

ASSESSMENT OF GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS IN BLACKGRAM (*VIGNA MUNGO* L. HEPPER) GERMPLASM

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ABSTRACT

Black gram is a self-pollinated, leguminous, pulse crop which is rich in lysine amino acid and consist of protein content of about 25 to 28%. The study was conducted at Field Experimental Center, Department of Genetics and Plant Breeding, Sam Higginbottom Institute of Agriculture, Technology & Sciences, Allahabad on thirty genotypes of black gram including one check, T-9 during *kharif* seasons 2015-2016 to estimate analysis of variance, genetic variability, correlation and genetic diversity. All the genotypes of black gram were planted in randomized block design with three replications. Analysis of variance showed that all traits observed were significant and ensures presence of variability among genotypes. Genetic variability observed showed that values of phenotypic coefficient of variation was higher as compared to genotypic coefficient analysis. High heritability along with high genetic advance as a percent of mean was observed for traits, branches/plant, number of seeds/pod and seed yield/plant. Correlation coefficient analysis was measured at both genotypic and phenotypic level. In phenotypic correlation, seed yield per plant exhibited positive and significant correlation with harvest index and biological yield/plant. In genotypic correlation, seed yield per plant showed positive and significant correlation with biological yield/plant followed by number of clusters/plant, harvest index and 100 seed weight. Genetic diversity was estimated *via* Mahalanobis D² method. All the genotypes were clustered into six groups by Tocher's method. Maximum intra-cluster distance was observed in cluster II and highest Inter cluster distance was observed between cluster V and cluster VI followed by cluster IV and cluster V. Hence, genotypes in cluster V and VI will be efficient as a parent for hybridization program.

KEYWORDS: Blackgram, Genetic Variability, Heritability, Genetic advance, Correlation and path coefficient analysis

INTRODUCTION

Black gram (*Vigna mungo* L. Hepper) commonly referred as urd is a pulse crop belonging to family Leguminosae, exhibits self-pollination. Black gram with chromosome number $2n = 24$ is believed to be originated in India. It is the third most important pulse crop after chickpea and pigeon pea. Black gram contains protein (25-28%), oil (1-1.5%), carbohydrate (60-65%), fibre (3.5-4.5%) (Lavanya *et al.*, 2022 and Patial *et al.*, 2022). Black gram is rich in lysine amino acid which can be more beneficial for balanced diet when consumed with rice. Like most of the crops under Leguminosae family black gram also have nitrogen fixing ability in soil *via* symbiotic association with nitrogen fixing bacteria. It can be used as a green manure or to feed milch animals. Urd can be grown during *kharif*, *rabi* and summer. According to DA&FW current production of black gram is 17.14 lakh tonnes (2025-2026).

Assessing genotypes for any breeding program, must show variability first. Hence, genetic variability is a basic requirement for selection process. Genetic variability is governed by genotypic, phenotypic and environmental factors. In any breeding or agronomy programs the major output is yield for a crop. Yield is a polygenic trait which defines that selection alone on the basis of yield will be not successful as a result correlation coefficient comes in role. Correlation analysis determines the association between the traits and yield and among the traits under study. Genetic diversity is a pre-requisite for hybridization programs. For obtaining segregating

generation it is important to identify genotypes that are highly diverse and can be used as a parent for creation of elite varieties.

MATERIAL AND METHOD

The experiment was conducted on 30 genotypes of Black gram during *kharif* season 2015-2016 at the Field Experimental Centre, Department of Genetics and Plant Breeding, Sam Higginbottom Institute of Agriculture, Technology & Sciences, Allahabad. The field experiment centre is located at 25.28°N latitude and 81.54°E longitude, with an elevation of 98 m above sea level. The genotypes were sown in Randomized Block Design (RBD) with three replications. Each genotype was planted in a plot size of 0.55×2m with row to row and plant to plant distance of 30×10cm. All the agronomical measures were taken during trial period like, thinning application of fertilizer, irrigation. Total number of thirteen observations were made, plant height (cm), number of branches per plant, days to 50% flowering, days to 50% pods setting, days to maturity, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length (cm), seed yield per plant (g), biological yield, seed index (g), harvest index (%). For recording observations five plants were selected from each genotype except for days to 50% flowering and days to 50% pods setting.

For statistical analysis ANOVA, genetic variability, correlation and genetic diversity were estimated. Analysis of Variance was calculated as per as Fisher (1938). For estimation of genetic variability various measures were observed, phenotypic and genotypic coefficient of variation was calculated according to Burton and De vane (1953) and was categorised as high (more than 20 percent), medium (10-20 percent) and low (less than 10 percent) according to Sivasubramanian and Madhava Menon (1973) the broad sense heritability (h^2b) was categorized as per as scale suggested by Johnson *et al.*, 1955, low (less than 30 percent) moderate (30 to 60 percent) and high (more than 60 percent) and the genetic advance as a percent of mean was categorised as low (0-10 percent), moderate (10-20 percent) and high (>20 percent) as per as Johnson *et al.*, (1955). Correlation Coefficient Analysis at both genotypic and phenotypic level were calculated using formula suggested by Al-Jibouri *et al.* (1958). Diversity analysis among thirty genotypes were estimated using Mahalanobis's D^2 Statistics (Mahalanobis, 1936) and grouping of genotypes was done using according to Tocher's method given by Rao, 1952.

RESULT AND DISCUSSION-

Analysis of variance under present study revealed to have significance at 1% for every trait except number of clusters/plant and number of pods per plant, which are significant at 5% level of significance (Table 1). This suggests that the selected germplasm lines have significant genetic variability, which insures enough of scope for crop improvement (Bharathi *et al.*, 2022; Kumawat *et al.*, 2023). High coefficient of variation (CV) is a result of good degree of variation in genotypes, which is why the scope for selection is significant. PCV and GCV values at higher end showed sizeable variation, but low difference between GCV and PCV values illustrates less influence of environmental factors.

A wide range of phenotypic coefficient of variation (PCV), was observed for all the traits, from 2.58 to 22.90 (Table 2). Estimate of PCV was high for number of branches/plant (22.90). Moderate PCV was observed in seed yield/plant (19.90), biological yield/plant (18.63), harvest index (18.15), number of clusters/plant (16.52), number of seeds/pod (15.98), number of pods/plant (14.59), plant height (11.78), 100 seed weight (10.34). Low PCV was seen for pod length (9.12), days to 50% pod setting (3.46), days to 50% flowering (2.66) and days to maturity (2.58) suggested for a limited scope of selection for improvement of these traits. Similar result for high PCV for number of branches/plant and Moderate PCV for traits like number of seeds/pods, pods/plant, plant height was observed by Kumawat *et al.*, 2023. Low PCV was recorded by Deekshith *et al.*, 2022 for pod length, days to 50% flowering and days to maturity.

A wide range of genotypic coefficient of variation (GCV) was observed for all the traits ranged from 1.77 to 18.20 (Table 2). Estimate of GCV were moderate for number of branches/plant (18.20) followed by biological yield/ plant (16.57), seed yield /plant (15.79), harvest index (13.53), number of seeds/pod (12.79). Low estimate of GCV was observed in number of clusters/plant (9.13), number of pods/plant (7.14), pod length (6.48), plant height (6.42), 100 seed weight (6.12), days to 50% pod setting (2.38), days to maturity (2.15) and days to 50% flowering (1.77). Comparable results for days to maturity, days to 50% flowering and 100 seed weight was described by Gnanasekaran *et al.*, 2025 and results for all the traits with low estimates of GCV showed resemblance with Praneetha *et al.*, 2025.

Estimates of heritability (%) in broad sense for 13 characters studied (Table 2), which range from 23.9% to 79.11% (Table 2). Seed yield/plant (79.11%), days to maturity (69.4%), number of seeds/pod (64.17%), 100 seed weight (62.85%), number of branches/plant (62.5%) showed high heritability. Moderate heritability was recorded for biological yield/plant (55.61%) days to 50% pod setting (47.16%), pod length (46.15%), days to 50% flowering (44.78%), seed index (35.29%). Furthermore, low heritability was noted in number of clusters per plant (29.89%), plant height (29.74%) and number of pods per plant (23.9%). Study conducted by Gnanasekaran *et al.*, 2025 deduced similar results for days to 50% flowering, days to maturity, 100 seed weight, Seed yield/plant.

A perusal of genetic advance (Table 2) revealed that it was highest in biological yield/plant (12.44) followed by harvest index (4.58), plant height (3.24), days to maturity (2.54), seed yield/plant (2.30), days to 50% pod

setting (1.95), number of pods/plant (1.79), days to 50% flowering (1.17), number of seeds/pod (1.08), number of clusters/plant (0.62), number of branches/plant (0.52), pod length (0.38) and 100 seed weight (0.30). High estimate of genetic advance as percent of mean (GAM) was registered for biological yield/plant (30.36), number of branches/plant (29.82), seed yield/plant (25.80), number of seeds/pod (21.10), harvest index (20.79) (Table 2). Number of clusters/plant (10.41) was the only character exhibiting moderate estimate of genetic advance as percent of mean (GAM). Low estimate of genetic advance as percent of mean (GAM) was illustrated in pod length (9.49), 100 seed weight (7.46), plant height (7.22), number of pods/plant (7.19), days to maturity (3.69), days to 50% pod setting (3.36) and days to 50% flowering (2.44). Similar result was procured by Deekshith *et al.*, 2022 for number of clusters/plant, pod length, days to 50% flowering and days to maturity. Genotype selection by variability shown in traits can lead to poor results as variability may get influenced by environmental factors but, selection on the basis of high broad sense heritability combined with high GAM, like number of branches/plant, number of seeds/pod and seed yield/plant may prove beneficial.

Correlation Coefficient Analysis

For selecting a suitable plant type, correlation studies would provide reliable information, extent and direction of selection, especially when the breeder needs to combine high yield potential with desirable agronomic characters and grain quality. During the correlation study, associations between yield and yield contributing features were assessed.

In phenotypic correlation, Seed yield per plant exhibited positive and significant correlation with harvest index (0.562) and biological yield/plant (0.534). Whereas 100 seed weight (0.270), number of clusters/plant (0.240), days to maturity (0.153), number of seeds/pod (0.100), number of pods/plant (0.084), days to 50% flowering (0.068) and pod length (0.068) showed positive non-significant correlation with seed yield. The character number of branches/plant (-0.071), plant height (-0.038) and days to 50% pod setting (-0.002) had negative non-significant correlation with seed yield (Table 3). Study conducted by Kumar *et al.*, 2022 and Priyanka *et al.*, 2022 deduced resembling results for positive and significant correlation for harvest index and biological yield/plant. Comparable result for number of branches/plant was observed by Mishra and Lavanya, 2021.

In genotypic correlation, seed yield per plant exhibited positive and significant correlation with biological yield/plant (0.612) followed by number of clusters/plant (0.519), harvest index (0.426) and 100 seed weight (0.397). Whereas pod length (0.236), days to maturity (0.190), days to 50% pod setting (0.143), number of seeds/pod (0.133), number of pods/plant (0.056), plant height (0.044), days to 50% flowering (0.009) showed positive non-significant correlation with seed yield. Number of branches/plant (-0.178) and had negative non-significant correlation with seed yield/plant (Table 4). Similar results for all positive significant correlation were observed by Radhikaben and Bala, 2020. Comparable results for days to 50% flowering, number of pods/plant, pod length were procured by Priyanka *et al.*, 2022.

D² Genetic Diversity Analysis

In a breeding program, choosing diverse parents assists in finding transgressive segregants. Genetic diversity can be used to estimate inherent capacity of a cross for heterosis and the frequency of desired recombinants in subsequent generations. Genetic distance is important because superior genotypes in segregating populations necessitate diversity in parent genotypes.

Clustering of genotypes

Clustering genotypes according to their similarities or differences is essential for delivering accurate information on several genotypes. Genotypes within the same cluster were regarded as more closely related than those in other clusters (Bhagat *et al.*, 2025). The 30 black gram genotypes were grouped into 6 clusters (Table 5). Cluster II had maximum number of genotypes i.e. 19, while cluster I showed presence of 7 genotypes. Cluster III, IV, V, VI are mono-genotypic, indicating genetic distinctiveness within germplasm. Mono-genotypic clusters reveal that though present solitary, these genotypes tend to be diverse from other genotypes of any clusters (Sreenivas *et al.*, 2023)

Inter and Intra Cluster Divergence

Inter and intra cluster distance shows presence or absence of genetic homogeneity within the group. Maximum intra-cluster distance was observed in cluster II (12.50), followed by in cluster I (6.36) and lowest was found in cluster III, IV, V, VI (0.00). As for the inter cluster distance, it revealed that the highest genetic variation was noted in cluster V and cluster VI (76.32), followed by cluster IV and cluster V (46.61) (Table 6). This denotes, parent selection from these clusters will be beneficial for acquiring good amount of heterosis in F₁ generation and a high probability of transgressive segregants with wide genetic base (Prasanna *et al.*, 2024; Korattukudy *et al.*, 2022; Reni *et al.*, 2022). Lowest inter cluster distance was observed in cluster I and cluster III (10.78), followed by cluster I and cluster II (12.70). Parent selection from these clusters should be avoided since it might lead to F₁ with a narrow genetic base (Prasanna *et al.*, 2024). Similar results were drawn from previous studies by Korattukudy *et al.*, 2022; Prasanna *et al.*, 2024; Reni *et al.*, 2022; Sreenivas *et al.*, 2023.

Cluster Mean

The cluster mean analysis revealed trait-specific advantage (Vengatesh *et al.*, 2026). By examining cluster means it can be pointed out that cluster VI showed superior mean value for number of seed yield/plant (11.91g). This cluster also displayed advantageous values for pods/plant, biological yield/plant justifying the advantageous seed yield/plant (Table 7). Mean values of cluster II and V were found to be intermediate (inferior) as compared to the other clusters. Cluster IV exhibited low means for days to 50% flowering, representing early flowering among genotypes with elevated values for plant height, number of clusters/plant,

pod length, number of seeds/pod, seed index and harvest index, supporting its utility as a donor for improving seed yield and harvest index. Meanwhile, cluster I and III showed low mean values for days to 50% pod setting but only cluster I revealed to have low value for days to maturity in genotypes. These genotypes can be used in areas where early maturity allows escape from biotic and abiotic stress.

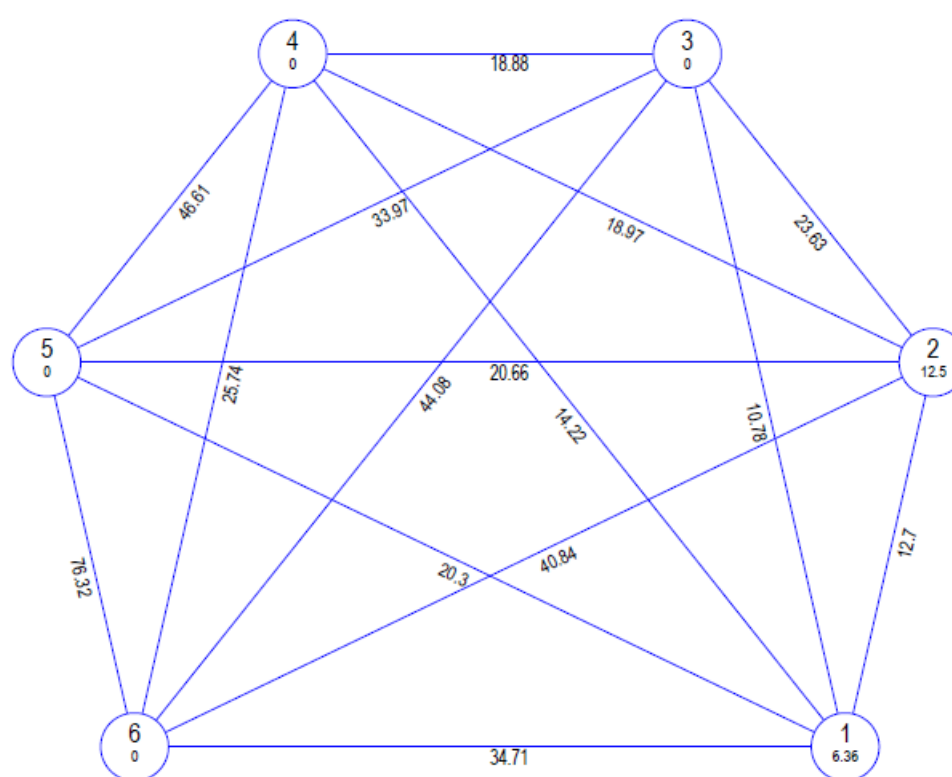
Percent contribution of each character to total divergence

Genetic diversity is one of the basic objectives of any breeding programme. The highest contribution in the manifestation of genetic divergence was exhibited by biological yield per plant (27.59%) by ranking first 120 times, followed by grain yield per plant (14.94%) by ranking at top for 65 times, number of seeds per pod (12.64%) by ranking first for 55 times and pod length (10.57%) by ranking at top for 46 times, suggesting scope for improvement in these characters. On the contrary, traits with lowest contribution to the divergence are 100 seed weight (0.23%) by ranking at top for only a single time, plant height (1.61%) by ranking first for 7 times and days to 50% podding (1.84%) by ranking first for 8 times (Table 8). Emphasis on traits which were good contributors to the total divergence helps in finding and selecting genetically diverse parents for wide genetic base of further generations. (Preethi *et al.*, 2022)

CONCLUSION

Black gram is a self pollinated crop originated in India and belongs to family Leguminosae. For selection among genotypes on basis of traits observed various statistical analysis was done like, ANOVA, genetic variability, correlation and genetic diversity. ANOVA suggests that there is variability among genotypes for all traits observed, and by the genetic variability analysis selection of traits like branches/plant, number of seeds/pod and seed yield/plant will be beneficial for crop improvement as it is governed by additive gene effect. Correlation analysis revealed that with increase in harvest index and biological yield, seed yield per plant increases simultaneously in both at genotypic and phenotypic level. Genetic diversity estimates that, biological yield per plant had highest contribution to genetic divergence by ranking first for 120 times. All the genotypes were grouped into six cluster in which cluster II holds most of the genotypes. Inter cluster distance revealed that the cross between NDU-5-7 (cluster V) and IC-250188 (cluster VI) and NDU-5-7 (cluster V) and IPU-96-1 (cluster IV) may produce the heterotic progeny.

Figures



Mahalanobis Euclidean Distance (Not to the Scale)

Fig 1. Intra and inter cluster distance in blackgram genotypes

Tables: Table 1. Analysis of variance for 13 different quantitative characters in 30 genotypes of blackgram.

S. No.	Characters	Mean sum of squares		
		Replications (d.f.= 2)	Treatments (d.f.= 29)	Error (d.f.= 58)
1	Days to 50% flowering	1.68	3.09**	0.91
2	Days to 50% pod setting	1.63	7.87**	2.14
3	Plant height	37.21	44.78**	19.72
4	Number of branches per plant	0.08	0.37**	0.06
5	Number of clusters per plant	0.47	1.56*	0.67
6	Pods per plant	3.06	19.55*	10.06
7	Pod length	0.14	0.27**	0.07
8	Number of seeds per pod	0.35	1.54**	0.24
9	Days to maturity	0.34	7.58**	0.98
10	Seed index	2.71	7.13**	1.17
11	Harvest index	8.94	33.88**	7.12
12	Biological yield	8.38	150.51**	12.17
13	Seed yield per plant	0.09	0.30**	0.11

Significant at 5%* & 1%** level of significance.

Table 2. Genetic parameters for 13 biometrical characters of 30 blackgram genotypes

S.No.	Characters	Genotypic Variance (V g)	Phenotypic Variance (V p)	GCV	PCV	Heritability (%) (bs)	GA	GAM
1	Days to 50% flowering	0.73	1.63	1.77	2.66	44.78	1.17	2.44
2	Days to 50% pod setting	1.91	4.05	2.38	3.46	47.16	1.95	3.36
3	Days to maturity	2.20	3.17	2.15	2.58	69.40	2.54	3.69
4	Plant height	8.35	28.07	6.42	11.78	29.74	3.24	7.22
5	Number of branches/ plant	0.10	0.16	18.20	22.90	62.50	0.52	29.82
6	Cluster /plant	0.29	0.97	9.13	16.52	29.89	0.62	10.41
7	Pods /plant	3.16	13.22	7.14	14.59	23.90	1.79	7.19
8	Seed /pod	0.43	0.67	12.79	15.98	64.17	1.08	21.10
9	Pod length	0.06	0.13	6.48	9.12	46.15	0.38	9.49
10	Biological yield /plant	46.11	58.28	16.57	18.63	55.61	12.44	30.36
11	Harvest index	8.92	16.04	13.53	18.15	35.29	4.58	20.79
12	100-seed weight	0.06	0.17	6.12	10.34	62.85	0.30	7.46
13	Seed yield /plant	1.98	3.15	15.79	19.90	79.11	2.30	25.80

Table 3. Correlation coefficient between yield and its related traits in 30 blackgram genotypes at phenotypic level.

Character	Days to 50% Flowering	Days to 50% podding	Days to maturity	Plant height	Number of branches/plant	Clusters / plant	Pods/plant	Seeds/pod	Pod length	Biological yield	Harvest Index	100-SW	Seed yield/plant
Days to 50% Flowering	1.000	0.633*	0.661**	-0.128	-0.023	-0.049	-0.056	-0.128	-0.219	0.086	-0.005	-0.052	0.000
Days to 50% podding		1.000	0.717**	-0.005	-0.109	0.081	-0.217	0.020	0.003	-0.066	0.068	0.142	-0.000
Days to maturity			1.000	-0.021	0.116	0.116	0.002	0.021	-0.037	0.098	0.066	0.053	0.000
Plant height				1.000	-0.138	0.042	-0.078	0.252	-0.056	-0.131	0.062	0.267	-0.000
Number of branches/plant					1.000	-0.074	0.068	0.148	0.041	-0.269	0.186	-0.148	-0.000
Clusters/plant						1.000	0.089	0.272	0.350*	0.146	0.091	0.225	0.000
Pods/plant							1.000	0.307*	-0.064	0.149	-0.054	-0.280	0.000
Seeds/pod								1.000	0.279	-0.097	0.191	0.494*	0.000
Pod length									1.000	-0.033	0.126	0.146	0.000
Biological yield										1.000	-0.383*	0.050	0.000
Harvest Index											1.000	0.262	0.000
100-Seed Weight												1.000	0.000
Seed yield/plant													1.000

significant levels of 5%* and 1%** respectively

Table 4. Correlation coefficient between yield and its related traits in 30 blackgram genotypes at genotypic level.

S.N.	Characters	Days to 50% Flowering	Days to 50% podding	Days to maturity	Plant height	Number of branches/plant	Clusters / plant	Pods/plant	Seeds/ Pod	Pod length	Biological yield
1	Days to 50% Flowering	1.000	0.786**	0.792**	-0.497**	-0.020	-0.119	-0.157	-0.235	-0.500**	0.000
2	Days to 50% podding		1.000	0.894**	-0.153	-0.164	0.162	-0.282	0.051	-0.270	0.000
3	Days to maturity			1.000	-0.220	0.087	0.016	-0.114	0.065	-0.215	0.000
4	Plant height				1.000	-0.240	0.369*	-0.398*	0.665**	0.088	-0.000
5	Number of branches/plant					1.000	-0.253	0.166	0.180	-0.027	-0.000
6	Clusters/plant						1.000	-0.377*	0.751**	0.649**	0.000
7	Pods/plant							1.000	0.636**	0.079	0.000
8	Seeds/pod								1.000	0.455**	-0.000
9	Pod length									1.000	0.000
10	Biological yield										1.000
11	Harvest Index										
12	100-SeedWeight										
13	Seed yield/plant										

significant levels of 5%* and 1%** respectively

Table 5. Distribution of 30 blackgram genotypes into different clusters

S. No.	Cluster No.	No. of genotypes	Genotypes included
1	I	7	IPU-96-1, UN-85-5, PGRU-99022, UN-82-83, KPU-131991, IC-140816, Shekhar 2
2	II	19	Pant U-19, T-9, Uttara, IC-24129, IC-91567, IP-140815, VG-27, PLU-710, Shekhar 1, IPU-7-3, IC-250190, IC-250189, IC-106194, IC-56048, Pant U-30, IC-140814, GC-9120, IC-250187, IPU-99-60
3	III	1	Azad-1
4	IV	1	IPU-96-1
5	V	1	NDU-5-7
6	VI	1	IC-250188

Table 6. Intra and inter cluster averages distances in blackgram genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	6.36	12.70	10.78	14.22	20.30	34.701
Cluster II		12.50	23.63	18.97	20.66	40.84
Cluster III			0.00	18.88	33.97	44.08
Cluster IV				0.00	46.61	25.74
Cluster V					0.00	76.32
Cluster VI						0.00

Table 7. Cluster mean values for different component characters in blackgram

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Mean
Days to 50 % Flowering	48.04	47.50	47.80	47.16	49.16	47.66	48.04
Days to 50 % Pod Setting	57.00	57.83	57.000	58.00	60.11	58.00	58.007
Plant height	43.16	47.65	46.17	49.22	42.33	42.09	44.96
Primary Branches/ Plant	1.64	1.83	1.90	1.40	1.82	1.33	1.76
Clusters/ Plant	5.52	5.47	6.48	6.97	5.59	6.07	5.96
Pods/ Plant	26.73	22.60	25.21	24.10	23.65	27.93	24.92
Pod Length	3.82	4.22	4.14	4.37	3.84	4.03	4.03
Seeds/ Pods	4.36	5.38	5.61	6.36	4.84	4.06	5.14
Days to Maturity	67.57	67.83	68.90	68.67	70.94	69.33	68.86

Seed index	3.82	4.37	4.00	4.76	4.00	4.02	4.06
Harvest index	20.49	25.72	21.54	25.87	21.68	18.31	22.06
Biological Yield/ Plant	40.35	32.95	41.74	44.44	40.58	65.16	40.93
Seed Yield/ Plant	8.17	8.44	8.99	11.33	8.74	11.91	8.93

Table 8. Percent contribution of 13 characters to genetic divergence

S.No.	Characters	Times Ranked 1st	Contribution %
1	Days to 50% Flowering	15	3.45%
2	Days to 50% podding	8	1.84%
3	Days to maturity	33	7.59%
4	Plant height	7	1.61%
5	Primary branches/plant	36	8.28%
6	Clusters/plant	9	2.07%
7	Pods/plant	19	4.37%
8	Seeds/pod	55	12.64%
9	Pod length	46	10.57%
10	Biological yield	120	27.59%
11	Harvest Index	21	4.83%
12	100-Seed Weight	1	0.23%
13	Seed yield/plant	65	14.94%

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