



### Short Communication

## Genetic Diversity for Yield and Its Components in Blackgram (*Vigna mungo* L.)

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### Abstract

Seventy five genotypes of blackgram were subjected to genetic divergence by using  $D^2$  statistic. The genotypes were grouped into seven clusters by  $D^2$  analysis. Cluster V consisted maximum accessions (21) followed by cluster VI (19) and VII (13) and cluster I consisted only 1 accession. The inter-cluster distances were greater than intra-cluster distances, revealing that considerable amount of genetic diversity existed among the accessions. Plant height, seed yield per plant, number of seeds per plant, number of seeds per pod and 1000-seed weight were major traits causing genetic divergence among accessions. Cluster II had highest mean value for number of pods per plant, 1000-seed weight and seed yield per plant, cluster IV had highest value for number of seeds per plant and number of seeds per pod. The accessions IU-65-2-1 and IU-73-2-1 may serve as potential parents for hybridization programme in the improvement of yield.

**Keywords:** Divergence, Yield attributes, black gram.

### Introduction

Multivariate analysis by  $D^2$  statistic is a powerful tool in quantifying the degree of divergence among all possible pairs of population at genotypic level<sup>1</sup>. The availability of genetically diverse germplasm is the basic need for the progress in plant breeding. Choice of parents for hybridization is one of the important considerations for creating new variability. Several biometrical approaches have been shown to be useful in selecting parents for successful hybridization programmes.  $D^2$  analysis has been found most effective and, therefore, widely used for the classification of parental lines.

The present study was therefore, undertaken to estimate the amount of genetic diversity in Seventy five 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.

### Material and Methods

The material under investigation consisted of seventy five genotypes of black gram Gram (*Vigna mungo* L. Hepper) were grown in Kharif 2009-10 and evaluated in a randomized block design with two replications at Regional Research Centre on Pulses, College of Agriculture, Indore MP. All the recommended package of practices were followed for raising healthy crop.

Observations were recorded on plot as well as on single plant basis. Observations on plot basis were recorded for days to 50% flowering and days to maturity. For recording single plant

observations, five competitive plants from each plot were randomly selected. Average of these five plants in respect of plant height, number of primary branches per plant, number of pods per plant, number of seeds per plant, number of seeds per pod, 1000-seed weight and seed yield per plant was used for statistical analysis. Mahalanobi's  $D^2$  statistic was employed to assess the genetic diversity.

### Result and 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 75 accessions of black gram for these characters (table-1).

The multivariate analysis giving the  $D^2$  values between 75 accessions, all these entries can be grouped into seven clusters (table 2). The estimates of  $D^2$  values varied substantially from 1.47 to 670.86. The highest  $D^2$  value of 670.86 was recorded between accession IU-65-2-1 and IU-73-2-1. A cross between these two accessions is expected to give heterotic hybrid and wide spectrum of variability.

Intra and inter cluster  $D^2$  values were worked out from divergence analysis (table 3). The inter-cluster distances were greater than intra-cluster distances, revealing that considerable amount of genetic diversity existed among the accessions. Same result also reported by<sup>2,3</sup>. Average intra-cluster distance revealed that cluster VII, which contained 13 accessions, had little intra-cluster distance. It indicated these accessions were closely related in their evolutionary process and passed through similar evolutionary factors.

**Table-1**  
**ANOVA showing values of mean squares for different characters in black gram**

S. No.	Source of variation	Replication	Accessions	Error
	d.f.	01	74	74
	↓ Characters	Mean sum of square		
1	Days to 50% flowering	1.7031	18.6681**	3.1121
2	Days to maturity	23.1875	13.2323*	8.8421
3	Plant height (cm)	0.0156	1275.00**	4.0270
4	Number of primary branches / plant	0.1870	1.1939**	0.1401
5	Number of pods / plant	19.6406	65.6060**	9.5122
6	Number of seeds / plant	31.7500	2663.577**	319.8007
7	Number of seeds / pod	2.1118	8.0205**	1.8943
8	Thousand-seed weight (g)	22.875	123.8062**	6.5629
9	Seed yield / plant (g)	1.2509	12.7314**	1.3696

\* - Significant at p = 0.05    \*\* - Significant at p = 0.01

**Table-2**  
**Clustering pattern of 75 accessions of the black gram on the basis of genetic divergence**

Cluster number	Number of accessions	Constituent accessions
I	1	40 (IU-65-2-1)
II	7	1 (99-V-42), 15 (IU-10-6), 46 (IU-69-4), 47 (IU-73-2), 48 (IU-73-2-1), 49 (IU-77-4), 56 (IU-83-2)
III	9	12 (IU-421), 13 (IU-421-1), 18 (IU-20-23), 27 (IU-25-22), 28 (IU-25-22-1), 34 (IU-62-2), 41 (IU-67-2), 62 (IU-86-9), 65 (MGS-1)
IV	5	9 (IU-8-38), 54 (IU-78-2), 58 (IU-83-3), 64 (MGS-1), 71 (IU-994-23-1)
V	21	17 (IU-20-11), 30 (IU-37-28-1), 31 (IU-43-12), 32 (IU-63-02), 33 (IU-63-02), 35 (IU-62-3), 36 (IU-62-3-1), 37 (IU-65-3), 38 (IU-65-1), 39 (IU-65-2), 42 (IU-67-2-1), 43 (IU-67-2-2), 44 (IU-68-5), 45 (IU-68-5-1), 57 (IU-83-2-1), 66 (IU-92-4), 67 (IU-92-41), 68 (IU-79-8), 69 (IU-994-9), 70 (IU-994-23), 75 (IU-994-27)
VI	19	2 (99-V-42-1), 3 (99-V-43), 4 (99-V-43-1), 5 (IU-8-6-130), 6 (IU-8-36-2), 7 (IU-8-36-2-1), 8 (IU-8-36-2-2), 10 (99-U-46), 11 (99U-47), 14 (99-U-42), 16 (99-U-41), 22 (IU-31-13), 23 (IU-31-13-1), 24 (IU-31-13-2), 50 (IU-77-4-1), 51 (IU-77-5), 53 (IU-78-1), 55 (IU-78-2-1), 60 (IU-83-4)
VII	13	19 (IU-20-23-1), 20 (IU-30-13), 21 (IU-30-13-1), 25 (IU-32-8), 26 (IU-32-8-1), 29 (IU-37-8), 52 (IU-77-5), 59 (IU-83-3-1), 61 (IU-4-6-9), 63 (IU-88-2), 72 (IU-994-24), 73 (IU994-25), 74 (IU-994-25-1)

The maximum inter-cluster distance of 8.026 was recorded between cluster I and IV followed by between cluster I and II, clusters I and VI, clusters I and VII, clusters I and III and between clusters III and IV. It is suggested that if the diverse accessions from these diverse groups are used in breeding programme, it is expected to produce a wide range of genetic variability in the population. The minimum inter-cluster distance between cluster V and VII indicates that the accessions of these clusters are genetically less diverse and were almost with same genetic makeup.

Cluster means for the 9 traits of all the 7 clusters were worked out (table 4). It was found that cluster I had lowest mean value for days to maturity and plant height. Cluster II had highest mean value for number of pods per plant, 1000-seed weight and

seed yield per plant, cluster IV had highest value for number of seeds per plant and number of seeds per pod. Cluster VI had highest mean value for plant height and number of primary branches per plant while cluster VII had lowest mean value for days to 50% flowering. To improve any particular trait donor for hybridization could be chosen from an appropriate cluster and that should be utilized in breeding Programme. The pattern of distribution of genotypes into various clusters indicates that geographical diversity, which was in agreement with earlier reports in blackgram<sup>4,5</sup>.

To improve seed yield, number of pods per plant and 1000-seed weight accessions from cluster II, viz., IU-73-2 and IU-73-2-1 would be right choice.

**Table-3**  
**Average inter and intra (diagonal) cluster D<sup>2</sup> values**

Clusters	I	II	III	IV	V	VI	VII
I	0.000	57.897	36.639	64.417	28.016	47.679	42.693
II		3.327	27.196	15.785	14.448	8.381	22.184
III			3.501	34.340	6.250	10.349	6.574
IV				3.193	17.148	14.815	14.326
V					4.326	8.168	5.226
VI						4.933	6.170
VII							2.563

**Table-4**  
**Cluster means for the characters under study in black gram**

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches /plant	Number of pods/ plant	No. of seeds /plant	No. of seeds /pod	1000 seed weight (g)	Seed yield/ plant (g)
I	46.50	65.50	24.50	3.40	26.20	150.45	5.75	13.00	1.95
II	43.57	68.43	34.31	4.61	31.38	190.53	6.29	61.08	11.62
III	40.17	66.39	37.94	3.46	22.08	80.86	3.83	52.22	4.21
IV	39.00	68.10	39.50	4.32	17.90	194.71	11.60	55.78	10.88
V	42.05	68.17	29.36	3.61	20.92	129.69	6.36	50.05	6.52
VI	39.97	66.34	42.05	4.91	25.49	141.96	5.75	56.61	8.02
VII	37.58	67.08	38.31	4.22	16.41	114.52	7.06	52.34	5.98

## Conclusion

The following conclusions are drawn from this present work. The analysis of variance showed significant differences among the accessions for all the characters studied. The pooled divergence for all the characters within the accessions was significant. Seventy-five accessions of black gram were grouped into seven clusters by D<sup>2</sup> analysis. The accessions IU-65-2-1 and IU-73-2-1 may serve as potential parents for hybridization programme in the improvement of yield. The accessions, IU-67-2-1 and IU-83-3 for early in days to 50% flowering; IU-77-5 for early in maturity; IU-62-3, IU-62-3-1 and IU-67-2-1 for dwarf; IU-77-5 for number of primary branches per plant; IU-73-2 and IU-73-2-1 for number of pods per plant; IU-73-2, IU-73-2-1, IU-78-2 and IU-83-3 for number of seeds per plant; IU-83-3 for number of seeds per pod; IU-73-2, IU-73-2-1 and IU-83-3 for 1000-seed weight; and 99-V-42, IU-73-2, IU-73-2-1, IU-78-2 and IU-83-3 for seed yield per plant may be used as suitable parents.

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