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Study on Genetic Variability and Correlation in Blackgram (*Vigna mungo* L. Hepper)

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Abstract

The present investigation was conducted to examine the 25 blackgram genotypes along with one check (T-9) to study the genetic variability, correlation. The observation were recorded randomly selected plants to each treatment and replication for 12 quantitative characters viz., days to 50% flowering, days to maturity, plant height, number of branches per plant, clusters per plant, pods per plant, pod length, seeds per plant, seed index, biological yield per plant, harvest index, seed yield/plant to estimate the variability, heritability and genetic advance as % mean, correlation among seed yield and its related traits. Analysis of variance showed highly significant differences among 25 blackgram genotypes for 12 quantitative characters studied. Maximum genotypic and phenotypic variance was recorded for harvest index, plant height and pods/plant. Maximum GCV and PCV were recorded for harvest index, pods/plant and seed yield /plant. High heritability was recorded for pods/plant, biological yield/plant, days to maturity, days to 50% flowering, harvest index, seed yield/plant. High heritability coupled with high genetic advance as percent of mean was recorded for pods/plant. Correlation coefficient analysis revealed that seed yield/plant exhibited significant and positive correlation both at genotypic and phenotypic level with harvest index and pods/plant.

Keywords: Blackgram, Genetic Variability, Correlation

Introduction

Blackgram is one of the important pulse crops in India. Blackgram (*Vigna mungo* L. Hepper), a dicotyledonous plant belongs to family leguminosae. It is annual legume and self- pollinated crop having chromosome no $2n= 22$. Blackgram was originated in India. Blackgram is commonly referred to as urd bean. Blackgram is basically a tropically crop but it is grown in both *Kharif* and *Zaid*. In 2014-2015, 1.61 million tonnes Urd production in the country is largely concentrated in five states viz., Uttar Pradesh, Maharashtra, Madhya Pradesh, Andhra Pradesh, and Tamil Nadu. These five states together contribute for about 70% of total Urd production in the country (Ministry of agriculture, Govt, of India, 2015). Black gram contains sulphur containing amino acids, methionine and cysteine and also contains lysine, which are excellent component of balanced human nutrition. The study of genetic variability is the pre-requisite for any crop improvement programme, success in a recombination breeding depends on the exploitation of genotypes as parents for obtaining high heterotic crosses and transgressive segregants for this, the presence of genetic variability in a base population is essential. Correlation coefficient analysis measure the mutual relationship between various plant characters and determines component characters on which selection can based for improvement in the economically important character.

Therefore, present study was planned to investigate the genetic variability, correlation coefficient and path analysis to identify the best trait to be used for future exploitation.

Metarials and Methods

The present investigation was carried out at the Field Experimentation Centar, Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Science, Allahabad, U.P. during *Zaid*-2017. The experimental materials constituted 25 blackgram genotypes along with one check (T9) of Blackgram (*Vigna mungo* L. Hepper), received from Department of Genetics and Plant Breeding, SHUATS, Allahabad. The experiment was laid out in the Randomised Block Design with three replication of 1×1 m² size plots and has four rows with spacing of row to row 25 cm and plant to plant 10 cm. The genotypes were sown by hand dibbling in each plot by imposing randomisation in each replication along with check T9.

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Results and Discussion

Analysis of variance revealed highly significant to significant differences ($p < 0.01$) among genotypes for all 12 quantitative characters studied (Table 1). In the present study, variation among the characters is estimated by Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV). The magnitude of phenotypic coefficient of variation was higher than genotypic coefficients for all characters under study, indicating the interaction of genotypes with the environment (Table 2). High GCV and PCV were maximum in case of harvest index (32.48 and 33.24) followed by pods per plant (31.28 and 31.33) and seed yield/plant (29.76 and 30.49). High heritability in the broad sense is not only enough to make sufficient improvement through selection unless accompanied by the amount of genetic advance. The estimates of heritability (broad sense) was observed for pods per plant

(99.71%), biological yield per plant (99.28%) followed by days to maturity (96.68%), days to 50% flowering (95.75%), harvest index (95.44%), seed yield per plant (95.29%) indicating preponderance of additive gene action in the expression of these traits and they can be improved through individual plant selection. High heritability coupled with high genetic advance as percent of the mean was recorded for pods per plant, biological yield/plant, days to maturity, harvest index, seed yield per plant. Indicate the preponderance of additive gene action in controlling gene expression. Seed index, plant height had moderate estimates of heritability, GCV, PCV and genetic advance indicating reasonable improvement under selection. These findings are in accordance with Rao *et al.* (2006) [8] and Makeen *et al.* (2007) [5].

Table 1: Analysis of variance for 12 different quantitative characters in 26 genotypes of blackgram.

Source of variation	d.f.	Days for 50% Flowering	Plant height(cm)	Number of branches/plant	Clusters /plant	Pods/Plant	Pod length	Number of Seeds/pod	Days to maturity	Biological yield/plant	Harvest index	Seed index	Seed Yield/plant
Replications	2	0.82	14.19	0.01	0.36	1.45	1.45	0.03	44.84	20.97	0.92	0.18	0.08
Treatments	25	48.96**	186.42**	0.53**	16.31**	114.35**	114.35	0.76**	1.01**	31.97**	299.09**	31.48**	12.10**
Error	50	0.71	53.77	0.06	0.30	0.10	0.02	0.04	0.50	10.49	4.68	0.75	0.19

**Significant at 1% level.

Table 2: Genetic parameters for 12 biometrical characters of 26 blackgram genotypes

S. No	Characters	Genotypic Variance (V _g)	Phenotypic Variance (V _p)	Genotypic Coefficient of variation	Phenotypic coefficient of variation	Heritability (%) (broad sense)	Genetic advance	Genetic advance as % of mean
1.	Days to 50% flowering	4.01	4.09	7.35	7.51	95.75	8.08	14.82
2.	Days to maturity	3.84	3.90	4.57	4.64	96.68	7.78	9.26
3.	Plant height	6.64	9.89	20.34	30.28	45.12	9.20	28.14
4.	Number of branches/plant	0.39	0.47	25.08	29.66	71.51	0.69	43.70
5.	Cluster /plant	2.29	2.36	26.05	26.78	94.60	4.60	52.19
6.	Pods /plant	6.17	6.17	31.28	31.33	99.71	12.69	64.36
7.	Seed /pod	0.48	0.53	7.58	8.31	83.14	0.91	14.24
8.	Pod length	0.32	0.35	7.56	8.30	83.03	0.61	14.20
9.	Biological yield /plant	3.23	3.24	14.47	14.53	99.28	6.64	29.71
10.	Seed Index	0.12	0.24	3.47	6.67	27.13	0.13	3.73
11.	Harvest index	9.90	10.14	32.48	33.24	95.44	19.93	65.37
12.	Seed yield /plant	1.99	2.04	29.76	30.49	95.29	4.00	59.85

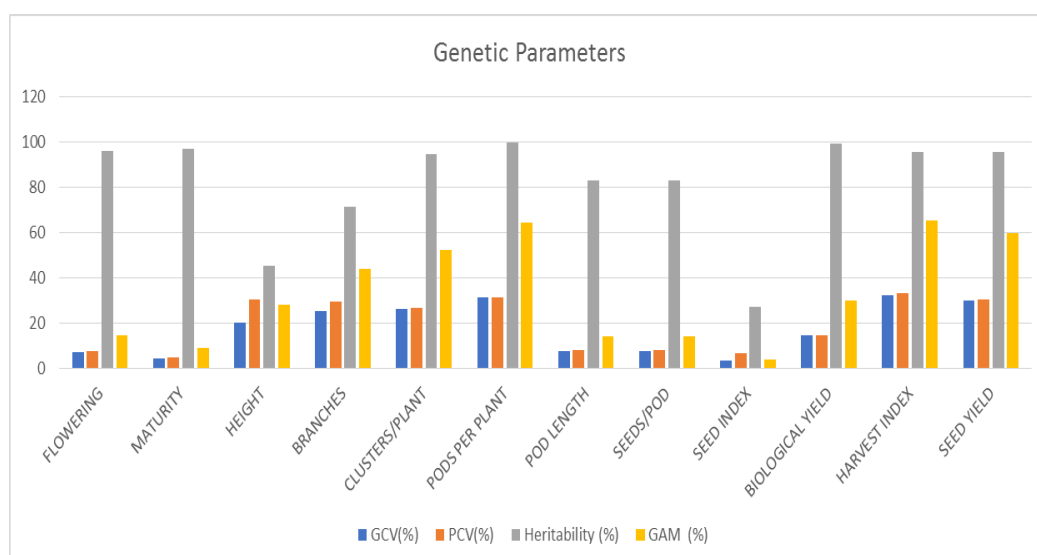


Fig 1: Genetic parameters for 12 biometrical characters of 26 blackgram genotypes

Table 3: Genotypic and Phenotypic correlation coefficients of 12 characters in Blackgram.

Characters		Days to 50% flowering	Days to Maturity	Plant Height	Number of Branches/plant	Clusters/plant	Pods/plant	Pod length	Seeds/pod	Seed index	Biological yield/plant	Harvest index	Seed yield/plant
Days to 50% flowering	r _g	1	0.969**	-0.099	0.168	-0.263*	-0.189	-	-0.320*	-0.304*	-0.193	-0.208	-0.322*
	r _p	1	0.953**	-0.073	0.143	-0.050	-0.185	-	-0.262*	-0.132	-0.183	-0.210	-
Days to maturity	r _g		1	-0.166	0.252*	-0.030	-0.125	-0.230*	-0.229*	-0.267*	-0.169	-0.113	-0.213
	r _p		1	-0.103	0.199	-0.041	-0.121	-0.203	-0.203	-0.151	-0.163	-0.119	-0.214
Plant height	r _g			1	0.040	-1.846**	0.028	0.164	0.163	-0.059	0.510**	-0.056	0.134
	r _p			1	0.021	-0.091	0.019	0.072	0.072	-0.021	0.338**	-0.041	0.080
Number of branches/plant	r _g				1	0.707**	-0.031	0.128	0.128	-0.072	0.320**	-0.013	0.125
	r _p				1	0.008	-0.031	0.096	0.097	0.016	0.282*	0.009	0.129
Clusters/plant	r _g					1	-0.585*	0.216	0.219	0.241*	3.122**	-1.180*	-0.040
	r _p					1	-0.043	-0.006	-0.007	0.158	0.199	-0.065	0.010
Pods/plant	r _g						1	-0.072	-0.073	0.294*	-0.156	0.761*	0.782*
	r _p						1	-0.068	-0.069	0.167	-0.154	0.741*	0.761*
Pod length	r _g							1	1.000*	0.340*	0.291**	-0.195	-0.093
	r _p							1	1.000*	0.072	0.262*	-0.181	-0.089
Seeds/pod	r _g								1	0.339*	0.291**	-0.195	-0.093
	r _p								1	0.073	0.263*	-0.181	-0.089
Seed index	r _g									1	0.174	0.123	0.220
	r _p									1	0.099	0.069	0.125
Biological yield/plant	r _g										1	-0.388*	-0.028
	r _p										1	-	0.382*
Harvest index	r _g											1	0.926*
	r _p											1	0.928*
Seed yield/Plant	r _g												1
	r _p												1

r_g = Genotypic correlation coefficient. r_p = Phenotypic correlation coefficient. *Significant at 5% level, **Significant at 1% level.

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