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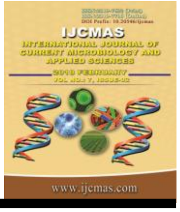

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Variability, Heritability and Genetic Advance for Quantitative Characters in Rice Fallow Blackgram [*Vigna mungo* (L.) Hepper]

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ABSTRACT

Keywords

Variability, Heritability, Genetic advance, Blackgram and quantitative traits

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An investigation was carried out with thirty six blackgram genotypes in rice fallow situation, to assess the variability, heritability and genetic advance for yield and yield attributing characters. The results revealed that high PCV and GCV for number of clusters per plant and high PCV coupled with moderate GCV for number of branches per plant and grain yield per plant exhibiting wider range of variability. Whereas, number of pods per plant and 100 seed weight recorded moderate variability. High heritability coupled with high genetic advance as per cent of mean was observed for number of branches per plant, number of clusters per plant, number of pods per plant, 100 seed weight and grain yield per plant indicating that the heritability was due to additive gene effects which may be exploited through breeding methods involving simple selection like pedigree method, mass selection, ear-to-row methods for the improvement of these traits.

Introduction

Blackgram [*Vigna mungo* (L.) Hepper], was popularly known as Urdbean, urid or mash. It was domesticated from *V. mungo var. silvestris* (Lukoki *et al.,* 1980). Blackgram is one of the most ancient and important legume crop of India, the primary centre of origin of Urdbean and about 70% of the world's Urdbean production and contributes 70% of world's total production (Priyanka *et al.*, 2016). Urdbean consists of good nutritional values of high seed protein (25-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins. Hence, it is usually known as "poor man's meat" particularly in the vegetarian population of the Indian subcontinent (Chubatemsu and Malini, 2017). It has the ability to restore the soil fertility through symbiotic nitrogen fixation and suitable for various crop rotation practices and well suited in both dry and irrigated conditions. This is one of the most important short duration legume crop utilized in the food, fodder, soil conservation, integrated farming systems, reclaiming of degraded pastures and symbiotic nitrogen fixation. It is essential to understand the genetic architecture and nature of gene action governing yield and its component traits for increasing the yield per unit area. Yield is the resultant product of various morphological, physiological and biological components. The yield of pulses in general and black gram in particular remains at low level and there is a need for improvement.

The success of any breeding programme depends upon the quantum of genetic variability present in the population. Wider range of genetic variability helps in selecting desired genotypes. Variability is one such estimate provides a clear-cut idea about a particular traits on which greater emphasize should be given during selection. In addition to the genetic variability, knowledge on heritability and genetic advance helps the breeder to employ the suitable breeding strategy. Heritability of a character provides an idea of the extent of genetic control for the expression of a particular character (Priyanka *et al.*, 2016). Moreover, heritability serves as a guide to the reliability of phenotypic variability in the selection program and hence determines its success. Johnson *et al.*, 1995, reported that heritability estimates along with genetic advance are more reliable than heritability alone to the predict effect of selecting the best individuals. Genetic advance indicates the magnitude of the expected genetic gain from one cycle of selection. In this regards, the present investigation was undertaken to evaluate variability, heritability and genetic advance of 10 quantitative characters in 36 black gram genotypes to provide necessary information that could be useful to improve yield traits.

Materials and Methods

Thirty six blackgram (*Vigna mungo* (L.) Hepper) genotypes of diverse origin were raised in rice fallow situation in a Randomized Block Design in three replications, each of 4 rows of 4 meters length with spacing of row to row 30 cm and plant to plant of 10 cm at Agricultural Research Station, Ghantasala, Krishna District, during *Rabi*, 2016-17. All the recommended package of practices was followed to raise a good crop.

Observations were recorded for 10 quantitative characters *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g) and grain yield per plant (g). Data was recorded from five randomly selected plants of each genotype per replication and the average was taken for analysis. Standard statistical procedures were used for the analysis of genetic variability estimates of quantitative traits such as PCV, GCV, heritability and genetic advance were worked out as per Johnson *et al.*, (1955) and Hanson (1963).

Results and Discussion

The mean sum of squares due to genotypes were highly significant at 1% level of significance for days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g) and grain yield per plant (g). This indicated the existence of considerable variability for all characters studied among the genotypes.

Hence, it offers a better scope for further improvement of breeding material by the selection of promising genotypes in Blackgram breeding programme. The mean sum of squares of various characters is presented in Table 1.

Table.1 Mean performance of 36 genotypes of rice fallow blackgram [*Vigna mungo* (L.) Hepper] for yield and yield component characters

S. No	Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches per plant	No. of clusters per plant	No. of pods per plant	Pod length (cm)	No. of seed per pod	100 Seed weight (g)	Grain yield per plant (gm)
1	LBG 623	46.50	77.50	21.96	2.50	4.50	26.50	3.04	6.00	4.61	6.42
2	VBG 4-008	45.00	75.50	18.48	2.50	5.50	36.00	4.02	7.00	4.41	9.09
3	VBG 4-14	45.00	76.50	21.07	3.00	7.00	33.00	4.05	6.50	4.35	7.58
4	Uttara	40.00	69.50	19.98	1.50	4.50	30.50	4.03	6.00	3.60	6.52
5	LBG 17	46.00	75.50	19.15	3.00	3.50	21.50	4.06	5.50	4.40	4.95
6	TGBG 40	46.50	79.50	23.25	2.50	4.50	27.00	4.05	5.50	4.55	6.46
7	LBG 402	48.00	80.00	21.87	3.00	3.50	23.50	4.07	6.50	4.65	6.64
8	KKB 05011	48.50	79.00	24.27	3.00	5.00	29.00	4.08	7.00	4.10	7.93
9	TU 94-2	42.50	74.00	24.90	3.50	6.50	36.00	4.06	7.00	4.20	8.96
10	LBG 787	41.00	72.50	24.41	3.00	6.00	33.50	4.02	7.00	3.85	8.15
11	TGBG 26	46.00	76.00	22.97	3.00	5.50	35.00	4.06	7.00	5.00	9.72
12	TGBG 344	40.50	71.50	21.85	3.00	3.50	24.50	4.06	6.50	4.35	6.31
13	TGBG 74	43.50	73.00	21.22	3.00	4.50	28.50	4.02	5.50	3.75	5.54
14	TGBG 143	42.50	74.00	22.50	3.00	4.00	24.50	4.08	5.50	4.50	5.72
15	TGBG 281	44.00	75.00	21.71	2.50	4.50	27.50	4.08	6.50	3.50	5.86
16	KUG 216 X BG 018-2	40.00	70.50	20.99	2.00	6.00	33.50	4.05	7.00	4.10	8.34
17	OPU 88 31 X VBG 4-008	40.00	71.00	21.14	4.00	6.00	37.00	4.05	6.50	3.65	7.85
18	LBG 645	44.50	75.00	24.55	3.00	4.00	26.00	5.03	6.00	4.65	6.85
19	TBG 104	42.00	73.50	23.36	2.50	5.50	33.50	4.05	7.00	4.10	8.24
20	WBG 108	43.50	73.50	20.08	2.00	6.50	34.00	4.02	7.00	4.30	8.36
21	KUG 216 X PU 40	38.00	69.50	14.62	3.00	6.00	32.50	4.07	7.00	3.62	7.78
22	LBG 648	48.00	78.50	25.13	2.90	3.00	21.00	4.05	5.50	3.05	3.46
23	PU 40	41.50	71.50	25.13	3.50	4.50	29.00	4.03	7.00	4.80	8.51
24	TU 18	46.50	76.00	25.55	3.00	4.50	26.50	4.08	6.00	4.18	6.41
25	LBG 685	45.50	75.00	23.28	2.00	3.00	27.50	4.06	6.50	4.99	8.34
26	PU 31	40.00	70.00	18.74	3.00	5.50	34.00	4.05	7.00	3.95	7.92
27	TGBG 258	40.00	72.50	18.97	2.00	4.00	26.50	4.07	6.50	4.57	7.07
28	IPU 2-43	44.50	74.00	23.85	3.00	5.50	29.50	4.03	6.00	4.03	6.99
29	LBG 788	44.50	75.00	23.40	1.50	4.50	28.50	4.05	7.00	4.62	7.76
30	KUG 216 X SPS 5	40.00	71.00	20.19	3.00	6.00	28.00	4.08	6.50	3.54	6.13
31	TGBG 136	42.50	74.00	23.90	4.00	5.50	33.50	4.08	6.00	4.35	7.93
32	T 9	45.00	75.00	19.79	2.50	6.00	30.00	4.02	6.50	4.15	6.94
33	TGBG 401	43.00	73.50	19.59	2.50	3.50	24.00	4.03	6.00	3.22	4.57
34	LBG 752	46.50	76.00	21.60	3.00	4.50	27.50	4.04	6.00	3.99	6.51
35	LBG 709	40.00	70.50	19.95	3.00	7.00	36.00	4.09	7.00	3.86	8.25
36	LBG 20	39.00	71.00	20.55	2.00	7.00	38.50	4.04	7.00	4.12	9.33
Mean		43.33	74.04	21.78	2.76	5.01	29.81	4.05	6.44	4.16	7.20
C.V.		2.40	1.71	6.65	13.89	11.91	6.66	1.00	6.91	2.48	8.78
S.Em		0.73	0.90	1.02	0.27	0.42	1.40	0.03	0.32	0.07	0.45
C.D. 5%		2.11	2.57	2.94	0.78	1.21	4.03	0.08	0.90	0.21	1.28

Table.2 Analysis of variance for grain yield and yield component characters of 36 genotypes in rice fallow blackgram [*Vigna mungo* (L.) Hepper]

Source of Variations	df	Days to 50% flowering	Days to maturity	Plant height (cm)	No.of branches per plant	No. of clusters per plant	No.of pods per plant	Pod length (cm)	No.of seed per pod	100 Seed weight (g)	Grain yield per plant (gm)
Mean sum of squares											
Replications	1	0.222	0.347	0.000	0.376	0.014	0.056	0.001	0.056	0.001	0.090
Treatments	35	16.457**	15.896**	11.307**	0.669**	2.642**	41.865**	0.113**	0.594**	0.438**	3.833**
Error	35	1.079	1.604	2.098	0.147	0.357	3.941	0.002	0.198	0.011	0.400
Total	71	17.759	17.848	13.406	1.191	3.013	45.862	0.116	0.848	0.450	4.322

** Significant at 1% level * Significant at 5% level

Table.3 Estimates of variability, heritability and genetic advance as per cent of mean for grain yield, yield components of 36 genotypes in rice fallow blackgram [*Vigna mungo* (L.) Hepper]

S.No	Character	Mean	Range		Coefficient of variation (%)		Heritability in broad sense (h^2_b) (%)	Genetic advance (GA) (%)	Genetic advance as per cent of mean (GAM)
			Min.	Max.	Phenotypic coefficient of variation (PCV)	Genotypic coefficient of Variation (GCV)			
1	Days to 50% flowering	43.33	38.00	48.50	6.83	6.40	87.70	5.35	12.34
2	Days to maturity	74.04	69.50	80.00	4.00	3.61	81.70	4.98	6.72
3	Plant height (cm)	21.78	14.62	25.55	11.89	9.85	68.70	3.66	16.82
4	No.of branches per plant	2.76	1.50	4.00	23.13	18.50	64.00	0.84	30.48
5	No. of clusters per plant	5.01	3.00	7.00	24.42	21.32	76.20	1.92	38.34
6	No.of pods per plant	29.81	21.00	38.50	16.06	14.61	82.80	8.16	27.38
7	Pod length (cm)	4.05	3.04	5.03	5.92	5.84	97.10	0.48	11.86
8	No.of seed per pod	6.44	5.50	7.00	9.77	6.90	49.90	0.65	10.04
9	100 Seed weight (g)	4.16	3.05	5.00	11.39	11.12	95.30	0.93	22.35
10	Grain yield per plant (gm)	7.20	3.46	9.72	20.20	18.19	81.10	2.43	33.75

The parameters of genetic variability such as mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as percentage of mean (GA) were estimated for all the quantitative characters are presented in Table 2.

The days to 50% flowering ranges from 38.00 to 48.50 days with mean of 43.33 days, days to maturity from 69.50 to 80.00 days with mean of 74.04 days, plant height varied from 14.62 to 25.55 cm with an mean of 21.78 cm, number of branches per plant ranged from 1.50 to 4.00 with mean of 2.76, number of clusters per plant from 3.00 to 7.00 with a mean of 5.01, number of pods per plant varied from 21.00 to 38.50 with mean of 29.81, number of seeds per pod ranged from 5.50 to 7.00 with mean of 6.44, 100 seed weight varied from 3.05 to 5.00 g with mean of 4.16 g and grain yield per plant varied from 3.46 to 9.72 g with mean of 7.20 g, which indicates that sufficient variability is present in the genotypes for above characters.

The phenotypic coefficient of variance (PCV) was slightly higher in magnitude than genotypic coefficient of variance (GCV) for all the characters studied indicating the influence of environment on expression of these traits. Number of clusters per plant showed high PCV (24.42) and GCV (21.32). While, high PCV and moderate GCV was observed for number of branches per plant and grain yield per plant, whereas number of pods per plant and 100 seed weight exhibited moderate PCV, GCV. Plant height recorded moderate PCV and low GCV. However, low PCV, GCV were recorded for days to 50% flowering, days to maturity, pod length and number of seeds per pod (Table 3). Similar results were reported by Anu Bishnoi *et al.,* (2017), Kondagari *et al.,* (2017), Gowsalya *et al.,* (2016), Monika *et al.,* (2016) and Punia *et al.,* (2014).

High heritability coupled with high genetic advance as per cent of mean was observed for the characters viz., number of branches per plant, number of clusters per plant, number of pods per plant, 100 seed weight and grain yield per plant, indicating that the heritability was due to additive gene effects, which may be exploited through breeding methods involving simple selection like pedigree method, mass selection, ear-to-row method etc. are to be followed to improve these traits. Whereas high heritability and moderate genetic advance as per cent of mean was recorded for the days to maturity, plant height, pod length. While, number of seeds per plant exhibited moderate heritability, genetic advance as per cent of mean, reveals that heritability was due to additive gene effects and selection may be effective. Days to maturity showed high heritability coupled with low genetic advance as per cent of mean, indicative of non-additive gene action and heritability was being exhibited due to favorable influence of environmental conditions rather than genotype and selection for this trait may not be rewarded. These results are in accordance with Anu Bishnoi *et al.,* (2017), Monika *et al.,* (2016), Kondagari *et al.,* (2017), Gowsalya *et al.,* (2016) and Punia *et al.,* (2014).

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