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Research Article

Genetic variability and association analysis in F_3 progenies of IC 436656 x KKB14045 in black gram (*Vigna mungo* L. Hepper) for agro-morphological traits

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Abstract

The present experiment was undertaken on 140 F_3 progenies developed from the cross IC 436656 x KKB14045 in black gram (*Vigna mungo* L. Hepper) for genetic variability and association analysis. There is a lesser extent of variance between the PCV and GCV for all nine quantitative traits which represents the minor effect of the environment. Plant height, Days to 50% flowering, no. of primary branches/plant, no. of clusters/ plant, no. of pods/plant, 100 seed weight and yield were having high heritability and high genetic advance hinting additive gene action. No. of primary branches/ plant, no. of clusters/plant and no. of pods/plant having a significantly high positive correlation with single plant yield. From path analysis, no. of pods/plant having a high direct effect on yield. Therefore, the selection of these characters is important for developing high yielding varieties.

Keywords

Black gram, F_3 population, variability, association analysis.

INTRODUCTION

Legumes are considered as the universal source of protein in a vegetarian diet. Black gram (*Vigna mungo* (L.) is one of the important food legumes and it contains approximately 25% protein, 60% carbohydrates, fat, minerals, amino acids and vitamins. It is an autogamous, short duration crop which is cultivated largely in the Indian subcontinent as a rice-fallow. Being a leguminous plant, it fixes atmospheric nitrogen symbiotically and improves soil fertility. It can be used as a forage, fodder for milch animals. Black gram is grown as a rainfed crop and also prone to biotic and abiotic stresses results in yield reduction. One of the major constraints in improving the yield potential in blackgram is lack of appropriate ideotypes and disease susceptibility. It is important to estimate the variability present in the population for the success of the breeding program. Presence of wider variability leads to a greater chance of selection improvement in the characters. The genetic variability study includes the parameter such as Genotypic coefficient of variation, Phenotypic coefficient of variation, Environmental coefficient of variation, genetic advance and heritability and needed for a better breeding method (Sarkar *et al.,* 2014, Bandi *et al.,* 2018). This present study presents the results of selection based on yield and related characters in F_3 progenies derived from the cross IC 436656 x KKB 14045.

MATERIALS AND METHODS

In the present study, 140 F_3 progenies developed from the cross IC 436656 x KKB14045 were evaluated at Dept. of PBG, AC and RI, Killikulam during Kharif 2019. All 140 progenies were raised in 4m length row in two replications with a spacing of 30x10cm. Observation on biometrical traits *viz.* days to 50% flowering (days), plant height (cm), no. of primary branches/plant, no. of clusters/ plant, no. of pods/plant, pod length (cm), no. of seeds/ pod, 100 seed weight (g) and single plant yield (g) were recorded in 5 plants from each progeny. Genetic variability parameters *viz.,* genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as per cent of the mean (GAM) were obtained by using the formula mentioned in Johnson *et al.* (1955). GENRES statistical software was used to perform correlation and path coefficients.

RESULTS AND DISCUSSION

PCV was greater than GCV for all traits. Single plant yield was recorded the highest PCV (45.29%) and GCV 47.36%). This result indicated a high variability (direct selection may be followed) of these traits which were similar to the studies Panigrahi *et al*. (2014), Sathees *et al*. (2019) and Vadivelu *et al*. (2019). GCV and PCV were moderate for traits including days to 50% flowering (10.05% and 10.29%) which were similar to the study by Partab *et al.* (2019). Plant height (19.36% and 19.52%), no. of seeds/pod (10.93% and 15.02%) and 100 seed weight (15.35% and 16.19%) respectively for GCV and PCV and which was similar to the study by Patidar *et al.* (2018). GCV and PCV were the lowest in pod length (9.48% and 9.81%) which was mentioned by Hemalatha *et al*. (2017) and Priya *et al*. (2018).

High heritability (above 60%) and genetic advance (above 20%) were mentioned in **table 1**. All traits showed high heritability except no. of seeds/pod (52.97%) which is similar to the result by Bandi *et al*. (2018), Patidar *et al*. (2018) and Vadivelu *et al*. (2019).

Table 1. Variability parameters in F_3 progenies developed from the cross IC 436656 x KKB14045

Characters	GCV(%)	PCV(%)	H(%)	GAM(%)
Days to 50%flowering (DFF)	10.05	10.29	95.43	20.23
Plant height (PH)	19.36	19.52	98.32	39.54
No. of primary branches/plant (NPBP)	36.37	38.95	87.19	69.96
No. of clusters/plant (NCP)	37.43	38.40	94.99	75.14
No. of pods/plant (NPP)	35.40	36.36	94.77	70.99
No. of seeds/pod (NSP)	10.93	15.02	52.96	16.39
Pod length (PL)	9.48	9.81	93.41	18.88
100 seed weight (HSW)	15.35	16.19	90.01	30.01
Single plant yield (SPY)	45.29	47.36	91.44	89.21

(PCV= Phenotypic coefficient of variation, GCV=Genotypic coefficient of variation, H(%)=Heritability, GAM= Genetic advance as per cent of the mean)

Table 2. Genotypic (Geno) and phenotypic (Pheno) correlation coefficients between yield components in F_3 progenies developed from the cross IC 436656 x KKB14045

Characters		DFF	PH	NPB	NCP	NPP	NSP	PL	HSW	SPY
DFF	Geno	1.0	.035	-.064	-.088	-.086	-.273**	-.162*	-.199*	-.196*
	Pheno	1.0	.035	-.057	-.081	-.081	-.198*	-.156	-.184*	-.181*
PH	Geno		1.0	.620**	.567**	.501**	.053	.125	.203*	.448**
	Pheno		1.0	.572**	.546**	.483**	.039	.121	.192*	.424**
NPB	Geno			1.0	.906**	.899**	.164*	.157	.331**	.841**
	Pheno			1.0	.877**	.861**	.119	.144	.285**	.786**
NCP	Geno				1.0	.975**	.151	.138	.29**	.897**
	Pheno				1.0	.964**	.102	.134	.267**	.862**
NPP	Geno					1.0	.184*	.157	.268**	.914**
	Pheno					1.0	.120	.151	.247**	.887**
NSP	Geno						1.0	.708**	.221**	.409**
	Pheno						1.0	.490**	.116	.412**
PL	Geno							1.0	.209**	.327**
	Pheno							1.0	.196**	.305**
HSW	Geno								1.0	.544**
	Pheno								1.0	.512**
SPY	Geno									1.0
	Pheno									1.0

*significance at 5% level, ** significance at 1% level

Genotypic and phenotypic correlation between yield and its component characters are listed in **Table 2**. The characters plant height (0.448), the number of primary branches per plant (0.841), the number of clusters per plant (0.897), the number of pods per plant (0.914), the number of seeds per pod (0.409), hundred seed weight (0.544) and pod length (0.327) were significantly positive correlation with single plant yield and days to fifty per cent flowering (-0.196) was significant and negatively correlated with single plant yield in both genotypic and phenotypic level. This indicated that yields could be increased by an improvement of positively correlated traits. These results were in agreement with Sathees *et al*. (2019) and Partap *et al*. (2019), Blessy *et al*. (2018), Priya *et al.* (2018).

From the inter correlation studies, no. of primary branches/plant, no. of clusters/plant and no. of pods/plant are positively correlated among them. DFF was not in correlation with the yield parameters which is also reported in Sushmitharaj *et al*. (2017).

In both phenotypic and genotypic levels, plant height had positive significance with the number of primary branches per plant, the number of clusters per plant, the number of pods per plant and hundred seed weight. Number of clusters per plant had positive significance with number of pods per plant and hundred seed weight. Number of seeds per pod and pod length were positively significant with hundred seed weight. Number of seeds per pod had significant highly positive correlated with pod length.

Table 3. Path coefficients of different charecters on yield in F_3 progenies developed from the cross IC 436656 x KKB14045

Characters	DFF	PH	NPB	NCP	NPP	NSP	PL	HSW	SPY
DFF	**-0.013**	-0.001	0.001	-0.011	-0.061	-0.053	-0.001	-0.056	-0.196
PH	0.000	**-0.038**	-0.009	0.071	0.356	0.010	0.001	0.057	0.448
NPB	0.001	-0.024	**-0.015**	0.113	0.639	0.032	0.001	0.094	0.841
NCP	0.001	-0.022	-0.013	**0.125**	0.693	0.029	0.001	0.082	0.897
NPP	0.001	-0.019	-0.013	0.122	**0.711**	0.035	0.001	0.076	0.914
NSP	0.003	-0.002	-0.002	0.019	0.131	**0.192**	0.005	0.063	0.409
PL	0.002	-0.005	-0.002	0.017	0.112	0.136	**0.007**	0.059	0.327
HSW	0.003	-0.008	-0.005	0.036	0.191	0.043	0.002	**0.283**	0.544

Residual effect= 0.171
*values in bold letters represent the direct effect

[DFF - Days to 50% flowering (days), PH - Plant height (cm), NPBPP - Number of primary branches per plant, NCPP - Number of clusters 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)]

Direct and indirect effects of various characters on yield are shown in **Table 3**. No. of pods/plant (0.711) had the highest positive direct effect on yield. These results were in identical with Sathees *et al*. (2018), Bandi *et al*. (2018), Konda *et al.* (2008), Sohel *et al*. (2016) and Shivade *et al*. (2011). No. of pods/plant had a high positive indirect effect on yield through plant height (0.356), no. of primary branches/plant (0.639), no. of clusters/plant (0.693). Sathees *et al*. (2018) obtained the same results.

Residual effect (0.171) represents the characters influences single plant yield excluding the traits studied in this experiment. In this study, nearly 83% of the yield contributing characters was investigated. Among the yield contributing characters, the yield is majorly influenced by no. of pods/plant which has a high positive direct effect on yield. So, the improvement of this character ultimately results in a higher yield.

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REFERENCES

Bandi, H.R.K., Rao, K.N., Krishna, K.V. and Srinivasalu, K. 2018. Correlation and Path- Coefficient estimates of yield and yield component traits in rice fallow black gram (*Vigna mungo* (L.) Hepper. *Int. J. Curr. Microbiol. App. Sci.*, **7**(3): 3304-3309. [Cross Ref]

Blessy, V. and Naik, B.P. 2018. Studies on Correlation and Path Analysis in Black gram (*Vigna mungo* (L.) Hepper). *Int. J. Curr. Microbiol. App. Sci.*, **7**(8): 1991-1997. [Cross Ref]

Hemalatha, K., Lal, S.S. and Lal, G.M. 2017. Study on Genetic Variability and Correlation in Black gram (*Vigna mungo* L. Hepper). *J. Pharmacogn. Phytochem.*, **6**(4): 674-676.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Estimate of genetic and environmental variability in Soybeans. *Agron. J.*, **47**(7): 314 – 318. [Cross Ref]

Konda, C.R., Salimath, P.H. and Mishra, M.N. 2008. Correlation and path coefficient analysis in blackgram (*Vigna mungo* (L.) Hepper). *Legum. Res.,* **31**(3): 202-205.

Panigrahi, K.K., Baisakh, B., Kar, M. and Mohanty, A. 2014. Genetic divergence in mutants and land races of black gram (*Vigna mungo* [L.] Hepper) from Odisha. *Electron. J. Plant Breed.*, **5**(3): 567-572.

Partap, B., Kumar, M., Kumar, V. and Kumar, A. 2019. Genetic variability and correlation studies of seed yield and its components in black gram Blackgram (*Vigna mungo* (L.) Hepper). *J. Pharmacogn. Phytochem.*, **8**(3): 2035-2040.

Patidar, M., Sharma, H. and Haritwal, S. 2018. Genetic variability studies in Blackgram (*Vigna mungo* (L.) Hepper). *Int. J. Chem. Stud.*, **6**(2):1501-1503.

Priya, L., Arumugam Pillai, M., Shoba, D., Merina prem Kumari, S. and Aananthi, N. 2018. Genetic variability and correlation studies in black-gram [*Vigna mungo* (L.) Hepper]. *Electron. J. Plant Breed.,* **9**(4): 1583-1587. [Cross Ref]

Sarkar, M., Ghosh, S. and Kundagrami, S. 2014. Genetic Variability and Character Association of Yield and Yield Components in Mungbean [*Vigna radiata* (L.) Wilczek]. *J. Agroecol. Nat. Resour. Manag.*, **1**(3):161-165.

Sathees, N., Shoba, D., Saravanan, S., Merina prem Kumari, S. and Arumugam Pillai, M. 2019. Studies on Genetic Variability, Association and Path Coefficient Analysis in Black Gram (*Vigna mungo* L. Hepper). *Int. J. Curr. Microbiol. App. Sci.*, **8**(6): 1892-1899. [Cross Ref]

Shivade, H.A., Rewale, A. P. and Patil, S.B. 2011. Correlation and path analysis for yield and yield components in black gram (*Vigna mungo* (L.)Hepper). *Legum. Res.,* **34** (3): 178-183.

Sohel, M.H., Miah, M.R., Mohiuddin, S.J., Islam, A.K.M.S., Rahman, M.M. and Haque, M.A. 2016. Correlation and path coefficient analysis of black gram (*Vigna mungo* L.). *J. Biosci. Agric. Res.*, **7**(02): 621-629. [Cross Ref]

Sushmitharaj, D.V., Shoba, D. and Pillai, M.A. 2018. Genetic variability and correlation studies in black gram (*Vigna mungo* [L.] hepper) with reference to YMV resistance. *Int. J. Curr. Microbiol. App. Sci.*, Special Issue **6**: 2849-2856.

Vadivelu, K., Manivannan, N., Mahalingam, A., Satya, V.K., Vanniarajan, C. and Saminathan, V.R. 2019. Assessment of variability for seed yield, component characters and MYMV disease resistance in segregating populations of black gram [*Vigna mungo* (L.) Hepper]. *Electron. J. Plant Breed.,* **10** (2): 732-735. [Cross Ref]