

GENETIC VARIABILITY AND CHARACTER ASSOCIATION FOR YIELD AND ITS COMPONENTS IN BLACK GRAM [*VIGNA MUNGO* (L.) HEPPER]

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ABSTRACT

Forty six genotypes of black gram were studied in randomized block design with two replications for genetic variability, correlations, and direct and indirect effects for twelve quantitative characters. Analysis of variance revealed significant differences among 46 genotypes for all the 12 characters. Plant height had shown highest heritability coupled with genetic advance, followed by seed yield per plant, pod length. Correlation coefficient at phenotypic level revealed that grain yield per plant had a high positive and significant association with number of pods per plant ($r=0.712$), followed by number of secondary branches per plant (0.552), number of clusters per plant (0.551). The results of path analysis revealed that days to 50 per cent flowering (0.080), days to maturity (0.110), plant height (0.115), number of secondary branches per plant (0.324), branch height(0.136), number of pods per plant (0.604), number of seeds per pod (0.022), and hundred seed weight (0.134) had positive direct effects on grain yield. While the characters viz., number of primary branches per plant (-0.156), number of clusters per plant (-0.063) and pod length (-0.088) had negative direct effects on grain yield. On grain yield indicating importance of these characters and can be strategically used to improve the yield of black gram.

INTRODUCTION

Black gram (*Vigna mungo* L. Hepper, $2n=22$) is one of the nutritious pulse crops, popularly known as urbean. It is an important short duration pulse crop and self pollinated grain legume grown in many parts of India. This crop is grown in cropping systems as a mixed crop, catch crop, sequential crop besides growing as sole crop under residual moisture conditions after the harvest of rice and also before and after the harvest of other summer crops under semi irrigated and dry land conditions. Its seeds are highly nutritious with protein (25-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins. Like other pulses, it also enriches the soil fertility, improves the soil structure and used as green fodder for cattle (Parveen *et al.*, 2011). According to Vavilov, 1926 black gram has originated from Indian subcontinent. Though it is grown in different countries of South and South East Asia, India is the most important producer of black gram. The present productivity levels of black gram in India are very low. Efforts to genetically improve the crop are still at low ebb. Further, it has been the least studied crop among the pulses and no international system under the CGIAR has this as a mandate crop (Ghafoor, *et al.*, 2000).

An assessment of the genetic diversity of pulses is an important first step in a program to improve crop yield. The proper estimate of nature and magnitude of diversity in a crop is

essential to infer about extent of variation available for yield and its component traits. The selection of highly genetically divergent parents is expected to throw superior and desirable segregants following crossing (Bhatt, 1973). It is also known that germ plasm collections have some valuable genes which provide tolerance to various diseases, hence characterization and evaluation of such local germ plasm provides useful material for breeding good varieties. A throughout knowledge of existing genetic variation and degree of association between yield and yield contributing traits is essential for developing high yielding genotypes in black gram. The observed variability is a combined measure of genetic and environment causes. Correlation studies provide an opportunity to study the magnitude and direction of association of yield with its components and also among various components. To accumulate optimum combination of yield contributing characters in a single genotype, it is essential to know the implication of interrelationship of various characters along with path coefficient. Hence the present investigation was taken up to study the genetic divergence, variability and character association for yield components of 46 black gram genotypes for their better use in getting transgressive segregants.

MATERIALS AND METHODS

The material comprised of 46 black gram genotypes. These were evaluated at KVK, UAHS, Shimoga during *kharif* 2013.

The experiments were laid out in a homogeneous block following randomized complete block design (RCBD) with two replications of 4 m length with inter row spacing of 30 cm and intra row spacing of 10 cm. Recommended agronomic practices were followed to raise the crop.

Observations on 12 quantitative characters viz., days to fifty per cent flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, branch height, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length, hundred seed weight, grain yield per plant were recorded on five randomly selected plants in each treatment and were used for statistical analysis.

The genotypic and phenotypic correlation co-efficient, path co-efficient analysis was done to partition the genotypic correlation co-efficient into direct and indirect effects. Knowledge of the relationship among yield components is essential for the formulation of breeding programmes aimed at achieving the desired combinations of various components of yield. The estimates of correlation coefficients among the different characters indicate the extent and direction of association. The correlation co-efficient provide a reliable measure of association among the characters and help to differentiate vital associations useful in breeding from those of the non-vital ones (Falconer, 1981). For analyze character association, data were subjected to correlation coefficient (Burton and Devane, 1953) and path analysis (Dewey and Lu, 1959).

RESULTS AND DISCUSSION

The analysis of variance for randomized block design revealed

highly significant differences among accessions for all the characters under investigation thereby indicating the presence of a considerable magnitude of genetic variability among 46 genotypes of black gram for these characters. This suggested adequate amount of variability among germ plasms that may be helpful for trait improvement by selection. (Table 1).

The genetic parameters viz; environmental, genotypic and phenotypic variances, phenotypic and genotypic coefficients of variation, heritability estimates and predicted genetic advance as percent of mean for characters studied and discussed (Table 2).

All the genotypes under the study displayed considerable amount of differences in their mean performance with respect to characters studied. An assessment of heritable and non-heritable components in the total variability is indispensable in adopting suitable breeding procedure. The heritable portion of the overall observed variation can be ascertained by studying the components of variation such as coefficients of genotypic and phenotypic variability, heritability and predicted genetic advance. Presence of narrow gap between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for all the characters under study suggested that expression of these traits have low environmental influence.

The genotypes exhibited higher PCV and GCV values for seed yield per plant (29.85,28.38), number of pods per plant (25.74,22.16) and number of clusters per plant (24.27,15.82) suggesting that these characters are under the influence of genetic control and there is a possibility of improvement through direct selection for the traits. These results are in accordance with Shah and Patel (1981) in black gram, Borah

Table 1: ANOVA for yield and its component traits in Black gram

SV	Df	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12
Replications	1	113.08	143.75	42.32	12.12	0.14	14.40	41.11	109.78	0.17	1.24	1.73	5.83
Treatments	45	1.73**	3.92**	3.68**	1.84**	2.70**	4.36**	2.10**	44.37**	1.94**	1.85**	4.99**	1.88**
Error	45	2.12	0.86	3.10	0.45	3.08	3.17	3.25	64.67	0.29	0.29	7.29	0.02
Sem +		1.48	0.93	1.76	0.67	1.75	1.78	1.80	8.04	0.53	0.53	2.67	0.14
C.V.(%)		3.48	1.33	6.21	12.20	17.43	10.37	20.34	24.17	9.86	8.06	25.19	2.08
C.D. (5 %)		2.99	1.87	3.54	1.36	3.53	3.58	3.63	16.19	1.07	1.07	5.43	0.29
C.D.(1 %)		3.99	2.49	4.73	1.81	4.71	4.79	4.85	21.62	1.44	1.44	7.26	0.39

X1 = Days to 50per cent flowering, X2 = days to maturity, X3 = Plant height, X4 = Primary branches, X5 = Secondary branches, X6 = Branch height, X7 = No. of clusters per plant, X8 = No. of pods per plant, X9 = Pod length, X10 = seeds per pod, X11 = yield per plant, X12 = hundred seed weight

Table 2: Genetic variability parameters for quantitative traits in Blackgram

Character	Mean	Range	Variable	h ²	GCV	PCV	GAM
PI H	28.34	24.50-30.70	6.20	95.40	16.32	16.71	32.84
DFF	42.56	40.00-45.00	5.00	73.15	2.56	3.00	4.52
BrH	17.16	15.80-21.50	5.30	58.64	9.56	13.12	17.54
PB	5.52	5.00-7.30	2.30	50.68	11.33	15.91	16.61
SB	10.60	9.00-12.20	3.20	56.18	9.13	12.56	15.86
CL/PL	8.86	7.00-11.10	4.10	42.49	15.82	24.27	21.25
P/PL	33.27	20.60-40.00	19.40	74.12	22.16	25.74	39.31
PLNTH	5.42	5.00-5.70	0.70	80.30	3.06	3.42	5.66
S/POD	6.62	6.00-7.50	1.50	56.63	4.06	5.39	6.29
DAM	69.51	68.00-71.00	3.00	73.08	6.02	7.05	10.61
100SWT	6.91	6.00-7.90	1.90	54.39	6.75	9.16	10.26
Y/PL	10.71	7.00-13.00	6.00	90.37	28.38	29.85	55.57

Where, PI H = Plant height, DFF = Days to 50% flowering, Br H = Branch height, PB = Primary branches, SC = Secondary branches, CL/PL = Clusters/plant, P/PL = Pods/plant, PLNTH = Pod length, S/POD = Number of seeds/pod, DAM = Days to maturity, 100SWT = 100 Seed weight, Y/PL = Yield/plant

Table 3: Phenotypic correlation analysis of 46 black gram genotypes

	DFF	DAM	PH	PRI B	SEC B	BR HT	NO. CLUS	NO. PODS	POD LNTH	SEED S/P	100 S/P
DFF	1										
DAM	-0.4057 **	1									
PH	-0.0244	-0.0418	1								
PB	-0.0322	0.2545 *	0.4431 **	1							
SEC B	0.0148	-0.083	0.075	0.2894 **	1						
BR HT	-0.0474	0.0844	0.4620 **	0.5089 **	0.1848	1					
NO.CLUS	0.0775	0.0634	0.3500 **	0.5974 **	0.6130 **	0.4677 **	1				
NO.PODS	-0.0695	-0.0557	0.3275 **	0.3422 **	0.5062 **	0.3374 **	0.7050 **	1			
POD LNTH	-0.0633	-0.0194	0.2667 *	0.3241 **	0.1115	0.3837 **	0.2161 *	0.2328 *	1		
SEEDS/P	-0.156	0.0146	0.4412 **	0.4533 **	0.1206	0.4500 **	0.2930 **	0.3277 **	0.6753 **	1	
100SEED	0.2683 **	-0.0754	0.0825	-0.1321	-0.0917	-0.0247	-0.1602	-0.1236	0.0184	-0.0553	1
YEILD/PL	0.0272	-0.028	0.3002	0.2165	0.5528	0.3228	0.5517	0.7129	0.1178	0.2044	0.0771

Similarly positive association of plant height with primary branches (rp = 0.443), branch height (rp = 0.462), number of clusters per plant (rp = 0.350), number of pods per plant (rp = 0.327), pod length (rp = 0.266), seeds per pod (rp = 0.441). Significance Levels 0.05 0.01 0.005 0.001, if correlation r² 0.2049568 0.26728890.2902839 0.3375

Table 4: Phenotypic Path coefficient analysis of 46 black gram genotypes.

	DFF	DAM	PH	PRI B	SEC B	BR HT	NO. CLUS	NO. PODS	POD LNTH	SEEDS/ P	100 SEED
DFF	0.080	-0.032	-0.002	-0.002	0.001	-0.003	0.006	-0.005	-0.005	-0.012	0.021
DAM	-0.044	0.110	-0.004	0.028	-0.009	0.009	0.007	-0.006	-0.002	0.001	-0.008
PH	-0.002	-0.004	0.115	0.051	0.008	0.053	0.040	0.037	0.030	0.050	0.009
PRI B	0.005	-0.039	-0.069	-0.156	-0.045	-0.079	-0.093	-0.053	-0.050	-0.070	0.020
SEC B	0.004	-0.026	0.024	0.093	0.324	0.059	0.198	0.164	0.036	0.039	-0.029
BR HT	-0.006	0.011	0.062	0.069	0.025	0.136	0.063	0.045	0.052	0.061	-0.003
NO.CLUS	-0.004	-0.004	-0.022	-0.037	-0.038	-0.029	-0.063	-0.044	-0.013	-0.018	0.010
NO. PODS	-0.042	-0.033	0.198	0.206	0.306	0.204	0.426	0.604	0.140	0.198	-0.074
POD LNTH	0.005	0.001	-0.023	-0.028	-0.009	-0.033	-0.019	-0.020	-0.088	-0.059	-0.001
SEEDS/P	-0.003	0.001	0.009	0.010	0.002	0.009	0.006	0.007	0.014	0.022	-0.001
100SEED	0.036	-0.010	0.011	-0.017	-0.012	-0.003	-0.021	-0.016	0.002	-0.007	0.134
YEILD/PL	0.027	-0.028	0.300	0.216	0.552	0.322	0.551	0.712	0.117	0.204	0.077
Partial R ²	0.002	-0.003	0.034	-0.033	0.179	0.043	-0.034	0.431	-0.010	0.004	0.010

R SQUARE = 0.6237 RESIDUAL EFFECT = 0.6134, *Significant at 5per cent level; **Significant at 1per cent level Diagonals = Direct effect ; Off diagonals = Indirect effect

and Hazarika (1995) in green gram, and Meshram *et al.*, (2013) in blackgram. However, in the present investigation, plant height, days to 50% flowering, pod length, number of seeds per pod, days to maturity had low values of GCV and PCV for genotypes indicated that improvement for these traits can be achieved up to some extent. These results are in accordance with Medhi *et al.* (1980) in greengram. The GCV and PCV values for plant height, number of branches per plant were moderate. Heritability estimates reveals the heritable portion of variability present in different characters. The knowledge of heritability enables the plant breeder to decide the course of selection procedure to be followed under a given situation. However, heritability values coupled with genetic advance would be more reliable (Johnson *et al.*, 1955) and useful in formulating selection procedure. In the present study, heritability estimates in broad sense and genetic advance as per cent of mean were estimated.

Heritability estimates were high for all the characters studied, except for number of primary branches per plant, number of secondary branches per plant, branch height, number of clusters per plant, number of seeds per pod and test weight. These results are in accordance with Shah and Patel (1981), Ramakrishna and Jairaj (1981), Patel and Shah (1982), Kumar and Reddy (1986), Singh *et al.* (1987) in blackgram, and

Deepshikha *et al.* (2014) in blackgram.

In the present study, high heritability coupled with high genetic advance as per cent over mean was observed for the characters like plant height, number of pods per plant, seed yield per plant, these results are in line with Patel *et al.*, (2014) in greengram. This indicates the lesser influence of environment in expression of these characters and prevalence of additive gene action in their inheritance, hence are amenable for simple selection. The high genetic advance over mean coupled with moderate to high heritability suggested the importance of additive gene action for these traits. The moderately high heritability and low genetic advance for remaining characters indicating the presence of non-additive gene action and role of environment in expression of these traits. Therefore, priority should be given to those traits which recorded higher estimates of genetic advance as per cent mean while deciding selection strategies and selection based on these characters may be useful in realizing better gain by selection. Black gram is a self-pollinated species hence there must be preponderance of additive genes. Correlation coefficient is a statistical measure, which denotes the degree and magnitude of association between any two casually related variables. This association is due to pleiotropic gene action or linkage or more likely both. In plant breeding correlation coefficient analysis measures the mutual relationship between two characters and

it determines character association for improvement yield and other economic characters. Since the association pattern among yield components help to select the superior genotypes from divergent population based on more than one interrelated characters. Thus information on the degree and magnitude of association between characters is of prime important for the breeder to initiate any selection plan.

In the present investigation the data on all the twelve traits which showed significant differences among the entries were subjected to statistical analysis and the results on correlation analysis in present genotypes indicated that the highest positive correlation was observed in number of pods and yield ($r_p=0.712$) followed by number of clusters and number of pods ($r_p=0.705$), pod length and seeds per pod ($r_p=0.675$), secondary branches and number of clusters ($r_p=0.613$). On contrary, highest negative correlations were observed in days 50% flowering and days to maturity ($r_p=0.405$), as less number of days to flowering reduces the crop duration, this helpful in terms of economic cultivation of blackgram. More over it helps the crop to escape terminal drought, hence the selection can be practiced for early flowering genotypes with high grain yield to suit for scanty rain fall areas (Table 3).

Hence these traits could be selected indirectly in order to improve the seed yield per plant. Similar kind of significant positive association of clusters per plant and pods per plant with seed yield was reported earlier by Makeen *et al.* (2009), Konda *et al.* (2008), Mallikarjuna Rao *et al.* (2006), Bhagowati and Hazarika (2006) and Pan *et al.* (2014).

The coefficients of correlation between 100 seed weight was significant with remaining other traits in the population. It indicates that genotypes with bold seed produces higher grain yield. It attracts consumer's preference. Hence selection for bold grain size helps the farmers to cultivate bold seeded types it will fetch higher market price for their produce. The trait pod length was also significantly associated with number of pods per plant in the population. These results are in line with the earlier reports of Bhagowati and Hazarika (2006).

Path coefficient analysis is simply a standardized partial regression coefficient which splits the correlation coefficient into the measures of direct and indirect effects. In the present investigation indicates that the highest positive direct effect on seed yield per plant was shown by number of pods per plant ($P=0.604$) followed by secondary branches ($P=0.324$), branch height ($P=0.136$), hundred seed weight ($P=0.134$), plant height ($P=0.115$), days to maturity ($P=0.110$), days to 50% flowering ($P=0.080$), seeds per pod ($P=0.022$) (Table 4). These positive direct effects observed with seed yield were in accordance with the reports of Zubair and srinivas (1986) for 1000 seed weight and pods per plant, Singh and Singh (1994), khattak *et al.*, (1995) for 100 seed weight and pods/plant. On contrary, number of clusters per plant, pod length and primary branches recorded negative direct effect on seed yield. These findings were in accordance with the reports of Gopikrishnan *et al.*, (2002) character clusters/plant and pods/plant had negative direct effect on seed yield. Hence for increasing the seed yield in present genotypes, direct selection based on these traits would be rewarding.

The present investigation has indicated the importance of plant

height, number of pods per plant, branch height, number of clusters per plant which are important traits for improving the yield. Therefore, due emphasis should be given to these traits in the selection programme to evolve high yielding genotypes in blackgram

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