



RESEARCH ARTICLE

# Genetic Variability, Association and Path Coefficient Analyses in Segregating Populations of Black Gram (*Vigna mungo* (L.) Hepper)

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## ABSTRACT

The experiment was conducted at the National Pulses Research Centre, Vamban, during *Kharif* 2020. F<sub>2</sub> generation of four crosses was utilized in this study. Around 150-200 single plants per cross were used for observation. The traits viz., plant height, number of branches per plant, number of cluster per plant, number of pods per cluster, number of pods per plant, 100 - seed weight and seed yield per plant recorded high PCV, GCV, high heritability along with high genetic advance as per cent of the mean. It indicated that these traits were less influenced by the environment and possessed high genetic variability. Also, these traits had a positive and significant correlation with seed yield in most of the crosses. The trait number pods per plant recorded positive and high direct effects on seed yield. Hence, based on correlation and path analyses, the number of pods per plant can be considered as a selection index for seed yield improvement programme in blackgram. However, population-specific selection indices are preferred as the association of traits varies with the populations.

**Keywords :** *Blackgram; Segregating population; Variability studies; Correlation analysis; Path analysis*

## INTRODUCTION:

Blackgram is an important food legume that is widely cultivated in Asia as a short-duration crop. It is suitable for all cropping seasons and is also cultivated as intercrop, mixed crop, catch crop, and bund crop. The nutritional quality of blackgram was high. It has high seed protein (25-26%), carbohydrates (60%), minerals, vitamins and is also rich in sulphur-containing amino acids (Bandi *et al.*, 2018). Blackgram has a symbiotic association with *Rhizobium* bacteria; hence it can fix atmospheric nitrogen and improve soil fertility. As the world's population rises, the demand for grain legumes is also growing and agriculture is struggling to meet the increasing demands. High yielding genotypes need knowledge about existing genetic variation and the association among yield contributing characters. The development of a suitable plant breeding program is dependent on the presence of genetic variability. Heritability is an important parameter that determines the extent of expressivity of a trait. Heritability estimation and genetic advance as per cent of mean (GAM) are more useful in assessing the gain under selection than predicted heritability alone (Falconer, 1960). Yield is a highly complex trait because the number of component traits governs it.

So, an assessment of the interrelationship between the yield components and seed yield will be helpful in selecting a suitable and effective breeding program. Association analysis provides measures of relationship between the traits and assesses the chance for the mutual improvement of two desirable characters by common selection programme (Kumar *et al.*, 2003). Estimation of correlation coefficient enables to eliminate the characters with little or no importance during selection. Path coefficient analysis suggested by Dewey and Lu (1959) proves helpful in partitioning the correlation coefficient into its direct and indirect effects. If the correlation is due to direct effect, it reflects a true and perfect relationship and such characters can be directly subjected to selection for improving yield. Hence, the present investigation was proposed to estimate the genetic variability and determine the character association by employing correlation coefficients and path analysis for obtaining a higher yield.

## MATERIAL AND METHODS

The present research work was carried out at the National Pulses Research Centre, Vamban, during *Kharif* 2020. Four different cross combinations in F<sub>2</sub> generation viz., VBN (Bg) 4 x CO 5, VBN (Bg) 4 x APK

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1, VBN (Bg) 4 x Mash 1008, and CO 5 x TU 68 along with their parents were studied. In each  $F_2$  cross combination, around 150 plants were maintained. Observations were recorded on plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, the total number of pods, pod length (cm), number of seeds per pod, 100-seed weight (g) and seed yield per plant (g). Observations were recorded on all single plants of cross combinations and parents. For each character, phenotypic and genotypic coefficients of variability (PCV and GCV) were computed based on the method given by Burton (1952). Heritability in a broad sense was estimated by the method suggested by Lush (1949). The expected genetic gain under selection was estimated by the method suggested by Johnson *et al.* (1955). As suggested by Dewey and Lu (1959), path coefficient analysis was carried out. The TNAUSTAT software (Manivannan, 2014) analyzed the variability, correlation, and path coefficients.

## RESULT AND DISCUSSION

Variability analysis helps to identify the significant variation present among genotypes for a trait. Phenotypic Coefficient of Variation, Genotypic Coefficient of Variation, heritability and Genetic Advance as percent of mean of the four  $F_2$  populations are presented in Table 1. The trait *viz.*, number of branches per plant PCV=45.99 - 91.70; GCV=27.51 - 77.36), number of clusters per plant (PCV=44.39 - 56.00; GCV=38.93 - 52.88), number of pods per plant(PCV=52.80 - 66.91; GCV=44.83 - 61.28) and seed yield per plant (PCV=53.85 - 65.89; GCV=39.76 - 49.27) had high PCV and GCV for all the four crosses. Similarly, Thirumalai and Murugan (2020) recorded higher PCV for plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, and seed yield per plant. Sathees *et al.* (2019) observed higher GCV for the number of branches per plant, number of clusters per plant, number of pods per plant, and seed yield per plant. Days to first flowering recorded low PCV and GCV for all the crosses. The other traits *viz.*, plant height, number of pods per cluster, pod length, number of seeds per pod, and hundred seed weight, recorded a higher phenotypic coefficient of variation than the genotypic coefficient of variation for most of the crosses. Similarly, Sushmitharaj *et al.* (2018) reported moderate PCV for number of seeds per pod. Moderate GCV for plant height and 100-seed weight was previously observed by Sushmitharaj *et al.* (2018). Bishnoi *et al.* (2017) observed the low GCV for pod length and number of seeds per pod.

**Table 1. Variability parameters of yield components on yield per plant in  $F_2$  generations of various crosses**

Character	Crosses	PCV (%)	GCV (%)	Heritability (%)	GAM (%)
Days to first flowering	C1	8.23	7.68	86.98	14.53
	C2	7.69	7.24	88.52	13.82
	C3	8.22	7.57	84.70	14.14
	C4	7.69	7.09	84.98	13.27
Plant height (cm)	C1	22.86	22.63	97.98	46.14
	C2	21.65	16.43	57.58	25.68
	C3	21.12	18.16	73.95	32.17
	C4	28.90	22.79	62.19	37.02
Number of branches per plant	C1	55.41	37.31	45.34	51.75
	C2	52.19	34.88	44.65	48.01
	C3	91.70	77.36	71.17	134.44
	C4	45.99	27.51	35.78	33.90
Number of clusters per plant	C1	44.39	43.30	95.16	87.01
	C2	54.48	47.07	74.63	83.77
	C3	49.42	38.93	62.06	63.18
	C4	56.00	52.88	89.15	102.84
Number of pods per cluster	C1	34.35	23.72	47.67	33.73
	C2	28.43	18.69	43.20	25.30
	C3	28.73	16.72	33.85	20.04
	C4	26.09	17.39	44.44	23.88
Number of pods per plant	C1	52.80	52.63	99.38	108.09
	C2	64.99	55.77	73.62	98.57
	C3	60.13	44.83	55.59	68.86
	C4	66.91	61.28	83.89	115.63
Pod length (cm)	C1	19.14	12.56	43.07	16.98
	C2	19.27	11.07	33.00	13.10
	C3	20.15	11.63	33.33	13.83
	C4	12.90	5.06	15.38	4.09
Number of seeds per pod	C1	13.54	12.93	91.28	25.46
	C2	15.73	7.02	19.90	6.45
	C3	16.60	10.29	38.43	13.14
	C4	12.09	1.55	1.64	0.41
100-seed weight (g)	C1	21.90	16.04	53.61	24.19
	C2	15.85	7.76	23.96	7.82
	C3	19.11	8.59	20.18	7.94
	C4	15.11	12.42	67.65	21.05
Seed yield per plant (g)	C1	53.85	48.76	81.99	90.96
	C2	64.03	49.27	59.21	78.10
	C3	65.89	43.55	43.70	59.31
	C4	65.66	39.76	36.67	49.60

C1-VBN(Bg) 4 x CO 5; C2-VBN(Bg) 4 x APK 1; C3-VBN(Bg) 4 x Mash 1008; C4-CO 5 x TU 68

High heritability coupled with low genetic advance indicates the presence of non-additive gene action and selection for such traits may not be rewarding. High heritability and high genetic advance and low

heritability accompanied with high genetic advance indicate the presence of additive gene effect. Selection may be effective in such cases (Nadarajan *et al.*, 2018). Low heritability with low genetic advance suggests that the environment highly

affects the trait. In such instances, selection would be ineffective. Days to first flowering recorded high heritability with moderate GAM for all four crosses. Plant height recorded high heritability with high GAM for all the crosses except VBN(Bg) 4 x APK 1.

**Table 2. Simple correlation coefficient between yield and yield attributes in F<sub>2</sub> generations of various crosses in blackgram**

Character	Crosses	DFF	PH	NBPP	NCPP	NPPC	NPPP	PL	NSPP	HSW
Plant height (cm)	C1	0.04								
	C2	-0.05								
	C3	0.11								
	C4	0.02								
Number of branches per plant	C1	-0.08	0.41**							
	C2	0.03	0.42**							
	C3	-0.03	0.18*							
	C4	0.08	0.41**							
Number of clusters per plant	C1	-0.12	0.55**	0.68**						
	C2	-0.07	0.50**	0.74**						
	C3	-0.03	0.30**	0.73**						
	C4	-0.03	0.49**	0.53**						
Number of pods per cluster	C1	-0.14	0.31**	0.18**	0.25**					
	C2	-0.15	0.18*	0.26**	0.30**					
	C3	0.16	0.21*	0.20*	0.26**					
	C4	0.02	0.26**	0.29**	0.34**					
Number of pods per plant	C1	-0.11	0.62**	0.62**	0.86**	0.54**				
	C2	-0.04	0.23**	0.36**	0.45**	0.14				
	C3	0.09	0.14	0.53**	0.67**	0.51**				
	C4	-0.02	0.49**	0.55**	0.92**	0.43**				
Pod length (cm)	C1	0.02	0.00	0.04	-0.01	0.03	0.04			
	C2	-0.23	-0.13	0.02	0.04	0.01	0.18*			
	C3	0.13	-0.02	-0.03	-0.02	0.11	0.05			
	C4	0.08	0.28**	0.33**	0.29**	0.16*	0.34**			
Number of seeds per pod	C1	-0.04	-0.02	0.07	0.07	0.06	0.09	0.81**		
	C2	-0.05	-0.14	0.00	-0.02	0.04	0.20**	0.75**		
	C3	0.03	-0.10	0.08	0.09	0.12	0.10	0.47**		
	C4	0.14	0.26**	0.31**	0.40**	0.26**	0.41**	0.72**		
100-seed weight (g)	C1	-0.02	0.42**	0.38**	0.52**	0.30**	0.57**	0.05	0.06	
	C2	0.02	0.04	-0.05	0.15	0.00	0.30**	0.04	0.18**	
	C3	0.05	0.11	0.42**	0.44**	0.24**	0.43**	0.11	0.13	
	C4	-0.08	0.13	-0.05	-0.15	-0.09	-0.12	0.11	0.06	
Seed yield per plant (g)	C1	-0.12	0.60**	0.60**	0.83**	0.50**	0.94**	0.06	0.13	0.66**
	C2	-0.07	0.21*	0.34**	0.41**	0.16	0.94**	0.19*	0.21	0.29**
	C3	0.12	0.17*	0.62**	0.62**	0.31**	0.70**	-0.01	0.05	0.67**
	C4	-0.03	0.49**	0.53**	0.84**	0.49**	0.92**	0.35**	0.45**	0.00

C1-VBN(Bg) 4 x CO 5; C2-VBN(Bg) 4 x APK 1; C3-VBN(Bg) 4 x Mash 1008; C4-CO 5 x TU 68

\*,\*\* Significant at 5 % and 1 % level of probability, respectively.

Similarly, Sushmitharaj *et al.* (2018) recorded high heritability and high GAM for the trait plant height. High heritability with high GAM was observed for the trait number of branches per plant for the

cross VBN(Bg) 4 x Mash 1008. The remaining crosses recorded moderate heritability with high GAM. Thirumalai and Murugan (2020) recorded high heritability and high GAM for number of branches

per plant. The number of clusters per plant, number of pods per plant recorded high heritability and high GAM for all the cross except VBN(Bg) 4 x Mash 1008. Sushmitharaj *et al.* (2018) also observed the high heritability and GAM for number of clusters per plant and number of pods per cluster. Pod length recorded

moderate heritability and moderate GAM for most of the crosses. The traits number of seeds per pod and 100-seed weight recorded various levels of heritability and GAM. Seed yield per plant recorded moderate heritability and high GAM. Similar results were observed by Anuradha *et al.* (2020)

**Table 3. Direct and indirect effect of yield components on yield per plant in F<sub>2</sub> generations of various crosses**

Character	Crosses	DFP	PH	NBPP	NCPP	NPPC	NPPP	PL	NSPP	HSW	Simple correlation coefficient with seed yield per plant (g)
Days to first flowering	C1	<b>-0.03</b>	0.00	0.00	0.00	0.00	-0.08	0.00	0.00	0.00	-0.12
	C2	<b>-0.04</b>	0.00	0.00	0.00	0.00	-0.03	0.00	0.00	0.00	-0.07
	C3	<b>0.08</b>	0.00	-0.00	0.00	-0.01	0.04	-0.00	-0.00	0.01	0.11
	C4	<b>-0.02</b>	0.00	0.00	0.00	0.00	-0.01	0.00	0.01	-0.01	-0.03
Plant height(cm)	C1	0.00	<b>0.02</b>	0.01	0.02	0.00	0.47	0.00	0.00	0.08	0.60**
	C2	0.00	<b>0.00</b>	0.01	-0.02	0.01	0.21	0.00	0.00	0.00	0.21*
	C3	0.01	<b>0.04</b>	0.04	-0.01	-0.01	0.06	0.00	0.00	0.04	0.17*
	C4	0.00	<b>0.01</b>	0.01	0.03	0.03	0.38	-0.01	0.02	0.01	0.49**
Number of branches per plant	C1	0.00	<b>0.01</b>	<b>0.02</b>	0.03	0.00	0.48	0.00	0.01	0.07	0.60**
	C2	0.00	<b>0.00</b>	<b>0.04</b>	-0.03	0.01	0.33	0.00	0.00	0.00	0.34**
	C3	-0.00	<b>0.01</b>	<b>0.23</b>	-0.02	-0.01	0.24	0.00	0.00	0.17	0.62**
	C4	0.00	<b>0.00</b>	<b>0.02</b>	0.04	0.03	0.43	-0.01	0.02	-0.01	0.53**
Number of clusters per plant	C1	0.00	<b>0.01</b>	<b>0.01</b>	<b>0.04</b>	0.00	0.66	0.00	0.01	0.09	0.83**
	C2	0.00	<b>0.00</b>	<b>0.03</b>	<b>-0.05</b>	0.01	0.42	0.00	0.00	0.00	0.41**
	C3	-0.00	<b>0.01</b>	<b>0.17</b>	<b>-0.03</b>	-0.02	0.31	0.00	0.00	0.18	0.62**
	C4	0.00	<b>0.00</b>	<b>0.01</b>	<b>0.07</b>	0.04	0.71	-0.01	0.03	-0.02	0.84**
Number of pods per cluster	C1	0.00	<b>0.01</b>	0.00	<b>0.01</b>	<b>0.01</b>	0.42	0.00	0.01	0.05	0.50**
	C2	0.01	<b>0.00</b>	0.01	<b>-0.01</b>	<b>0.03</b>	0.13	0.00	0.00	0.00	0.16
	C3	0.01	<b>0.01</b>	0.05	<b>-0.01</b>	<b>-0.07</b>	0.24	-0.01	0.00	0.10	0.31**
	C4	0.00	<b>0.00</b>	0.01	<b>0.02</b>	<b>0.12</b>	0.33	0.00	0.02	-0.01	0.49**
Number of pods per plant	C1	0.00	<b>0.01</b>	0.01	0.04	<b>0.00</b>	<b>0.76</b>	0.00	0.01	0.10	0.94**
	C2	0.00	<b>0.00</b>	0.01	-0.02	<b>0.00</b>	<b>0.93</b>	0.01	0.00	0.01	0.94**
	C3	0.01	<b>0.01</b>	0.12	-0.02	<b>-0.03</b>	<b>0.46</b>	0.00	0.00	0.18	0.70**
	C4	0.00	<b>0.00</b>	0.01	0.06	<b>0.05</b>	<b>0.78</b>	-0.01	0.03	-0.01	0.92**
Pod length (cm)	C1	0.00	<b>0.00</b>	0.00	0.00	0.00	<b>0.03</b>	<b>-0.07</b>	0.08	0.01	0.06
	C2	0.01	<b>0.00</b>	0.00	0.00	0.00	<b>0.17</b>	<b>0.03</b>	-0.01	0.00	0.19*
	C3	0.01	<b>0.00</b>	-0.01	0.00	-0.01	<b>0.02</b>	<b>-0.05</b>	-0.01	0.05	-0.01
	C4	0.00	<b>0.00</b>	0.01	0.02	0.02	<b>0.26</b>	<b>-0.02</b>	0.05	0.01	0.35**
Number of seeds per pod	C1	0.00	<b>0.00</b>	0.00	0.00	0.00	<b>0.07</b>	<b>-0.05</b>	<b>0.10</b>	0.01	0.13
	C2	0.00	<b>0.00</b>	0.00	0.00	0.00	<b>0.19</b>	<b>0.02</b>	<b>-0.01</b>	0.00	0.21*
	C3	0.00	<b>0.00</b>	0.02	0.00	-0.01	<b>0.05</b>	<b>-0.02</b>	<b>-0.03</b>	0.05	0.05
	C4	0.00	<b>0.00</b>	0.01	0.03	<b>0.03</b>	<b>0.32</b>	<b>-0.02</b>	<b>0.08</b>	0.01	0.45**
100-seed weight (g)	C1	0.00	0.01	0.01	0.02	0.00	0.44	0.00	<b>0.01</b>	<b>0.18</b>	0.66**
	C2	0.00	0.00	0.00	-0.01	<b>0.00</b>	0.28	0.00	<b>0.00</b>	<b>0.02</b>	0.29**
	C3	0.00	0.00	0.10	-0.01	<b>-0.02</b>	0.20	-0.01	<b>0.00</b>	<b>0.41</b>	0.67**
	C4	0.00	0.00	0.00	-0.01	<b>-0.01</b>	<b>-0.09</b>	<b>0.00</b>	<b>0.00</b>	<b>0.11</b>	0.00

Residual effects: 0.30 (C1); 0.33 (C2); 0.54 (C3); 0.37 (C4)

C1-VBN(Bg) 4 x CO 5; C2-VBN(Bg) 4 x APK 1; C3-VBN(Bg) 4 x Mash 1008; C4-CO 5 x TU 68

\* Bold figures denote direct effects.

\*,\*\* Significant at 5 % and 1 % level of probability, respectively.

Association studies used to select the desirable yield attributing traits to improve the seed yield. In this study, the traits viz., plant height, number of branches per plant, number of clusters per plant, number of pods per plant recorded significant and positive correlation with seed yield per plant in all four crosses (Table 2). These results are in close agreement with Sathya *et al.* (2018) for plant height, Dheeraj *et al.* (2020) for number of branches per plant, Sridhar *et al.* (2019) for the number of clusters per plant, and Teja and Lal (2021) for the number of pods per plant. The number of pods per cluster recorded a positive and significant correlation with seed yield in all the cross except VBN(Bg) 4 x APK 1. Reddy *et al.* (2020) observed a similar finding. Pod length recorded a significant and positive correlation with yield in VBN(Bg) 4 x APK 1 and CO 5 x TU 68. Similar results were reported by Sathees *et al.* (2019). Number of seeds per pod recorded a significant and positive correlation with seed yield in only one cross CO 5 x TU 68. Gomathi *et al.* (2020) observed similar findings. The trait 100-seed weight recorded a significant and positive correlation with seed yield per plant in all the crosses except CO 5 x TU 68. These results are in close agreement with Radhikaben and Bala (2020).

Path coefficient analysis helps partition the correlation coefficient into its direct and indirect effects (Table 3). In the present study, number of pods per plant had a high and positive direct effect on seed yield in all four populations. The trait 100-seed weight recorded a high and positive direct effect on seed yield in the cross VBN(Bg) 4 x Mash 1008 alone. Number of branches per plant recorded moderate and positive direct effect on seed yield in the cross VBN(Bg) 4 x Mash 1008. Number of pods per cluster and number of seeds per pod recorded low and positive direct effect on seed yield in CO 5 x TU 68 and VBN(Bg) 4 x CO 5, respectively. The residual effect of all four crosses, was ranged between 0.30-0.54. It clearly explains the observed characters were more appropriate for the path analysis on seed yield per plant. These results are in close agreement with Sathya *et al.* (2018) for high direct effect on number of pods per plant, Gomathi *et al.* (2020) for high direct effect on 100 - seed weight. Among various traits, number of pods per plant alone showed high to moderate and positive indirect effects for most of the characteristics. Saran *et al.* (2020) reported a positive and high indirect effect on seed yield per plant via the number of pods per cluster and pod length.

## CONCLUSION

Based on the previous discussion, it can be concluded that there was sufficient genetic variability in the segregating populations studied

for all the characters. The traits viz., plant height, number of cluster per plant, number of pods per cluster, number of pods per plant, and seed yield per plant indicated high heritability along with high genetic advance as per cent of mean. Hence, the environment influenced these traits and possessed high genetic variability. Hence, selection can be practiced for these traits in these populations. Association studies revealed the plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant and 100-seed weight were positive and significant association with seed yield per plant. The path analysis indicated that number of pods per plant had positive and high direct effects. Most of the traits also had high to moderate positive indirect effects via number of pods per plant. However other characteristics like 100-seed weight and number of branches per plant had high or moderate and positive direct effect in the cross VBN(Bg) 4 x CO 5 alone. Hence, based on correlation and path analyses, it can be concluded that the number of pods per plant can be considered as selection index for the seed yield improvement programme in blackgram. However, population-specific selection indices are preferred as the association of traits varies with the populations.

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### Ethics approval

The author declares that the study performed is true with novelty in the interpretations.

### Conflicts of interest/Competing interests:

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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