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Studies on Variability, Heritability, Correlation and Path Analysis in Segregating Population of Black Gram [*Vigna mungo* (L.) Hepper]

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ABSTRACT

Back ground: Pulses are an important source of protein in the human diet and black gram is a popular pulse crop in India. The black gram breeding program faces various drawbacks due to narrow genetic diversity accompanied by biotic and abiotic diseases which seriously affect the yield potential of the crop. Hence it is important to understand the gene action and to frame the efficient breeding program in black gram for yield improvement.

Methods: The present experiment was conducted during 2018-2019. Sixty-nine F_2 plants of the cross ADT3 × KKB14-052 were raised and nine biometrical traits were recorded. Genetic variability and association analysis were carried out.

Result: High PCV and GCV were obtained for the traits *viz.,* number of primary branches/ plant, number of clusters/plant, number of pods/plant and single plant yield. High heritability and high GAM were obtained for the traits *viz.,* plant height, number of primary branches/plant, number of clusters/plant, number of pods/plant, hundred seed weight, pod length and single plant yield. All the characters under the study were significantly positive correlation with yield except days to 50% flowering. Number of pods/plant showed a high positive, direct effect on single plant yield. Hence, these characters would be mainly focused in black gram breeding programs for yield improvement.

Key words: Black gram, Correlation, Path analysis, Variability.

INTRODUCTION

Black gram [*Vigna mungo* (L.) Hepper] is one of the important nutritious legumes widely cultivated in India as a short duration crop. Grain legumes play a critical position in meeting the necessities of dietary proteins in India. Black gram can easily fit into any cropping pattern as a sole crop, intercrop, mixed crop and catch crop. Black gram belongs to Leguminosae family and a self-pollinating crop. By fixing the atmospheric nitrogen in the soil it can improve the soil fertility level. Black gram seeds include excessive protein and lysine content than in cereals. Pulses are generally cultivated in marginally poor soils, normally in rainfed situations which results in low yield and hence yield improvement in black gram is the prime objective of a plant breeder. The achievement of high yield mainly depends on the magnitude of yield contributing traits and nature of genetic variability present in the crop (Johnson and Bernard, 1962). 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 (Bishnoi *et al.,* 2017). The correlation coefficient estimates, the degree and direction of association between a pair of characters were proved useful for simultaneous improvement of the correlated traits through selection (Panigrahi *et al.*, 2014). Path coefficient analysis, on the other hand, is an efficient statistical technique specially designed to quantify the interrelationship of different components and their direct and indirect effects on seed yield (Senthamizhselvi *et al*., 2019). Henceforth, present study targeted on genetic variability studies, correlation and path coefficient analysis for effective selection in the F_2 derivative cross of ADT3 × KKB14-052 in black gram.

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MATERIALS AND METHODS

The present experiment was conducted at Department of Plant Breeding and Genetics at Agricultural College and Research Institute, TNAU, Killikulam during 2019-2020. The experimental material used in this study consisted of

69 F_2 plants derived from the cross ADT3 × KKB14-052. Observations on biometrical traits *viz.,* plant height (cm), days to fifty per cent flowering, number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length (cm), hundred seed weight (g) and single plant yield (g) were recorded.

The pedigree information of the parents is given below.

Parents	Pedigree	Source
ADT3 (female)	Pure line selection from Tirunelveli local	Tamil Nadu Rice Research Institute, Aduthurai, TN, India.
KKB14-052 (male)	Cross derivative from PU06-20 × 2-107	Agricultural College and Research Institute, Killikulam, TN, India.

Along with the parents, all the 69 F_2 plants were raised in a spacing of 30 × 10 cm^2 in 3m length row and all the agronomic practices were carried out properly. The statistical techniques recommended by Johnson *et al.* (1955) for diverse genetic variability parameters *viz.,* genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as percent of mean (GAM) had been executed. Genotypic correlation coefficient was calculated by the formulae given by AL-Jibouri *et al.* (1958). Correlation and path coefficient analysis were carried out using TNAUSTAT software (Manivannan, 2014). Path analysis was also computed as direct and indirect effects of different components on yield using the procedure given by Dewey and Lu (1959). The R software program was used for preparing correlation chart (R Core Team, 2019).

RESULTS AND DISCUSSION

Variability studies

Estimation of phenotypic and genotypic coefficient of variation is important to find out the environmental interaction on various traits. Values of GCV and PCV for all the nine characters are furnished in Table 1. High PCV and GCV were obtained for single plant yield (65.70% and 64.33% respectively) followed by number of clusters per plant (46.14% and 45.06% respectively), number of pods per plant (43.64% and 42.48% respectively), number of primary branches per plant (30.45% and 24.37% respectively). These results were found in agreement with Sathees *et al.* (2019), where they studied 162 F_2 plants of a cross between IC 436656 × KKB 14045. Moderate PCV and GCV were obtained for plant height (17.73% and 16.74% respectively), 100 seed weight (19.64% and 19.36% respectively), pod length (12.50% and 12.30% respectively). These results are in agreement with Panigrahi *et al.* (2014), where they studied 19 genotypes of black gram. High PCV coupled with moderate GCV obtained for number of seeds per pod (21.28% and 14.24% respectively).

High heritability was recorded for the characters *viz.,* pod length (96.84%), hundred seed weight (97.21%), single plant yield (95.86%), number of clusters per plant (95.34%), number of pods per plant (94.72%), days to 50% flowering (89.86%), plant height (89.14%) and number of primary branches per plant (64.06%). Reddy *et al.* (2018) studied 30 black gram genotypes and reported high heritability for days to 50% flowering, plant height, number of clusters per plant, number of pods per plant and single plant yield. Konda *et al.* (2009b) reported high heritability for days to 50% flowering, plant height and hundred seed weight. High GAM was recorded for single plant yield (129.74%) followed by number of clusters per plant (90.62%), number of pods per plant (85.16%), number of primary branches per plant (40.18%), hundred seed weight (39.33%), plant height (32.55%) and pod length (24.94%). Number of seeds per pod (19.63%) and days to 50% flowering (14.11%) were exhibiting moderate GAM. These results are in harmony with the finding of Bandi *et al.* (2018) for the traits *viz.,* number of clusters per plant, number of pods per plant, number of primary branches per plant, hundred seed weight, single plant yield, days to 50% flowering and number of seeds per pod and number of seeds per pod which in 36 black gram genotypes of diverse origin.

High heritability coupled with high GAM was obtained for plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, hundred seed weight, pod length and single plant yield. Panigrahi *et al.* (2014) studies revealed that plant height, number of clusters per plant, number of pods per plant, hundred seed weight and pod length had high heritability coupled with high GAM. Bandi *et al.* (2018) reported high heritability coupled with high GAM for single plant yield.

Table 1: Variability parameters in F_2 derivatives of the cross ADT3 × KKB14-05.

Characters	PCV(%)	GCV(%)	(h^2)(%)	GAM (%)
Days to 50% flowering	7.62	7.23	89.86	14.11
Plant height	17.73	16.74	89.14	32.55
No. of primary branches per plant	30.45	24.37	64.06	40.18
No. of clusters per plant	46.14	45.06	95.34	90.62
No. of pods per plant	43.64	42.48	94.72	85.16
No. of seeds per pod	21.28	14.24	44.78	19.63
100 seed weight	19.64	19.36	97.21	39.33
Pod length	12.50	12.30	96.84	24.94
Single plant yield	65.70	64.33	95.86	129.74

Konda *et al.* (2009b) studied 40 genotypes and obtained similar result for plant height. High GAM coupled with high heritability refer to the presence of additive gene action for these traits which indicated the scope of improvement of these traits *via* selection.

Correlation

Correlation between different yield component traits are furnished in Table 2 and Fig 1. From the intra correlation studies, the characters plant height (0.39), number of primary branches per plant (0.68), number of clusters per plant (0.72), number of pods per plant (0.89), number of seeds per pod (0.67), hundred seed weight (0.41) and pod length (0.35) were significantly positive correlation with single plant yield and days to fifty per cent flowering was negatively correlated with single plant yield. This clearly exhibited that improvement of all the characters except days to fifty per cent flowering will ultimately increase the seed yield and particularly number of clusters per plant, number of pods per plant had greater association with yield. These results are in accordance with the earlier finding Sathees *et al.* (2019). Konda *et al.* (2009a) reported that positive significant association of single plant yield with number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per plant and pod length. Senthamizhselvi *et al.* (2019) also observed positive significance of number of pods per plant, plant height, number of primary branches per plant, number of clusters per plant and hundred seed weight.

From the inter correlation studies, days to 50% flowering was negative significant association with number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod and hundred seed weight. Plant height had positive significant with number of primary branches per plant (0.41), number of clusters per plant (0.38), number of pods per plant (0.46), number of

Table 2: Correlation coefficients among yield components in F_2 derivatives of the cross ADT3 × KKB14-052.

Characters	DFF	PH	NPBPP	NCPP	NPPP	NSPP	HSW	PL	SPY
DFF	1	0.06	-0.29**	-0.21*	-0.30**	-0.27**	-0.39**	-0.17	-0.41**
PH		1	0.41**	0.38**	0.46**	0.27**	0.09	0.23**	0.39**
NPBPP			1	0.65*	0.73**	0.36**	0.30**	0.09	0.68**
NCPP				1	0.86**	0.32**	0.11	0.16	0.72**
NPPP					1	0.44**	0.17	0.21*	0.89**
NSPP						1	0.24**	0.23**	0.67**
HSW							1	0.37**	0.41**
PL								1	0.35**
SPY									1

*Significance at 5% level, **Significance at 1% level.

(DFF- Days to 50% flowering (days), PH- Plant height (cm), NPBPP- Number of primary branches per plant, NCPP- Number of cluster per plant, NPPP- Number of pods per plant, NSPP- Number of seeds per pod, HSW- Hundred seed weight (g), PL- Pod length (cm), SPY- Single plant yield (g).

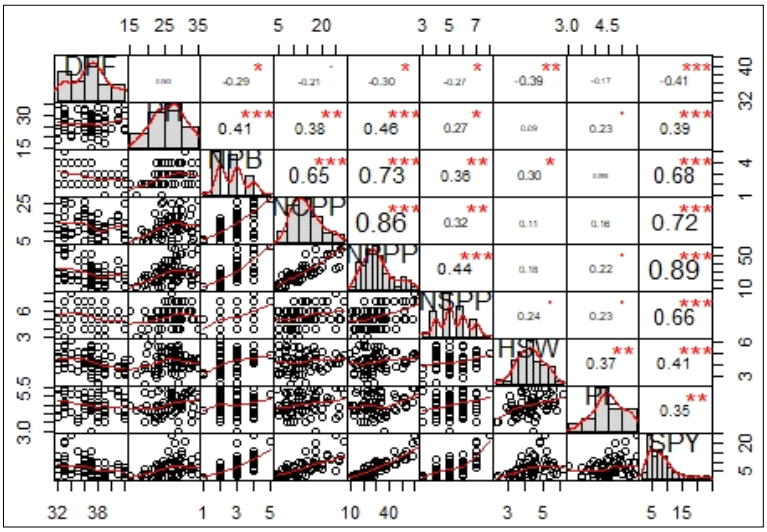


Fig 1: Correlation matrix chart for different traits in F_2 derivatives of the cross ADT 3 × KKB14-052.

DFF- Days to 50% flowering, PH- Plant height, NPB- Number of primary branches, CPP- Number of cluster per plant, PPP- Number of pods per plant, NSPP- Number of seeds per pod, HSW- Hundred seed weight, PL- Pod length, SPY- Single plant yield.

***Significant at 0.001 level, **Significant at 0.01 level, *Significant at 0.05 level, ˙Significance at 0.1 level).

Table 3: Direct and indirect effects of different traits on yield in F_2 derivatives of ADT 3 × KKB14-052.

Characters	DFF	PH	NPBPP	NCPP	NPPP	NSPP	HSW	PL	SPY
DFF	**-0.018**	-0.003	0.008	0.017	-0.250	-0.077	-0.075	-0.009	-0.408
PH	-0.001	**-0.053**	-0.011	-0.031	0.380	0.080	0.018	0.013	0.394
NPBPP	0.005	-0.022	**-0.027**	-0.052	0.606	0.106	0.059	0.005	0.680
NCPP	0.004	-0.020	-0.018	**-0.080**	0.708	0.093	0.021	0.009	0.716
NPPP	0.005	-0.024	-0.020	-0.069	**0.825**	0.127	0.034	0.012	0.890
NSPP	0.005	-0.015	-0.010	-0.026	0.360	**0.291**	0.046	0.013	0.665
HSW	0.007	-0.005	-0.008	-0.009	0.145	0.069	**0.194**	0.020	0.413
PL	0.003	-0.012	-0.003	-0.013	0.178	0.068	0.072	**0.055**	0.348

(Residual effect= 0.248).

seeds per pod (0.27) and pod length (0.23). Number of primary branches per plant had positive significance with number of clusters per plant (0.65), number of pods per plant (0.73), number of seeds per pod (0.36) and hundred seed weight (0.30). Number of clusters per plant had positive significance with number of pods per plant (0.86) and number of seeds per pod (0.32). Number of pods per plant had positive significance with number of seeds per pod (0.44) and pod length. Number of seeds per pod had positive significance with hundred seed weight (0.24) and pod length (0.23). Hundred seed weight had positive significance with pod length (0.37). Suguna *et al.* (2017) reported that positive significance of hundred seed weight with pod length in 4 genotypes and their 12 hybrids. The results of inter-correlation studies were closely harmony with the results of Sathees *et al.* (2019). Priya *et al.* (2018) observed that number of primary branches per plant had positive significance with number of pods per plant, number of seeds per pod and hundred seed weight from 120 germplasm lines.

Hence, choice of these characters might improve the plant yield significantly. In correlation matrix chart (Fig 1), association of different traits with the yield is clearly displayed *i.e.*, the distribution of variables was displayed on the diagonal, bivariate scatter plots with fitted line were shown on the bottom of the diagonal.

Path analysis

Direct and indirect effects of various traits on the yield are furnished in Table 3. The trait number of pods per plant showed high direct effect (0.825) on single plant yield. Number of seeds per pod (0.291), hundred seed weight (0.194) and pod length (0.055) exhibited positive direct effects on single plant yield. These results had harmony with the findings of Sathees *et al.* (2019). Sathya *et al.* (2018) reported that high direct effect on single plant yield by number of pods per plant and low positive effect by hundred seed weight in F_2 populations of five crosses *viz.,* VBN (Bg) 4 × Mash 114, VBN (Bg) 4 × Mash 1008, VBN 8 × Mash 114, VBN 8 × Mash 1008 and VBN 8 × VBG11-053. Veeramani *et al.* (2005) revealed similar results for number of pods per plant, number of seeds per pod and pod length.

Days to 50% flowering had positive indirect effect on yield through number of primary branches per plant and number of clusters per plant. Plant height had a positive indirect effect on yield through number of pods per plant, number of seeds per pod, hundred seed weight and pod length. Number of primary branches per plant and number of clusters per plant had a positive indirect effect on yield through days to 50% flowering, number of pods per plant, number of seeds per pod, hundred seed weight and pod length. Number of pods per plant had a positive indirect effect on yield through days to 50% flowering, number of seeds per pod, hundred seed weight and pod length. Number of seeds per pod had a positive indirect effect on yield through days to 50% flowering, number of pods per plant, hundred seed weight and pod length. Hundred seed weight had a positive indirect effect on yield through days to 50% flowering, number of pods per plant, number of seeds per pod and pod length. Pod length had a positive indirect effect on yield through days to 50% flowering, number of pods per plant, number of seeds per pod and hundred seed weight. Among all the characters, number of pods per plant alone showed high positive indirect effect on yield. The residual effect (0.248) indicated that the characters which are included in the path analysis explained nearly 75% of the total variation on the dependent variable *i.e.* seed yield.

CONCLUSION

In the present experiment, phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters indicating the presence of environmental influence on the traits. Plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, hundred seed weight, pod length and single plant yield having high heritability coupled with high GAM revealed that the presence of additive gene action and selection is rewarded for enhancing the seed yield. Analysis of correlation shows, number of pods per plant, number of clusters per plant, number of primary branches per plant, number of seeds per pod, hundred seed weight, plant height and pod length were significantly positive correlation with single plant yield. Among the yield contributing characters, number of pods per plant has high positive direct effect on yield followed by number of seeds per pod, hundred seed weight and pod length. Selection of these characters will be effective in improvement of yield in black gram breeding program.

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