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GENETIC DIVERSITY STUDIES OF BLACKGRAM GENOTYPES GROWING IN NORTHERN INDIA

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KEYWORDS

Blackgram

D² analysis

Diversity

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ABSTRACT

Current study was carried out to assess the diversity of thirty-eight black gram (*Vigna mungo*) genotypes by using D² statistics for thirteen quantitative characters. All studied genotypes formed six clusters by using D² statistics, among these cluster I formed the largest and containing twenty three genotypes in it, followed by cluster III contains five genotypes, cluster IV contains four genotypes, cluster V contains three genotypes, cluster II contains two genotypes and cluster VI contains only one genotype. The highest inter-cluster distance is found between cluster V and cluster VI followed by cluster II and VI, cluster I and VI, cluster III and IV, cluster V and VI, showing that the effective breeding program can be started to increase productivity and other yield-related traits by exploiting heterosis breeding. Cluster V has the maximum mean values for seed yield for the plant, harvest index, number of pods per plant and plant height. Cluster II has the highest mean values for seed yield, seed index, pod length and number of seeds per pod, number of clusters per plant. The hybridization programme has been suggested based on inter-cluster divergence and cluster means for the characters studied.

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1 Introduction

Blackgram or urdbean (*Vigna mungo* [L.] Hepper) is an important pulse crop with easily palatable protein and less flatulence contents. The genus *Vigna* (Leguminosae) consists of seven subgenera and has about 150 species (Verdcourt, 1970). The genus *Vigna* is a large leguminous taxon comprising 104 described species spread over tropical and subtropical regions of Africa, Asia, America, and Australia (Lewis, 2005). Pulses are a vital part of various diets around the globe and have copious potential to improve human health, conserve soils, guard the environment and contribute to world food security. It is grown in kharif as well as dry (zaid) season. Black gram seeds have high nutritive value with protein (25- 26%), carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins (Singh & Singh, 2013). Seed yield of blackgram is about 600-800 kg/ha (Indiastat, 2020). To increase potential productivity of blackgram, it is essential to study and exploit the genetic diversity of this crop. The selection of genetically diverged parents is likely to produce superior and desirable segregates following the crossing between them. Several biometrical methods have been used for selecting parents for successful hybridization programmes. Among these, D^2 analysis has been most effective and widely used (Dasgupta & Das, 1984; Elangaimannan et al., 2008; Neelavathi & Govindarasu, 2010; Rao et al., 2019) for the classification of parental lines for developing high yielding genotypes in black gram. For generating population for different breeding programmes or for varietal selection, it is essential to identify genetic materials that contain desirable traits. Hence, it is of great interest to categorize or group the genotypes according to their trait scores or genetic structure. The objective of this study is to classify the blackgram genotypes into different clusters using morphological traits data.

2 Materials and Methods

The thirty-eight genotypes were evaluated in the experimental farm of department of genetics and plant breeding, SHUATS, Prayagraj, Uttar Pradesh, India. The experiment was carried out in randomized block design (RBD) with three replications. Each genotype was

represented by five rows of one-meter length with a spacing of 30 cm x 10cm. A fertilizer dose of 20:40:20 kg NPK/ha was applied and need based plant protection measures were followed. The observations were recorded on the randomly taken five plants in each entry. The observations were recorded on thirteen quantitative traits viz., days to 50% flowering (DFF), days to 50% pod setting (DFPS), plant height (PH), number of primary branches per plant (NPBP), number of clusters per plant (NCP), number of pods per plant (NPP), number of seeds per plant (NSP), pod length (PL), days to maturity (DM), seed index (SI), biological yield (BY), harvest index (HI) and seed yield per plant (SY). Assessment of genetic D^2 divergence was done using Mahalanobis D^2 statistics (Mahalanobis, 1936) and the genotypes were grouped into different clusters using Tocher's method as described by (Rao, 1952). The statistical analysis was performed using TNAU STAT (Manivannan, 2014).

3 Results and Discussion

Analysis of variance showed significant differences among the genotypes for all the thirteen studied characters. The thirty-eight genotypes were grouped into six clusters (Table 1). Distance between all genotypes were calculated using squared Euclidean distance technique and the genotypes were grouped or clustered based on Tocher's method (Rao, 1952). Among the six clusters, clusters I had highest number of genotypes consists twenty-three genotypes indicates that crossing among the genotypes in this cluster may give transgressive segregants, this was followed by cluster III with five genotypes and cluster IV with four genotypes. Clusters V, II and VI has three, two and one genotypes in each cluster respectively. The single genotype present in the cluster VI indicates that it could be more divergent from the other genotypes and crossing with the genotypes of other different clusters would be suitable for obtaining heterosis for some of the important traits. It is observable that the genotypes have clustered into different groups irrespective of their geographical origins. Similar results were observed by various researchers (Senapati & Misra, 2009; Panigrahi et al., 2014; Patel et al, 2014; Rao et al., 2019).

Table 1 Distribution of the blackgram genotypes into different clusters

Clusters	Number of clusters	Genotypes
Cluster I	23	IC-250188, MDU8-5-7, PLU-710, IC-250187, SHEKHAR-3, PLU-648, IC-140816, SPS-33, UH82-83, IC-250190, IPU-199-60, IC-91567, PKG U3, UH-10, UH-82-35,UTTARA, STNP2, IPU9 94-10, PLU 826, UH 81-89, PANT U-30, IC-106194, PU-31
Cluster II	2	P-1, IC- 56048
Cluster III	5	T-9, UH82-15, UG-27, UH-85-5, U-9
Cluster IV	4	IC-24129, PLU-277, PGRV-99022, IPU 99-16
Cluster V	3	IPU 7-3, IPU-96-1, U-5
Cluster VI	1	AZAD-1

Table 2 Average intra (diagonal and bold) and inter-cluster distance

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	269.4943	350.5999	626.6422	777.963	746.9949	2616.358
Cluster II		179.2026	879.4133	957.3473	1338.804	3460.555
Cluster III			333.4702	1759.66	794.8365	1363.093
Cluster IV				305.9564	1131.975	3939.922
Cluster V					194.9215	1568.584
Cluster VI						0

Table 3 Cluster wise mean values of thirteen quantitative traits of blackgram

	DFP	DFPS	PH	NPBP	NCP	NPP	PL	NSP	DM	SI	BY	HI	SY
Cluster I	49.29	58.34	53.82	2.30	5.16	24.04	4.28	5.69	68.43	3.69	55.80	15.46	8.42
Cluster II	47.33	57.66	49.70	2.57	5.33	26.40	4.48	5.83	65.33	4.86	66.81	14.76	9.86
Cluster III	47.87	58.00	52.55	2.22	4.88	24.55	4.67	5.33	67.27	4.07	42.31	18.71	7.80
Cluster IV	48.25	58.00	43.54	1.86	5.58	19.34	3.61	4.60	67.25	3.73	57.81	15.63	8.96
Cluster V	50.44	59.44	58.12	2.66	5.22	26.72	3.86	4.78	66.77	3.98	40.03	25.08	10.07
Cluster VI	48.33	58.00	48.30	1.66	7.33	24.36	4.64	6.30	66.66	4.59	48.96	28.17	7.76

The greater inter cluster distance than the intra cluster distance revealed that substantial amount of genetic diversity was existed among the studied genotypes (Table 2). The inter cluster distance was reported between ranged of 350.59 to 3939.92 while intra cluster distance is ranged from 0.00 (cluster VI) to 333.47 (cluster III). Minimum intra cluster distance exists with cluster VI (0.00) due to the presence of single genotype while highest intra cluster distance was observed in cluster III (333.47), followed by cluster IV (305.95), cluster I (269.49), cluster V (194.92) and cluster II (179.20) which suggesting that genotypes of these clusters may useful as parents for hybridization programme because crosses between genetically divergent parents will generate transgressive segregants. The highest inter cluster distance was observed between clusters IV and VI (3939.92), clusters II and VI (3460.55), clusters I and VI (2616.35).

The wide range of variation was observed among the cluster mean values for thirteen traits in black gram genotypes (Table 3). Cluster II and V has minimum and maximum period for days to 50% flowering respectively. Cluster VI and I has minimum and maximum period for days to maturity respectively. Minimum and maximum plant height was observed in cluster IV and V respectively. The highest primary braches per plant was observed in cluster V followed by cluster II, I and III. The

maximum number of clusters per plant was observed in cluster VI followed by IV, II, V and I. Maximum pods per plant was observed in cluster V followed by clusters II, III, VI and I. The maximum pod length was observed in cluster III followed by clusters VI, II and I. The maximum seeds per pod was observed in cluster VI followed by II, I and III. Maximum seed index was observed in cluster II followed by clusters VI and III. The maximum harvest index was observed in cluster VI followed by cluster V. The maximum seed yield per plant was observed in cluster V followed by cluster II, IV and I. Characters such as number of primary branches per plant, number of clusters per plant, pod length, pods per plant, seed index, seeds per pod and harvest index were having positive correlation with direct and dominant role in higher seed yield (Rajasekhar et al., 2017). So, genotypes belonging to cluster II, III and V were promising for the hybridization programme.

The characters contributing to maximum divergence needs greater emphasis for deciding the clusters for the purpose of selection of parents for further hybridization (Table 4). Among all the yield contributing traits, the maximum contribution towards divergence was made by pod length (41.28%) followed by seed yield per plant (40.25%), harvest index (8.58%), plant height (6.92%) and number of pods per plant (2.56%).

Table 4 Percent contribution of different traits headed for diversity in blackgram genotypes

Trait codes	Contribution (%)
DFF	0
DFPS	0
PH	6.92
NPBP	0.25
NCP	0
NPP	2.56
PL	41.28
NSP	0
DM	0
SI	0
BY	0.12
HI	8.58
SY	40.25

Conclusion

For developing breeding program, it is suggested to choose the clusters which have more intra cluster distance because diverse parents within heterotic group may give desirable segregants. Diversity had important implications on establishment of heterotic patterns among varieties and lines. In the present study, it revealed that the maximum cluster distance was found between cluster V and VI. It is expected that maximum heterosis will be demonstrated in cross combinations involving the parents belonging to most divergent clusters.

Conflict of interest

The authors declare that they have no conflict of interest

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