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Identification of Elite Genotypes of Blackgram (*Vigna Mungo* (L.) Hepper)

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ABSTRACT

Field experiment was conducted to study variability and genetic diversity among 32 blackgram genotypes for selection of elite genotypes suited to Allahabad. Analysis of variance indicated the presence of substantial genetic variability among genotypes. Higher magnitude of phenotypic coefficient of variation (PCV) was recorded for harvest index followed by number of pods per plant and biological yield. High genotypic coefficient of variation (GCV) was recorded for harvest index, number of pods per plant and biological yield. High heritability coupled with high genetic advance as per cent of mean was recorded for number of pods per plant, biological yield, harvest index and number of clusters per plant. Thirty two genotypes were grouped into six clusters, indicating a wide range of variation among the genotypes studied. The cluster IV was the largest consisting of 11 genotypes, followed by cluster I and cluster III with nine and four genotypes respectively, while cluster II and IV with three genotypes each. Inter cluster distance (D^2) was found maximum between cluster III and V (6045.625). Hybridization between the desirable genotypes from these divergent clusters *i.e.,* cluster III and V may produce transgrassive segregants in blackgram.

Key words : Elite genotypes,Genetic advance, Genetic diversity, Genetic variability, Heritability.

Blackgram (*Vigna mungo* (L.) Hepper) is one of the important pulse crops of India. It is grown in an area of 1.92 million hectares with an annual production of 1.11million tones with productivity of 578 kg ha^{-1} (Anonymous, 2010). It is a short duration crop of about 90 days. These days in india, pulses production is less and demand is very high. To meet the higher demand identification and cultivation of high yielding genotypes is prime important. Study of genetic variability and diversity plays an important role in identification of better genotypes. Selection of diverse parents in breeding programme helps in isolation of superior recombinants. D^2 analysis, cluster analysis, principal component analysis and metroglyph analysis have been shown to be useful in selecting genetically distant parents for the hybridisation programmes to develop new varieties with distinguishable characters.

MATERIAL AND METHODS

The experimental material comprised of 32 genotypes of blackgram, collected from Indian Institute of Pulses Research, Kanpur. Experiment was conducted at Field Experimentation Center, Department of Genetics and Plant Breeding Allahabad during *kharif* 2009. The blackgram genotypes (UG 27, IPU 99-31, SPS35, T9, IC16-54, B.LOCAL, PU 19, STY 2468, IPU 99-236, TPU 4, TAU 94-2, TPU 99-167, TPU 94-1, GP 98, DPU 88-31, T 65, U 8-10, UH 86-5, PDU 103, KARS 114, PU 232, IPU 02-43, NSM 74, VKG 30/28, PLU 384, NO.11/13, PLU 1077, NP 3, UH 86-32, LBG 623, PLU 302 and IPU 2002-1) were sown in randomized block design with three replications. Test plots were managed following the recommended site specific standard agronomic practices. The plot size was $2m^2$ and spacing between rows and plants was 30 and 10 cm, respectively. Observations were recorded on five randomly selected plants from each plot for 10 characters *viz*., days to 50% flowering, plant height (cm), number of primary branches $plant^{-1}$, number of clusters $plant^{-1}$, number of pods $plant^{-1}$, days to maturity, biological yield (g), harvest index, 100 seed weight (g) and seed yield $plant^{-1}$ (g). Means were computed and data were subjected to Analysis for variance (Fisher, 1936), phenotypic and genotypic coefficients of variation (Burton, 1952) and heritability (broad sense) as the ratio of genotypic to phenotypic variance (Lush, 1946). The procedure of Johnson *et al.* (1955) was followed for calculating the expected genetic advance and genetic advance as per cent of mean. The mean data was also used for

Table 1. Analysis of variance for 10 different quantitative characters in blackgram

S. No.	Characters	Mean sum of square		
		Replication	Treatment	Error
		d. f.=2	d. f.= 31	d. f.= 62
1.	Days to 50% flowering	7.198	15.295**	2.111
2.	Plant height	0.717	400.318**	3.551
3.	No. of branches plant^{-1}	0.174	14.304**	0.198
4.	No. of clusters plant^{-1}	1.588	83.546**	1.804
5.	No. of pods plant^{-1}	2.822	891.572**	0.888
6.	Days to maturity	5.323	36.267**	4.387
7.	Biological yield	0.130	271.269**	0.545
8.	Harvest index	8.363	755.566**	5.679
9.	100 seed weight	0.152	0.407**	0.012
10.	Seed yield plant^{-1}	0.278	24.421**	0.198

significant at 1% level of significance

Table 2. Estimates of genetic variability parameters for 10 different characters in blackgram.

S. No.	Characters	Genetic parameters				
		Phenotypic coefficient of variation	Genotypic coefficient of variation	Heritability (%)	Genetic advance	GA as % of Mean
1.	Days to 50% flowering	4.67	3.84	67.50	3.55	6.50
2.	Plant height	23.23	22.93	97.40	23.38	46.61
3.	No. of branches plant^{-1}	16.01	15.68	95.90	4.38	31.65
4.	No. of clusters plant^{-1}	27.46	26.59	93.80	10.41	53.05
5.	No. of pods plant^{-1}	36.37	36.31	99.70	35.44	74.69
6.	Days to maturity	5.18	4.36	70.80	5.65	7.56
7.	Biological yield	29.85	29.76	99.40	19.51	61.12
8.	Harvest index	37.03	36.61	97.80	32.20	74.59
9.	100 seed weight	8.82	8.45	91.70	0.72	16.67
10.	Seed yield plant^{-1}	22.50	22.24	97.60	5.78	45.26

estimating genetic distance among the genotypes using D^2 statistics (Mahalanobis, 1936) and the genotypes were formed into different clusters using Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

The analysis of variance indicated the presence of significant differences among the genotypes for all characters under study (Table1). Estimates of genetic variability and genetic parameters for different characters are presented in Table 2. Higher magnitude of phenotypic coefficient of variation (PCV) was recorded for harvest index (37.03), followed by number of pods per plant (36.37), biological yield (29.85) and number of clusters per plant (27.46). However, plant height (23.23), seed yield per plant (22.50) and number of primary branches per plant (16.01) exhibited moderate values of PCV, while low values were observed for days to maturity (5.18) and days to 50% flowering (4.67). High magnitude of genotypic coefficients of variation (GCV) was recorded for harvest index (36.61), followed by number of pods per plant (36.31), biological yield (29.76) and number of clusters per plant (26.59). However, plant height (22.93), seed yield per plant (22.24) and number of primary branches per plant (18.68) exhibited moderate values of GCV, while low values were observed for days to maturity (4.36) and days to 50% flowering (4.36). Bakshi and Ghoshdastidar (2004) reported higher phenotypic and genotypic coefficients of variation for number of pods per plant and seed yield per plant.

In the present study, highest estimates of heritability were observed for number of pods per plant (99.7) followed by biological yield (99.4), harvest index (97.8), seed yield per plant (97.6), plant height (97.4), number of primary branches per plant (95.9), number of clusters per plant (93.8) and 100 seed weight (91.7). Days to maturity (70.8), and days to 50% flowering (67.5) recorded moderate heritability. The above results are in accordance with the findings of Isaacs *et al*. (2000). Therefore, selection can be practiced based on these characters as the additive gene action is predominant in their expression. The highest genetic advance was recorded for number of pods per plant (35.44) followed by harvest index (32.20) and plant height (23.38). However, moderate value of genetic advance was recorded for biological yield (19.51) and number of clusters per plant (10.41), while lower values of genetic advance were observed for days to 50% flowering (3.55) and 100 seed weight (0.72).

In the present study, high heritability coupled with high genetic advance as per cent of mean recorded for number of pods per plant (99.7, 74.69), biological yield (99.4, 61.12), harvest index (97.8, 74.59), number of clusters per plant (93.8, 53.05). Bakshi and Ghoshdastidar (2004) reported high heritability coupled with high genetic advance as per cent of mean for number of pods per plant and seed yield per plant. High heritability with high genetic advance may be attributed to the action of additive genes. These characters also recorded high GCV. Therefore, phenotypic selection of these characters would be effective for yield improvement (Sharma *et al*., 2006).

Thirty two genotypes were grouped into six clusters using Mahalanobis D^2 statistics and Tocher's method indicating, a wide range of variation among the genotypes studied (Table 3). The cluster IV was the largest consisting 11 genotypes followed by clusters I and III with nine and four genotypes, respectively and clusters II and IV with three genotypes each. The pattern of group constellation proved the existence of significant amount of variability. From the clustering pattern, it was found that the genotypes collected from different regions were independent of their genetic origin (Lavanya *et al.,* 2007). Hence, the genotypes studied are reliable enough for hybridization and selection. The present study also suggested that there is no relationship between geographic and genetic diversity as genotypes chosen from different eco-geographical regions are found to be in different clusters.

Intra (diagonal) and inter-cluster average distances (D^2) in blackgram are presented in Table 4. The intra-cluster distance was registered maximum for cluster VI (1306.324) followed by cluster IV (558.451), minimum intra cluster distance was recorded for cluster I (273.012) (Table 4). Inter cluster distances (D^2) was found maximum between cluster III and cluster V (6045.625) followed by cluster II and cluster V (4941.061) and cluster II and VI (4671.772).

Mean performance of different clusters for different characters in blackgram are presented in Table 5. Cluster I recorded moderate mean values for all the characters under study. Clusters II registered high mean value for harvest index (72.248) and lower mean value for 100 seed weight (4.043). Cluster III showed high mean value for the characters, number of clusters per plant (23.067) and number of pods per plant (75.098). Cluster IV recorded moderate mean values for all the characters studied. Cluster V showed lowest mean value *i.e.,* earliness for days to maturity (72.111). Cluster VI recorded high mean value for the characters number of branches per plant (15.917), 100 seed weight (4.930) and seed yield per plant (18.700).

Table 3. Distribution of 32 genotypes of blackgram in different clusters D^2 analyses

Cluster No.	Genotypes included	No. of genotypes
1	UG 27, TPU 4, B.LOCAL, No.11/32, UH 86-5, T 65, IPU 99-31, IC 16-54 and KARS 114	9
2	SPS 5, IPU 99-167, and IPU 99-236	3
3	DPU 88-31, PLU 384, IPU 2002-1 and T 9	4
4	PU 19, IPU 02-43, PDU 103, UH 86-32,U 8-10, VKG 30/28, STY 2468, PU 232,TAU 94-1, PLU 302 and TAU 94-2	11
5	GP 98, NSM 74 and LBG 623	3
6	PLU 1077,and NP 3	2

Table 4. Intra (diagonal) and inter-cluster average distances (D^2) in blackgram

Cluster No.	I	II	III	IV	V	VI
I	273.012 (16.523)	965.320 (31.069)	831.205 (28.205)	1005.995 (31.717)	3053.168 (46.763)	2186.794 (46.763)
II		486.555 (22.057)	1156.206 (34.003)	1852.315 (43.038)	4941.061 (70.293)	4671.772 (68.350)
III			286.623 (16.929)	2699.550 (51.957)	6045.625 (77.753)	3616.307 (60.135)
IV				558.451 (23.631)	1344.644 (36.669)	2428.70 (49.281)
V					386.790 (19.666)	2554.590 (50.542)
VI						1306.324 (36.143)

D values presented in parenthesis

Table 5. Clusters mean performance for different characters in blackgram

Cluster No.	Days to 50% flowering	Plant height	Primary branches plant^{-1}	Clusters plant^{-1}	Pods plant^{-1}	Days to maturity	Biological yield	Harvest index	100 seed weight	Seed yield plant^{-1}
I	54.056	53.789	13.972	21.844	51.853	73.889	33.517	35.177	4.257	11.667
II	54.500	57.442	12.825	23.067	75.098	75.250	33.850	36.379	4.337	12.217
III	54.292	39.754	13.654	16.908	33.813	74.125	25.975	51.605	4.231	12.983
IV	54.417	45.175	12.717	11.050	22.450	72.833	42.658	38.338	4.599	15.875
V	55.556	49.267	14.900	22.000	59.089	77.333	16.644	72.248	4.043	11.822
VI	61.000	83.267	18.667	28.267	58.200	87.333	55.467	31.007	4.740	17.200

From the present experiment, it can be concluded that the characters having high genotypic and phenotypic coefficients of variation, along with high heritability and genetic advance as per cent of mean (harvest index and number of pods per plant) may be used as indices during selection. Hybridization between the elite genotypes from divergent clusters *i.e.,* cluster III (T 9 and DPU 88-31) and cluster V (LBG 623 and NSM 74) may produce transgressive segregants in blackgram. The genotypes included in the diverse clusters can be used as promising parents in intermating for obtaining high heterotic response and better segregants (Singh, 2001).

LITERATURE CITED

Anonymous 2010. Agricultural Ministry of India, NB Research.

Bakshi A and Ghoshdastidar K K 2004. Studies on genetic variability in blackgram (Vigna mungo (L.) Hepper). *Indian Agriculturist* 48 (3/4): 149-152.

Burton F W 1952. Quantitative inheritance in grasses. Proceeding of 6th International Grassland Congress 1: 222-283.

Fisher R A 1936. Statistical Methods for Research Workers, ISBN-0-05-002170-2.

Isaacs S M, Jebaraj S and Ganesh S K 2000. Estimates of genetic variability and heritability in blackgram (*Vigna mungo* (L.) Hepper). *Research on Crops* 1(1): 37 – 39.

Johnson H W, Robison H F and Comstock R E 1955. Estimates of genetic and environmental variability in soybean and their implications in selection. *Agronomy Journal* 47: 314-318.

Lush J L 1949. Heritability and qualitative traits in farm animals. Proceedings of 8th International Genetic Congress, Heriditas (Suppl.) 336-357.

Lavanya G R, Toms B and Suresh B G 2007. Evaluation of mungbean germplasm for genetic diversity. *Journal of Plant Genetic Resources* 20(3): 240-242.

Mahalonobis P C 1936. On the generalized distance in statistics. *Proceedings of National Institution of Sciences* 2: 49-55.

Rao C R 1952. The utilization of multiple measurement of problems in biological classification. **Journal of Rural Statistics Society** 10(13): 159 – 203.

Sharma D K, Billore M and Shrivastava M 2006. Estimation of variability parameters in blackgram (*Vigna mungo* L. Hepper) in western Madhya Pradesh. *Biosciences, Biotechnology Research Asia* 3(1a): 283 – 284.

Singh B 2001. Genetic divergence in blackgram (*Vigna mungo* L. Hepper). *Legume Research* 24(1): 54 – 56.

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