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REGULAR ARTICLE

STUDIES ON GENETIC DIVERSITY IN *VIGNA MUNGO* L. HEPPER IN YMV HOTSPOT

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ABSTRACT

The present investigation was conducted to examine the 41 blackgram genotypes along with one check (T-9) to study the genetic diversity. Analysis of variance showed highly significant differences among 41blackgram genotypes for 9 quantitative characters studied. Maximum genotypic and phenotypic variance was recorded for percentage of disease infection, single plant seed yield, and number of pods per plant. Minimum GCV and PCV were recorded for pod length, days to 50% flowering, number of seeds per pod. High heritability was recorded for percentage of disease infection, single plant seed yield, and number of pods per plant. High heritability coupled with high genetic advance as percent of mean was recorded for percentage of disease infection, single plant seed yield. Genetic diversity estimated in 41 blackgram genotypes using Mahalanobis's D^2statistic. Forty one genotypes were grouped into seven clusters by Tocher method (Mahalanobis Euclidean Distance) cluster analysis. The maximum inter-cluster distance was observed between cluster VI and cluster VII and maximum intra-cluster distance was observed in cluster VI. Cluster VII showed maximum cluster mean value for seed yield per plant. Among all the characters, seed yield per plant and percentage of disease infection contributes maximum.

Keywords: Blackgram, Genetic diversity, D^2statistic and cluster analysis

INTRODUCTION

Blackgram (*Vigna mungo* L. *Hepper*) belong to family leguminoseae with chromosome number 2n=2x=22. It is a short duration, self-pollinated, diploid grain legume (2n = 22) with a small genome size estimated to be 0.56pg/1C (574 Mbp) [1]. India, blackgram contribute 10 per cent of total pulses production [2-4]. Blackgram is a cheap source of dietary protein (24%). It also contributes 76% carbohydrate, 3-5% Fibre, 1.74% Fat and a major portion of lysine in the vegetarian diet. It is the richest sources of phosphoric acid being 5-10 times richer than other crops. Many factors are responsible for the low productivity of blackgram ranging from plant ideotype to various biotic and abiotic stresses [5]. The selection pressure in case of pulses have been focused on the adaptation to both biotic and abiotic stresses. Pulses have been traditionally cultivated in marginal lands with least inputs [6]. Hence, genetic variability for yield contributing characters were lost during the course of evolution. Yellow Mosaic Virus (YMV) belongs to the genus Begomo virus and is transmitted by the vector whitefly, *Bemisia tabaci* [7]. An assessment of the genetic diversity of pulses is an important step in a programme to improve crop yield. Hence proper estimate of nature and magnitude of diversity in a crop is essential to understand the extent of variation available for yield and its component traits. Besides, it could be of interest to know the magnitude of variation due to heritable component, which in turn would be a guide for selection for the improvement of a population.

MATERIALS AND METHODS

The study was conducted at Panmozhi village of Tirunelveli District, Tamil Nadu during summer 2017. Fourty one genotypes of urd bean obtained from various geographical locations. The data were recorded on five randomly selected plants of each replication for all character but in case of days to 50% flowering the observations were recorded in all plants the rows. Other traits were taken during pre harvest namely, Days to 50% flowering, Plant height (cm), Number of primary branches per plant, Number of clusters per plant, Number of pods per plant, No. Of seeds per pod, Pod length (cm), percentage of diseases infection, and Seed yield per plant (g). Mean values were computed and data were analyzed for analysis of variance as suggested Fisher [8], Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) as per Burton [9], Heritability in broad sense as per Lush [10] and Burton and Devane [11], Genetic advance as per Lush [12] and Johnson *et al.* [13] and Genetic divergence as per Mahalanobis [14].

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RESULTS AND DISCUSSION

The Genetic diversity based on Mahalanobis D2 statistic grouped the 41 genotypes into seven clusters by Non-Hierarchical Euclidean cluster analysis. Maximum of 22 genotypes were found in Cluster VIII (AUBG 6, AUBG 7, AUBG 8, AUBG10, AUBG11, AUBG13, AUBG14,AUBG15, AUBG16, AUBG17, AUBG19, AUBG20, AUBG22, AUBG24,AUBG27 AUBG29, AUBG30, AUBG31, AUBG32, AUBG34, AUBG36, AUBG37) followed by clusters I with six genotypes (AUBG1, AUBG2, AUBG3, AUBG4, AUBG26, AUBG35) and cluster VII with three genotypes (AUBG5, AUBG28, AUBG40). The cluster II (AUBG18, AUBG33), cluster III (AUBG39, AUBG41), cluster IV (AUBG21, AUBG23) and cluster V (AUBG12, AUBG9) had two genotypes each. The intra-cluster (D^2) distance ranged from 44.94 to 4302.98. Cluster II showed minimum intra cluster distance (44.94) and Maximum Intra cluster distance was exhibited by cluster VII (4302.98). Maximum Inter-cluster distance (D2) was found between cluster VI and VII (5575.09). Minimum inter-cluster distance was found between Cluster IV and V (141.23). The results indicated that there is close genetic similarity between the cultivars of blackgram based on the study. The highest contribution of characters in the manifestation of genetic divergence was exhibited by seed yield per plant (53.20%) followed percentage of disease infection (44.24%), days to 50% flowering (0.60%) suggesting scope for improvement in these characters.

The inter-cluster distance was observed between clusters VI and VII (D2 =5575.09) indicating high divergence of genotypes included in these two clusters. The lowest inter-cluster distance was observed between IV and V (D2 =141.23) indicating that genotypes included in them were closely related. According to Rahman *et al.,* [15], crossing between highly divergent genotypes would produce a broad spectrum of variability. Thus, selection of genotypes from these clusters for a crossing programme will produce desirable transgressive segregants. The genotypes of cluster VII had recorded the highest seed yield per plant-1 while the genotypes of cluster II recorded the lowest seed yield. The genotypes of cluster III had more number of pods per plant-1. Cluster VI included the genotypes having longest pod length. The promising genotypes viz., with high mean values for above traits from divergent clusters were AUBG 30, AUBG3, AUBG 4, AUBG 13, and AUBG 25 may be selected as parents for hybridization programme to develop high yielding blackgram varieties. Among all the characters, grain yield plant-1 (53.20%) contributed the maximum towards genetic divergence followed by number of seed per pods (0.48%) and plant height (0.73%). The maximum contribution of seed yield per plant-1 and number of seed per pods in blackgram were reported by Arivoli *et al.* [16] which corroborated the results of the present study. Therefore, the genotypes from the clusters having maximum inter-cluster distance can be selected to yield superior segregants [17,18]. In the present study, genotypes from cluster I, VII and VIII can be selected for crossing programme to get desirable transgressive segregants. The other genotypes viz., AUBG 3, AUBG 40 and AUBG30 were also found superior for yield and most of the component characters studied. Hence, these genotypes were selected for further improvement through hybridization and selection.

The results indicated that there is close genetic similarity between the cultivars of blackgram based on the study. Whereas the percent contribution of thirteen characters towards total genetic divergence has the highest contribution in the manifestation of genetic divergence was exhibited by seed yield per plant (53.20%) followed by percentage of disease infection (44.14%).

On the basis of results of the experiment it can be conclude that, the genotypes AUBG-3, followed by AUBG-40 were identified as the genotypes for high seed yield at the hot spot region. The present investigation registered that high seed yield along with high genetic advance as % of mean should be given top priority for effective selection. The present investigation further revealed that Cluster VIII and Cluster V were the most divergent clusters. Therefore, genotypes present in these clusters are suggested to provide broad spectrum variability in segregating generations. Our results are in agreement with previous reports [19-22].

It is observed that no cluster contained at least one genotype with all the desirable traits which ruled out the possibility of selecting directly one genotype for immediate use therefore hybridization between the selected genotype from divergent clusters is essential to judiciously combine all the targeted traits. The genotype from the cluster having high mean value may be used as parent in future hybridization programme.

Table 1: Analysis of variance from 9 different quantitative characters in 41 genotypes of blackgram

S. No.	Character	Mean sum of square		
		Replication df=2	Treatment df=40	Error df=80
1	Days to 50 % flowering	40.92	15.69**	0.59
2	Plant height (cm)	37.66	138.45**	7.02
3	Number of primary branches	5.09	2.24**	1.31
4	Number of clusters per plant	11.7	6.91**	2.77
5	Number of pods per plant	44.47	210.51**	3.83
6	Pod length (cm)	0.28	0.26**	0.17
7	Number of seeds per pod	0.13	1.06**	0.08
8	% of disease infection	76.77	1013.44**	0.34
9	Single plant seed yield (g)	4.03	0.34**	1.65

Table 2: Magnitude of variability and estimates of heritability and genetic advance for various characters in 41 blackgram genotypes

S. No.	Characters	GCV (%)	PCV (%)	ECV (%)	Hertibility	GA as percent of mean
1.	Days to 50 % flowering	6.07	6.42	2.09	89%	11.82
2.	Plant height (cm)	18.55	19.98	7.42	86%	35.48
3.	Number of primary branches	9.09	20.79	18.69	19%	8.20
4.	Number of clusters per plant	13.74	23.85	19.49	33%	16.32
5.	Number of pods per plant	28.19	28.97	6.65	94%	56.53
6.	Pod length (cm)	3.80	9.68	8.90	15%	3.07
7.	Number of seeds per pod	8.40	939	4.19	80%	15.49
8.	% of disease infection	56.36	56.39	1.78	99%	49.05
9.	Single plant seed yield (g)	34.00	34.57	6.25	96%	45.89

Table 3: Distribution of 41 blackgram genotypes into different clusters

Clusters	Number of genotypes	Name of genotypes
I	6	AUBG 1,AUBG 2,AUBU 3,AUBG 4,AUBG 26,AUBG 35
II	2	AUBG 18,AUBG 33
III	2	AUBG 39,AUBG 41
IV	2	AUBG 21,AUBG 23
V	2	AUBG 9,AUBG 12
VI	2	AUBG 25,AUBG 38
VII	3	AUBG 5,AUBG 28, AUBG 40
VIII	22	AUBG 6,AUBG 7,AUBG 8,AUBG 11,AUBG 13,AUBG 14, AUBG 15,AUBG 16,AUBG 17,AUBG 19, AUBG 20,AUBG 22,AUBG 24,AUBG 27,AUBG 29,AUBG 30,AUBG 31,AUBG 32,AUBG34,AUBG 36,AUBG 37

Table 4: Inter-cluster and intra-cluster (diagonal) average of D^2 (parenthesis) and D values for 41 blackgram genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII
I	35.055 (1228.882)	24.753 (612.694)	35.023 (1226.638)	28.717 (824.684)	34.330 (1178.549)	25.055 (627.729)	70.575 (4980.806)	48.061 (2309.896)
II		6.704 (44.946)	25.084 (629.211)	18.824 (354.334)	26.122 (682.357)	16.338 (266.922)	66.850 (4468.932)	42.675 (1821.156)
III			6.901 (47.627)	17.269 (298.216)	13.282 (176.418)	36.099 (1303.138)	49.418 (2442.104)	42.506 (1806.798)
IV				7.494 (56.162)	11.884 (141.230)	26.748 (715.474)	56.104 (3147.659)	41.034 (1683.823)
V					7.704 (59.348)	35.028 (1226.946)	50.168 (2516.878)	42.309 (1790.015)
VI						8.282 (68.598)	74.667 (5575.094)	46.479 (2160.256)
VII							65.597 (4302.985)	69.286 (4800.584)
VIII								57.858 (3347.509)

Table 5: Cluster means of 41 blackgram genotypes for various characters

Clusters	Days to 50% flowering	Plant height (cm)	Number of primary branches	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	% of disease infection	Single plant seed yield (g)
I	37.325	37.128	5.906	8.167	29.239	4.740	6.800	25.389	22.556
II	36.712	39.350	6.867	10.083	31.800	4.835	6.300	25.175	12.077
III	39.178	31.483	5.983	9.283	38.933	4.632	7.100	37.175	15.752
IV	35.652	39.383	6.517	7.183	17.033	5.092	7.450	34.252	18.682
V	37.345	30.083	5.667	10.367	18.017	4.755	6.517	38.868	19.360
VI	35.520	30.483	6.717	7.417	29.700	4.347	6.900	20.633	24.028
VII	37.276	40.122	6.422	10.756	37.522	4.699	7.100	54.041	27.821
VIII	36.803	35.365	6.039	8.198	29.452	4.659	6.776	32.277	19.940

Table 6: Contribution of 9 different characters to genetic divergence

S. No.	Characters	Contribution (%)
1	Days to 50%Flowering	0.609
2	Plant Height	0.731
3	Number of Primary Branches	0.112
4	Number of Clusters per Plant	0.097
5	Number of Pods per Plant	0.487
6	Pod length	0.122
7	Number of Seeds per Pod	0.487
8	Percentage of disease infection	44.146
9	Single plant seed yield	53.204

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