



Research Article

GENETIC DIVERSITY STUDY IN BLACKGRAM (*Vigna mungo* L.Hepper) GENOTYPES

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Received: June 30, 2016; Revised: July 13, 2016; Accepted: July 14, 2016; Published: October 21, 2016

Abstract- The present investigation comprised 30 genotypes of black gram to assess the genetic divergence based on 13 traits including seed yield. Based on Non-Hierarchical Euclidean cluster analysis, these genotypes were grouped into six clusters. Ten genotypes falls in Cluster III, forming the largest cluster followed by cluster I comprised seven genotypes, cluster VI comprised six genotypes and cluster II comprised four genotypes. Among these six clusters, cluster VI was noted as mono genotypic cluster. The maximum inter-cluster distance was observed between cluster II and cluster VI, where as the maximum intra-cluster distance was observed in cluster V. Cluster VI showed maximum cluster mean value for seed yield per plant. Therefore, Superior genotypes may be developed by hybridization between genotypes belonging to different clusters. Genotype IC-250188 showed more diverse than others because it fall in cluster VI, clustering by Ward and Tocher methods. Among all the characters, biological yield/plant (27.64%) contributes maximum followed by seed yield/plant (14.94%) and seeds/pod (12.64%).

Keywords- Black gram, Divergence, D² analysis, Cluster

Citation: Gupta Priyanka, et al., (2016) Genetic Diversity Study in Blackgram (*Vigna mungo* L. Hepper) Genotypes. International Journal of Agriculture Sciences, ISSN: 0975-3710 & E-ISSN: 0975-9107, Volume 8, Issue 49, pp.-2056-2058.

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Academic Editor / Reviewer: Dr Ramanuj Maurya

Introduction

Blackgram is an important nutritious pulse crop, belongs to family *leguminaseae*. It is cultivated throughout the year in different geographical regions of India. It is a predominantly autogamous crop and no information is available suggesting a change in its breeding behaviour under varied environmental conditions. Due to highly nutritious and multipurpose nature of this crop, still it faces so many problems due to its narrow genetic base. A successful breeding programme is based on parents having more genetic diversity, may be used in hybridization. It also helps in improving economic characters. The breeders always trying to broadening the genetic base of blackgram. To achieve this goal, selection of desirable/ suitable parents is still a difficult task. Most of the researchers considering the geographic diversity as a measure but several researchers performed several statistical analyses. Genetic diversity is a basic tool to determine the diverse genotype and it represents the diverse forms [1]. Here we perform Non-Hierarchical Euclidean cluster analysis to measure the genetic diversity analysis and to group the genotypes.

Materials and Methods

The present investigation comprised of 30 genotypes of blackgram including check namely (T-9). Randomized block design was used for experiment with three replications during kharif 2015 at research farm of SHIATS, Allahabad (U.P.), India. All agronomical practices were done to raise a healthy crop. Observation recorded for all the 10 traits namely plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length (cm), seed yield per plant (gm.), biological yield, seed index, harvest Index were based on five randomly selected plants in each replication while three characters namely days to 50% flowering, days to 50% Pods setting and days to maturity were recorded on plot basis. The genetic divergence analysis was performed using Windostat version 9.1.

Results and discussion

Cluster Analysis by Ward method:

The pattern of clustering proved the existences of significant amount of variability. It is obvious that the genotypes have grouped into different cluster irrespective of their geographical origins. It means that the genetic constitution of the varieties was more important than their origin and distribution [2]. Genetic divergence analysis was widely used to determine the genetic relationship among the genotypes and find out the suitable genotypes for future breeding programme. Genetic diversity analysis also helps in tagging and elimination of the duplicate accessions from genetic stock. On the basis of divergence 30 genotypes under investigation have been grouped into six distinct clusters [Table-1], indicating a wide range of diversity in the experimental materials. Cluster III had maximum 10 genotypes followed by cluster I with 7 whereas cluster IV were di-genotypic. Cluster VI was noted as solo genotypic cluster, indicated their uniqueness of this genotype. This unique genotype may be used in breeding programme for blackgram improvement. Several researchers viz., [3-5] also gave the emphasis on mono genotypic cluster in breeding programmes. The genotypes included in a cluster were diverse geographical origin; it shows that geographic divergence need not important related to genetic diversity. The divergence within the cluster indicates the divergence among the genotypes in the same cluster. On the other hand inter cluster divergence suggests the distance (divergence) between the genotypes of different two clusters. Critical assessment of clusters showed that clusters were heterogeneous within them and between each other based on major character relation. The lower D value between their characters suggested that the genetic constituents of these genotypes in one cluster were in close proximity with those genotypes in other cluster. Similar result was reported earlier by [6].

The composition of cluster and values of inter and intra cluster distances are given in [Table-2]. The inter cluster distance were greater than the intra cluster distance revealing that significant amount of diversity existed among the genotypes. The

intra cluster distance (D2) ranged from 0.00 (cluster VI) to 30.46 (cluster V). Inter-cluster distance (D2) was found maximum between cluster II and cluster VI (161.61) followed by cluster IV and clusters VI (118.67) and cluster I and VI (118.47), indicating the possibility of blackgram improvement through crossing between members of these clusters. Minimum inter-cluster distance was found between cluster I and III (38.19) followed by between clusters I and II (40.13) indicating that the genotypes were divergent but extent of divergence is lower than the others. But crossing between members of these close clusters might be useful for trait manipulation.

Table-1 Distribution of 30 blackgram genotypes into different clusters following Ward method

S. No.	Cluster No.	No. of genotypes	Genotypes included
1	I	7	Shekhar 1, IPU-7-3, IC-24129, IC-91567, IC-250190, IP-140815, VG-27
2	II	4	Pant U-19, T-9(check), Uttara, NDU-5-7
3	III	10	Shekhar 2, IC-140816, IC-140814, IPU-96-1, UN-85-5, PGRU-99022, KPU-131991, GC-9120, IC-56048, Pant U-30
4	IV	2	UN-82-83, Azad-1
5	V	6	IC-106194, PLU-710, IPU-99-60, IC-250187, IC-250189, IPU-96-1
6	VI	1	IC-250188

Table-2 Intra and inter cluster averages distances Ward method

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	24.65	40.13	38.19	68.59	43.14	118.47
Cluster II		26.24	42.21	55.78	60.33	161.61
Cluster III			27.82	37.38	43.19	116.97
Cluster IV				14.42	70.71	118.67
Cluster V					30.46	102.07
Cluster VI						0.00

Table-3 Cluster mean values for different component characters by Ward method

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Mean
Days to 50 % Flowering (DF)	48.04	47.50	47.80	47.16	49.16	47.66	48.04
Days to 50 % Pod Setting(DP)	57.00	57.83	57.000	58.00	60.11	58.00	58.01
Plant Height (PH)	43.16	47.65	46.17	49.22	42.33	42.09	44.96
Primary Branches/ Plant (PB)	1.64	1.83	1.90	1.40	1.82	1.33	1.76
Clusters/Plant (CP)	5.52	5.47	6.48	6.97	5.59	6.07	5.96
Pods/ Plant (PP)	26.73	22.60	25.21	24.10	23.65	27.93	24.92
Pod Length (PL)	3.82	4.22	4.14	4.37	3.84	4.03	4.03
Seeds/ Pods (SP)	4.36	5.38	5.61	6.36	4.84	4.06	5.14
Days to Maturity (DM)	67.57	67.83	68.90	68.67	70.94	69.33	68.86
100-SW	3.82	4.37	4.00	4.76	4.00	4.02	4.06
Harvest index (HI)	20.49	25.72	21.54	25.87	21.68	18.31	22.06
Biological Yield/ Plant (BY)	40.35	32.95	41.74	44.44	40.58	65.16	40.93
Grain Yield/ Plant (GY)	8.17	8.44	8.99	11.33	8.74	11.91	8.93

The cluster means of the quantitative traits helps to identify the diverse genotypes for genetic manipulation. Concerning days to 50 per cent flowering and maturity, all the clusters exhibited similar mean values thus suggesting common crop duration for the genotypes under study [Table-3]. Plant height varied from 42.09 (cluster VI) to 49.22 cm (cluster IV) suggesting that these clusters could be considered for improvement of plant height of blackgram. However, both positive and negative correlations of plant height with seed yield have been reported by various researchers. For example [7,8] observed the negative association between plant height and seed yield per plant, whereas [9] reported positive association between plant height and seed yield per plant. When, the plant height is used as selection criteria for yield improvement, the average intermodal distance and stem diameter must be taken under consideration but they were not included in the present study. Since improvement in yield is the prime objective in any breeding scheme, cluster means for seed yield per plant and its major components should be considered for selection of genotypes. Accordingly, cluster VI consisting of genotype IC-250188 and showing the highest cluster mean for yield per plant, number of pods per plant and moderately early maturing appears a desirable parent. Genotypes belonging to cluster III and V were found suitable for improvement of number of clusters per plant. The pod length and 100 seed weight appeared non-deviating. Cluster V and VI appeared promising for pods per plant thus the genotypes under these clusters would be useful in breeding.

Cluster Analysis by Tocher method

The nonhierarchical Euclidean clustering grouped the genotypes into five distinct clusters [Fig-1]. The clustering pattern of genotypes confirmed the presence of wide diversity. The largest cluster II included nineteen genotypes followed by cluster I comprising seven genotypes, suggesting existence of wide diversity among the genotypes used in the study. Interestingly, Cluster III, Cluster IV, Cluster V and Cluster VI contained only one genotype, each which may be due to

its notable distinctness from the other genotypes in terms of the traits chosen for this study. The composition of cluster and values of inter and intra cluster distances are given in [Fig-2]. The inter cluster distance were greater than the intra cluster distance revealing that considerable amount of genetic diversity existed among the genotypes. Maximum intra cluster distance was found cluster II (12.50) followed by cluster I (6.36). Minimum intra cluster distance had been recorded with cluster III (0.00) cluster IV (0.00) cluster V (0.00) cluster VI (0.00) due to the presence of solitary genotypes. It indicated that these genotypes were closely related in their evolutionary process and passed through similar evolutionary factor. These genotypes within the cluster were less divergent. This might be due to the unidirectional selection practiced in past and that has resulted in uniformity and less divergent between these genotypes. The maximum inter cluster distance was observed between cluster IV and V (46.61) followed by cluster III and VI (44.08) and cluster II and VI (40.84), suggesting that the genotypes belonging to these cluster may further be used as parents for hybridization programme to develop desirable hybrids because crosses between genetically divergent parents will generate transgressive segregants[10].

The cluster mean values were estimated over genotypes for ten yield attributing characters in blackgram 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 IV. A maximum day to 50% flowering was recorded in cluster IV. Earliest maturing entries were belonged to cluster V followed by cluster I. Genotypes requiring longest period to mature belonged to cluster IV. Highest mean value for plant height was recorded with cluster III. Cluster IV had lowest mean value for plant height. Number of primary branches/plant was more with the genotypes of cluster V. The maximum number of cluster/plant was observed in cluster III. Genotypes belonged to cluster VI had maximum pod/plant. Similarly genotypes belonged to cluster III had maximum seed/pod. Highest mean values for pod length and 100 seed weight were more in genotypes of cluster III. Cluster

VI registered with highest yield/plant followed by cluster III and cluster IV.

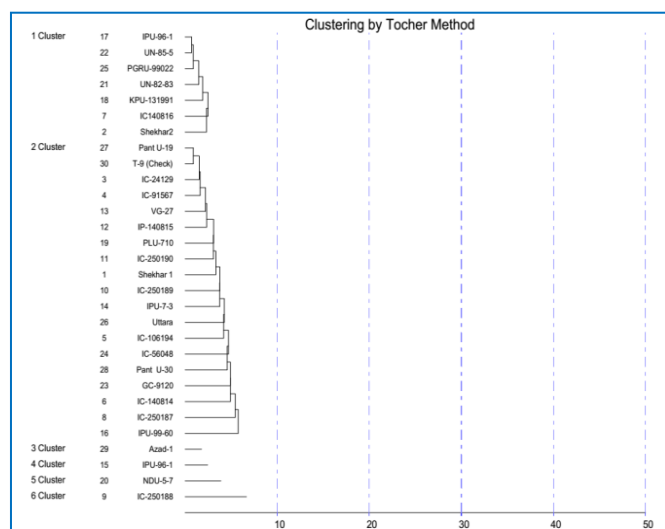


Fig-1 Clustering pattern of blackgram genotypes following Tocher clustering method

Present contribution

The number of times each of the yield component characters appeared first in rank and its respective percent contribution towards genetic divergence was presented in [Table-4]. Character contribution towards divergence was calculated

for each trait studied and ranked in descending order of magnitude in each of the combination. The highest contribution in the manifestation of genetic divergence was exhibited by biological yield (27.59%) followed by grain yield per plant (14.94%), seeds per pod (12.64%) and pod length (10.57%) suggesting scope for improvement in these characters. In other words, selection for these characters may be rewarding. The contribution of traits towards divergence varies with crop to crop even with breeding material. Genotypes belonging to different clusters having high means for desired characters and with maximum divergence may be successfully used in hybridization programmes.

Table-4 Percent contribution of 13 characters to genetic divergence

S.No.	Characters	Times Ranked 1 st	Contribution %
1	50% Flowering	15	3.45%
2	50% podding	8	1.84%
3	Days to maturity	33	7.59%
4	Plant Height	7	1.61%
5	Primary branches/plant	36	8.28%
6	Clusters/plant	9	2.07%
7	Pods/plant	19	4.37%
8	Seeds/pod	55	12.64%
9	Pod length	46	10.57%
10	Grain yield/plant	65	14.94%
11	Biological yield	120	27.59%
12	Harvest Index	21	4.83%
13	100-SW	1	0.23%

Table-5 Cluster means values for different component characters by Tocher method

	DF	DP	DM	PH	PB	CP	PP	SP	PL	GY	BP	HI	100-SW
Cluster I	47.67	57.57	68.62	46.38	1.84	6.64	25.23	5.53	4.16	10.21	43.66	23.54	4.10
Cluster II	48.18	58.12	68.89	44.72	1.75	5.66	24.89	4.95	3.96	8.06	38.83	21.08	3.99
Cluster III	47.33	59.33	69.67	47.85	1.30	7.73	24.40	6.47	4.53	11.53	40.73	28.37	4.89
Cluster IV	50.33	61.67	71.67	41.75	1.57	5.80	23.33	5.00	3.81	11.61	48.83	23.78	4.25
Cluster V	47.00	55.67	65.67	42.90	2.43	5.33	22.40	5.80	4.21	8.13	31.04	26.06	4.15
Cluster VI	47.67	58.00	69.33	42.09	1.33	6.07	27.93	4.07	4.03	11.91	65.16	18.31	4.02

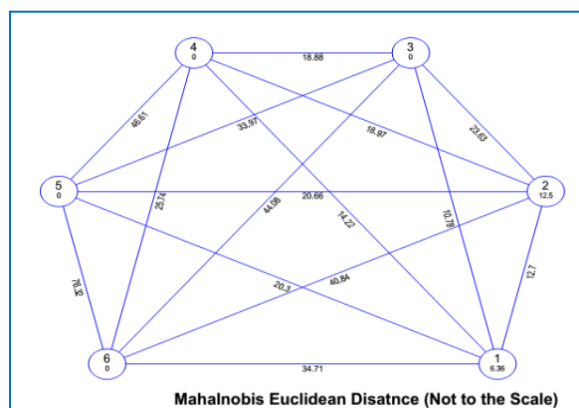


Fig-2 Intra and inter cluster average distances among clusters following Tocher method

Conflict of Interest: None declared

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