Assessment of Genetic Variability, Character Association and Path Analysis for Yield and Yield Attributes in Blackgram (*Vigna mungo* (L.) Hepper)

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ABSTRACT

The current investigation was conducted with an objective to estimate the extent of variability, genotypic and phenotypic correlation and path coefficient analysis among forty-five blackgram genotypes for fourteen yield and yield attributing traits at Genetics and Plant Breeding farm, Anand Agricultural University, Anand during *kharif* 2021 using Randomized Complete Block Design. The analysis of variance revealed significant differences among genotypes for all fourteen characters. The high heritability coupled with high genetic advance was recorded for plant height, clusters per plant, pods per plant, pods per cluster, seeds per pod, seed yield per plant, biological yield per plant, harvest index and protein content which indicated that selection would be effective for improvement due to predominance of additive gene action in the expression of these characters. The estimates of correlation coefficient revealed that days to 50% flowering, clusters per plant, pods per plant, seeds per pod, 100 seed weight, biological yield per plant, harvest index and protein content exhibited significant positive correlation with seed yield per plant at genotypic as well as phenotypic levels. The path analysis estimates revealed that biological yield per plant and harvest index had a very strong positive direct effect on seed yield per plant whereas seeds per pod, pods per plant, pods per cluster and clusters per plant showed high negative direct effects. The positive indirect effects of pods per plant and clusters per plant were quite substantial via biological yield per plant.

Keywords Black gram, Correlation, Genetic variability, Heritability, Path analysis.

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INTRODUCTION

Blackgram is the fourth important pulse crop that occupies unique position in Indian agriculture (Malik *et al.* 1994). It is a highly self-pollinated, short-duration grain legume and belongs to the family Fabaceae and sub-family Papilionaceae (Naik *et al.* 2017). Blackgram seeds are rich in protein (25-26%), carbohydrate (60%), fat (1.5%), minerals, amino acids and vitamins (Parveen *et al.* 2011). Genetic variability is the basic requirement for making progress in crop breeding. The effectiveness of selection depends upon the nature, extent and magnitude of genetic variability present in the experimental material and the heritability of the character. Correlation

Table 1. Analysis of variance for different characters of blackgram genotypes. * Significance at 5% level, ** Significance at 1% level.

Sl. No.		df	Mean squares		
	Characters	Replication 2	Genotype 44	Error 88	
1	Days to 50% flowering	7.49	74.25**	8.51	
2	Days to maturity	0.06	48.38**	16.29	
3	Plant height (cm)	53.75	543.03**	26.08	
4	Primary branches per plant	0.37	0.73**	0.13	
5	Clusters per plant	1.55	137.63**	2.40	
6	Pods per cluster	0.32	1.44**	0.17	
7	Pods per plant	46.84	1614.07**	74.38	
8	Pod length (cm)	0.24*	0.56**	0.05	
9	Seeds per pod	0.47	2.35**	0.27	
10	Seed yield per plant (g)	1.43	139.77**	1.76	
11	100 seed weight (g)	0.18*	0.33**	0.05	
12	Biological yield (g)	32.88	993.96**	11.89	
13	Harvest index (%)	3.00	179.00**	9.77	
14	Protein content (%)	1.07	72.92**	0.71	

coefficients generally show relationships among independent characters and the degree of linear relationship which provides basis for selection of traits. Though correlation provides the extent and direction of association between particular character and yield, this alone does not provide a complete picture about how these components alter the yield and it can be achieved by assessment of path coefficients in which correlation coefficient partitioned into components of direct and indirect effects. By using path coefficient analysis, one variable's direct and indirect effect on another can be estimated which would be helpful in formulating the selection criteria and make possible an overall improvement in single plant yield directly.

MATERIALS AND METHODS

The present investigation was conducted at Genetics and Plant Breeding Farm, BA College of Agriculture, Anand Agricultural University, Anand during *kharif* 2021. Seeds of 45 blackgram genotypes were collected from Pulses Research Station, Vadodara and

Table 2. Estimates of variance components and other genetic parameters for different characters in blackgram. GCV = Genotypic Coefficient of Variation, h^2(b) = Broad Sense Heritability, PCV = Phenotypic Coefficient of Variation, GAM = Genetic Advance as per cent Mean.

| Sl. No.	Character	Mean	Range	$\sigma^2 g$	$\sigma^2 p$	GCV	PCV	$h^2 b$	GAM
1	Days to 50% flowering	42.35	32.33-53.67	21.91	30.42	11.05	13.02	72.00	19.31
2	Days to maturity	77.02	67.00-84.67	10.70	26.99	4.25	6.75	39.60	5.50
3	Plant height	62.35	37.80-88.96	172.32	198.40	21.05	22.59	86.90	40.41
4	Primary branches per plant	4.91	4.07-6.00	0.20	0.33	9.17	11.68	61.70	14.88
5	Clusters per plant	20.85	10.53-34.68	45.07	47.48	32.2	33.05	94.90	64.65
6	Pods per cluster	4.28	2.80-5.87	0.42	0.59	15.23	18.04	71.20	26.43
7	Pods per plant	84.96	41.47-144.33	513.23	587.61	26.67	28.53	87.30	51.33
8	Pod length	4.58	3.79-5.57	0.17	0.22	9.02	10.37	75.70	16.17
9	Seeds per pod	6.01	4.57-8.03	0.69	0.96	13.87	16.31	72.30	24.3
10	Seed yield per plant	18.87	9.23-38.11	46.00	47.76	35.93	36.62	96.30	72.64
11	100 seed weight	3.73	3.19-4.54	0.09	0.14	8.12	10.21	63.20	13.41
12	Biological yield per plant	52.73	23.20-102.71	327.36	339.25	34.31	34.93	96.49	69.44
13	Harvest index	36.45	21.24-56.31	56.41	66.18	20.61	22.32	85.20	39.18
14	Protein content	22.52	13.63-32.36	24.07	24.78	21.79	22.11	97.10	44.23
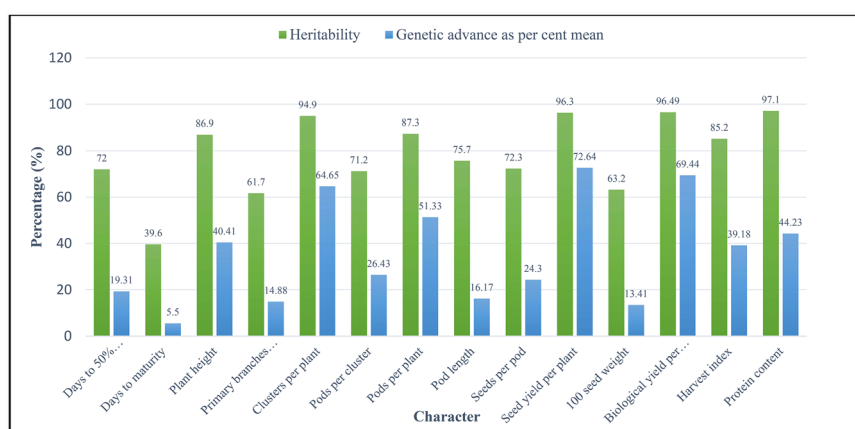
Fig. 1. Graphical representation of broad sense heritability and genetic advance as per cent of mean.

Navsari Agricultural University. The experiment was laid out in Randomized Complete Block Design with three replications and recommended agronomic practices were followed to raise the crop. Each genotype was grown in a single row with inter-row spacing of 45 cm and intra-row spacing of 15 cm. Observations for plant height (cm), primary branches per plant, clusters per plant, pods per cluster, pods per plant, pod length (cm), seeds per pod, seed yield per plant (g), 100 seed weight (g), biological yield per plant (g), harvest index (%) and protein content (%) were recorded from five randomly selected plants. The data were subjected to statistical analysis by the usual method of analysis of variance (Panse and Sukhatme 1978). Genotypic (GCV) and phenotypic (PCV) co-efficient of variation were calculated based on the formula given by Burton (1952). Heritability in broad sense was calculated according to Allard (1960) and was expressed in percentage. The genetic advance (GAM) as per cent of mean was classified according to Johnson *et al.* (1955). Phenotypic and genotypic correlations were worked out using the formulae suggested by Singh and Choudhary (1985). The direct and indirect effects of yield attributing traits on seed yield were calculated through path co-efficient analysis as suggested by Wright (1921) and used by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Analysis of variance exhibited significant differences among 45 genotypes for all fourteen characters,

indicating the presence of ample genetic variability among the genotypes (Table 1). The genotypic coefficients of variation for all characters except for days to maturity were lesser than phenotypic coefficient of variation indicating masking effects of environment (Fig. 1). The high genotypic and phenotypic coefficient of variation was observed for plant height (cm), clusters per plant, pods per plant, seed yield per plant (g), biological yield per plant (g), harvest index (%) and protein content (%) indicated the presence of adequate variability for these traits in the population studied. The estimates of GCV and PCV were moderate for days to 50% flowering, pods per cluster and seeds per pod whereas days to maturity, primary branches per plant, pod length and 100 seed weight exhibited lower estimates of GCV and PCV.

Variance components and other genetic parameters are given in Table 2. The high heritability coupled with high genetic advance were recorded for plant height (h^2b=86.9%, GAM=40.41%), number of clusters per plant (h^2b=94.90%, GAM=64.65%), pods per plant (h^2b=87.30%, GAM=51.33%), pods per cluster (h^2b=71.20%, GAM=26.43%), seeds per pod (h^2b=72.30%, GAM=24.3%), seed yield per plant (h^2b=96.30%, GAM=72.64%), biological yield per plant (h^2b=96.49%, GAM=69.44%), harvest index (h^2b=85.20%, GAM=39.18%) and protein content (h^2b=97.10%, GAM=44.23%) which indicated that selection would be effective for improvement due to predominance of additive gene action in the expression of these characters (Fig. 1). Days to 50%

768

Table 3. Genotypic correlation coefficients and phenotypic correlation coefficients among different characters in blackgram. *p <0.05 and **p <0.01. Note = DFF- Days to 50% flowering, DM- Days to maturity, PH- Plant height, PBPP- Primary branches per plant, CPP- Clusters per plant, PPC- Pods per cluster, PPP- Pods per plant, PL- Pod length, SPP- Seeds per pod, SYPP- Seed yield per plant, SW- 100-seed weight, BY- Biological yield per plant, HI- Harvest index and PC- Protein content.

Character		DFF	DM	PH	PBPP	CPP	PPC	PPP	PL	SPP	SYPP	SW	BY	HI	PC
DFF	rg	1.00	0.30*	0.51**	0.43**	0.53**	-0.20	0.51**	-0.01	0.08	0.43**	0.32*	0.53**	-0.12	0.38*
	rp	1.00	0.16	0.40**	0.31**	0.44**	-0.13	0.42**	-0.01	0.055	0.36**	0.18*	0.44**	-0.08	0.32**
DM	rg		1.00	0.35*	0.06	0.15	0.15	0.28	-0.10	-0.40**	-0.01	-0.06	0.19	-0.28	0.09
	rp		1.00	0.19*	0.08	0.12	0.16	0.20*	0.01	-0.22*	-0.01	-0.03	0.10	-0.15	0.04
PH	rg			1.00	0.01	0.33*	0.14	0.50**	0.21	-0.05	0.40**	0.31*	0.48**	-0.07	0.29
	rp			1.00	0.042	0.30**	0.12	0.41**	0.17	-0.03	0.38**	0.22**	0.43**	-0.03	0.27**
PBPP	rg				1.00	0.49**	-0.23	0.44**	-0.15	0.39**	0.56**	0.34*	0.47**	0.24	0.29
	rp				1.00	0.36**	-0.19*	0.31**	-0.09	0.25**	0.44**	0.21*	0.34**	0.22*	0.24**
CPP	rg					1.00	-0.56**	0.84**	-0.13	0.07	0.70**	0.30*	0.80**	-0.08	0.53**
	rp					1.00	-0.43**	0.77**	-0.10	0.07	0.67**	0.24**	0.76**	-0.07	0.50**
PPC	rg						1.00	0.03	0.12	-0.04	0.02	0.07	-0.21	0.35*	-0.23
	rp						1.00	0.017	0.08	-0.04	0.02	0.07	-0.18*	0.29**	-0.19*
PPP	rg							1.00	-0.09	0.09	0.88**	0.33*	0.85**	0.13	0.44**
	rp							1.00	-0.06	0.07	0.80**	0.24**	0.79**	0.08	0.40**
PL	rg								1.00	-0.06	-0.11	0.21	-0.12	0.05	0.25
	rp								1.00	-0.07	-0.10	0.12	-0.10	0.04	0.21*
SPP	rg									1.00	0.55**	0.25	0.16	0.64**	0.25
	rp									1.00	0.46**	0.11	0.13	0.50**	0.22**
SYPP	rg										1.00	0.54**	0.79**	0.38*	0.45**
	rp										1.00	0.42**	0.78**	0.38**	0.44**
SW	rg											1.00	0.49**	0.15	0.35*
	rp											1.00	0.38**	0.11	0.29**
BY	rg												1.00	-0.23	0.47**
	rp												1.00	-0.24**	0.45**
HI	rg													1.00	0.11
	rp													1.00	0.09
PC	rg														1.00
	rp														1.00

flowering (h^2b=72.00%, GAM=19.31%), primary branches per plant (h^2b=61.70%, GAM=14.88%), pod length (h^2b=75.70%, GAM=16.17%) and 100 seed weight (h^2b=63.20%, GAM=13.41%) exhibited high heritability coupled with moderate genetic advance as percent of mean indicating that these characters are governed by non-additive gene action and hence, population improvement approach would be effective for improvement of this character.

Similar findings had been reported by Hemalatha and Lal (2017), Senthamizhselvi *et al.* (2019) and Saran and Sharma (2021), where clusters per plant, pods per plant and seed yield per plant exhibited high heritability coupled with high genetic advance as per cent of mean.

Estimation of correlation coefficients between different pair of traits (Table 3) under study revealed that seed yield was positively correlated with all the characters viz Biological yield per plant (rg = 0.79** and rp = 0.78**), harvest index (rg = 0.38* and rp = 0.38**), 100 seed weight (rg = 0.54** and rp = 0.415**), clusters per plant (rg = 0.70** and rp = 0.666**), plant height (rg =0.40** and rp = 0.377**), pods per plant (rg = 0.88** and rp = 0.802**), seeds per pod (rg = 0.55** and rp = 0.457**), primary branches (rg = 0.56** and rp = 0.436**), days to 50 % flowering (rg = 0.43** and rp = 0.357**) and protein content (rg = 0.45** and rp = 0.436**) except with pod length (rg = -0.11 and rp = -0.099) and days to maturity (rg= -0.01and rp= -0.01) both at genotypic and phenotypic level (Table 3). Clusters per plant was positively and significantly correlated with pods per plant (rg=0.84** and rp=0.766**) whereas it was negatively correlated with pods per cluster
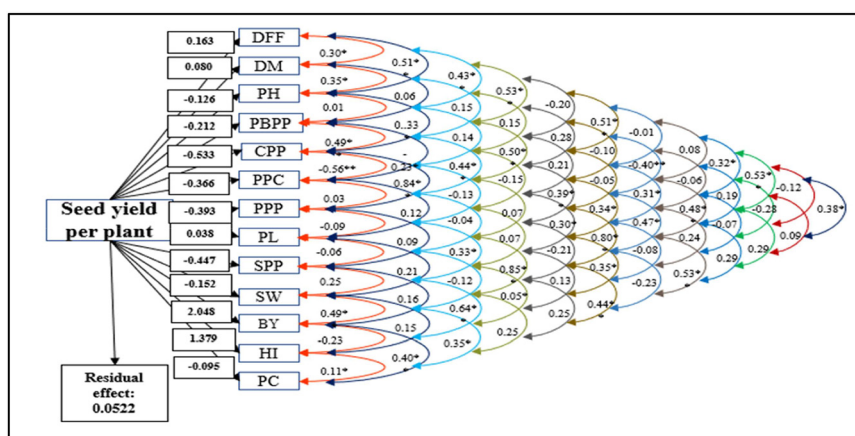
Fig. 2. Path diagram showing direct effect (values in square box) and correlation among various traits (values in curve arrow). Note: DFF- Days to 50% flowering, DM- Days to maturity, PH- Plant height, PBPP- Primary branches per plant, CPP- Clusters per plant, PPC- Pods per cluster, PPP- Pods per plant, PL- Pod length, SPP- Seeds per pod, SYPP- Seed yield per plant, SW- 100-seed weight, BY- Biological yield, HI- Harvest index and PC- Protein content.

(rg=-0.56**and rp=-0.43**). A highly significant and positive correlation was observed between seeds per pod and harvest index (rg= 0.64** and rp= 0.501**).

Days to 50% flowering exhibited high positive and significant correlation at both phenotypic and genotypic levels with plant height (rg=0.51** and rp=0.396**). Biological yield per plant was significantly and positively correlated with pods per plant (rg=0.85** and rp=0.79**), clusters per plant (rg=0.80** and rp=0.76**), plant height (rg=0.48** and rp=0.43**), days to 50% flowering (rg=0.53** and rp=0.44**) and protein content (rg=0.47** and rp=0.45**) whereas it was negatively associated with harvest index (rg=-0.23 and rp=-0.24**). Similar findings were reported by Mohanlal *et al.* (2018) where seed yield per plant was positively correlated with plant height, clusters per plant, pods per plant and seeds per pod and same as in the study carried out by Shanthi *et al.* (2019) where seed yield per plant was positively correlated with pods per plant and clusters per plant. In an evaluation carried out by Sathees *et al.* (2019) seed yield per plant was positively associated with plant height, primary branches, pods per plant, clusters per plant, number of seeds per pod and hundred seed weight.

Direct and indirect effects are depicted in Table 4. The characters viz., plant height (-0.126), prima-ry branches per plant (-0.212), clusters per plant (-0.533), pods per cluster (-0.366), pods per plant (-0.393), seeds per pod (-0.447), hundred seed weight (-0.152) and protein content (-0.095) showed significant positive correlation and negative direct effect on seed yield per plant (Fig. 2). All the characters except pods per cluster, pod length and harvest index showed high positive indirect effect on seed yield per plant *via* biological yield per plant whereas, days to 50% flowering (-0.283), primary branches per plant (-0.258), pods per plant (-0.445), biological yield per plant (-0.428) and protein content (-0.281) showed high negative indirect effects on seed yield per plant *via* clusters per plant. Clusters per plant showed high negative indirect effect on seed yield per plant *via* pods per plant (-0.328) while biological yield per plant showed high negative indirect effect *via* pods per plant (-0.334) and clusters per plant (-0.428). Primary branches per plant (0.328)), pods per cluster (0.484), pods per plant (0.177), seeds per pod (0.882), 100 seed weight (0.206) and protein content (0.145) showed high positive indirect effect *via* seed yield per plant.

It is extremely difficult to obtain complete knowledge of all yield component qualities in plant breeding. The residual effect at the genotypic level in the current study was 0.052, revealing that the study included major yield contributing characteristics (Table 4). Considering the magnitude of character

Table 4. Genotypic path coefficient analysis showing direct and indirect effects of different characters on seed yield in blackgram. Diagonal values indicate direct effects.   Residual effect = 0.0522, Note = DFF- Days to 50% flowering, DM- Days to maturity, PH- Plant height, PBPP- Primary branches per plant, CPP- Clusters per plant, PPC- Pods per cluster, PPP- Pods per plant, PL- Pod length, SPP- Seeds per pod, SYPP- Seed yield per plant, SW- 100-seed weight, BY- Biological yield per plant, HI- Harvest index and PC- Protein content.

Cha-racter	DF	DM	PH	PBPP	CPP	PPC	PPP	PL	SPP	SW	BY	HI	PC	rg
DF	**0.163**	0.024	-0.064	-0.090	-0.283	0.072	-0.199	0.000	-0.036	-0.049	1.090	-0.160	-0.036	0.43 **
DM	0.048	**0.080**	-0.045	-0.013	-0.082	-0.054	-0.109	-0.004	0.180	0.009	0.381	-0.391	-0.009	-0.01
PH	0.082	0.028	**-0.126**	-0.002	-0.174	-0.052	-0.197	0.008	0.020	-0.047	0.978	-0.090	-0.027	0.40 **
PBPP	0.069	0.005	-0.001	**-0.212**	-0.258	0.085	-0.172	-0.006	-0.173	-0.052	0.971	0.328	-0.027	0.56 **
CPP	0.086	0.012	-0.041	-0.103	**-0.533**	0.206	-0.328	-0.005	-0.032	-0.046	1.647	-0.113	-0.050	0.70 **
PPC	-0.032	0.012	-0.018	0.049	0.299	**-0.366**	-0.011	0.004	0.017	-0.010	-0.427	0.484	0.022	0.02
PPP	0.082	0.022	-0.063	-0.093	-0.445	-0.011	**-0.393**	-0.003	-0.041	-0.051	1.742	0.177	-0.041	0.88 **
PL	-0.002	-0.008	-0.026	0.031	0.069	-0.044	0.035	**0.038**	0.026	-0.032	-0.250	0.075	-0.023	-0.11
SPP	0.013	-0.032	0.006	-0.082	-0.038	0.014	-0.036	-0.002	**-0.447**	-0.038	0.332	0.882	-0.024	0.55 **
SW	0.052	-0.005	-0.039	-0.072	-0.161	-0.024	-0.131	0.008	-0.112	**-0.152**	1.006	0.206	-0.034	0.54 **
BY	0.087	0.015	-0.060	-0.101	-0.428	0.076	-0.334	-0.005	-0.072	-0.075	**2.048**	-0.313	-0.044	0.79 **
HI	-0.019	-0.023	0.008	-0.050	0.044	-0.129	-0.050	0.002	-0.286	-0.023	-0.464	**1.379**	-0.010	0.38 *
PC	0.062	0.007	-0.036	-0.060	-0.281	0.086	-0.172	0.009	-0.113	-0.054	0.956	0.145	**-0.095**	0.45 **

association, as well as their direct and indirect impacts, it is reasonable to conclude that simultaneous improvement of seed yield per plant is achievable *via* manifestation of biological yield per plant, harvest index and days to 50% flowering.

CONCLUSION

Existence of variability among the blackgram genotypes illustrates that the selection will be effective in enhancing the seed yield. Plant height, number of clusters per plant, number of pods per plant, pods per cluster, number of seeds per pod, seed yield per plant, biological yield per plant, harvest index and protein content showed high heritability coupled with high genetic advance which indicated that these characters are governed by additive gene action and thus selection would be effective. Correlation studies illustrated that pods per plant and clusters per plant were economically significant and were positively associated with seed yield and hence enhancing these characteristics would improve seed yield. Path analysis estimates confirmed that biological yield per plant and harvest index had a true relationship with seed yield per plant by establishing a strong positive association and a very high positive direct effect on seed yield per plant. As a result, biological yield and harvest index should be given integral importance during the selection process in order to increase seed yield per plant in blackgram.

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