

ANALYSIS OF VARIABILITY AND DIVERSITY IN RICE FALLOW BLACKGRAM [*VIGNA MUNGO* (L.) HEPPER]

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ABSTRACT

Seventy four diverse genotypes of blackgram were studied under rice fallow condition for yield and its component traits. High genotypic variability was observed for branches per plant, clusters per plant, pods per plant, biological yield and seed yield along with high heritability and genetic advance, suggesting effective improvement of these characters through a simple selection programme. The genotypes were grouped into five clusters by Mahalanobis' D^2 analysis. Rice fallow cultivation restricted the fullest expression of genetic diversity among the genotypes. Based on cluster mean values, the genotypes, OBG 4 and KKB 98001 were identified as the suitable parents for hybridization programme. The characters, pods per plant, 100 seed weight and biological yield contributed more for genetic divergence.

Key words : Rice fallow blackgram, Variability, Heritability, Genetic gain, Diversity.

INTRODUCTION

Blackgram [*Vigna mungo* (L.) Hepper], an important pulse crop is widely grown in *kharif*, *rabi* and summer seasons in India. In the states of Tamil Nadu and Puducherry, this crop is mostly cultivated as rice fallow crop particularly in canal irrigated area. The yield level of this rice fallow blackgram is very low as it utilizes only the residual moisture and nutrients of previous rice crop. Breeding efforts undertaken to improve the productivity level of this rice fallow blackgram are negligible. Information on the genetic variability is an important prerequisite for realizing response to selection. The breeder should be able to distinguish the genetic and nongenetic component of variability. The choice of genetically diverse parents for hybridization are an important feature of crop improvement programme for getting desirable segregants. The D^2 analysis proposed by Mahalanobis (1936) is an effective tool in quantifying the degree of genetic divergence among

the parents. In the present investigation, variability and diversity were estimated in blackgram genotypes grown under rice fallow condition.

MATERIAL AND METHODS

The study was conducted with 74 genetically diverse genotypes of blackgram obtained from different sources. The experiment was laid out under rice fallow condition at Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal in randomized block design with three replications. Sowing was taken on the day of harvest of rice crop. With the residual moisture, the blackgram seeds were dibbled in lines. Two seeds were sown per hill and thinned to single plant per hill on 8th day after sowing. Irrigation and soil fertilization were not given during the entire crop growth period. Only foliar application of two per cent diammonium phosphate was given at two stages, one at initiation of flowering and second at 15 days after first application. Each genotype was sown in

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a single row of 3 m length with row to row and plant to plant spacing of 30 and 10 cm, respectively. Observations were recorded on five random competitive plants from each genotype for 10 quantitative traits (Table 1). The data obtained from 74 true breeding genotypes were subjected to various statistical analyses. The phenotypic and genotypic coefficient of variation (PCV and GCV), heritability in broad sense (h^2) and genetic advance as per cent of mean (GA) were computed as per the standard procedures. The data were subjected to Mahalanobis' D^2 diversity analysis. Clustering of genotypes was done following the Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

Analysis of variance revealed highly significant differences among the genotypes for all the traits studied. The 74 genotypes were evaluated for their performance under rice fallow cultivation. The top five ranking genotypes for each of the ten characters are listed in Table 1. It is observed that high performance for six out of ten characters studied was noticed in OBG 4, which recorded the highest values for seed yield, pods per cluster and pods per plant. Besides these, it ranked second for branches per plant and clusters per plant and fourth for harvest index. Hence, out of 74 genotypes evaluated, OBG 4 may be selected as the best genotype for seed yield and many important yield component characters under rice fallow cultivation. The next best genotype would be IU 31-13, which registered higher performance for seed yield, clusters per plant and biological yield. The genotype, OBG 16 also exhibited good performance by recording higher values for seed yield and biological yield. The above three genotypes are identified as suitable for rice fallow cultivation.

Variability parameters worked out for the ten traits are presented in Table 2. As GCV represents the heritable component variation and PCV includes the effect of environment also, it would be more appropriate to use GCV for comparing variability of different characters (Johnson *et al.*, 1955). In the

Table 1 : First five ranking genotypes for ten characters in blackgram under rice fallow cultivation.

Rank	Branches per plant	Clusters per plant	Pods per cluster	Pods per plant	Pod length (cm)	Seeds per pod	100 Seed weight (g)	Harvest index	Biological yield (g)	Seed yield (g)
1	Ramnadu (13.33)	LBG 14 (9.99)	OBG 4 (3.27)	OBG 4 (28.64)	OBG 11 (5.72)	ADT 4 (8.02)	KKB 98001 (6.01)	ADB 2109 (0.46)	LBG 709 (16.19)	OBG 4 (6.08)
2	OBG 4 (13.01)	OBG 4 (9.35)	VBG 67 (3.20)	LBG 402 (22.42)	VBG 42 (5.65)	ADT 5 (7.77)	VBG 52 (5.60)	LBG 17 (0.45)	KBG 98005 (14.08)	APK 1 (5.81)
3	ADB 3268 (11.34)	IU 31-13 (8.30)	VBG 55 (3.13)	VBG 55 (21.68)	ADT 5 (5.51)	VBN 1 (7.76)	VBG 49 (5.31)	VBG 57 (0.45)	IU 31-13 (14.05)	IU 31-13 (5.56)
4	DU 94-6 (11.05)	Ramnadu (8.27)	LBG 402 (3.12)	DU 94-6 (21.05)	KKB 98001 (5.45)	VBG 42 (7.70)	LBG 20 (5.29)	OBG 4 (0.44)	OBG 16 (13.92)	OBG 16 (5.40)
5	T 9 (11.03)	LBG 17 (7.96)	VBG 23 (3.06)	VBG 33 (20.73)	OBG 8 (5.39)	Tenkasi 2 (7.36)	PDU 1 (5.22)	ADB 2045 (0.44)	LBG 402 (13.90)	ADB 2003 (5.38)
Mean	7.84	6.13	2.73	16.19	4.77	6.30	4.49	0.36	10.22	3.64
CD (5%)	0.67	0.88	0.25	0.64	0.36	0.46	0.11	0.01	0.77	0.39

Table 2 : Variability parameters for ten characters in under rice fallow blackgram

Character	PCV	GCV	h ²	GA
Branches per plant	25.41	24.83	95.46	50.02
Clusters per plant	23.07	20.96	83.37	33.12
Pods per cluster	11.02	9.33	71.67	16.29
Pods per plant	21.82	21.67	98.71	44.41
Pod length	9.00	7.64	72.06	13.37
Seeds per pod	12.02	11.08	85.01	21.06
100 Seed weight	10.74	10.63	97.82	21.68
Harvest index	14.77	14.49	96.15	29.30
Biological yield	23.27	22.77	95.77	45.96
Seed yield	24.99	23.05	92.60	47.73

present study, branches per plant, clusters per plant, pods per plant, biological yield and seed yield showed high GCV estimates. Higher GCV for these traits were also reported by Savithamma *et al.* (1999) and Kumar *et al.* (2000). Hence, selection for these characters having high genetic variability would facilitate successful isolation of desirable types for these characters.

High heritability combined with high genetic advance would indicate the predominance of additive gene action on the trait and as such that trait is likely to respond effectively for phenotypic selection. In the present investigation, all the traits except pods per cluster and pod length were found to exhibit high heritability coupled with high genetic advance, indicating the predominance of additive gene action on the characters, branches per plant, clusters per plant, pods per plant, seeds per pod, 100 seed weight, harvest index, biological yield and seed yield and these characters would respond effectively for phenotypic selection. These results are in conformity with that of Patil *et al.* (1999) and Kumar *et al.* (2000).

Burton (1952) suggested that GCV together with heritability and genetic advance would give the best picture of the extent of advance expected by selection. In the present study also the three parameters were considered together for the characters under study which indicated that

branches per plant, clusters per plant, pods per plant, biological yield and seed yield recorded high genetic variability along with high heritability and genetic advance. It revealed the greater scope for improving these characters by simple phenotypic selection in rice fallow blackgram.

The D² analysis grouped 74 genotypes studied into five clusters (Table 3). The clustering pattern revealed that the cluster I and II were found to include genotypes from different states, indicating that genetic diversity is not related to geographical diversity. Such a grouping of genotypes of diverse geographical regions in one cluster was reported by Singh (2001) and Chauhan *et al.* (2008). This may be due to the fact that the unidirectional selection for a particular trait specifically yield practiced in several places results in aggregation of genotypes irrespective of their geographical origin. All the clusters, except V had the genotypes from Tamil Nadu, revealing that variable environment within the same region could have caused such diversity. Such a wide diversity among the genotypes of same geographic region is desirable for selecting parents with similar adaptability for pedigree method of breeding.

Sixty three out of seventy four, representing 85% of the total genotypes studied were grouped together in the cluster I. This suggests that under rice fallow cultivation, the expression of diversity

Table 3 : Clustering pattern of seventy four genotypes of blackgram under rice fallow condition.

Table 4 : Intercluster divergence (D value) among the five clusters

Cluster	II	III	IV	V
I	24.77	24.54	29.33	35.45
II		25.41	37.57	48.99
III			42.76	50.06
IV				35.92

among different genotypes is restricted in blackgram. The absence of tillage, irrigation and soil fertilization under rice fallow cultivation might have provided an environment not conducive for better expression of potential genetic diversity among the genotypes.

The extent of diversity among the genotypes may be understood from the genetic distance between clusters. Cluster V, which included only one type OBG 4 was found to be highly divergent from other clusters (Table 4). Similarly, cluster IV which also had only one type KKB 98001 had high divergence with clusters II, III and V. However, the highest intercluster divergence was recorded between cluster V and III. Hence, genotype included

in cluster V can be used for crossing with those of the other clusters, in particular with clusters III and II to generate variability.

The cluster mean values were used for selecting parents for hybridization. The cluster V (OBG 4) recorded the highest mean values for most of the characters under study viz. seed yield, branches per plant, clusters per plant, pods per cluster, pods per plant, harvest index and biological yield (Table 5). Another monogenotypic cluster IV (KKB 98001) exhibited maximum mean values for per pod and 100 seed weight. These two genotypes could be used as parents for hybridization programme for developing superior variety(s) for rice fallow cultivation.

The study was also utilized for identifying characters that contributed more for total divergence. The character pods per plant followed by 100 seed weight and biological yield made high contribution, accounting for 81.29% of total genetic divergence (Table 3). This indicates that these traits were responsible for differentiating the genotypes

Table 5. Cluster mean values and contribution of traits for divergence

grown under rice fallow condition into different clusters. Thus, these characters may be very useful for choosing diverse parents for hybridization programme for improving rice fallow blackgram.

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Cluster/ Character	Branches per plant	Clusters per plant	Pods per cluster	Pods per plant	Pod length (cm)	Seeds per pod	1 se we (
I	7.93	6.16	2.75	16.50	4.76	6.29	4
II	7.59	5.47	2.45	12.52	4.79	6.32	4
III	3.06	5.10	2.60	10.67	4.58	5.83	4
IV	8.37	7.33	2.93	20.46	5.45	7.04	6
V	13.01	9.35	3.26	28.64	4.74	6.69	4
Contribution towards divergence (%)	8.95	0.29	0.02	38.80	0.11	2.51	30