



STUDIES ON GENETIC DIVERSITY FOR YIELD AND ITS COMPONENTS IN BLACKGRAM (*VIGNA MUNGO L.* HEPPER) GENOTYPES

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ABSTRACT

The experiment was conducted during *kharif* season 2017 on crop research farm of department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology & Sciences, Randomized Block Design with three replications. The present investigation was conducted to examine the 51 blackgram genotypes along with one check (Shekhar-2) to study the genetic Diversity. Analysis of variance showed highly significant differences among 51 blackgram genotypes for 13 quantitative characters studied. Number of branches/plant, biological yield/plant and seed yield /plant, significant differences were observed among the genotypes for all the characters studied. Genetic diversity estimated in 51 blackgram genotypes using Mahalanobis's D^2 statistic. 51 genotypes were grouped into eight clusters by Non-Hierarchical Euclidean cluster analysis. The maximum inter-cluster distance was observed between cluster V and cluster V. The maximum intra-cluster distance was observed in cluster I Cluster VI showed maximum cluster mean value for seed yield per plant among all the characters, biological yield/plant, seed yield/plant and seeds/pod contributes maximum. The accessions KU-14001 and KU-961, may serve as potential parents for hybridization programme in the improvement of yield.

KEY WORDS: Blackgram, Yield attributes, Genetic Diversity and cluster.

INTRODUCTION

Blackgram (*Vigna mungo* (L.) Hepper) is an important nutritious pulse crop occupying unique position in Indian Agriculture, belongs to family leguminosae with chromosome number $2n=2x=22$ (Malik, 1994). In India alone, it occupies about 3.7 million hectare and annual production of urdbean in India is about 1.5 to 1.9 million tons (Ministry of Agriculture, GOI). In U.P Black gram is grown in about 3.91 lakh hectares with a total production of 1.87 lakh tones (DMR Annual Report, 2014-15). Among the states of India, Orissa ranks first in area 777 thousand hectares and production 396 thousand tones. However Punjab is a leading state in productivity with 856.9 kg/hectare. (FAO STAT, 2014-15). The present study was therefore, undertaken to estimate the amount of genetic diversity in 51 genotypes of black gram Gram (*Vigna mungo* L. Hepper) and to identify genetic diverse parents for hybridization programme aimed at yield improvement in this crop. Association studies give an idea about the contribution of different characters towards seed yield and it reveals the type, nature and magnitude of correlation between yield components with yield and among the selves. In other words, for the improvement in any crop species, the knowledge of genetic variability for characters of economic importance and their heritability and genetic advance is of utmost importance in planning future breeding programme. Singh *et al.* (2007). The creation of variability is difficult through hybridization due to its high self-pollination and flower droop (Deepalakshmi and Anandakumar, 2004). Besides the major constrains in achieving higher yield of blackgram is

absence of suitable ideotypes for different cropping system, poor harvest index and susceptibility to disease (Souframanien and Gopalakrishnan, 2004). In order to improve yield and other polygenetic characters, mutation breeding can also be effectively utilized (Deepalakshmi and Anandakumar, 2004). Therefore genetic variability is the basic requirement for making progress in crop breeding (Appalaswamy and Reddy, 2004). The correlation coefficient gives a measure of the relationship between traits and provides the degree to which various characters of crop are associated with productivity. Keeping the above factor in view, the present investigation is prepared with the following to evaluate the black gram genotypes for the yield and yield contributing traits. To estimate genetic diversity in black gram genotype using D^2 analysis.

MATERIALS & METHODS

The experimental material for the present investigation consisted of 51 genotypes the present experiment was conducted in randomized block design at Field Experimentation Centre, Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology & Sciences, Allahabad during *kharif*, 2017. 51 genotypes of Blackgram were grown in this 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. five competitive plants from each plot were randomly selected. Average of these five plants in respect of 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) Mahalanobi's D2 statistic was employed to assess the genetic diversity. All the 51 blackgram genotypes based on statistical differences were

used for genotypes classification in different clusters, results of inter and intra clusters D2 values between clusters, as well as mean of intra-clusters D2 values of different clusters are presented in tables 1–4 and figures 1 and 2.

RESULTS & DISCUSSION

The analysis of variance for randomized block design revealed highly significant differences among accessions for all the characters under investigation thereby indicating the presence of a considerable magnitude of genetic variability among 51 accessions of black gram for these characters (Table-1).

TABLE 1: Analysis of variance for 13 different quantitative characters in 51 genotypes of black gram

S. No.	Characters	Mean sum of squares		
		Replications (d.f.=2)	Treatments (d.f.= 50)	Error (d.f.= 100)
1	Days to 50% flowering	0.74	5.02**	1.54
2	Days to 50% pod setting	0.99	3.96**	0.85
3	Plant height	7.11	143.84**	4.73
4	Number of branches per plant	0.10	0.54**	0.07
5	Number of clusters per plant	0.80	1.09**	0.36
6	Pods per plant	1.68	12.60**	2.92
7	Pod length	0.05	0.28**	0.03
8	Number of seeds per pod	0.12	1.10**	0.14
9	Days to maturity	3.93	58.85**	2.18
10	Seed index	0.001	0.60**	0.09
11	Harvest index	0.22	49.64**	0.69
12	Biological yield	9.41	254.69**	4.89
13	Seed yield per plant	0.01	12.34**	0.08

**Significant at 1% level of Significance

The present study, 51 genotypes were grouped into seven clusters by Non-Hierarchical Euclidean cluster analysis (Table-2). Cluster III comprised Seventy genotypes (KU-1386, KU-1389, KU-1531, KU-1272, KU-1446, KU-9912, KU-1402, KU-9922, KU-9986, KU-1518, KU-1588, KU-1399, KU-1429, KU-1425, KU-1254, KU-1598, KU-1591) evolving the maximum genotype, followed by clusters IV with Towel genotypes (KU-8896, KU-1590, KU-8890, KU-9926, KU-1609, KU-1586, KU-1538, KU-97-5, KU-1603, KU-1611, KU-8891, KU-97-9), and II cluster with seven genotypes (KU-8893, KU-1587, KU-1593, KU-1607, KU-8870, KU-1597, KU-97-8), clusters I with seven genotype (KU-1424, KU-14001, KU-9919, KU-1256, KU-1286, KU-961, SHEKHAR-2 (check), cluster V with five genotype (KU-1521, KU-1528, KU-1526, KU-1472, KU-1595), cluster VI comprised also One genotype (KU-1453), and cluster VII comprise also One genotype (KU-9923), cluster VIII comprise also One genotype (KU-1363) the pattern of group constellation proved the existence of significant amount of variability.

The intra and inter-cluster average distance among Eight clusters were variable (Table-3). The maximum intra-cluster (D^2) was registered for, Cluster V (45.07), followed Cluster III (36.96), cluster IV (35.14), Cluster I (21.27), Cluster II (20.54), and Cluster VI (0.00), Cluster VII (0.00), Cluster VIII (0.00). Inter-cluster distance (D^2) was found maximum between cluster I and IV (202.27) followed by Cluster I and II (166.57), Cluster IV and VI

(158.44). Minimum inter-cluster distance was found between Cluster I&VI (30.74). The results indicated that there is close genetic similarity between the cultivars of black gram based on the study. This might be due to the high degree of commonness in their pedigrees. The narrow genetic base of the black gram cultivars was revealed in the present study.

A comparison of the mean value of thirteen characters of different clusters has been presented in the (Table-4) Considerable differences in cluster mean values were evident for all the characters. Cluster I comprised of Seven genotypes, it showed high mean value for days to maturity (66.50), biological yield (57.38), days 50% pod setting (57.43), days to 50% flowering (47.69) and low mean value for primary branches (2.32). Cluster II comprised of seven genotypes, Cluster registered maximum mean performance for days to maturity (75.43), plant height (58.04) and low mean value for primary branches (2.22) Cluster III comprised seventy genotypes that showed high mean performance for days to maturity (68.76), days to 50 % pod setting (57.36) and low mean value for primary branches (2.18) Cluster IV comprised towel genotypes, that showed high mean performance for days to maturity (73.43), biological yield (44.81), days to 50% pod setting (58.31), and low mean value for primary branches (2.26) Cluster V comprised five genotypes. Showed high mean performance for days to maturity (72.74), days to 50% pod setting (57.82) and lowest mean value for primary branches (2.17) Cluster VI comprised

only one genotype showed high mean performance for days to maturity (71.), days to 50% pod setting (57.46) and biological yield (61.60) and low mean value for primary branches (1.80) Cluster VII comprised of one showed high mean performance for days to maturity (64.06), days to 50% pod setting (58.86) and biological yield (57.93) and

low mean value for primary branches (3.20). Cluster VIII comprised of one showed high mean performance for days to maturity (66.53), days to 50% pod setting (56.66) and biological yield (65.46) and low mean value for primary branches (1.93).

TABLE 2: Distribution of 51 black gram genotypes into different clusters

S. No.	Cluster No.	No. of genotypes	Genotypes included
1	I	7	KU-1424, KU-14001, KU-9919, KU-1256, KU-1286, KU-961, SHEKHAR-2(C)
2	II	7	KU-8893, KU-1587, KU-1593, KU-1607, KU-8870, KU-1597, KU-97-8
3	III	17	KU-1386, KU-1389, KU-1531, KU-1272, KU-1446, KU-9912, KU-1402, KU-9922, KU-9986, KU-1518, KU-1588, KU-1399, KU-1429, KU-1425, KU-1254, KU-1598, KU-1591
4	IV	12	KU-8896, KU-1590, KU-8890, KU-9926, KU-1609, KU-1586, KU-1538, KU-97-5, KU-1603, KU-1611, KU-8891, KU-97-9
5	V	5	KU-1521, KU-1528, KU-1526, KU-1472, KU-1595
6	VI	1	KU-1595
7	VII	1	KU-9923
8	VIII	1	KU-1363

TABLE 3: Intra and inter cluster averages distances in black gram genotypes

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster	7 Cluster	8 Cluster
1 Cluster	21.27	166.57	60.01	202.27	85.75	30.74	146.96	123.29
2 Cluster		20.55	80.63	60.23	90.33	97.23	40.70	91.14
3 Cluster			36.97	92.67	45.29	47.91	72.00	69.40
4 Cluster				35.15	81.68	158.45	59.92	102.77
5 Cluster					45.07	76.18	92.77	74.13
6 Cluster						0.00	106.69	123.77
7 Cluster							0.00	84.40
8 Cluster								0.00

TABLE 4: Cluster mean values for different component characters in blackgram

Character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Days to 50 % Flowering	47.69	47.92	46.83	47.85	47.56	46.40	48.33	46.33
Days to 50 % Pod Setting	57.43	57.78	57.36	58.31	57.82	57.46	58.86	56.66
Plant height	53.13	58.04	50.78	49.90	45.62	63.26	58.60	29.93
Primary Branches/ Plant	2.32	2.22	2.18	2.26	2.17	1.80	3.20	1.93
Clusters/ Plant	5.414	4.99	4.95	5.02	5.25	5.60	5.86	4.86
Pods/ Plant	25.96	26.80	25.80	24.60	25.20	26.33	25.33	26.33
Pod Length	4.22	4.52	4.29	4.45	4.29	4.46	4.44	4.43
Seeds/ Pods	4.98	5.55	5.23	5.12	5.44	5.20	5.33	5.60
Days to Maturity	66.50	75.43	68.76	73.43	72.74	71.66	64.06	66.53
Seed index	3.94	3.72	4.20	3.95	4.15	4.00	3.32	3.77
Harvest index	17.01	6.54	13.45	9.57	14.97	13.64	8.23	8.54
Biological Yield/ Plant	57.38	62.77	53.63	44.81	47.64	61.60	57.93	65.46
Seed Yield/ Plant	9.64	4.12	6.99	4.12	6.67	8.31	4.74	5.56

Genetic diversity for yield and its components in blackgram

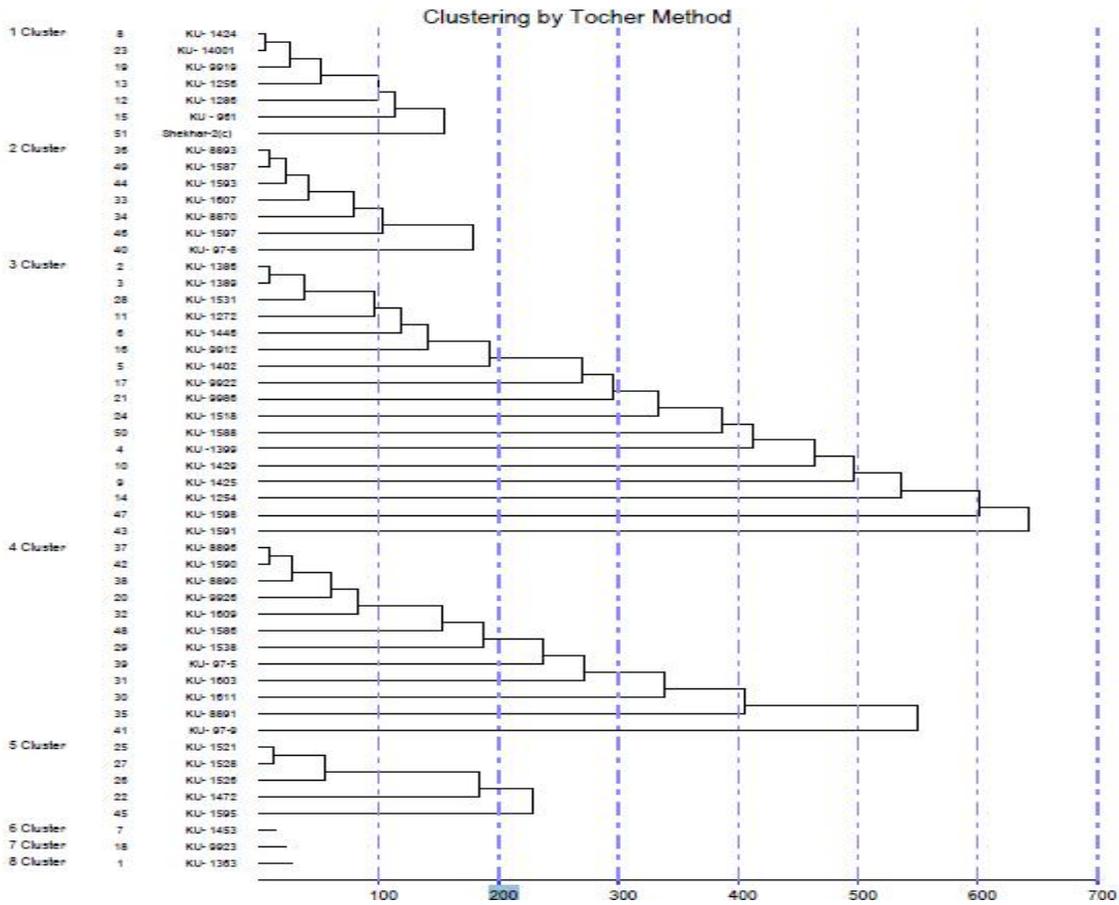


FIGURE 1: Clustering pattern of 51 blackgram genotypes on the basis of D^2 statistic by Tocher method

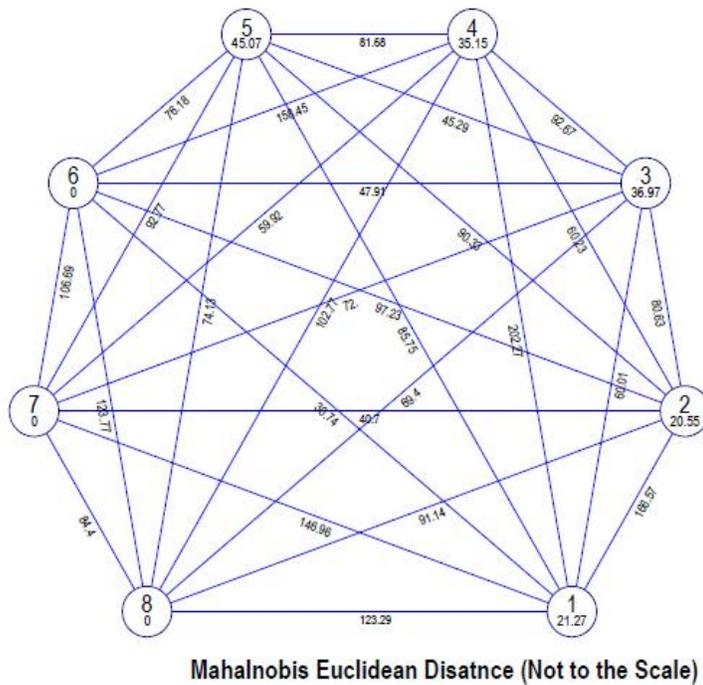


FIGURE 2: Mahalanobis Euclidean Disatnce among the 8 Clusters of 51 blackgram genotypes

CONCLUSION

The present investigation entitled “Studies on genetic diversity in black gram (*Vigna mungo* L. Hepper) genotype” were identified as the genotypes for seed yield at Allahabad region. Genotypes were carried out with the objective to collect the basic information on genetic variability, genetic advance and genetic diversity for 13 quantitative characters. The present investigation the highest contribution in manifestation of genetic divergence was exhibited by Seed yield/plant (52.63), biological yield (23.69%), followed by plant height cm (9.57) and pod length cm (2.12). On the basis of results of the experiment it can be conducted that, the genotypes KU-14001, followed by KU -961, KU-9919, KU-1286, and KU-1424, were identified as the genotypes for seed yield at Allahabad region. The present investigation registered high along with high genetic advance as a 5 % of mean for seed yield per plant which should be given top priority for effective selection, the present investigation further revealed that Cluster I and Cluster IV 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 to develop desirable genotype.

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