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STUDIES ON GENETIC DIVERSITY IN BLACKGRAM (*Vigna mungo* L. Hepper) GERMPLASM

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ABSTRACT
The present investigation was conducted to examine the genetic diversity existing among 32 genotypes of blackgram, during *kharif-2016* under randomized block design with three replications. The data was recorded for thirteen quantitative characters to obtain estimates of variability, heritability, genetic advance and divergence. Analysis of variance showed significant differences between genotypes for all the 13 characters studied. High estimates of GCV and PCV were observed for seed index followed by clusters per plant, number of branches per plant, plant height and seed yield per plant. High heritability coupled with minimum genetic advance was recorded for seed index. The 32 genotypes were grouped in to six heterogeneous clusters. Among these clusters, cluster II have a maximum number of genotypes (11). On the basis of mean performance genotypes BG-6 followed by IC-140016 were found to be the best genotypes in Allahabad agro-climatic conditions. The characters such as plant height and seed yield per plant which should be given top priority for effective selection. Percent contribution towards the total divergence was maximum through seed index followed by number of branches per plant and clusters per plant. The present investigation revealed that cluster III and V are most diverse to each other and the genotypes constituted in these clusters may be used as parents for future hybridization programme.

KEY WORDS: Blackgram, Genetic Diversity, D^2 statistic and cluster

INTRODUCTION

Blackgram (*Vigna mungo* L. Hepper) popularly known as urdbean or mash, is a grain legume domesticated from *V. mungo var. silvestris* (Lukoki, 1980). It belongs to family leguminoseae with chromosome number 2n=2x=22. Blackgram is reported to be originated in India (Zukovskiji, 1962). India is the world's largest producer as well as consumer of blackgram. It produces about 1.5 to 1.9 million tons of blackgram annually from about 3.5 million hectares of area, with an average productivity of 500 kg per hectare. Blackgram output accounts for about 10% of India's total pulse production (*Ministry of Agriculture, Govt. of India, 2015*). In 2014-2015, 1.61 million tonnes Urd production in the country is largely concentrated in five states *viz*, Uttar Pradesh (UP), Maharashtra, Madhya Pradesh, Andhra Pradesh and Tamil Nadu. These five states together contribute for about 70% of total urd production in the country (*Ministry of Agriculture, Govt. of India, 2015*). In U.P. Blackgram is grown in about 3.91 lakh hectares with a total production of 1.72 lakh tones (Annual Report 2014-2015). Among the states of India, Orissa ranks first in area 777 thousand hectares and production 396 thousand tones. However, Bihar is a leading state in productivity with 898 kg/hectare (Pulses in India, Ministry of Agriculture and Farmer welfare, Govt. of India, 2015). Per capita availability of pulses per day is only 47g as against the minimum requirement of 104g as recommended by nutritional experts of World Health Organization/Food and Agriculture Organization (Hariprasanna and Bhatt, 2002). Generally, pulses are rich in those amino acids (Lysine and Tryptophan) which are present in traces in cereals. It is a cheap source of dietary protein 23-24%. It also contributes 76% carbohydrate, 3-5% Fiber, 1.74% Fat and a major portion of lysine in the vegetarian diet (Elangaimannan, 2008). It is also an important protein source for people it is rich in phosphoric acid among pulses (Rao and Suryawanshi, 1988). Being 5-10 times richer than other crops. Besides, being used as food for inexpensive source of dietary protein it is better to use for bean sprouts than mungbean for its longer shelf life (Mishra and Khan, 2001). Blackgram is predominantly a self-pollinated and widely cultivated grain legume (Nag *et al*., 2006). It is an annual, tendency for twining in the upper branches, leaves are trifoliate with basal appendages, stipules minute and leaflets entire ovate, inflorescence is auxiliary or terminal raceme with 10–20 flowers crowed on long peduncle, flower are either light yellowish, olive or olive yellow; hermaphrodite, zygomorphic, 5 sepals, 5 petals, 10 stamens in diadelphous (9+1) condition, single carpelled ovary with style. Generally, Pod length 3-7 cm long and 6-9 seeds with blackish cotyledons (Ram, 2011). The productivity of pulse crop is very low when compared to cereals, which have been selected for high grain yield under high input conditions while the selection pressure in case of pulses have been focused in the adaptation to both biotic and abiotic stresses. The reason for low yield is; i) adaption of crop to marginal lands of rain fed nature. The crop has been traditionally cultivated under less fertile soils with

least inputs, ii) unavailability of cultivars with high potential, iii) stress to disease insects and environmental fluctuations, etc. Hence, large parts of the genetic variability for yield contributing characters were lost during the course of evolution. Lack of stable varieties for higher yield is a major bottleneck for growing of this crop Therefore for increasing the productivity of Blackgram collection and characterization of germplasm from different regions of cultivation need specific emphasis. The improvement in this crop is confined to pure line selection and to a limited extent through hybridization. In the past, there have been attempts to increase the production and productivity of the crop using conventional breeding approaches in different agriculture research centers (Ali and Kumar, 2006).

Quantitative traits provide an estimate of genetic diversity and numerical taxonomic techniques including principle component and cluster analysis have been successfully used to classify and measure the pattern of genetic diversity in germplasm, as in blackgram (Shanmugam and Shreerangaswwamy, 1982; Dasgupta and Das, 1984 and 1985; Ghafoor *et al.,* 2001), mungbean (Singh, 1988; Ramana and Singh, 1987), pea (Amurrio *et al.,* 1995), soyabean (Perry and Melntosh,1991), alfalfa (Smith *et al.,* 1995), chickpea (Naghavi and Jahansouz). Among pulses, black gram is the least researched crop ad no international centre has listed it as a mandate crop. Although it been identified as a potential crop in number countries, but no systematic research information is available on crop improvement using biometrical techniques except few report in recent years (Ghafoor *et al*., 2003). The creation of variability is difficult through hybridization due to its high self-pollination and flower dropping (Deepalakshmi and Anandkumar, 2004), Besides the major constraints in achieving higher yield of blackgram is absence of suitable ideotypes for different cropping system, poor harvest index and susceptibility to disease (Souframanien and Gopalkrishnan, 2004) in order to improve yield and other polygenetic characters, mutation breeding can be effectively utilized (Deepalakshmi and Anandkumar, 2004). Therefore, genetic variability is the basic requirement for making progress in crop breeding (Appalaswamy and Reddy, 2004). Progenies originating from the crosses involving diverse parents exhibit greater heterosis and provide broad spectrum variability in segregating generations. Such crosses not only result in inducing variation but also provide new recombination of the genes in the gene pool, which may have great impact on future breeding programme. Choice of parents is not only based on desirable agronomic traits, components of yield and extent of diversity but also heritability of yield contributing traits. The environment, in which selection is made, is also important because heritability and genetic advance estimates vary with change in environment (Baradhan and Thangavel., 2011).

The study of genetic variability is the pre-requisite for any crop improvement programme. Success in recombination breeding depends on the suitable exploitation of genotypes as parents for obtaining high heterotic crosses and transgressive segregants for this, the presence of genetic variability in a base population is essential. It is well known that all the plant breeding programmer involve selection at one stage or the other. The effectiveness of selection depends on the existence of genetic variability within or among the population, which is subjected to selection. While the existing variability can be augmented and new variability generated through appropriate genetic or breeding technique (Joshi and Dhawan., 1986). Selection of superior parents exhibiting better heritability and genetic advance for various characters is an essential prerequisite for any yield improvement programme (Khan and Malik, 2005). The major function of heritability estimate is to provide information on transmission of characters from the parents to the progeny. The efficiency of selection depends upon the magnitude of genetic variability for yield and yield contributing traits in the breeding material. The knowledge of heritability and genetic advance guides the breeder to select superior parents to initiate an effective and fruitful crossing programme (Johnson *et al.,* 1955). The assessment of variation provides us a correct picture of the extent of variation, further helping us to improve the genotypes. Genetic diversity is one of the criteria of parent selection in the hybridization program. The availability of transgressive segregant in any breeding program depends upon the diversity between the parents involves. The quantification of genetic diversity through biometrical procedures such as Mahalanobis's D^2-statistic has made possible to choose genetically diverged parents. Recent works indicated that the Mahalanobis generalized distance (D^2-statistic) may be an efficient tool in the quantitative estimation of genetic diversity (Mahalanobis, 1936). The divergence analysis has a definite role to play in an efficient choice of divergent parents for hybridization to exploit maximum heterosis.

MATERIALS & METHODS

The present experiment was undertaken at Field of Department of Genetics and Plant Breeding, Naini Agriculture Institute, Sam Higginbottom University of Agriculture, technology and Sciences Allahabad, U.P. during *kharif* 2016. 32 genotypes of urd bean were grown in this experiment. Experiment was done according to randomized block design with three replications, and recommended package of practices were followed to raise the crop. Seeds were sown with row to row spacing of 30 cm and plant to plant spacing of 10 cm. The data were recorded on five randomly selected plants of each replication for all characters but in case of days to 50% flowering and days to maturity, the observations were recorded on plot basis, pre-harvest observations are Days to 50% flowering, Days to 50% pods setting, Plant height (cm), Number of primary branches per plant, Number of clusters per plant, Number of pods per plant, Days to maturity and Post harvest observations are No. Of seeds per pod, Pod length (cm), Seed index (g), Biological yield (g) and Seed yield per plant (g). Mean values were computed and data were analyzed for analysis of variance as suggested Fisher (1936) given in table :1. phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were given by Burton (1952). Heritability in broad sense was given by Lush (1949) and Burton and Devane (1953). Genetic advance was given by Lush (1949) and Johnson *et al.* (1955). Genetic divergence was given by Mahalanobis (1936).

RESULTS & DISCUSSION

The mean sums of squares of 13 different traits are presented in [Table-1]. High significant differences for all characters under study among the 32 blackgram genotypes were found in analysis of variance, at 1 % and 5 % level of significance indicating the presence of sufficient variability among different genotype Maximum seed yield per plant was recorded for BG-6, (10.80g) followed by IC-140016 (10.78 g) [Table-2], moderate magnitude of GCV was recorded for number of clusters per plant (16.72), number of branches per plant (15.26). Whereas plant height (11.05), seed yield per plant (10.47), Number of pods per plant (9.61), harvest index (9.15), biological yield per plant (7.09), days to 50% flowering (6.92), seeds per pod (6.67), pod length per plant (6.43), days to 50% pod setting (4.41) and days to maturity (2.91) depicted low genotypic coefficient of variation [Table-3].

TABLE-1 Analysis of variance for different 13 quantitative characters in blackgram

S. No.	Characters	Mean sum of squares		
		Replication (d.f.= 2)	Treatments (d.f.= 31)	Error (d.f.= 62)
1	Days to 50 % Flowering	1.38	31.67**	2.37
2	Days to 50 % Pod Setting	1.16	19.65**	2.08
3	Plant Height (cm)	38.18	135.10**	16.82
4	Number of Branches/Plant	0.004	1.15**	0.024
5	Clusters/ Plant	1.62	34.80**	1.25
6	Pods/ Plant	0.50	77.05**	1.94
7	Pod Length/ Plant	0.04	0.27**	0.03
8	Seeds/ Pod	0.01	0.58**	0.05
9	Days of Maturity	5.29	15.63**	3.90
10	Seed Index (gm)	0.04	1.78**	0.03
11	harvest Index	0.003	39.29**	3.02
12	Biological Yield/ Plant (g)	0.25	9.53**	0.55
13	Seed Yield/ Plant	0.29	2.93**	0.13

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

Phenotypic coefficient of variation (PCV) ranged from 4.12 (days to maturity) to seed index (19.46). Moderate magnitude of PCV was recorded for number of clusters per plant (17.64), Number of branches per plant (15.76), plant height (13.19), seed yield per plant (11.19), harvest index (10.23). Whereas pods per plant (9.97), pod length per plant (7.83), day to 50% flowering (7.72), biological yield (7.72), seeds per pod (7.66), days to 50% pod setting (5.13) and days to maturity (4.12) exhibited low phenotypic coefficient of variation [Table-3]. On an average, the higher magnitude of GCV and PCV were recorded for seed index, clusters per plant, Number of branches per plant, plant height, seed yield, pods per plant and harvest index suggesting sufficient variability and thus scope for genetic improvement through selection for these traits, similar finding was also reported by Neelavati and Govindarasu, (2010). All characters show maximum heritability in 32 genotypes (table :3). The estimates of heritability (%) in broad sense for 13 characters studied, which range from 50.03 to 94.88. Higher estimates of heritability in broad sense were recorded for seed index (94.88) followed by number of branches per plant (93.80), pods per plant (92.80), clusters per plant (91.86), seed yield per plant (87.61), biological yield per plant (84.43), harvest index (82.04), seeds per pod (75.82), Days to 50% pods setting (74.79), plant height (70.09). The traits like, pods length per plant (67.37) and days to maturity (50.03) exhibited moderate value of heritability [Table-3]. Wani *et al.,* (2007) reported high heritability coupled with high genetic advance for number of pod per plant, number of pods per clusters, plant height and seed yield per plant suggested the additive genetic control in the inheritance of these characters.

The genetic advance (as percent of mean) varied from 4.24 to 38.04%. Maximum genetic advance was recorded for seed index (38.04) followed by Clusters per plant (33.14), whereas minimum genetic advance was recorded for Days 50% pod setting (7.80) followed by Days to maturity (4.24) [Table-3]. Johnson *et al.,* (1955) showed that high heritability should be accompanied by high genetic advance to arrive at more reliable conclusion. In Genetic diversity (Mahalanobis D^2 statistics) In the present study, 32 genotypes were grouped into six clusters [fig 2] by Non-Hierarchical Euclidean cluster analysis [Table- 4], clustering pattern indicate that II is the largest comprised 11 out of 32 genotypes (LBG-645, M-198, RASHMI, UH-85-5, IC-91567, M-104, PLU-648, IPU-96-1, SPS-33, UH-82-83, IC-250190). Cluster III with 6 genotypes (DU-1, IC-456048, PKG-U-3, UH-10, U-5, IC-436724) and IV comprised 6 genotypes (BG-8, IPU-199-60, KU-10-625, IC-436566, M-291, MBG-105.), cluster V comprised 4 genotypes (HAIR KSS, IPU-7-3, IC-140016, AZAD-1), cluster I comprised 3 genotypes (IC-398958, BG-6, T-9 (CHECK)) and cluster VI comprised 2 genotypes (UH-82-15, UG-27), the pattern of group constellation proved the existence of significant amount of variability.

The average intra cluster distance ranged from 46.66 to 117.35. The maximum intra cluster distance was recorded for cluster VI (117.35) followed by cluster I (112.29), cluster IV (84.43), cluster III (74.47) and cluster II (66.20) while the minimum intra cluster distance was recorded for cluster V (46.66).

TABLE: 2 (a) Mean performance of 32 blackgram genotypes for 13 quantitative characters

No	Character	Days to 50% Flowering	Days to 50% Pods Setting	Plant Height (cm)	Branches / Plant	Clusters/ Plant	Pods /Plant	Pod Length (cm)	Seeds/ Pod	Days to Maturity	Seed Index (g)	Seed Yield/ Plant (g)	Biological Yield (g)	Harvest Index (%)
1	LBG-645	38.66	51.00	55.33	3.48	16.66	50.53	4.53	7.13	65.33	4.24	39.82	22.18	8.83
2	M-198	40.66	52.66	52.46	3.94	17.13	51.26	4.42	6.26	67.66	3.88	42.43	20.82	8.83
3	BG-8	39.66	50.33	58.06	4.19	16.80	50.53	4.29	6.66	66.33	4.26	40.79	24.90	9.68
4	RASHMI	43.33	53.66	48.73	4.35	17.86	52.86	3.94	6.06	63.66	4.82	38.17	23.13	8.83
5	HAIR KSS	40.66	50.33	49.93	4.48	18.93	55.46	4.41	6.06	66.33	4.68	43.01	24.44	10.49
6	DU-1	43.66	53.66	80.73	3.63	20.73	46.63	4.34	7.06	69.00	3.63	34.51	25.77	8.89
7	UH-85-5	48.00	57.00	57.06	4.60	20.80	53.88	4.70	6.13	68.33	4.06	36.30	25.96	9.37
8	IPU-199-60	46.33	54.33	57.00	4.55	17.33	54.23	4.09	6.73	66.00	3.82	34.85	26.08	9.08
9	IC-398958	41.33	52.00	66.93	4.80	22.20	60.66	4.03	5.46	70.33	4.40	37.87	26.24	9.93
10	IC-91567	47.66	57.00	57.93	4.17	15.73	52.46	4.14	6.13	69.66	3.56	40.84	23.71	9.66
11	KU-10-625	39.33	50.33	55.53	4.37	20.53	55.53	4.31	6.66	65.00	3.33	39.26	20.11	7.89
12	M-104	43.33	55.00	56.26	3.23	19.13	46.08	3.76	5.60	63.66	4.67	36.02	22.37	8.05
13	IC-436566	45.66	55.33	55.66	4.34	20.20	54.75	3.93	6.46	66.66	3.43	36.52	25.67	9.38
14	IC-456048	48.00	57.66	54.93	4.08	18.33	50.33	4.64	6.20	68.00	3.44	31.63	27.20	8.60
15	PKG-U-3	49.00	58.00	58.06	3.26	19.13	44.41	4.72	6.53	70.66	3.23	36.00	22.29	8.03
16	UH-10	48.00	57.66	52.93	3.09	19.66	42.43	4.43	6.00	69.00	3.73	32.25	23.54	7.59
17	U-5	47.00	57.00	50.60	3.11	20.40	41.21	4.68	5.40	68.66	3.49	30.17	23.71	7.14

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TABLE: 2 (b) Mean performance 32 blackgram genotypes for 13 quantitative characters

No	Character	Days to 50% Flowering	Days to 50% Pods Setting	Plant Height (cm)	Branches / Plant	Clusters/ Plant	Pods /Plant	Pod Length (cm)	Seeds/ Pod	Days to Maturity	Seed Index (g)	Seed Yield/ Plant (g)	Biological Yield (g)	Harvest Index (%)
18	M-291	47.00	56.66	59.46	4.17	26.40	52.85	4.12	6.06	70.66	3.57	36.26	24.61	8.92
19	IC-436724	40.66	50.66	58.93	3.50	19.66	44.79	4.27	6.66	68.66	3.71	31.81	25.77	8.20
20	MBG-105	45.00	53.66	57.13	4.31	21.73	52.91	4.11	6.40	71.33	3.16	35.09	25.35	8.75
21	BG-6	47.33	57.66	66.66	5.13	28.33	60.66	4.68	6.66	73.66	3.67	42.91	25.16	10.80
22	PLU-648	47.66	57.00	55.06	4.16	20.00	53.51	4.26	5.40	71.00	3.48	37.00	25.66	9.49
23	IPU-7-3	48.66	56.66	60.20	4.79	22.26	58.01	5.08	6.40	66.66	5.47	38.76	26.45	10.24
24	IPU-96-1	47.66	57.33	51.20	3.85	21.40	51.86	4.26	6.73	67.00	3.39	38.89	23.44	9.12
25	IC-140016	46.66	55.66	42.20	4.68	25.66	57.86	4.54	6.20	66.33	6.33	43.39	24.86	10.78
26	AZAD-1	46.33	57.33	50.13	4.00	16.13	53.13	4.54	6.60	66.66	5.82	39.63	26.15	10.36
27	SPS-33	46.33	55.33	56.40	3.68	18.73	50.14	4.32	5.80	67.66	4.38	39.05	25.60	9.98
28	UH-82-15	47.66	56.66	51.13	3.31	18.00	48.27	4.72	6.40	69.33	4.79	40.98	22.69	9.23
29	UH-82-83	47.66	56.00	60.06	3.29	21.60	52.11	4.66	5.93	68.00	3.27	37.67	26.08	9.86
30	UG-27	47.33	56.33	59.20	2.89	16.20	50.34	4.89	6.33	65.00	4.14	38.47	22.29	8.57
31	IC-250190	48.00	56.66	58.73	3.81	14.26	53.86	4.06	6.13	68.33	3.72	40.55	22.50	9.11
32	T-9 (CHECK)	40.33	51.66	64.40	5.30	28.06	62.80	4.54	6.60	67.00	3.55	36.93	25.64	9.47
	Mean	45.14	54.94	56.84	4.02	20.00	52.07	4.39	6.27	67.86	4.03	37.99	24.39	9.22
	S.E.	3.41	2.62	7.21	3.92	5.61	2.67	4.47	3.76	2.91	4.40	4.57	3.04	3.93
	C.D. 5%	13.33	9.44	8.03	46.37	27.63	39.66	7.19	10.40	4.00	56.56	12.98	17.26	22.20
	Range Lowest	38.66	50.33	42.20	2.89	14.26	41.21	3.76	5.40	63.66	3.16	30.17	20.11	7.14
	Range Highest	49.00	58.00	80.73	5.30	28.33	62.80	5.08	7.13	73.66	6.33	43.39	27.20	10.80

TABLE 3 Genetic parameters for 13 quantitative characters of 32 blackgram genotypes

S.No.	Characters	Genotypic Coefficient of variation	Phenotypic coefficient of variation	Heritability (%) (broad sense)	Genetic advance	Genetic advance as % of mean
1	Days to 50 % Flowering	6.92	7.72	80.44	5.77	12.79
2	Days to 50 % Pod Setting	4.41	5.13	74.79	4.28	7.80
3	Plant Height	11.05	13.19	70.09	10.83	19.05
4	Number of Branches / Plant	15.26	15.76	93.80	1.22	30.45
5	Clusters/ Plant	16.72	17.64	91.86	6.63	33.14
6	Pods/ Plant	9.61	9.97	92.80	9.93	19.07
7	Pod Length/ Plant	6.43	7.83	67.37	0.48	10.87
8	Seeds/ Pod	6.67	7.66	75.82	0.75	11.97
9	Days of Maturity	2.91	4.12	50.03	2.88	4.24
10	Seed Index	18.96	19.46	94.88	1.54	38.04
11	harvest Index	9.15	10.23	82.04	6.52	17.16
12	Biological Yield/ Plant	7.09	7.72	84.43	3.27	13.43
13	Seed Yield/ Plant	10.47	11.19	87.61	1.86	20.19

FIGURE1: Histogram depicting estimates of genetic parameters for 13 important agro-economic traits in blackgram

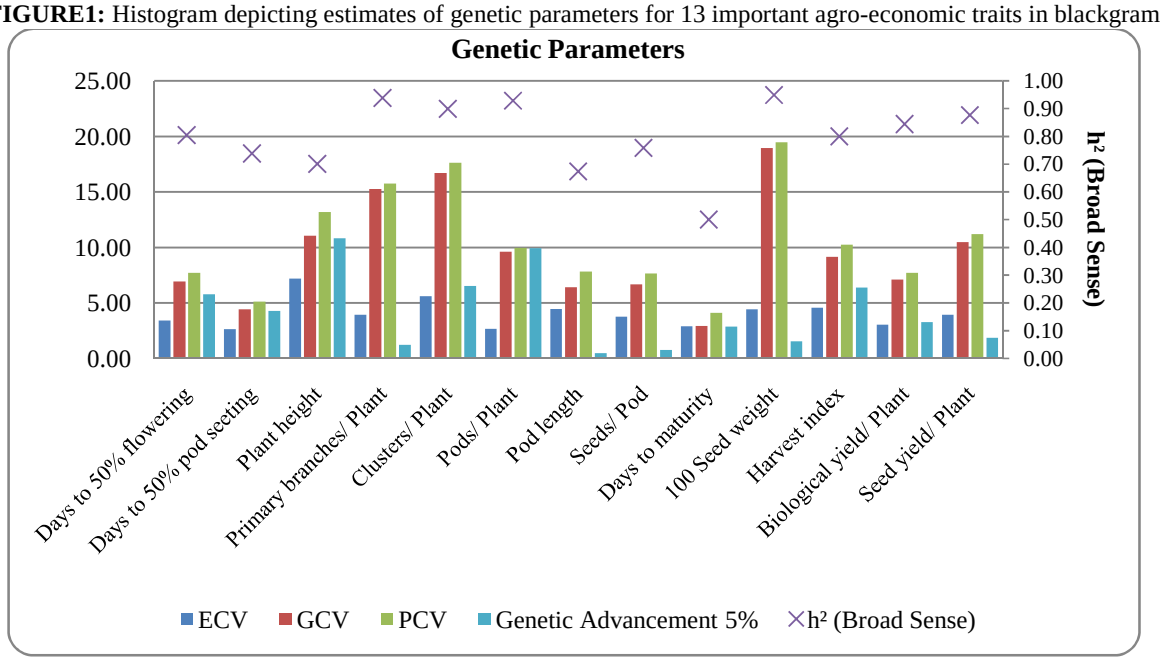


TABLE 4: Distribution of the 32 genotypes of blackgram into different clusters

Clusters / Characters	I	II	III	IV	V	VI
Days to 50 % Flowering	43.00	45.36	46.05	43.83	45.58	47.50
Days to 50 % Pod Setting	53.77	55.33	55.77	53.44	55.00	56.50
Plant Height	66.00	55.38	59.36	57.14	50.61	55.16
Number of Branches/Plant	5.07	3.87	3.44	4.32	4.49	3.10
Clusters/ Plant	26.20	18.48	19.65	20.50	20.75	17.10
Pods/ Plant	61.37	51.69	44.97	53.47	56.11	49.30
Pod Length/ Plant	4.42	4.28	4.51	4.14	4.64	4.81
Seeds/ Pod	6.24	6.12	6.31	6.50	6.31	6.36
Days to Maturity	70.33	67.30	69.00	67.66	66.50	67.16
Seed Index	3.87	3.95	3.54	3.59	5.58	4.46
harvest Index	41.84	38.79	32.73	37.13	41.20	39.73
Biological Yield/ Plant	25.68	23.77	24.71	24.45	25.47	22.49
Seed Yield/ Plant	10.73	9.19	8.07	8.95	10.47	8.90

TABLE: 5 Cluster mean values of 6 clusters for different quantitative characters in blackgram

S. No	Cluster numbers	Number of genotypes	Genotypes included
1	I	3	IC-398958, BG-6, T-9 (CHECK).
2	II	11	LBG-645, M-198, RASHMI, UH-85-5, IC-91567, M-104, PLU-648, IPU-96-1, SPS-33, UH-82-83, IC-250190.
3	III	6	DU-1, IC-456048, PKG-U-3, UH-10, U-5, IC-436724.
4	IV	6	BG-8, IPU-199-60, KU-10-625, IC-436566, M-291, MBG-105.
5	V	4	HAIR KSS, IPU-7-3, IC-140016, AZAD-1.
6	VI	2	UH-82-15, UG-27.

TABLE: 6 Intra (diagonal) and inter cluster average distances (D^2) for different quantitative characters in blackgram

	I Cluster	II Cluster	III Cluster	IV Cluster	V Cluster	VI Cluster
I Cluster	112.294	130.075	236.341	162.11	337.721	273.247
II Cluster		66.205	157.408	186.358	309.067	347.595
III Cluster			74.473	146.908	636.52	540.792
IV Cluster				84.433	598.367	320.810
V Cluster					46.666	388.689
VI Cluster						117.359

FIGURE: 2 Cluster diagram depicting intra and inter cluster distances

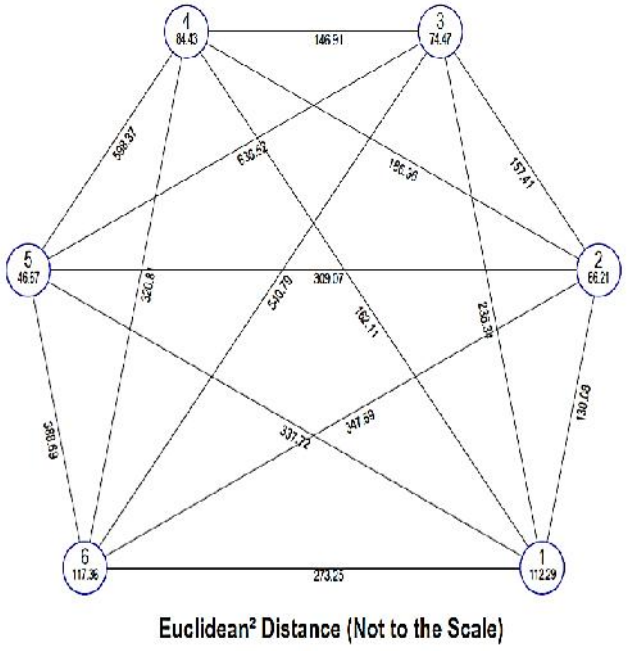
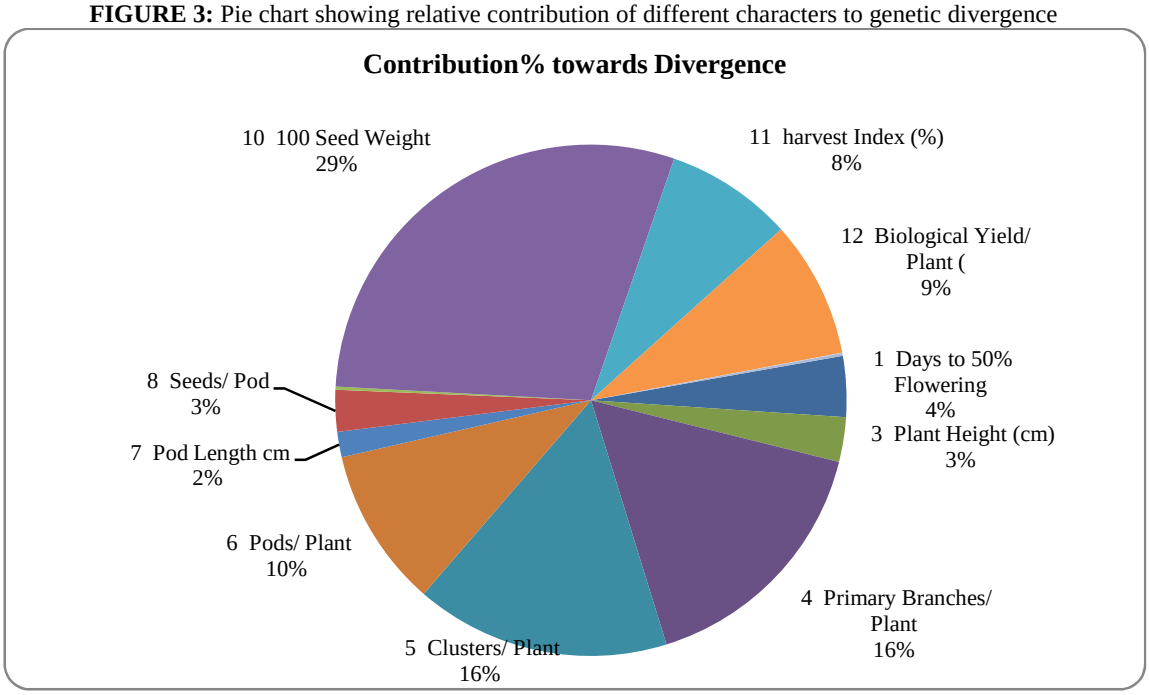


TABLE 7: Percent contribution of 13 different quantitative characters towards genetic divergence in blackgram genotypes

S. No.	Source	Contribution %
1	Days to 50 % Flowering	3.83
2	Days to 50 % Pod Setting	0.01
3	Plant Height	2.82
4	Number of Branches/Plant	16.33
5	Clusters/ Plant	16.13
6	Pods/ Plant	10.08
7	Pod Length/ Plant	1.61
8	Seeds/ Pod	2.62
9	Days to Maturity	0.20
10	Seed Index	29.44
11	harvest Index	8.06
12	Biological Yield/ Plant	8.67
13	Seed Yield/ Plant	0.20

FIGURE 3: Pie chart showing relative contribution of different characters to genetic divergence



The inter cluster D^2 value was maximum between cluster III and V (636.52) followed by cluster IV and V (598.36), cluster III and VI (540.79), cluster V and VI (388.68), cluster II and VI (347.59), cluster I and V (337.72), cluster IV and VI (320.81) and cluster II and V (309.06) [Table-6], suggesting that the genotype present in these clusters may be used as parents for hybridization programme to develop desirable type as heterosis can be best exploited and chance of getting transgressive segregants are maximum when generating diverse lines are crossed (Lal *et al.*, 2001). Whereas the percent contribution of thirteen characters towards total genetic divergence has the highest contribution in the manifestation of genetic divergence was exhibited by Seed index (29.44), number of branches per plant (16.33), clusters per plant (16.13), pods per plant (10.08), biological yield per plant (8.67), harvest index (8.06) and days to 50% flowering (3.83) suggesting scope for improvement in these characters [Table-7 & Fig-3]. In other words, selection for these characters may be rewarding. Similar results were reported by Pandey and Anurag, (2010) for biological yield and test weight.

CONCLUSION

On the basis of results the genotypes BG-6 exhibited maximum seed yield per plant followed by IC-140016 identified as the genotypes for seed yield at Allahabad region. The present investigation registered high heritability along with high genetic advance as a % of mean for clusters per plant and seed index are should be given top priority for effective selection the present investigation further revealed that cluster III and V are most diverse to each other. Therefore, genotypes present in these clusters are suggested to provide a broad-spectrum variability in segregating generations and may be used as parents for future hybridization programme to develop desirable genotypes.

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