Journal of AgriSearch, 9 (2): 133-135
An Open Access International Peer Reviewed Quarterly

ISSN : 2348-8808 (Print), 2348-8867 (Online)
https://doi.org/10.21921/jas.v9i02.10117

Genetic Diversity Analysis in Blackgram Genotypes

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ABSTRACT

An investigation was carried out during *kharif* 2018 by employing 35 genotypes of blackgram including two checks (*i.e.,* Pratap Urd-1 and Pant Urd-31) for the assessment of genetic diversity using D^2 statistics. Results revealed that all the genotypes were grouped into five clusters among them, cluster V was largest had maximum number of genotypes (17) followed by cluster I, cluster IV, cluster II and cluster III were comprising 5, 5, 4 and 4 genotypes respectively. Inter cluster distances were found greater than intra cluster distances. Highest inter cluster distance was observed between cluster I and cluster IV indicate that maximum genetic divergence was exists among genotypes of these cluster, while least between cluster III and cluster V. The cluster III had maximum intra cluster distance followed by cluster IV whereas cluster I had minimum. The relative contribution of traits towards genetic divergence found highest for number of seeds per pod followed by 100-seed weight. For most of the traits, maximum cluster mean was showed by cluster III.

Keywords: Blackgram, cluster, genetic diversity.

ARTICLE INFO

Received on	:	26.10.2021
Accepted	:	07.06.2022
Published online	:	16.06.2022

INTRODUCTION

Blackgram is one of the valuable pulse crops as it occupies an ample quantity of vegetarian protein and other substances *i.e.,* carbohydrates, minerals, vitamins, amino acids, etc. in its seed. India is a leading country in the production of blackgram although the productivity of this crop is very low because of genetic potential of cultivars is not too good. Hence, plant breeders should give more consideration to improve the productivity of blackgram by following various plant breeding strategies. Diversity analysis is one of them, helps in identification of more diverse genotypes from a population that can be used in a hybridization program to produce desirable and superior segregants by crossing between more diverse parents. The greater heterosis observed for the hybrids among genetically diverse parents than hybrids among more closely associated parents (Ramanujam *et al.,* 1974). An accurate assessment of genetic divergence among different genotypes is essential for better understanding of the pattern for varietal differentiation and evaluation as well as for assisting plant breeders in selecting the appropriate material for further genetic improvement and management of germplasm of blackgram (Shamim and Pandey, 2019). Thus, keeping all the aspects in view, the present study was proposed to assess the genetic diversity in blackgram genotypes.

MATERIALS AND METHODS

The thirty-five genotypes of blackgram including two checks *namely* Pratap Urd-1 and Pant Urd-31 were subjected to diversity analysis by using D^2 statistics. All the genotypes were grown during *Kharif* 2018 in Randomized Block Design with three replications at Instructional Research Farm, Department of Genetics and Plant breeding, Rajasthan College of Agriculture, MPUAT, Udaipur. Each genotype was sown in 2 rows of 4-meter length and row to row and plant to plant spacing were maintained at 30cm and 10cm respectively. Statistical data for plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, number of pods per cluster, pod length (cm), number of seeds per pod, seed yield per plant (g), biological yield per plant (g), harvest index (%), 100-seed weight (g) and seed protein content (%) were recorded on five randomly selected plants from each replication while days to 50 per cent flowering and days to 75 per cent maturity were recorded on entire plot basis. Wilk' (1932) was used for Multivariate analysis of variance (MANOVA). Genetic divergence estimated by Mahalanobis D^2 statistics (Mahalanobis, 1936) and grouping of genotypes into various clusters was done by Tocher's method as described by Rao (1952). The seed protein content was determined following Micro Kjeldhal's method (1883).

RESULTS AND DISCUSSION

Genetic divergence among different genotypes is the prime requirement of any successful plant breeding program. Collection and evaluation of genotypes of a crop offers a better scope for exploiting genetic diversity.

Thirty-five genotypes were resolved into five clusters by using Tocher's method (Table 1).

Similar results were observed by Vidya *et al*. (2018). The dendrogram represents the pattern of clustering was depicted

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Table 1: Distribution of blackgram genotypes in different clusters

Cluster	Number of genotypes	Members
I	5	KPU-1127, KU-16-87, KPU-514-75, AKU-11-21, AKU-12-3
II	4	KU-1695, AKU-11-23, KU-16-90, KU-16-96
III	4	KU-16-8, GP(U)KPU-1143, KU-16-92, AKU-1603
IV	5	KU-16-9, KU-16-97, AKU-1604, TBU-2, Pratap Urd-1 KPU-1098, KU-16-11, GP(U) KPU-1137, KU-1698, KPU-129-104, TBU-6,
V	17	KU-16-102, AKU-1302, AKU-14-02, AKU-13-3, AKU-11-3, AKU-11-9, KU-16-6, KU-16-3, KU-16-13, AKU-11-15, Pant Urd-31

in the fig. 1 showed that the significant amount of variability was present among genotypes. Grouping of genotypes by multivariate methods in the study is of practical value to the plant breeders. Representative genotypes may be chosen from particular clusters for hybridization program (Jayamani and Sathya, 2013). Among these five clusters, cluster V was largest which comprises maximum number of genotypes (*i.e.*, 17) followed by cluster I & IV (5 genotypes) and cluster II and III (4 genotypes).

Inter and intra cluster distances are presented in the table 2. It was recorded that inter cluster distances were higher than intra cluster distance indicates that ample genetic diversity was present among genotypes of different clusters in comparison to genotypes of same cluster. Gowsalya *et al.* (2017) also reported higher inter cluster distances than the intra cluster distance. The inter cluster distance ranged from 8.188 to 20.856. Among cluster I and IV (20.856) maximum inter cluster distance was recorded followed by cluster I and III (17.666) indicates plentiful diversity exists among genotypes hence, genotypes consisted by these clusters would be utilized in crossing programs to obtain better segregants. Whereas, minimum inter cluster distance found between cluster III and V (8.188) therefore selection of parents from these clusters is not useful for hybridization purpose. The intra cluster distance was recorded in range of 5.494 to 6.764. The cluster III had maximum intra cluster distance followed by cluster IV and V suggesting that genotypes involved in these clusters might have different genetic architecture whereas, least intra cluster distance was recorded for cluster I showed that all the genotypes of this cluster may have same gene pool (Bhareti *et al.*, 2019).

Table 2: Intra (in bold) and inter cluster distances between five clusters of blackgram genotypes

Cluster	I	II	III	IV	V
I	**5.494**	11.556	17.666	20.856	10.857
II		**5.676**	12.544	16.110	9.715
III			**6.764**	9.003	8.188
IV				**5.897**	10.558
V					

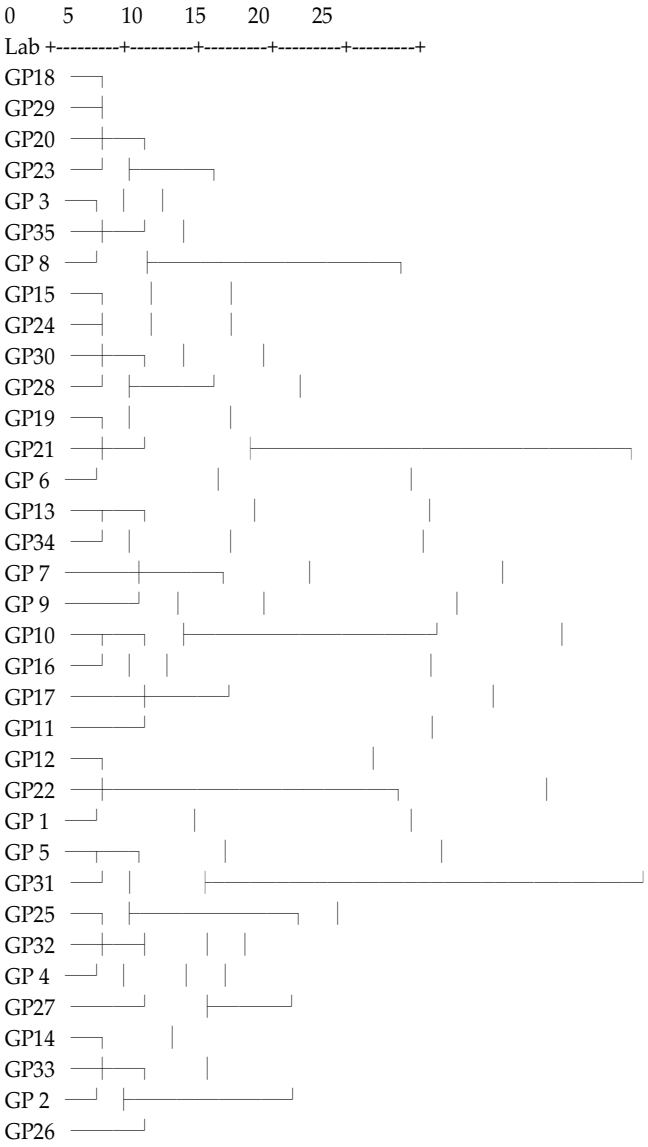

Fig. 1: Dendrogram represents the pattern of clusters of thirty-five genotypes of blackgram (Ward, 1963)

Per cent contribution of each character studied towards genetic divergence was presented in the table 3.

The maximum contribution towards genetic divergence was reported by number of seeds per pod followed by 100-seed weight. The yield per plant followed by100-seed weight contributed highest to the divergence (Vidya *et al.*, 2018). Traits *viz.*, number of branches per plant, number of clusters per plant, pod length, seed protein content and seed yield per plant also exhibited considerable contribution. The traits contributing maximum towards divergence will be considered during selection and choice of parents for hybridization. Days to 50% flowering was showed least contribution to the genetic divergence. Cluster mean of five clusters for various traits studied are presented in the table 3. Results revealed that the cluster III showed maximum cluster mean for days to 50 per cent flowering, days to 75 per cent maturity, number of branches per plant, number of clusters per plant, number of pods per plant, seed yield per plant, 100-seed weight and seed protein content whereas minimum

Table 3: Cluster means and Percent contribution of different characters to genetic diversity for seed yield and component traits of 35 genotypes of blackgram

Character	Cluster					Percent contribution
	I	II	III	IV	V	
Days to 50% flowering	39.73	42.00	42.34	41.53	42.00	1.13
Days to 75% maturity	72.47	73.50	74.42	72.60	73.71	1.42
Plant height (cm)	21.87	31.10	27.06	31.35	25.54	4.90
Number of branches / plant	7.05	10.10	11.33	9.10	8.41	10.95
Number of clusters/ plant	6.80	8.62	10.00	8.22	7.70	8.32
Number of pods/plant	17.30	20.98	23.27	20.24	19.71	1.64
Number of pods/cluster	2.55	2.49	2.35	2.49	2.59	2.54
Pod length (cm)	4.45	4.38	4.40	4.81	4.41	8.23
Number of seeds/pod	5.78	5.45	5.31	5.91	5.52	23.13
Seed yield/plant (g)	3.96	5.09	7.09	5.87	5.17	7.55
Biological yield / plant (g)	17.45	20.10	19.51	14.58	16.18	3.94
Harvest index (%)	22.84	25.58	36.82	40.59	32.11	1.98
100-seed weight (g)	4.93	4.62	5.31	4.59	4.65	16.55
Seed protein content (%)	22.84	22.99	23.42	22.87	23.17	7.74

cluster mean was reported for number of pods per cluster and number of seeds per pod. Highest cluster mean for number of pods per cluster was expressed by cluster V. Cluster IV had maximum cluster mean for plant height, pod length, number of seeds per pod and harvest index while minimum for biological yield per plant and 100-seed weight. Cluster II exhibited highest mean for biological yield per plant and minimum for pod length. For rest of the traits least cluster mean was exhibited by cluster I.

CONCLUSION

From the results of current investigation, it was concluded that cluster V was largest having maximum number of genotypes. Inter cluster distances were greater than intra cluster distance represents vast genetic diversity between genotypes of different clusters. Maximum inter cluster distance was found among cluster I and IV indicates genotypes of these clusters utilized in the crossing program for getting better transgressive segregants. Maximum intra cluster distance was observed for cluster III explained genotypes of different architecture within this cluster. The number of seeds per pod followed by 100-seed weight contributed utmost to the genetic divergence hence these traits should be considered at the time of selection and choice of parents for crossing. Cluster III had maximum while cluster I had minimum cluster means for most of the traits.

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Citation:
Saran R and Sharma PP. 2022. Genetic diversity analysis in blackgram genotypes. *Journal of AgriSearch* 9(2):133-135