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Genetic Divergence in Blackgram

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ABSTRACT

Genetic diversity in 70 genetypes of Blackgram (*Vigna mungo* (L.) Hepper) estimated using Mahalanobis' D^2 value, indicated considerable diversity in the material studied. The genotypes were grouped in 8 clusters using multivariate analysis. Cluster I was the largest with 55.6% genotypes from different states except Madhya Pradesh, New Delhi and Rajasthan. Cluster VI, VII and VIII were monogenotypic. Genotypes from Gujarat exhibited the maximum diversity and were represented in all the clusters except cluster V. However, no parallelism was observed between geographic diversity and genetic diversity. Cluster I showed much genetic divergence with cluster VI, VII and VIII. It was suggested that the genotypes GU 84-2, Valsad-1 and GU 84-1 can be utilized as parents in the hybridization programme to develop a high yielding blackgram with early maturity.

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INTRODUCTION

Blackgram (*Vigna mungo* (L.) Hepper) is an important legume crop, receiving importance due to short duration and widely grown as intercrop. A successful breeding programme in the crop would need information on the nature and degree of genetic divergence in the available genetic stocks with plant breeder in choosing the right parents for further improvement.

MATERIALS AND METHODS

Seventy popular geographically diverse genotypes of Blackgram from twelve states of India, were taken for present study. These genotypes were grown during *kharif* 1992-93 at Instructional Farm, Gujarat Agricultural University, Junagadh, in a randomized block design with three replications. The plot size consisted of single row of 4 m length following a spacing of 30 cm x 10 cm. The recommended agronomical practices and plant protection measures were followed to ensure a normal crop. Observations were recorded on five randomy selected plants in each entry replication wise for twelve characters viz., seed yield per plant (g), days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, number of clusters per plant, pods per cluster, seeds per pod, pod length (cm), 100-seed weight (g) and protein cotent (%). The analysis was carried out by using Mahalanobis' D^2 statistics. The grouping of the genotypes into clusters was made as per Tocher's method (Rao, 1952).

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TABLE 1

Composition of clusters and origin of blackgram genotypes.

Cluster	Genotypes	Origin
I	UPU 80-56, UPU 80-3-5, UPU 9-40-4, PDU 5, PDU 5, PDU 2, DPU 83-2, P 26, PU 19, PU 30, PDU 10.	Uttar Pradesh
	UG 370, UG 201, UG 378, UG 414, UG 298, UG 407, UG 301, UG 203.	Punjab
	GU 80-1, GU 87-7, GU 87-23.	Gujarat
	UH 80-4, UH 80-7, UH 81-7, UH 82-39, UH 84-39.	Hariyana
	JU 77-41, JU 78-3, JU 78-4, JU 78-27. No. 57, PG 16, RU 2	Maharashtra
	DU 5, DU 2	Bihar
	S 37, Samba 1	Jammu & Kashmir
	B 3-8-8	West Bengal
	NPRB 2	Tamil Nadu
II	GU 84-6, GU 84-8, GU 87-9, GU 87-11, GU 87-15, Zandewal	Gujarat
	L 35-5-2, UG 170, UG 170 UG 218	Punjab
	PDU 319, UPM 79-1-2	Uttar Pradesh
	DB 51	Rajasthan
	C 5-61-1	New Delhi
	KB 63	Tamil Nadu
III	P 16, T 9, UL 222, UPU 2-40-1	Uttar Pradesh
	A 5-31, GU 87-10, GU 87-17	Gujarat
	No 21	Maharashtra
	B 12-4-4	West Bengal
IV	S 10	Jammu & Kashmir
	Shapur 4	Gujarat
	PDU 12	Uttar Pradesh
V	TPU 4	Maharashtra
	PDU 401	Uttar Pradesh
VI	GU 84-2	Gujarat
VII	Valsad	Gujarat
VIII	GU 84-1	Gujarat

TABLE 2

Intra and Inter cluster distance (D^2) for 70 genotypes of blackgram.

Cluster	I	II	III	IV	V	VI	VII	VIII
I	4.96	57.26	32.06	44.64	49.64	84.45	83.07	76.34
II		5.06	38.51	33.20	33.95	38.45	38.65	39.03
III			4.67	32.39	34.77	64.65	63.24	57.89
IV				4.91	40.17	48.98	57.03	45.37
V					4.50	32.75	42.03	49.40
VI						00.00	29.85	31.63
VII							00.00	40.79
VIII								00.00

TABLE 3

Cluster means for different characters in black gram.

Cluster	Number of popu-lation	Seed yield per plant (g)	Days to 50 per cent flower-ing	Days to maturity	Plant height (cm)	Effec-tive number of branches per plant	Number of pods per plant	Number of cluster per plant	Number of pods per cluster	Number of seeds per pod	Pod length (cm)	100 seed weight	Protein content (%)
I	39	1.99	38.40	66.20	14.09	1.58	8.45	4.44	1.95	5.77	3.67	3.90	20.90
II	14	2.52	41.68	70.60	21.82	1.54	12.40	5.73	2.24	6.08	4.09	4.12	20.75
III	9	2.29	39.56	68.56	17.49	1.84	9.98	5.19	1.96	5.70	3.86	4.14	21.40
IV	3	2.88	38.67	68.22	17.26	1.51	13.63	6.30	2.18	5.76	3.55	3.94	19.48
V	2	3.37	43.17	72.50	21.37	2.22	8.22	5.37	1.56	5.85	3.84	4.30	18.39
VI	1	3.82	37.33	65.67	24.63	1.90	16.65	7.53	2.19	5.27	4.09	4.70	18.35
VII	1	3.60	41.67	70.33	27.40	1.53	11.50	5.93	1.94	6.70	4.30	4.50	17.95
VIII	1	3.03	37.33	65.67	23.40	1.77	13.60	10.07	1.35	5.67	3.99	4.20	18.13

RESULTS AND DISCUSSION

Analysis of variance revealed highly significant differences among the genotypes for all the characters studied, indicating existance of genetic diversity among the populations. All the 70 genotypes were grouped into 8 clusters on the basis of D^2 values (Table 1). Among these, cluster I was the largest having 39 genotypes representing Uttar Pradesh, Punjab, Gujarat, Haryana, Maharashtra, Bihar, Jammu and Kashmir, West Bengal and Tamil Nadu. Cluster II included 14 genotypes from six states. Cluster III was represented by 9 genotypes from four states. Cluster IV consisted of 3 genotypes from three states, cluster V possessed two genotypes consisting one each from Maharashtra and Uttar Pradesh. Cluster VI, VII and VIII had only one genotype originating from Gujarat. Thus, clustering pattern showed that genotypes of different states were clubbed into one cluster and also the genotypes of same state were grouped in different clusters. This indicated that there was no correspondence between genetic and geographical diversity. Similar findings were reported by Parameshwarappa *et al.* (1993) in blackgram.

Intra and inter-cluster average D^2 values (Table 2) indicated maximum distance between cluster I and VI (84.85) followed by cluster I and VII (83.07) and cluster I and VIII (76.34). The criterion used for selection of varieties as parent for hybridization using D^2 analysis is the inter-cluster distances. Those genotypes included in clusters with maximum inter-cluster distance are obviously genetically more divergent. Hence, it would be logical to incorporate genotypes from cluster I and VI, as parents in hybridization to obtain high heterotic combinations.

Cluster mean for different characters (Table 3) showed large differences for various traits. The cluster VI got desirable rating in respect of seed yield, days to 50% flowering, days to maturity, plant height, pods per plant and 100-seed weight whereas cluster VIII was good for earliness and cluster per plant, cluster VII for seeds per pod and pod length and cluster II, III and V for pods per cluster, protein content and branches per plant respectively. Therefore, inter crossing of such genotypes involved in these clusters would be useful for inducing variability in the respective traits. On the basis of genetic divergence and mean performance. The characters viz., plant height, pods per plant, clusters per plant, pod length and 1000-seed weight were found to be the main contributing characters for seed yield and thus are the basic attributes of plant architecture which need greater attention.

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