



Research Article

GENETIC DIVERSITY FOR YIELD AND YIELD RELATED TRAITS IN BLACKGRAM (*Vigna mungo* L. Hepper)

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Abstract- Blackgram (*Vigna mungo* L. Hopper) is an important food legume, it is widely cultivated and consumed in India. Utilization of divergent parents in hybridization results in promising recombinants. The present investigation was conducted to examine the 48 blackgram genotypes to study the genetic diversity. Analysis of variance showed highly significant differences among 48 genotypes for 13 quantitative characters studied. Maximum GCV and PCV variances was reported for seed yield per plant, pod per plant, harvest index and cluster per plant. High heritability coupled with high genetic advance as percent of mean was reported for seed yield per plant. Divergence analysis among forty eight genotypes for 13 Characters was carried out using Mahalanobis. D^2 statistics the genotypes were grouped into 7 clusters. The contribution of number of pods per plant was maximum (54.43%) followed by harvest index (14.98). The maximum intercluster distance was reported in cluster V and VI (229.034). The maximum intra cluster distance was reported in cluster V (39.119).

Keywords- Blackgram, D^2 , analysis, genetic diversity and cluster

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Introduction

Blackgram is third important food legume grown in India extensively. It is an excellent source of quality protein. Black gram restores fertility of soil too through symbiotic nitrogen fixation. Through India is the large producer of blackgram. The productivity is still low. D^2 statistic is one of the potent techniques of measuring genetic diversity in plant breeding. Genetic diversity plays an important role in crop improvement strategies. The selection of genetically diverged parents is expected to throw superior and desirable segregates following crossing, reported that the hybrid between genetically diverse parents yield greater heterosis than those between more closely related parents [1-3]. Analysis of genetic diversity in germplasm collection can facilitate reliable classification of accessions and identification of subsets of core accessions with possible utility for specific breeding purpose. Evaluation of divergence would help in identification of genotype which may be used in crossing programme to produce transgressive segregate. Hence the present study was under taken to identify the potential parents for hybridization programme.

Material and Method

The experiment materials for the present investigation comprised of 48 genotypes to divergence studies D^2 statistic. The experiment was conducted in Randomized Block design with the replication. Each entry was represented by 3 rows of 1.5 meter length with a spacing of 30x10 cm. A fertilizer dose of 20:40:20 kg/ha. NPK ha⁻¹ was applied and need based plant protection measures were followed at Horticultural farm, Bundelkhand University Jhansi during Kharif 2017-18. The mean values of three replication were used for statistical analysis. The observation was recorded on thirteen quantitative traits viz. Days to 50% flowering, Days to maturity, Plant Height, No. of Primary branches per plant, No. of cluster per plant, No. of pod per cluster. Pods per plant, Pod length, Pod length, Biological yield per plant, No. Of seed per pod, Seed yield per plant, 100 Seed weight and Harvest index. D^2 statistic and Tocher's method was used for Assessment of genetic divergence and the genotype was grouped into different cluster [4,5].

Result and Discussion

Analysis of variance revealed highly significant difference among the accessions for all the characters studied [Table-1]. Genetic divergence analysis was carried out by calculating D^2 values from the means of 48 genotypes of black gram for 13 characters. The genotypes were grouped into 7 clusters [Table-2]. Among 7 clusters, cluster -7 maximum numbers of 48 genotypes followed by cluster -4, cluster -5, cluster -6 and cluster -1 with 6 genotypes. The dendrogram depicting the clustering pattern was depicted in figure -1. The pattern of clustering indicates presence of significant amount of variability. The inter and intra cluster D^2 value are presented in [Table-3] in the present study, it is indicated that the inter cluster distance were greater than intra cluster distances which shows considerable amount of genetic diversity existed among genotype. Intra cluster distance ranged from 0.00 to 39.119 [6-10]. Cluster V recorded the maximum cluster distance of 39.119 followed clusters III, II & I 33.082, 22.641, 13.899 respectively. Three solitary cluster with no intra cluster value. The uniqueness of these genotypes placed then separately. The highest inter cluster distance was found between cluster V and VI (229.034) which was followed by cluster III and V (200.043) and V and VII (194.193) indicates wide divergence among the genotypes of these clusters. The magnitude of heterosis depends largely on the degree of genetic diversity in the parental lines. There for the genotypes from these diverse clusters could be used in the hybridization to get broad spectrum of genetic variability in the segregating generation. Genetic constitution of genotype in one cluster were in close proximity with the genotypes in the other cluster of pair. It was observed on the basis of least inter cluster distance which is found between cluster I and IV (35.151). Hence genotypes from these clusters may not be useful. This result is supported by other research findings in black gram [11-14]. The relative contribution of each character towards divergence was represented in the [Table-4] No. of pods per plant (54.43) contributed maximum towards genetic divergence followed by Harvest index % (14.98) and plant Height (7.80). The contribution of biological yield per plant, Clusters per plant and seed yield per plant 6.12, 4.17 and 3.90 respectively.

Table-1 Analysis of variance for 13 different quantitative characters in 48 genotypes of blackgram

S.No	Characters	Mean sum of squares		
		Replications (d.f.=2)	Treatments (d.f.= 47)	Error (d.f.= 94)
1	Days to 50 % Flowering	4.75	8.68**	4.79
2	Plant Height (cm)	1.88	64.69***	3.87
3	Primary Branches/ Plant	0.85	1.30***	0.48
4	Days to 50% Maturity	0.09	38.19***	4.72
5	Clusters Per Plant	1.48	94.61***	3.69
6	Pods Per Cluster	0.28	0.43***	0.17
7	Pods Per Plant	1.66	646.94***	4.64
8	Pod Length (cm)	0.02	0.14***	0.05
9	Biological Yield Per Plant (g)	9.25	187.52***	4.85
10	Seeds Per Pod	0.17	1.03***	0.11
11	Seed Yield Per Plant (g)	0.42	24.06***	0.70
12	100 Seed Weight (g)	11.51	31.86***	5.93
13	Harvest Index %	0.20	163.93***	7.78

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

Table-2 Distribution of 48 black gram genotypes into different clusters

SN	Cluster No	No. of genotypes	Genotypes included
1	1 Cluster	6	KU14-1, TU94-2, GBB1, KPU129-104, RBV-38, COBG11-03
2	2 Cluster	4	VBG11-031, TBG104, T-9, KU16-04
3	3 Cluster	3	AZAD-1, SHEHAKAR-2, ADBG13-004
4	4 Cluster	10	PU10-23, IU05-1, CDBG-10-06, TU-13, COBG11-03, IPU10-26, KU16-07, SHEHKHAR-1, PU10-23, KUG725
5	5 Cluster	7	LBG-752, LBG645, DKU98, WBU108, PU10-16, COBG11-053, IPU55
6	6 Cluster	7	TU22, RUG-55, IPU13-1, NDUK-159, MDOK-16-7, IPU-14-1, NIRB003
7	7 Cluster	11	MDUK-16, IPU-2000, KU96-7, SHEHAKAR-1, WBG12-061, RUG59, DBG11, DBG123, NRB004, AKU11-5, IU05-1

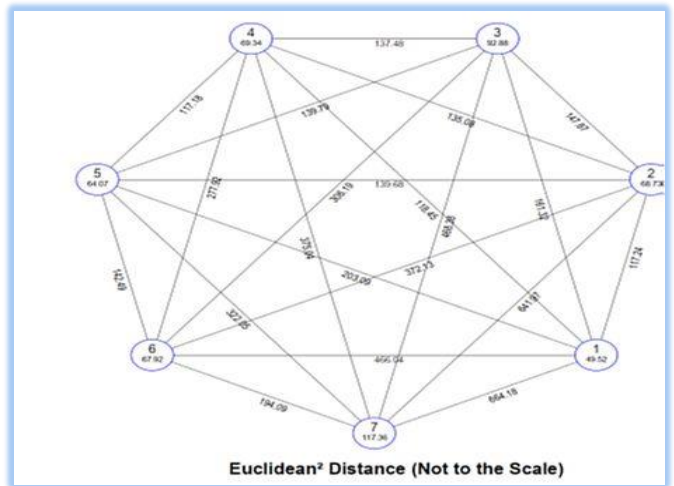


Fig-1 Mahalanobis Distance Cluster Diagram

Table-4 Percent contribution of 13 characters to genetic divergence

SN	Characters	Contribution %	Times Ranked 1st
1	Days to 50 % Flowering	0.09	1
2	Plant Height (cm)	7.8	88
3	Primary Branches/ Plant	0.09	1
4	Days to 50% Maturity	2.93	33
5	Clusters Per Plant	4.17	47
6	Pods Per Cluster	0.01	0
7	Pods Per Plant	54.43	614
8	Pod Length (cm)	0.18	2
9	Biological Yield Per Plant (g)	6.12	69
10	Seeds Per Pod	2.66	30
11	Seed Yield Per Plant (g)	3.9	44
12	100 Seed Weight (g)	2.66	30
13	Harvest Index %	14.98	169

Table-3 Intra (In Bold) and inter cluster averages of D^2 value among VII cluster

SN	Cluster No	I Cluster	II Cluster	III Cluster	IV Cluster	V Cluster	VI Cluster	VII Cluster
1	I Cluster	13.899	48.569	47.35	35.151	98.436	75.269	66.34
2	II Cluster		22.641	130.991	79.224	64.695	166.998	77.033
3	III Cluster			33.082	64.967	200.043	61.571	121.443
4	IV Cluster				0	72.969	98.215	149.373
5	V Cluster					39.119	229.034	194.193
6	VI Cluster						0	150.041
7	VII Cluster							0

Table-5 Cluster mean values for different component characters in blackgram

SN	Characters	I Cluster	II Cluster	III Cluster	IV Cluster	V Cluster	VI Cluster	VII Cluster
1	Days to 50 % Flowering	41.833	41.278	43.722	44	43.111	45.333	42.333
2	Plant Height (cm)	48.583	44.283	46.807	47.333	47.422	57.6	45.4
3	Primary Branches/ Plant	4.508	4.628	4.506	5.867	5.078	5.6	5.267
4	Days to 50% Maturity	63.167	62.833	63.583	62.667	62.333	84	62
5	Clusters Per Plant	19.206	27.433	15.561	21.6	27.533	18.133	23.933
6	Pods Per Cluster	2.711	2.872	2.272	2.167	2.711	1.9	2.733
7	Pods Per Plant	40.075	56.744	23.328	32.4	57.633	23.533	51.733
8	Pod Length (cm)	3.998	3.881	3.831	3.903	4.246	3.793	4.14
9	Biological Yield Per Plant (g)	32.442	37.267	26.028	42.667	49.178	28.667	25.6
10	Seeds Per Pod	5.792	5.744	5.28	5.633	6.111	5.967	6.367
11	Seed Yield Per Plant (g)	9.587	7.851	3.825	8.347	11.216	3.373	9.587
12	100 Seed Weight (g)	37.403	35.667	36.813	41.833	35.111	35.833	32.333
13	Harvest Index %	21.412	21.441	14.531	19.637	22.922	11.827	38.24

The cluster contributing maximum to the divergence should be given more importance for the purpose of further selection and the choice of parents for hybridization [15]. The cluster mean values were estimated over genotype for thirteen characters in black gram related to yield, which revealed that a wide range of variation [Table-5]. Minimum days to 50% flowering was observed in genotype of cluster II followed by cluster I. Maximum days of 50% flowering was recorded by cluster VI. Maximum Days to 50% maturity was recorded by cluster VI followed by cluster III. The highest mean for cluster per plant was recorded by cluster V and cluster II. Cluster V recorded the highest mean for Number of Pods per plant followed by cluster II and Cluster VII. Cluster V recorded the highest mean for pod length, seed yield per plant and cluster per plant Cluster IV recorded the highest mean values for 100 seed weight. Cluster V recorded the highest mean values for cluster per plant, pods per plant, pod length and seed yield per plant. Hence the genotypes in cluster were high yielding [16-18]. On the basis of results of experiment it can be concluded that the genotypes LBG752 followed by LBG645, DKU98, WBU108, PU10-16, COBG11-053 and IPU55 in cluster V had higher mean values for traits viz. Cluster per plant, pod per plant, pod length and seed yield per plant at Jhansi region.

Application of research: 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 the effective selection. Further it revealed that cluster V is most divergence to each genotypes are suggested to provide broad spectrum variability in segregating generations and may be used as parents for further hybridisation programme to develop desirable types of recombination's.

Research Category: Genetics and Plant Breeding

Abbreviations:

PCV: Phenotypic coefficient of variation

GCV: Genotypic coefficient of variation

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