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Research Article

ESTIMATES OF GENETIC VARIABILITY AND HERITABILITY FOR YIELD AND YIELD COMPONENT TRAITS IN BLACKGRAM (*Vigna mungo* L. Hepper)

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Abstract- In present study, thirty blackgram (*Vigna mungo* L. Hepper) genotypes were evaluated for thirteen economically important characters. The study showed considerable variability for these characters. Heritability in broad sense was high for all the characters studied except for primary branches/ plant and days to 50% maturity. High heritability coupled with high genetic advance as per cent mean was perceived for plant height and seed yield/ plant, specified the prevalence of additive gene action in the expression of the traits. While the remaining traits showed high to moderate heritability coupled with moderate to low genetic advance as percent of mean, suggesting prevalence of non-additive gene action in the expression of the traits, therefore may be potentially utilized in recombination breeding. Furthermore, based on them *per se* performance, the suitable genotypes for these traits could be isolated and utilize for blackgram improvement. The association analysis revealed that the genotypic correlation coefficients were higher than corresponding phenotypic ones for all the character combinations.

Keywords- Heritability, Traits, Blackgram.

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Introduction

Blackgram [*Vigna mungo* L. Hepper] is an important pulse crop and occupies as good position due to its high seed protein content and ability to store the soil fertility through symbiotic nitrogen fixation [1]. Thus, it contributed significantly to enhancing the yield of subsequent crops [2]. Like other pulses, it also enriches the soil fertility, improves the soil structure and used as green fodder for cattle [3]. Due to highly nutritious and multipurpose nature of this crop, still it faces so many problems due to its narrow genetic base for any crop improvement programme, selection of superior parents is an essential prerequisite especially for the traits showing higher heritability and genetic advance for various traits [4]. The study of inheritance of various developmental and productive traits through the estimation of different genetic parameters like components of variances, genotypic and phenotypic coefficients of variability, heritability and genetic advance is helpful for framing the effective breeding programme [5].

Materials and Methods

The present experiment comprised of a set of thirty blackgram genotypes including check *i.e.* T-9. The experiment was conducted in randomized block design (RBD) with three replications during *kharif* 2016 at Field Experimentation Centre, Department of Genetics and Plant Breeding, Faculty of Agriculture, SHUATS, Allahabad. To record the data on quantitative traits [except days to 50% flowering (DFF), days to pod setting (DPS) and days to maturity (DM)], *viz.,* plant height (PH), primary branches per plant (PBP), clusters per plant (CPP), pods per plant (PPP), pod length (PL), seeds per pod (SPP), seed index (SI), seed yield per plant (SYP), Harvest Index (HI) a total of five plants were selected randomly. These two traits were computed on plot basis. The data were subjected to analysis of variance, genetic parameters by using statistical package WINDOSTAT developed by Indostat Service Hyderabad.

Results and Discussion

The analysis of variance (ANOVA) showed highly significant differences ($P < 0.01$) among the genotypes for the entire yield and yield component traits studied [Table-1]. Similar patterns were also recorded by [6,7] in which highly significant genetic differences among genotypes were observed for DFF and yield. The success of any breeding programme relies upon the knowledge available on genetically heritable variation with good proportion of selection response of important yield component traits.

A wide range of variability was showed among all the traits considered in the present study [Table-2]. For example, DFF and DM ranged from LBG -11 (48.40 days) to T- 9 Check (35.07 days) and IC - 140816 (70.40) to LBG -648 (65.74) days, respectively [8]. However, none of the genotypes exhibited significant superiority in terms of these traits over check variety (T-9), whereas all the thirty genotypes showed at par *per se* performance for DFF and poor performance for DM. Similarly, another trait *i.e.* plant height varied from PU-19 (85.27 cm) to IC-140816 (41.56 cm) and more importantly, these genotypes *viz.,* PU-19, SHEKHAR-3, PLU-277, IC-250187 etc. were found to be superior over the better check (Taller than check) [9] also suggested the taller plant stature is beneficial for mechanical weeding and mechanical harvesting. Days to 50% pod varied from 54.74 to 41.74 days. Primary Branches/ Plant varied from 1.74 to 4.74. Clusters/ Plant varied from 6.07 to 22.40. Pods/ Plant varied from 34.74 to 63.40. Pod Length varied from 3.61 to 4.10. Seeds/ Pod varied from 4.07 to 5.74 Seed Index 2.75 (g) 3.85. Harvest Index (%) 30.43 to 41.92. Biological Yield (g) 26.67 to 38.77. Seed Yield/ Plant (g) 9.80 to 14.88. Yield is ultimate aim of any crop improvement programme and out of twenty one, nine genotypes showed significant superiority over check for SYP [10].

The genetic parameters on 13 yield and yield component traits have been presented in [Table-3]. The coefficient of variation (CV) revealed that the

magnitude of phenotypic coefficient of variation (PCV) were higher than the corresponding genotypic coefficient of variation (GCV) for all the traits studied which indicates the role of environment in manifestation of these traits. Clusters/ Plant and Primary Branches/ Plant showed high magnitude of GCV and PCV, suggested that these two traits were less influenced by the environment. Similar finding for PBP has earlier been reported by [11]. Genotypic coefficient of variation (GCV) ranged from 1.28 % to 13.35 %. Maximum GCV was recorded for Primary branches per plant (13.35%) followed by clusters per plant (13.08%) and plant height (12.80 %), while estimates for GCV were minimum for days to 50 % maturity (1.28%) followed by pod length (3.01%),Days to 50% pods Setting (4.29%) and seed per pod (5.71%). [12] also reported maximum GCV for seed yield per plant.

Phenotypic coefficient of variation (PCV) ranged from 2.67% to 30.38%. This deviation may be noted due to environmental fluctuation on these traits and/ or other traits which having more contribution in manifestation of SY. Maximum PCV was recorded for Primary branches per plant (30.38%) followed by Clusters per plant (22.39%) and Plant height (13.40%), while estimates for PCV were low for days to 50% maturity (2.67%) followed by Pod length (3.10%). [13] also reported maximum PCV for number of clusters per plant and seed yield per plant. SY exhibited low magnitude of GCV but moderate magnitude of PCV. Heritability is good index for identification of traits. It is important selection parameter and provides clues on possible improvement [12]. Here, the heritability (in broad sense) estimates were recorded to be in the range of 28.0% (primary branches per plant) and 81.00% (plant height). [6] also reported high heritability for plant height. Interestingly, almost all the traits showed high to moderate heritability estimates. In addition to heritability, the genetic advance (GA) offers a potential parameter for selection. In the context, in the present study GA estimates ranged from 0.23% (pod length) to 17.13% (plant height). [7] also reported high genetic advance for plant height. High heritability coupled with high GAM was recorded for plant height and seed yield/ plant, indicated the predominance of additive gene action in the expression of the traits which could be easy targets for phenotypic selection and consequently, may be improved genetically *via* simple plant selection methods. [11] also observed high GAM for NSP and PH. Rest traits showed high to moderate heritability coupled with moderate to low GAM suggesting the existence of non-additive gene action in the expression of the traits and may be exploited better in recombination breeding. Targeting selections based on *per se* performance of genotypes; the superior genotypes for these traits may be isolated and further utilized for blackgram genetic improvement.

Table-1 *Analysis of variance (ANOVA) for 13 quantitative characters in blackgram*

S. No.	Characters	Mean sum of squares		
		Replication (d.f.= 2)	Treatments (d.f.= 29)	Error (d.f.= 58)
1	Days to 50% Flowering (DFF)	21.196	35.000**	6.931
2	Days to 50% Pods Setting (DPS)	15.036	21.052**	7.731
3	Plant Height (PH)	17.983	234.268**	7.198
4	Primary Branches/ Plant (PBP)	1.346	1.046**	0.609
5	Clusters/ Plant (CPP)	9.052	26.150**	10.237
6	Pods/ Plant (PLP)	16.476	79.447**	7.431
7	Pod Length (PL)	0.0006	0.0415*	0.0008
8	Seeds/ Pod (SPP)	0.325	0.394**	0.166
9	Days to 50% Maturity (DM)	4.579	4.806**	2.527
10	Seed Index (SI)	0.102	0.223**	0.049
11	Harvest Index (HI)	16.476	20.471**	5.776
12	Biological Yield (BY)	9.943	21.665**	4.218
13	Seed Yield/ Plant (SYP)	0.209	4.367**	0.073

*** & ** Significant at 1 % & 5% level of significance, df has been given in parenthesis.**

Table-2 *Mean performance of blackgram genotypes for 13 quantitative characters*

Genotypes	DFF	DPS	PH	PBP	CPP	PPP	PL	SPP	DM	SI	HI	BY	SYP
IC-24129	46.74	51.40	63.83	3.07	18.40	61.40	3.99	5.07	68.40	3.19	39.48	32.80	12.95
IC-250188	40.40	48.74	52.88	2.41	15.74	60.07	4.04	5.07	69.07	3.36	40.22	28.84	11.60
IPU96-1	42.74	49.74	74.66	2.40	17.74	61.40	4.00	4.40	69.74	3.03	37.50	37.04	13.89
PLU-277	42.07	49.74	78.83	2.74	18.40	61.74	3.98	5.40	70.07	3.63	37.40	36.34	13.59
PGRV-99022	45.40	47.07	68.58	2.40	13.74	55.40	3.90	5.40	70.07	3.47	36.98	33.64	12.44
MDU8-5-7	43.40	47.74	74.23	3.07	15.40	59.40	3.97	4.74	66.07	3.57	38.82	35.50	13.78
PLU-710	42.40	48.40	72.51	3.07	16.40	58.40	3.86	5.07	67.74	3.76	39.94	35.80	14.30
IC-250187	43.40	52.40	74.80	3.40	16.07	62.74	3.90	4.74	68.07	3.73	39.05	36.67	14.32
SHEKHAR-3	45.40	50.40	82.39	4.74	19.74	63.07	4.03	5.40	67.40	3.82	38.15	38.77	14.79
P-1	41.40	51.40	70.10	2.74	19.74	57.07	3.61	4.74	67.40	3.75	38.74	35.70	13.83
PLU-648	36.74	48.74	73.77	3.07	17.07	60.07	3.83	4.74	67.74	3.28	31.81	35.37	11.25
IPU 7-3	38.40	47.74	74.97	3.07	13.40	62.40	3.82	4.40	68.07	3.37	38.65	36.77	14.21
IPU-96-1	39.40	41.74	64.18	3.07	18.07	61.74	3.80	5.07	67.07	3.24	38.02	33.80	12.85
IC-140816	40.74	52.40	41.56	1.74	6.07	34.74	3.61	4.07	70.40	2.75	36.75	26.67	9.80
T-9	35.07	44.74	56.26	2.40	19.74	61.74	3.94	4.40	67.74	3.68	40.39	29.14	11.77
KPU-18-192	39.07	47.74	69.13	3.07	18.74	61.40	3.84	4.74	66.74	3.28	39.61	35.80	14.18
PU-31	41.74	50.07	69.76	2.74	18.40	62.74	3.88	4.74	68.07	3.76	32.33	35.57	11.50
KPU-63-189	42.07	49.40	72.42	2.74	21.07	61.07	3.82	4.74	67.74	3.76	38.65	36.04	13.93
BDU-1	38.74	50.07	63.98	3.07	21.40	62.07	3.80	5.07	68.07	3.61	41.54	32.40	13.46
TAU-1	37.07	45.74	72.78	3.07	18.40	61.74	3.84	5.07	69.07	3.53	37.21	34.64	12.89
MU-44	37.74	46.74	68.74	2.74	18.40	61.74	3.81	4.74	67.07	3.31	38.68	35.50	13.73
VALLABH URD	41.07	47.74	63.05	2.40	17.74	61.07	3.82	4.74	66.40	3.77	37.03	34.84	12.90
KU-96-97	37.07	48.07	64.89	2.74	18.74	62.40	3.76	4.74	68.40	3.24	37.05	34.20	12.67
DKU-11	40.07	48.07	59.37	1.74	17.40	61.74	3.81	4.40	67.07	3.82	37.77	31.80	12.01
LBG-11	48.40	48.40	65.16	2.40	17.07	62.40	3.67	5.07	66.74	3.69	37.21	34.37	12.79
PU-38	45.40	53.74	72.05	3.40	17.74	62.07	3.88	4.74	66.74	3.82	30.43	37.20	11.32
NOVK-13-14	42.07	50.07	58.25	3.07	19.40	60.07	3.73	4.74	68.40	3.63	41.92	31.80	13.33
PU-09-37	46.07	48.40	65.99	2.40	16.74	61.74	3.84	4.74	70.40	3.32	37.49	34.97	13.11
LBG-648	43.40	51.74	64.47	2.74	18.74	63.07	3.90	4.40	65.74	3.44	40.94	35.10	14.37
PU-19	47.40	54.74	85.27	4.07	22.40	63.40	4.10	5.74	67.07	3.85	40.03	37.17	14.88
Mean	41.70	49.10	67.96	2.86	17.60	60.34	3.86	4.84	67.96	3.52	37.99	34.48	13.08
SE	2.15	2.27	2.19	0.64	2.61	2.23	0.02	0.33	1.30	0.18	1.96	1.68	0.22
CD5%	4.30	4.54	4.38	1.28	5.23	4.46	0.03	0.67	2.60	0.36	3.93	3.36	0.44
CV	6.31	5.66	3.95	27.30	18.18	4.52	0.50	8.42	2.34	6.31	6.33	5.96	2.06
Max	48.40	54.74	85.27	4.74	22.40	63.40	4.10	5.74	70.40	3.85	41.92	38.77	14.88
Min	35.07	41.74	41.56	1.74	6.07	34.74	3.61	4.07	65.74	2.75	30.43	26.67	9.80

Table-3 *Estimates of genetic parameters for 13 characters in blackgram genotypes.*

S. No.	Characters	Coefficient of variation		Heritability (%) (broad sense)	Genetic advance	Genetic advance as % of mean
		Genotypic	Phenotypic			
1	Days to 50% Flowering	7.33	9.68	57.45	4.78	11.45
2	Days to 50% Pods Setting	4.29	7.10	36.48	2.62	5.34
3	Plant Height (cm)	12.80	13.40	91.32	17.13	25.20
4	Primary Branches/ Plant	13.35	30.38	19.30	0.35	12.08
5	Clusters/ Plant	13.08	22.39	34.13	2.77	15.75
6	Pods/ Plant	8.12	9.29	76.36	8.82	14.62
7	Pod Length (cm)	3.017	3.106	94.353	0.233	6.037
8	Seeds/ Pod	5.71	10.17	31.50	0.32	6.60
9	Days to 50% Maturity	1.28	2.67	23.12	0.86	1.27
10	Seed Index (g)	6.85	9.31	54.06	0.36	10.37
11	Harvest Index (%)	11.33	12.98	76.25	7.75	20.39
12	Biological Yield (g)	7.00	9.19	57.96	3.78	10.97
13	Seed Yield/ Plant (g)	9.15	9.38	95.17	2.40	18.38

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Abbreviations

PCV : Phenotypic coefficient of variation
GCV : Genotypic coefficient of variation

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