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GENETIC DIVERSITY FOR YIELD AND ITS COMPONENTS IN BLACKGRAM (*Vigna mungo* L.)

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ABSTRACT

The present experiment was conducted at field experimentation centre, Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture Technology and Sciences, Allahabad during *kharif* 2017 in Randomized Block Design with three replications. The present investigation was prevailed to examine the 41 blackgram genotypes along with one check (T-9) to study the variability, heritability, genetic advance and divergence. Analysis of variance showed highly significant differences among 41 blackgram genotypes all the 13 quantitative characters studied. Maximum GCV and PCV were recorded for harvest index, seed yield/plant, clusters per plant. High heritability was recorded for days to maturity, pods/plant, days to 50% flowering, seeds yield/plant biological yield /plant. High heritability coupled with high genetic advance as percentage of mean was recorded for harvest index. Genetic diversity estimated in 41 blackgram genotypes using Mahalanobis's D^2 statistic. Forty-one genotypes were grouped into seven clusters by tocher method (Mahalanobis Euclidean Distance) cluster analysis. The maximum inter-cluster distance was observed between cluster VI and cluster VII. The maximum intra-cluster distance was observed in cluster VI. Cluster VI showed maximum cluster mean value for seed yield per plant among all the characters cluster per plant, seeds per pod, harvest index contributes maximum.

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

INTRODUCTION

Blackgram (*Vigna mungo* L.) popularly known as urdbean or mash, is a grain legume domesticated from *V. mungo var. silvestris* (Lukoki, 1980). It belongs to family leguminosae 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 2.1 million tons of blackgram annually from about 3.5 million hectares of area, with an average productivity of 500 kg ha^{-1}. Blackgram output accounts for about 10% of India's total pulse production (*Ministry of Agriculture, Govt. of India*, 2016).

In 2016-2017, 2.1 million tonnes Urad 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 urad production in the country (*Ministry of Agriculture, Govt. of India,* 2016). In U.P. Blackgram is grown in about 5.59 lakh hectares with a total production of 3.11 lakh tonnes (Annual Report 2015-2016). Among the states of India, M.P. ranks first in area 607 thousand hectares and production 276 thousand tonnes. However Bihar is a leading state in productivity with 898 kg ha^{-1} (Pulses in India: Retrospect and Prospects 2016).It is a cheap source of dietary protein (45%). It also contributes 45% carbohydrate, 3-5% Fibre, 1.74% Fat and a major portion of lysine in the vegetarian diet. It is the richest sources of phosphoric acid. 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).

An assessment of the genetic diversity of pulses is an important first step in a programme to improve crop yield. The study of inheritance of various developmental and productive traits through the estimation of different genetic parameters like components of variances, genotypic and phenotypic coefficients of variability, heritability and genetic advance is helpful for framing the effective breeding programme. Variability refers to the presence of differences among the individuals of plant population. It result due to difference either in the genetic constitution of the individual of a population or in the environment they have grown. The existence of variability is essential for improvement of genetic material. The study of genetic variability in any crop would help in the genetic improvement of yield and desirable characters. It will facilitate the identification of proper genotypes for a particular agro-climate. Identification, characterization and study of genotypes and genetic homology between them would provide a base for further studies for crop improvement. The observed phenotypic variation is the result of interaction of genotype and environment in which the individuals are grown. However, it is only genetic variation which is heritable and hence important in any selection programme. The knowledge of genetic diversity is useful tool in gene bank managements and planning experiments by identifying and or eliminating duplicates in the gene stock ultimately resulting in the development of core collective philosophy. In order to maintain, evaluate and utilize germplasm effectively, it is important to investigate the extent of generic diversity available. Smith *et al.* (1991) considered morphological characterization as an important step in description and classification of crop germplasm because a breeding

programme mainly depends on the magnitude of genetic variability.

D^2 Statistic is a powerful tool in quantifying the degree of divergence at genotypic level. Therefore, an attempt has been made in the present investigation with a view to estimate genetic divergence among a set of 41 genotypes of urdbean. In view of these facts, 41 blackgram genotypes were evaluated in this study to estimate genetic variability, heritability, genetic advance and divergence for selection of suitable genotype for exploitation in a breeding programme aimed at improving grain yield potential of blackgram.

MATERIALS & METHODS
The experiment were conducted in *kharif* season 2017-2018 at the Field Experimental Centre, Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology & Sciences, Allahabad, Uttar Pradesh, India. The experiment was done according to Randomized Block Design with 41 genotypes in 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 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 (%). Mean values were computed and data were analysed for analysis of variance as suggested Fisher (1935) 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 Burton and Devane (1953). Genetic advance was given by Lush and Johnson *et al.* (1955). Genetic divergence was given by Mahalonobis (1936).

RESULTS & DISCUSSION
The mean sum of squares values for all the 13 characters are presented in table 1. The mean sum of squares due to 41 genotypes were highly significant for all the characters studied, suggesting that the experimental materials were genetically divergent from each other. This indicates that here is ample scope for selection of promising lines for the present gene pool for yield and its components. The presence of large amount of variability might be due to diverse source of materials taken as well as environmental influence affecting the phenotypes.

TABLE-1 Analysis of variance for 13 different quantitative characters in 41 genotypes of Blackgram

S. No.	Characters	Mean sum of squares		
		Replications (d.f.=2)	Treatments (d.f.= 40)	Error (d.f.= 80)
1	Days to 50% flowering	2.15	46.86**	0.97
2	Days to 50% pod setting	2.32	45.43**	1.64
3	Plant height	2.87	96.10**	12.38
4	Number of branches per plant	0.21	0.84**	0.39
5	Number of clusters per plant	0.20	7.39**	0.78
6	Pods per plant	0.008	38.99**	0.76
7	Pod length	0.003	0.58**	0.007
8	Number of seeds per pod	0.23	1.61**	0.66
9	Days to maturity	0.52	25.65**	0.45
10	Seed index	0.36	1.17**	0.28
11	Seed yield per plant	0.67	10.54**	0.22
12	Biological yield	6.85	213.42**	4.75
13	Harvest index	1.08	44.47**	0.93

** Significant at 1%.

Wide ranges of genotypic coefficient of variation (GCV) were observed for all the traits ranged from days to maturity (4.22) to Harvest index (24.28). Higher magnitude of GCV were recorded for harvest index (24.28) followed by Seed yield/plant (21.56), cluster/plant (15.81), No. of branches/plant (15.06), Biological yield/plant (14.95), 100 seed weight (11.14), Seed/pod (10.70), pods/plant (10.50), Days to 50% flowering (10.22), Plant height (9.53), pod length (8.66).

A wide range of phenotypic coefficient of variation (PCV) were observed for all the traits ranged from days to maturity (4.33) to No. of branches per plant (28.68). Higher magnitude of PCV were recorded for No. of

branches per plant (28.68) followed by harvest index (25.05), Seed yield/plant (22.24), Seed/pod (18.94), cluster per plant (18.43), 100 seed weight (15.68), Biological yield/plant (15.45), plant height (11.46), pods/plant (10.81), days to 50 % flowering (10.54), pod length (10.42), the estimates of heritability (%) in broad sense for 13 characters studied, which range from (27.58 %) to (94.84 %). Days to maturity (94.84 %), pods/plant (94.37 %), Days to 50% flowering (93.99 %), seeds yield/plant (93.97 %), Biological yield /plant (93.60 %), Harvest index (93.93 %) and days to 50 % pod setting (89.89 %) showed high heritability**.**

TABLE 2(a): Mean performance of 41 Blackgram genotypes for 13 quantitative characters

Sr. 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	AKU 11-9	41.66	49.66	54.83	2.00	7.66	39.33	5.06	4.33	68.66	5.82	8.44	53.10	15.90
2	AKU 11-14	41.00	52.00	56.70	2.66	7.33	30.00	4.46	5.00	71.66	5.50	9.00	58.33	15.43
3	AKU 11-12	41.00	49.66	50.40	2.33	7.66	34.66	5.23	4.66	67.66	5.30	8.19	68.66	11.93
4	AKU 11-18	38.00	52.33	54.40	2.33	10.00	37.00	5.33	6.66	75.00	5.16	12.76	54.03	23.60
5	AKU 11-3	40.33	53.33	62.46	2.00	6.33	32.00	4.46	5.66	71.66	5.51	9.67	63.60	15.20
6	AKU 11-15	40.66	52.66	53.26	2.66	8.66	34.66	4.76	4.33	72.33	5.81	7.14	37.23	19.18
7	AKU 13-3	37.33	47.66	61.63	2.33	9.66	37.66	5.30	5.00	66.33	4.71	11.03	62.13	17.73
8	AKU 13-15	42.00	52.33	45.10	2.33	11.33	35.66	4.40	6.66	71.33	5.51	12.31	56.86	21.65
9	AKU 11-21	41.00	53.00	47.80	3.00	7.66	32.66	4.70	4.66	70.33	5.58	8.77	61.26	14.31
10	AKU 12-3	43.00	51.66	54.56	3.66	6.33	27.33	5.43	5.66	70.33	5.52	8.18	53.93	15.17
11	AKU 14-02	42.33	52.33	53.33	2.66	9.66	36.33	4.43	4.33	73.33	5.86	8.62	64.33	13.40
12	AKU 14-03	42.66	54.00	62.63	2.00	10.00	34.33	4.30	5.00	72.66	4.85	8.87	51.06	16.35
13	AKU 13-02	37.33	48.33	61.93	3.33	11.00	30.33	4.50	6.00	67.33	4.86	9.85	46.73	21.07
14	AKU-1601	31.00	45.33	49.56	3.00	9.66	38.00	4.03	4.66	66.33	4.73	7.88	68.66	11.48
15	AKU-1602	33.00	46.33	58.76	2.33	10.66	37.00	4.50	5.00	67.33	4.83	10.81	51.20	21.12
16	AKU-1603	42.00	55.00	49.96	2.33	9.33	33.33	4.70	6.00	65.66	5.43	10.83	53.43	20.89
17	AKU-1604	41.33	50.66	57.06	3.00	10.33	34.66	4.26	4.66	69.33	5.12	7.68	61.46	12.49
18	TBU-2	35.00	44.66	59.86	2.33	10.66	35.66	4.50	4.33	65.66	5.24	6.64	52.40	12.68
19	TBU-6	33.66	43.00	63.03	2.66	8.00	37.00	5.26	4.66	63.66	4.76	9.53	66.73	14.28
20	KU 96-3	35.00	45.33	59.80	3.00	9.33	28.33	4.56	5.00	69.00	3.68	6.32	60.66	10.42
21	AKU 11-23	42.33	50.66	59.10	3.00	10.66	33.66	5.53	4.66	69.66	4.90	11.82	67.96	17.39
22	KU 16-102	38.00	49.00	58.60	3.00	7.66	36.66	3.76	6.00	67.33	3.86	7.28	49.73	14.76
23	KU 16-90	31.66	43.00	54.46	2.00	11.33	39.00	4.50	4.33	66.66	4.65	6.47	62.66	10.33
24	KU 16-101	42.00	52.66	50.83	2.66	8.66	36.33	4.40	4.66	69.33	4.84	9.28	61.16	15.06
25	KU 16-100	35.66	46.00	52.90	3.66	10.66	33.66	4.56	5.00	69.00	3.84	7.81	58.00	13.47

TABLE 2(b): Mean performance of 41 Blackgram genotypes for 13 quantitative characters

Sr. 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 (%)
26.	KU 16-89	32.00	44.00	54.53	2.66	10.33	39.33	4.30	5.33	66.66	3.72	7.14	51.03	13.99
27	KU 16-95	40.00	52.00	43.03	2.66	12.66	39.33	5.40	5.33	69.66	4.91	11.59	49.06	24.95
28	KU 16-96	32.00	43.66	41.60	3.00	10.00	32.00	4.53	4.33	67.33	4.32	6.35	39.66	15.99
29.	KU 16-92	35.33	48.00	57.30	2.33	7.66	27.66	4.56	6.66	65.33	5.30	8.60	44.26	19.42
30.	KU 16-97	35.00	46.33	57.26	2.00	11.33	31.66	5.30	6.33	68.66	4.83	8.32	67.43	12.33
31.	KU 16-6	41.66	53.66	55.06	2.33	10.33	34.33	5.30	4.33	72.33	4.42	5.99	42.03	14.25
32.	KU 16-9	36.00	44.66	63.80	2.33	11.33	37.00	4.63	5.33	64.33	4.26	6.34	57.43	9.89
33.	KU 16-13	33.33	43.00	60.53	3.66	8.66	30.66	5.36	5.00	63.00	4.52	6.53	66.13	9.87
34.	KU 16-12	44.66	53.33	62.53	2.66	8.33	35.66	4.63	5.33	69.66	4.35	8.22	48.76	16.93
35.	KU 16-11	38.33	49.00	60.13	2.00	8.66	29.66	5.36	5.00	68.33	5.63	7.90	39.90	19.80
36.	KU 16-5	40.00	52.00	61.86	3.00	8.33	32.00	4.60	6.00	72.00	5.24	8.96	53.20	17.46
37.	KU 16-8	34.33	45.33	53.63	1.66	7.00	26.66	4.60	6.33	65.66	4.02	7.02	59.06	11.88
38.	KU 16-98	44.00	54.66	51.70	2.66	8.66	31.66	4.76	5.00	72.66	4.33	6.58	50.33	13.12
39.	KU 16-105	34.00	42.00	50.66	1.33	9.66	28.33	4.46	6.00	64.00	3.78	7.08	55.76	12.69
40.	KU 16-87	41.66	51.66	49.53	2.00	12.00	38.00	5.30	6.00	70.66	5.39	12.31	62.46	19.71
41.	T-9 (Check)	40.00	50.33	40.90	3.03	8.33	37.68	4.72	6.08	63.66	4.38	9.85	47.26	20.55
	Mean	38.42	49.22	55.19	2.58	9.35	34.08	4.74	5.25	68.64	4.86	8.65	55.58	15.85
	C.V.	2.58	2.60	6.35	24.40	9.46	2.56	5.78	15.63	0.98	11.03	5.46	3.90	6.16
	F ratio	47.87	27.68	7.76	2.14	9.36	51.27	7.72	2.40	56.18	4.05	47.71	44.90	47.46
	F Prob.	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	S.E.	0.57	0.73	2.03	0.36	0.51	0.50	0.15	0.47	0.39	0.31	0.27	1.25	0.55
	C.D. 5%	1.60	2.08	5.71	1.01	1.44	1.41	0.44	1.32	1.09	0.87	0.76	3.54	1.57
	C.D. 1%	2.13	2.76	7.58	1.35	1.91	1.88	0.59	1.76	1.45	1.15	1.01	4.70	2.08
	Range Lowest	31.00	42.00	41.60	1.33	6.33	26.66	3.76	4.33	63.00	3.68	5.99	37.23	9.87
	Range Highest	44.66	55.00	63.80	3.66	12.66	39.33	5.53	6.66	75.00	5.86	12.76	68.66	24.95

Estimates of heritability are useful in predicting the transmission of characters from parents to their offspring. It is a good index of transmission of characters from parents to their off spring (Falconer, 1981).
A perusal of genetic advance revealed that it were high for Biological yield/plant (16.62), plant height (9.06), days to 50% flowering (7.81), harvest index (7.61), days to 50% pod setting (7.46), pods/plant (7.14), days to maturity (5.81), seed yield/plant (3.70), clusters/plant (2.62), 100 seed weight (0.79), pod length (0.71), Seeds/pod(0.65),No. of branches per plant (0.42).
High estimate of genetic advance as percent of mean were registered for harvest index (48.47), seed yield/plant (43.05), biological yield/plant (29.79), clusters/plant (27.95), pods/plant (21.02), days to 50% flowering(20.40), plant height (16.35), No. of branches/plant (16.30), Seed index(16.30), days to 50% pod setting (15.20), pod length (14.84), seed/pod (12.45), and days to maturity (8.46).

TABLE- 3. Genetic parameters for 13 biometrical characters of 41 Blackgram genotypes

| Sr.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	10.22	10.54	93.99	7.81	20.40
2	Days to 50% pod setting	7.78	8.21	89.89	7.46	15.20
3	Plant height	9.53	11.46	69.27	9.06	16.35
4	Number of branches/ plant	15.06	28.68	27.58	0.42	16.30
5	Cluster /plant	15.81	18.43	73.60	2.62	27.95
6	Pods /plant	10.50	10.81	94.37	7.14	21.02
7	Pod length	8.66	10.42	69.16	0.71	14.84
8	Seed /pod	10.70	18.94	31.91	0.65	12.45
9	Days to maturity	4.22	4.33	94.84	5.81	8.46
10	100-seed weight	11.14	15.68	50.46	0.79	16.30
11	Seed yield /plant	21.56	22.24	93.97	3.70	43.05
12	Biological yield /plant	14.95	15.45	93.60	16.62	29.79
13	Harvest index	24.28	25.05	93.93	7.61	48.47
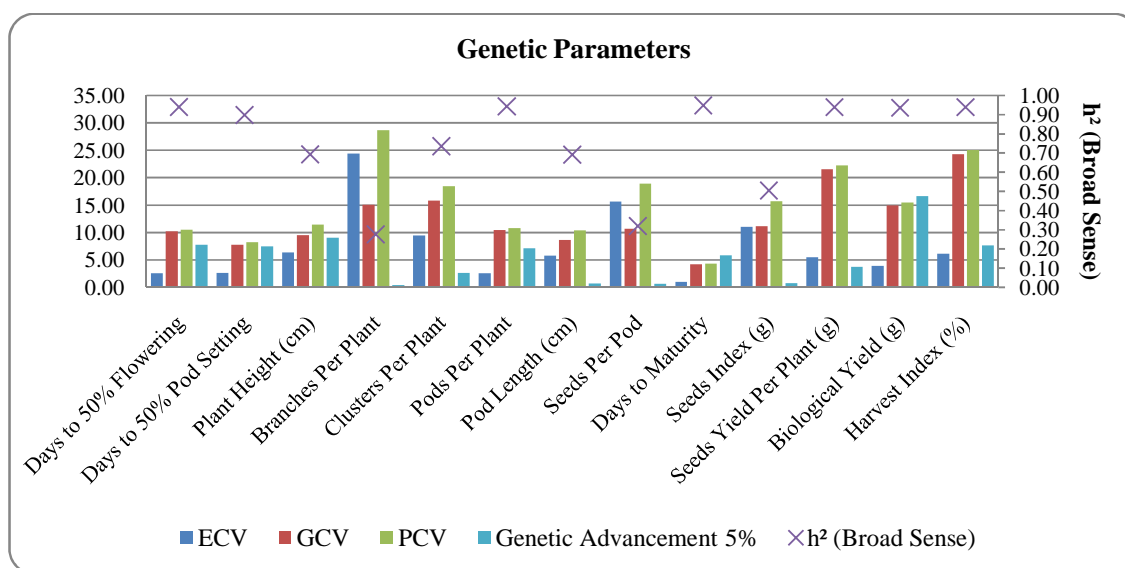
FIGURE 1- Histogram depicting estimates of genetic parameters for 13 important agro-economic traits in blackgram

TABLE 4: Distribution of 41 Blackgram genotypes into different clusters

S.No.	Cluster No.	No. of genotypes	Genotypes included
1	I	4	AKU 11-14, AKU 11-3, AKU 11-21, KU 16-5
2	II	4	KU 16-8, KU 16-105, KU 96-3, KU 16-97
3	III	9	AKU-1604, KU 16-101, AKU 14-02, AKU 14-03, KU 16-12, KU 16-98, AKU 11-9, KU 16-102, KU 16-6
4	IV	9	TBU-2, KU 16-9, KU 16-90,KU 16-89, AKU-1601, KU 16-100,TBU-6, AKU 13-3, AKU 11-12
5	V	1	AKU 12-3
6	VI	13	AKU 13-15, KU 16-87, KU 16-95, AKU 11-18, AKU-1603, AKU-1602, AKU 13-02, AKU 11-23, KU 16-11, KU 16-92, AKU 11-15, KU 16-96,T-9
7	VII	1	KU 16-13

TABLE 5: Cluster mean values for different component characters in Blackgram

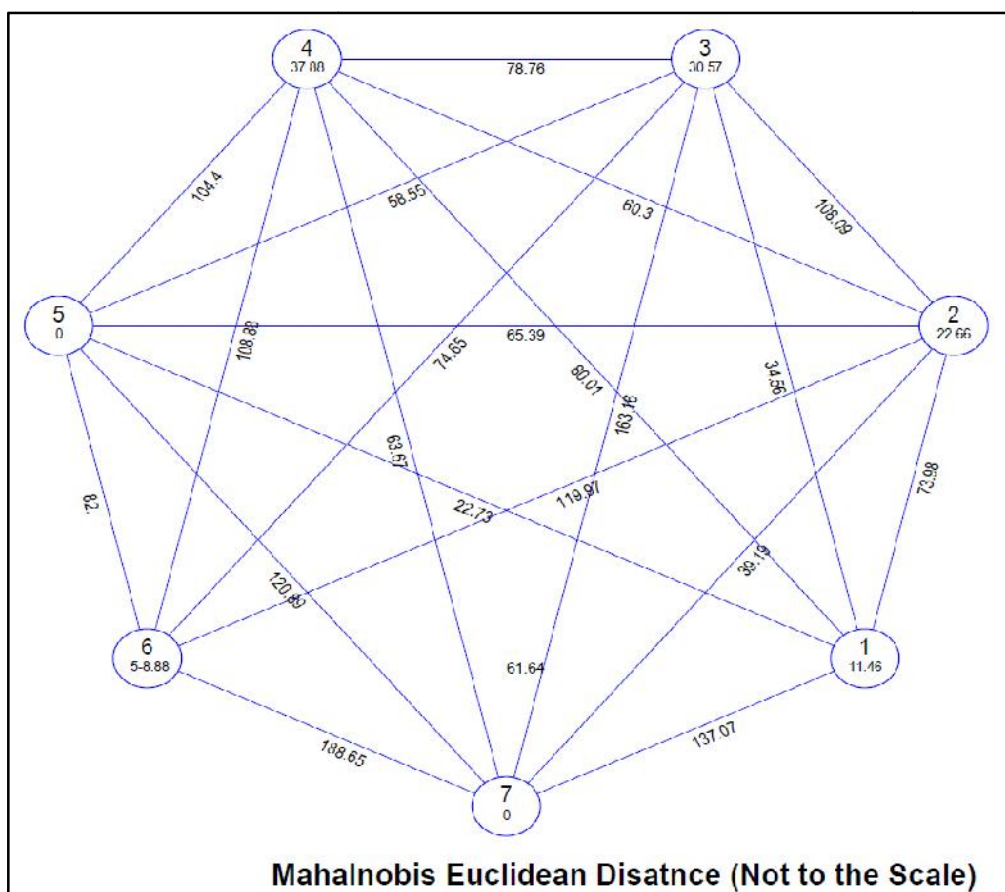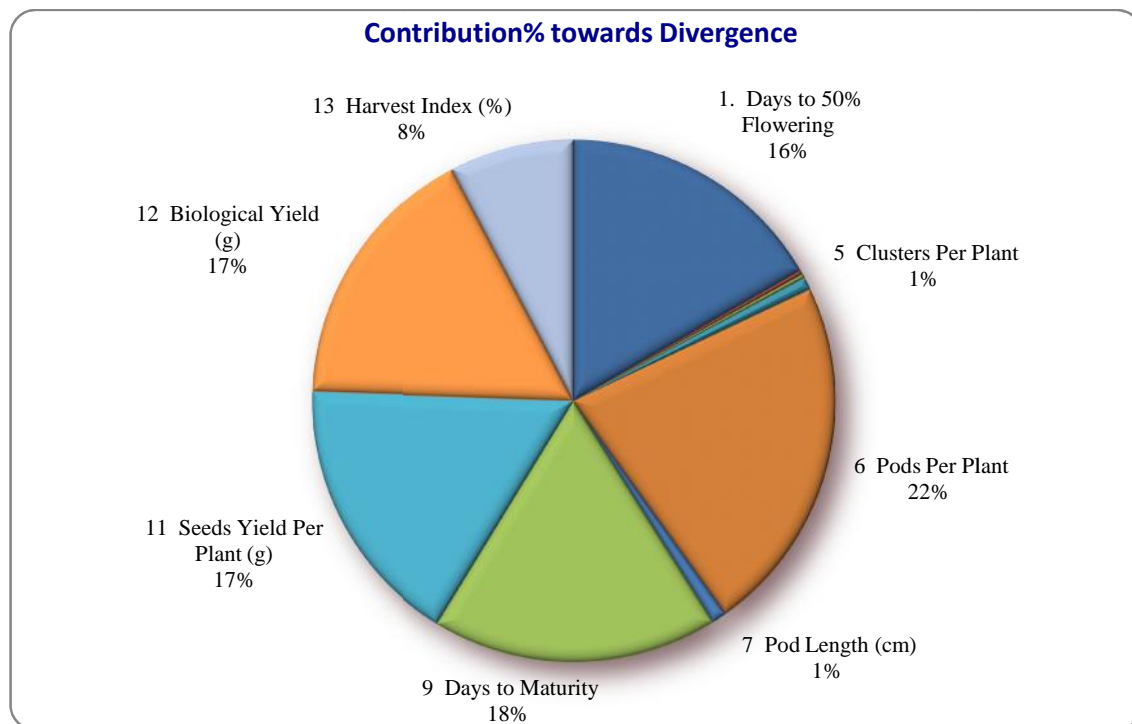|	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Days to 50 % Flowering	40.58	34.58	42.03	34.8	43.00	38.55	33.33
Days to 50 % Pod Setting	52.58	44.75	52.22	45.33	51.66	50.16	43.00
Plant height	57.20	55.34	56.28	56.68	54.56	52.84	60.53
Primary Branches/ Plant	2.66	2.000	2.55	2.59	3.66	2.52	3.66
Clusters/ Plant	7.41	9.33	9.03	9.92	6.33	10.22	8.66
Pods/ Plant	31.66	28.75	35.48	36.88	27.33	34.02	30.66
Pod Length	4.55	4.73	4.54	4.70	5.43	4.90	5.36
Seeds/ Pods	5.33	5.91	4.70	4.81	5.66	5.66	5.00
Days to Maturity	71.41	66.83	70.59	66.25	70.33	69.16	63.00
Seed index	5.46	4.07	4.83	4.58	5.52	5.17	4.52
Seed Yield/ Plant	9.10	7.18	7.88	7.89	8.18	10.19	6.53
Biological Yield/ Plant	59.10	60.73	53.55	60.85	53.93	50.23	66.13
Harvest index	15.60	11.83	14.69	12.86	15.17	20.40	9.87

FIGURE 2 : Cluster diagram depicting intra and inter distances

TABLE 6 : Intra and inter cluster averages distances in Blackgram genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	11.463	73.978	34.556	80.010	22.733	61.639	137.071
Cluster II		22.660	108.094	60.295	65.390	119.974	39.189
Cluster III			30.566	78.763	58.547	74.651	163.164
Cluster IV				37.884	104.396	108.882	63.669
Cluster V					0.000	82.000	120.886
Cluster VI						58.877	188.652
Cluster VII							0.000

TABLE 7: Percent contribution of 13 characters to genetic divergence

Sr. No.	Characters	Contribution %	Times Ranked 1st
1	Days to 50% flowering	16.67	130.00
2	Days to 50% Pod setting	0.26	2.00
3	Plant Height	0.26	2.00
4	Primary Branches Per Plant	0.01	0.00
5	Clusters/ Plant	0.77	6.00
6	Pods/ Plant	22.18	173.00
7	Pod Length	0.90	7.00
8	Seeds Per Pod	0.01	0.00
9	Days to Maturity	17.69	138.00
10	Seed Index	0.01	0.00
11	Seed Yield/ Plot	16.79	131.00
12	Biological Yield	16.79	131.00
13	Harvest Index	7.69	60.00
14.	Total	100	

FIGURE 3: Pie diagram: estimates of percent contribution of character to genetic divergence for 13 characters in Blackgram.

Inter-cluster distance (D^2) were found maximum between cluster VI and VII (188.65) followed by Cluster III and VII (163.16), Cluster I and VII (137.07), Cluster V and VII (120.88), Cluster II and VI (119.97) Minimum inter-cluster distance were found between Cluster I and Cluster V (22.73). The intra and inter-cluster average distance among seven clusters were variable (Table 6). The maximum intra-cluster (D^2) were registered for, Cluster VI (58.88), followed by Cluster IV (37.88), Cluster III (30.57), Cluster II (22.66), Cluster I (11.46), Cluster V (0) and Cluster VII (0).

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).

The percent contribution of thirteen characters towards total genetic divergence is presented in Table 7. The highest contribution in the manifestation of genetic divergence were exhibited by Pod/ Plant (22.18%) followed days to maturity (17.69%), Seed Yield/ Plot (16.79%), biological yield (16.79%) and days to 50% flowering (16.67%) suggesting scope for improvement in these characters. 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 of the experiment it is concluded that, the genotypes AKU 11-18, AKU 13-15 were identified as the best genotypes for seed yield at Allahabad region. The present investigation registered high heritability along with high genetic advance as % of mean

for harvest index which should be given top priority for effective selection, the present investigation further revealed that Cluster VI with VII are most divergence to each other. Therefore genotypes in these clusters are suggested to provide broad spectrum variability in segregating generations and may be used as parents for future hybridization programme.

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