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Studies on genetic diversity in blackgram (*Vigna mungo* L. Hepper) genotypes

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Abstract

30 Genotype of blackgram was evaluated in randomized block design was carried out to assess the analysis of variance, coefficient of variance, heritability, genetic advance, genetic advance as percent of mean using D2 analysis. The genotypes was grouped into six cluster. Cluster VIII consisted maximum accessions^[8] followed by cluster I and cluster IV^[7] and cluster V consisted^[4] and cluster VI consisted^[3] and cluster consist only accession. The inter cluster distance is greater than the intra cluster distance that considerable amount of genetic diversity existed among accessions. Maximum intra cluster distance was recorded for cluster IV (172.59) followed by, cluster V (148.37), cluster III (129.07) and cluster I (130.02) minimum for cluster V (25.12) and cluster VI (0.80). The character contributing maximum diversity towards in biological yield (16.32), plant height (16.02) cluster per plant (14.25), days to 50% (12.64) and seed per pod (9.89).

Keywords: Blackgram, genetic advance, D2 analysis

Introduction

Blackgram (*Vigna mungo* (L). Hepper) popularly known as urdbean, or blackgram is a grain legume, it belongs to family leguminoseae with chromosome number $2n=2x=22$. In India alone, it occupies about 3.3 million hectare and annual production of urdbean in India is about 1.37 million tones. In U.P Blackgram is grown in about 111.0 thousand hectares with a total production of 66.0 thousand tonne. An assessment of the genetic diversity is an important first step in a program to improve yield. The proper estimate of nature and magnitude is essential to infer about the extent of variation available for yield and its component traits. The selection of genetically divergent parent is expected to produce superior and desirable segregants following crossing. The availability of genetically divergent parent germplasm is the basic need for the progress in plant breeding. Choice of parents for hybridization is one of the important consideration for creating new varieties. D2 analysis have been found most effective consideration in biometrical approaches in selecting parents. Therefore this experiment was undertaken to estimate amount of genetic diversity among 30 genotype of blackgram and to identify genetic diverse parents for hybridization programmed at yield improvement in crop.

Materials and Methods

A field experiment was conducted during *kharib* 2015- 2016 at field experiment centre, department of genetic and Plant Breeding, SHIATS, ALLAHABAD, U.P. To identify the genetic diversity and variability among the genotype, divergence parent for future hybridization programme. The material consist 30 genotypes was sown in randomized block sign with three replications with distance of 30cm row to row and 10 cm plant to plant. Five plant each row was randomly selected to record the observations on plant height, number of primary branches per plant, seed weight, days to 50% flowering, days to 50% pod setting, days to maturity. The genetic divergence was estimated by using Mahalanobis D2 statistic genotype was grouped into clusters following the Tochers methods as described by Rao, 1952^[13].

Result and Discussion

30 genotype was grouped into six clusters. (Table.1). cluster III was the largest comprising of eight genotypes followed by cluster I and IV with seven genotypes each. Cluster V with four genotypes and cluster VI with three genotype. Cluster II with one genotype indicating high

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heterogeneity among the genotypes. Maximum intra cluster distance was observed in cluster IV (172.59) and VI (148.06) followed by, cluster V (140.06) and III (129.07) indicating that some divergence still existed among genotype, this could be made use in the yield improving through recombination breeding. From the inter cluster D₂ values highest divergence observed between cluster IV and VI (1460.76) followed by cluster II and VI (1081.6) II and IV cluster with (896.29) cluster II and V (760.30) the crosses involving varieties from this clusters would give wider desirable recombination (table 1.2). The minimum divergence was observed in I and III (250.30) I and V (212.11) it indicate that these cluster has maximum number of gene complexes. The genotypes of these clusters may be used as parents in the crossing program to generate breeding materials with diversity. The cluster means for each 13 character are presented in Table 3. the indicate that the cluster mean for plant height was observed maximum mean value in cluster II (63.25) and lowest in cluster IV (46.36), days to 50% flowering was highest in II (57.50) and lowest value in cluster VI (46.63). Days to maturity was highest in cluster I (68.52) and lowest in cluster

V (66.06). Primary branches per plant maximum mean was for cluster II (17.25) and lowest for cluster IV (13.89), cluster per plant maximum VI (22.84) and lowest was cluster IV (17.88), pod setting was maximum in cluster II (58.55) and minimum in cluster V (55.01). Pods per plant was highest in cluster II (62.56) and lowest in cluster IV (53.93), pod length per plant was highest in cluster IV (4.9) and lowest in cluster VI (4.1). Seeds per pod was highest in cluster II (5.63) and lowest in cluster V (4.68). Seed index was highest in cluster V (4.66) and lowest in cluster VI (3.99), harvest index was highest in cluster III (49.21) and lowest in cluster II (41.35). Biological yield highest in cluster II (26.38) and lowest in cluster VI (22.07). Seed yield was highest in cluster II and lowest in cluster IV (10.62). The result indicate that the selected genotype having high values for particular trait used in the future hybridization program. The maximum contribution towards genetic divergence was presented in table 1.4 according rank biological yield (16.32) was maximum contributed toward divergence followed by plant height (16.09), cluster per plant (14.25), days to 50% flowering (12.64) and seed yield per plant (9.89).

Table 1: Distribution of the 30 genotypes of blackgram into different clusters

S. No.	Cluster numbers	Number of genotypes	Genotypes included
1	I	7	KPU13-191, IC-250188, KPU13-299, GC-9120, KPU07-08, Shekhar1, KPU-13-200
2	II	1	KPU13-207
3	III	8	KPU13-183, KPU13-31, KPU 479, IC-56048, IC-140814, PGRU-99022, UG-27, GU-1
4	IV	7	IPU96-1, NDU-5-7, IC-56034, UTAE, PU2002×PU988-232, PLU 710, IPU-99-336
5	V	4	PLU-485, NP-3, IPU-99-60, PLU-384
6	VI	3	PLU86-7, IPU-199-60, IPU-7-3

Table 2: Intra (diagonal) and inter cluster average distances (D²) for different quantitative characters in blackgram

	I Cluster	II Cluster	III Cluster	IV Cluster	V Cluster	VI Cluster
I Cluster	103.021	406.35	250.303	281.98	212.11	378.87
II Cluster		0	510.422	896.29	760.30	1081.6
III Cluster			129.07	619.41	305.21	310.45
IV Cluster				172.59	253.63	1460.766
V Cluster					140.37	247.73
VI Cluster						148.06

Table 3: Cluster mean values of 7 clusters for different quantitative characters in blackgram

Characters	I	II	III	IV	V	VI
Days to 50 % Flowering	49.93	57.50	49.93	48.12	48.38	46.63
Days to 50 % Pod Setting	58.09	58.55	57.51	56.72	55.01	57.12
Plant Height	54.34	63.25	58.67	46.36	50.29	45.92
Primary Branches/Plant	15.05	17.25	16.39	13.89	14.73	16.00
Clusters/ Plant	21.83	20.26	22.79	17.88	21.20	22.84
Pods/ Plant	57.50	62.56	58.93	53.93	57.07	55.60
Pod Length/ Plant	4.50	4.53	4.51	43.95	4.23	4.15
Seeds/ Pod	5.47	5.63	5.11	4.79	4.68	5.12
Days to Maturity	68.52	68.14	66.88	67.85	66.06	67.00
Seed Index	4.34	4.34	4.36	4.05	4.66	3.99
harvest Index	48.44	41.35	49.21	47.79	47.79	48.81
Biological Yield/ Plant	24.32	26.38	24.23	22.49	23.23	22.07
Seed Yield/ Plant	11.74	11.71	11.8	10.62	11.12	10.73

Table 4: Percent contribution of different quantitative characters towards genetic divergence in blackgram genotypes

S. No.	Source	Contribution %
1	Days to 50 % Flowering	12.64
2	Days to 50 % Pod Setting	8.74
3	Plant Height	16.09
4	Primary Branches/Plant	1.84
5	Clusters/ Plant	14.25
6	Pods/ Plant	2.99
7	Pod Length/ Plant	2.07
8	Seeds/ Pod	9.89
9	Days to Maturity	1.64
10	Seed Index	3.22
11	harvest Index	1.15
12	Biological Yield/ Plant	16.32
13	Seed Yield/ Plant	9.89

Conclusion

On the basis of results the genotypes KPU 13-183 followed by KPU 13-31, KPU 479, KPU 13-207 and GU-1 was identified as the genotypes for seed yield at Allahabad region. The present investigation registered high heritability along with high genetic advance as a 5% of mean for seed yield per plant which should be given top priority for effective selection the present investigation further revealed that cluster IV and VI are most diverse to each other. Therefore, genotypes present in this cluster are suggested to provide broad spectrum variability in segregating generations and may be used as parents for future hybridization programme to develop desirable genotypes.

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