direct selection may not be profitable. For no. of pods per plant, number of clusters per plant, and yield per plant, Panigrahi et al. (2014), Patel et al. (2014), and Shoba (2018) found similar results. Kumar et al. (2015) found similar moderate GCV and PCV of seeds per pod. Chowdhury et al. (2020) found similar results for plant height, no. of



seeds per pod, days to 50% flowering, and black gram test weight. Gowsalya et al. (2016) reported higher GCV and PCV of branch length in a previous experiment. Lower GCV and PCV estimations for days to 50% flowering, days to maturity, hundred seed weight, and pod length matched the findings of Reddy et al. (2018), Bandi et al. (2018) and Bishnoi et al. (2017). The GCV for seed yield was found to be relatively high in this study, indicating that there is a lot of scope for yield increase by direct selection.

Table 4 – Estimates of Genotypic variance (V_g), Phenotypic variance (V_p), Genotypic coefficient of variation (GCV), Phenotypic coefficient of variation (PCV), Broad sense heritability (h^2_{bs}), Genetic advances (GA) and genetic advances as percent of mean (GAM) for growth, yield and its attributing traits of ten blackgram genotypes

Traits	V_g	V_p	GCV	PCV	h^2_{bs}	GA	GAM
Days to 50% flowering	4.10	5.24	7.31	8.26	0.78	3.69	13.31
No. of Primary branches	1.36	1.68	12.77	14.23	0.81	2.15	23.59
Branch length (cm)	106.60	112.75	31.75	32.65	0.95	20.68	63.59
No. of pod bearing Peduncle	27.49	31.70	34.46	37.01	0.87	10.06	66.11
Peduncle length (cm)	2.43	2.87	17.94	19.50	0.85	2.96	34.02
Days to 50% mature pods	13.61	15.01	7.05	7.40	0.91	7.24	13.83
Pod length (cm)	0.16	0.18	8.66	9.34	0.86	0.75	16.56
No. of pods per plant	143.10	221.86	37.30	46.44	0.65	19.79	61.70
No. of seeds per pod	0.67	0.72	12.93	13.48	0.92	1.61	25.55
1000 seeds weight (g)	11.58	13.02	7.70	8.16	0.89	6.61	14.96
Plant height at maturity (cm)	68.64	79.10	19.91	21.38	0.87	15.90	38.21
Yield per plant (g)	1.85	1.99	28.10	29.20	0.93	2.70	55.73

Note: V_g – genotypic variance, V_p – phenotypic variance, h^2_{bs} – heritability in the broad sense, GCV – genotypic coefficient of variation, PCV – phenotypic coefficient of variation, GA – genetic advance at 5% intensity of selection, GAM – genetic advance as per cent of mean

Heritability and genetic advance. The degree of similarity between parents and their offspring is determined by heritability. As proposed by Robinson et al. (1949), an attempt was made in this study to assess heritability in a broad sense and characterize it as low (50 %), moderate (50-70 %), and high (>70 %). For branch length and no. of pods per plant, the heritability estimates ranged from 0.945 to 0.645. Days to 50% flowering (78.2 %), number of primary branches (80.5 %), branch length (94.5 %), number of pod bearing peduncles (86.7 %), peduncle length (84.7 %), days to 50% mature pods (90.7 %), pod length (86.0 %), no. of seeds per pod (92.0 %), thousand seed weight (89.0 %), plant height (86.8%), and yield per plant (92.7 %) were among the traits studied with high heritability. Table 4 summarizes these findings. No. of pods per plant had the lowest heritability among the traits, which was similar to the findings of Siddique et al. (2006). The findings were similar to those of Panigrahi and Baisakh (2014) and Baisakh et al. (2014), except for no. of seeds per pod, which had low heritability. Blackgram previously found high heritability of pod length, seed yield, plant height, 100 seed weight, clusters per plant, no. of seeds per plant, and branches per plant (Kumar et al., 2015). Veni et al. (2015) also found that all nine quantitative traits evaluated had a high heritability, indicating less environmental influence. Kuralarasan et al. (2018) found that all of the studied traits, including peduncle length, have a high heritability. In a general sense, high heritability levels indicate that character is less influenced by environmental factors and that phenotype and breeding values may be more strongly associated.

Genetic advance and genetic advance as percent of mean. Under one cycle of selection at a given selection intensity, genetic advance (GA) under selection refers to the improvement of traits in genotypic value for the new population compared to the base population (Wolie et al., 2013). The genetic advance as a percent of the mean (GAM) ranged from 13.308 for days to 50% flowering to 66.107 for the number of pod bearing peduncles. Days to 50% flowering, number of branches, days to 50% mature pods, pod length, no. of seeds per pod, and thousand seed weight were all used to classify GAM as low (10%), medium (30%-10%), and high (>30%). GAM was high in branch length, no. of pod bearing peduncles, peduncle length, no. of pods per plant, plant height, and yield per plant. These findings are very similar to those of Sushmitharaj et al. (2018) and Gowsalya et al. (2016).



Seed yield per plant, clusters per plant, no. of pods per plant, plant height, test weight, days to 50% blooming, and days to 50% pod setting were all found to be identical by Aftab et al. (2018). A trait with a moderate to high GAM indicates that the character is governed by additive genes and that improvement of such traits will be favored by selection.

Heritability estimations combined with genetic advance is usually more accurate in predicting selection gain than heritability alone. Branch length, number of pods bearing a peduncle, peduncle length, plant height, and single plant yield all had high heritability and genetic advance as a percentage of the mean, indicating that these traits were controlled by additive gene action in inheritance and indicating the potential for improvement using simple selection procedures. For these traits, Gowsalya et al. (2016), Venkatesan et al. (2005) and Sushmitharaj et al. (2018) reported similar findings. Kuralarasan et al. (2018) also supported it for plant height, peduncle length, number of clusters per plant, and single plant yield.

Cluster analysis. Genetic divergence analysis was frequently utilized to establish the genetic relationship between genotypes and to identify the genotypes that would be appropriate for future breeding programs. Divergence was calculated for all twelve characters of ten blackgram genotypes. Table 5 and Figure 1 show all genotypes were divided into three clusters based on the traits.

Based on growth and yield traits, the 10 blackgram genotypes were divided into four groups (Table 5). Twenty-two black gram genotypes were grouped into five clusters by Vyas et al. (2018). Similarly, in a study conducted by Ahmadikhah et al. (2008), fifty-eight rice varieties were categorized into four clusters based on 18 morphological traits. Rahman et al. (2011) used 14 physiological traits to divide 21 rice varieties into five clusters. Anandan et al. (2011) also showed similar results in rice.

Table 5 – Grouping of ten blackgram genotypes by Euclidean average linkage method

Cluster number	No. of genotypes	Genotypes
1. Cluster1	6	BLG0061-2-2, BLG0066-1-1, BLG0036-1, BLG0035-1, Shekhar-1, BLG0041-1,
2. Cluster 2	1	BLG0092-1
3. Cluster 3	1	BLG0069-1,
4. Cluster 4	2	BLG0076-2, Khajura mash-1

Cluster1 was the largest one, having 6 genotypes, i.e., BLG0061-2-2, BLG0066-1-1, BLG0036-1, BLG0035-1, BLG0041-1 and Shekhar-1, which represented 60% of the genotypes. This cluster had the highest days to 50% flowering (28.33), branch length (35.91 cm), days to 50% mature pods (53.44), pod length (4.65 cm), seeds per pod (6.52) and plant height at maturity (44.58 cm) (Table 6). Cluster 2 consisted of BLG0092-1 and this cluster was characterized by the highest peduncle length (8.84 cm), yield per plant (5.32 g) with the lowest days to 50% flowering (26), branch length (23.07 cm), number of pods bearing peduncle (11.33), days to 50% mature pods (50.67) and plant height at maturity (34.33 cm) (Table 6). Cluster3 had one genotype, BLG0069-1. Genotypes grouped in this cluster had the highest number of pods per plant (49.40), thousand seed weight (47.79 g), peduncle length (10.62 cm) (Table 6). Cluster 4 had two genotypes, BLG0076-2 and Khajura mash-1. Genotypes grouped in this cluster had the highest number of primary branches (10.23), No. of pod bearing peduncles number (19.95) and yield per plant (5.42 g) (Table 6). Chakma et al. (2012) came up with similar results. For cluster 1, traits including days to 50% flowering, branch length, days to 50% mature pods, pod length, no. of seeds per pod, and plant height at maturity can be used to improve yield based on centroid values. Peduncle length and yield per plant can also be selected for cluster 2 to improve yield. Cluster 3 genotypes can be utilized for hybridization to increase economically important traits such as no. of pods per plant, thousand seed weight, and peduncle length. Furthermore, genotypes for a hybridization program can be chosen from clusters with a high inter-cluster distance and high genetic diversity. Selection between clusters with the shortest inter-cluster distance, on the other hand, may not be particularly useful in hybridization programs.

Distance between cluster centroids was found to be greater in between cluster 2 and cluster 3 (24.99) as presented in Table 7. Such genotypes can also be used in breeding programs for developing biparental crosses between the most diverse and closest groups to



break the undesirable linkages between yield and its associated traits. The distances between cluster centroids ranged from 13.95 to 24.99 (Table 7). The lowest distance between cluster centroids was found in the cluster 1 and cluster 4 (13.95) indicating genetic similarity and the highest was found in the cluster 2 (BLG0092-1) and cluster 3 (BLG0069-1) (24.99) indicating genetic dissimilarity (Table 7).

Table 6 – Cluster means for twelve traits of ten blackgram genotypes

Variable	Cluster1	Cluster2	Cluster3	Cluster4	centroid
Plant height at maturity	44.58	34.33	37.23	38.50	41.61
Days to 50% flowering	28.33	26.00	27.67	26.67	27.70
No. of primary branches	8.85	9.27	8.37	10.23	9.12
Branch length (cm)	35.91	23.07	25.93	30.38	32.52
No. of pod bearing peduncle number	14.53	11.33	13.73	19.95	15.21
Peduncle length (cm)	8.67	8.84	10.62	7.69	8.69
Days to 50% mature pods	53.44	50.67	50.67	50.67	52.33
Pod length (cm)	4.65	4.26	4.33	4.44	4.54
No. of pods per plant	29.78	25.27	49.40	38.68	33.07
No. of seeds per pod	6.52	5.50	5.87	6.30	6.31
1000 seeds weight (g)	44.29	44.31	47.79	42.20	44.22
Yield per plant (g)	4.63	5.32	4.40	5.42	4.84

Table 7 – Distances between cluster centroids in ten blackgram genotypes

	Cluster1	Cluster2	Cluster3	Cluster 4
Cluster1	-	17.77	23.75	13.95
Cluster2			24.99	18.25
Cluster3				14.84
Cluster4				-

Table 8 – Different statistics of Euclidean distance and cluster analysis of ten blackgram genotypes

Cluster	No. of genotypes	Within clusters sum of squares	Average distance from centroid	Maximum distance from centroid
Cluster1	6	316.79	6.86	10.77
Cluster2	1	0.00	0.00	0.00
Cluster3	1	0.00	0.00	0.00
Cluster4	2	25.16	3.55	3.55

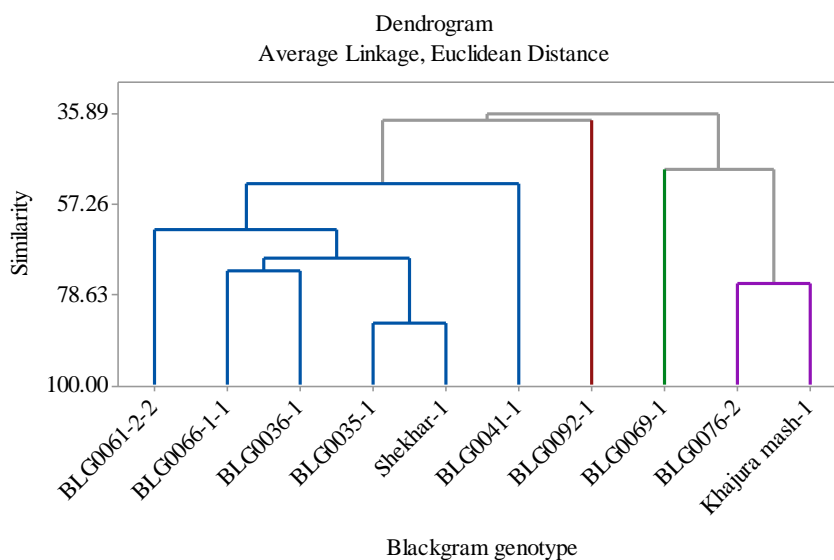


Figure 1 – Dendrogram of ten blackgram genotypes using Euclidean average linkage method



Similar results were found by Mohanlal et al. (2018) who found the highest intra- and inter-cluster distances between cluster III and cluster V in their multivariate analysis of 21 black gram genotypes. Anandan et al. (2011) and Latif et al. (2011) both found similar results in rice. Vennila et al. (2011) and Latif et al. (2011) proposed using distantly placed cluster genotypes in hybridization programs to get a wide spectrum of variation among genotypes. Cluster 1, the largest, is comprised of six genotypes, indicating all the genotypes had some similar characteristics and crossing among the genotypes in this cluster may give transgressive segregants. The genotypes present in cluster 2 and cluster 3 indicate that they could be more divergent from other genotypes and that crossing with the genotypes of other different clusters would be suitable for obtaining heterosis for some of the important traits.

The maximum distance of cluster 1 from centroids was 10.77 followed by cluster 2 (3.55) (Table 8). Chakma et al. (2012) discovered similar results.

CONCLUSION

Plant height at maturity, days to 50% flowering, number of primary branches, branch length, number of pods bearing peduncles, the longest peduncle length, pod length, number of seeds per pod, 1000 seed weight, and grain yield all differed significantly between genotypes. Such variation showed that the genotypes had great potential in future breeding programs when it came to selection. PCV was greater than GCV in all traits, showing that there was an environmental influence. Cluster 2 and cluster 3 had the greatest gap between cluster centroids, indicating genetic distance. BLG0076-2 and BLG0066-1-1 were the genotypes with the highest yield potential. These genotypes can be grown for higher production.

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