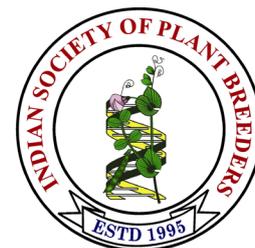


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Research Article



Genetic analysis in pre-breeding lines derived from inter sub-specific cross of blackgram (*Vigna mungo* (L.) Hepper)

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Abstract

One hundred and eighty nine stabilised lines obtained from the cross VBN (Bg) 5 and *Vigna mungo* var *silvestris* 22/10 were evaluated during *Rabi*, 2019. Analysis of variance for various traits exhibited significant differences among the lines for all the nine quantitative traits. The GCV was lower compared to the values of PCV which revealed the influence of the environment in deciding the expression of these lines. Moderate GCV was recorded for single plant yield (16.22 %), the number of pods per plant (12.60%), plant height (12.48 %), the number of primary branches per plant (11.75 %) and hundred seed weight (11.34%). High heritability was observed for the characters like hundred seed weight (96.99 %), plant height (78.33 %), days to 50 per cent flowering (72.98 %), single plant yield (72.44 %) and pod length (65.70 %). High heritability along with high genetic advance as per cent of mean was observed for hundred seed weight (96.99, 23.00), plant height (78.33, 22.76) and single plant yield (72.44, 28.44) indicates the possibility of improving these traits by selection since there is a wide range of variation and additive gene action exists for these traits. The maximum number of lines with a positive value over the mean was observed for pod length and 100 seed weight. Correlation analysis showed that the number of pods per plant, plant height, the number of seeds per pod, the number of primary branches per plant, the number of pods per cluster, pod length and hundred seed weight had positive significant association with single plant yield. A number of pods per plant and pod length had a high positive direct effect on single plant yield. Hence, the selection for these characters would improve seed yield in blackgram.

Key words: Blackgram, pre-breeding lines, genetic variability, heritability, genetic advance, correlation

INTRODUCTION

Blackgram (*Vigna mungo* (L.) Hepper), also well known as urdbean or mash bean, an important short duration self pollinated legume crop is an important constituent of the Indian diet every day. Blackgram is the economic source of protein for the poor (Main, 1976). It is cultivated in marginal lands under rainfed conditions. The major problems in the achievement of higher yield are the absence of genetic variability, ideal ideotypes suitable for different cropping systems and prone to pest and diseases. To overcome these constraints, one possible

way is to incorporate genes from wild species to cultivated ones through interspecific cross. The introgressed lines contribute more novel genes for yield improvement. To develop high yielding varieties, it is important to understand the nature and magnitude of genetic variability extant in the population which is indispensable to assume any breeding programme.

The estimation of genetic parameters *viz.*, phenotypic and genotypic coefficients of variation, heritability

and genetic advance helps to understand the mode of inheritance of quantitative traits and also helps to formulate selection criteria for improving seed yield in blackgram. The realization of inter relationship between yield and other traits is very much important for a breeder for making a selection where direct selection for yield is not much effective. Correlation measures the magnitude of relationship between yield and other yield contributing traits. Whereas, path coefficient analysis helps to split the correlation coefficient into direct and indirect effects of independent trait on the dependent trait. Keep in view of these points, the present study was conducted to assess the genetic variability available for different traits among the derivatives of inter sub-specific cross of blackgram and to determine the association of different traits with seed yield in blackgram.

MATERIALS AND METHODS

The present study was performed with one hundred and eighty nine stabilized lines (F_{10}) obtained from the cross VBN (Bg) 5 and *Vigna mungo* var *silvestris* 22/10. The lines were planted in a randomised block design (RBD)

with two replications at the Department of Pulses, Tamil Nadu Agricultural University, Coimbatore raised during *Rabi*, 2019. The lines were planted in a row of 4 m length with a spacing of 30 x 10 cm. The observations were taken on three randomly selected plants in each replication and recorded for nine quantitative traits like days to 50 per cent flowering, plant height (cm), the number of primary branches per plant, the number of pods per cluster, the number of pods per plant, pod length (cm), the number of seeds per pod, hundred seed weight (g) and single plant yield (g). The statistical analysis was done according to the procedure outlined by Panse and Sukhatme (1967). Genetic variability parameters like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), genetic advance and genetic advance as per cent of mean were estimated according to the procedure outlined by Johnson *et al.* (1955). Heritability in a broad sense was calculated according to the method given by Lush (1940). Correlation and path coefficient analyses were carried out based on the method proposed by Dewey and Lu (1959).

Table 1. Analysis of variance for biometrical traits in blackgram

Source	df	Days to 50 per cent flowering	Plant height	Number of primary branches per plant	Number of pods per cluster	Number of pods per plant	Pod length	Number of seeds per pod	Hundred seed weight	Single plant yield
Genotypes	188	6.56*	34.67*	0.31*	0.37*	57.12*	0.25*	0.49*	0.57*	3.96*
Replication	1	0.08	2.36	0.23	0.35	12.99	0.11	0.01	0.00	0.05
Error	188	1.03	4.21	0.12	0.22	20.93	0.05	0.23	0.01	0.63

* Significant at 5 per cent level

Table 2. Mean, Range, Coefficients of variation, heritability (broad sense), genetic advance and genetic advance as per cent of mean for different traits in blackgram

Character	Mean	Range	Number of lines above mean value	PCV %	GCV %	Heritability (h^2) %	Genetic advance	GA as percent of mean
Days to 50 per cent flowering	38	35-43	84	5.13	4.38	72.98	2.93	7.71
Plant height (cm)	31.26	22.58-47.35	77	14.10	12.48	78.33	7.12	22.76
Number of primary branches per plant	2.64	2.00-3.67	45	17.52	11.75	45.00	0.45	16.24
Number of pods per cluster	4.63	3.83-5.83	95	11.71	5.82	24.67	0.27	5.95
Number of pods per plant	33.76	22.50-52.50	89	18.51	12.60	46.36	5.96	17.67
Pod length (cm)	4.52	3.60-5.43	100	8.51	6.90	65.70	0.53	11.52
Number of seeds per pod	6.90	5.83-8.00	93	8.69	5.30	37.22	0.45	6.66
Hundred seed weight (g)	4.65	3.39-5.92	102	11.51	11.34	96.99	1.07	23.00
Single plant yield (g)	7.96	5.30-12.63	84	19.06	16.22	72.44	2.27	28.44

RESULTS AND DISCUSSION

Analysis of variance revealed that a vast range of variability was recorded for all the traits in blackgram lines (**Table 1**). The results on variability parameters are given in **Table 2**. Mean performance of all inter subspecific lines exhibited a wide range of variation for all the biometrical traits viz., days to 50 per cent flowering (35-43), plant height (22.58- 47.35 cm), the number of primary branches per plant (2.00-3.67), the number of pods per cluster (3.83-5.83), the number of pods per plant (22.50-52.50), pod length (3.60-5.43 cm), the number of seeds per pod (5.83-8.00), hundred seed weight (3.39-5.92 g) and single plant yield (5.30-12.63 g). Considering the mean performance, it was adjudged that a total of 112 lines with a lower mean value than the general mean (31.26 cm) for plant height are of short stature and could be exploited in intercropping system. The number of lines that exhibited more than the general mean values for yield attributing traits was : 95 lines for the number of pods per cluster, 89 lines for the number of pods per plant, 93 lines for the number of seeds per pod, 102 lines hundred seed weight and 84 lines for single plant yield. This showed that a significant amount of variation was observed for all the traits studied.

The genotypic coefficient of variation for various traits studied ranged from 4.38 to 16.22 per cent. Moderate GCV was found in the characters viz., single plant yield (16.22 %), the number of pods per plant (12.60 %), plant height (12.48 %), the number of primary branches per plant (11.75 %) and hundred seed weight (11.34 %). The low GCV values were found in the traits like pod length (6.90 %), the number of pods per cluster (5.82 %), the number of seeds per pod (5.30 %) and days to 50 per cent flowering (4.38 %). The genotypic coefficient of variation was found to be lower than the phenotypic coefficient of variation for all the traits studied. This showed that these characters are not only expressed by means of genotype but also influenced by the environment. Moderate GCV for plant height, the number of seeds per pod and hundred seed weight was observed by Manish *et al.* (2017); plant height, the number of branches per plant, the number of pods per plant, the number of pods per cluster, pod length, the number of seeds per pod and single plant yield was observed by Rajwanti *et al.* (2021) in blackgram.

The phenotypic coefficient of variation for various traits ranged from 5.13 to 19.06 per cent. The moderate PCV was found in the traits viz., single plant yield (19.06 %), the number of pods per plant (18.51 %), the number of primary branches per plant (17.52 %), plant height (14.10 %), the number of pods per cluster (11.71 %) and hundred seed weight (11.51 %). The difference between PCV and GCV ranged from 0.17 to 5.91 per cent. The lowest difference is exhibited by hundred seed weight indicating the highest contribution of genotypic value to the phenotype and low influence of environmental factors suggesting for a genetic gain for this trait through

selection. The moderate PCV for the number of branches per plant, hundred seed weight and plant height was observed by Panda *et al.* (2017); the number of pods per cluster, pod length and the number of pods per plant was observed by Vikky *et al.* (2020) in blackgram.

High heritability estimates help in the identification of transmissible traits from one generation to another and have minimal influence by the environment. High values of heritability estimates were obtained for the traits viz., hundred seed weight (96.99 %), plant height (78.33%), days to 50 per cent flowering (72.98 %), single plant yield (72.44 %) and pod length (65.70 %) whereas, moderate values of heritability were recorded for the number of pods per plant (46.36 %), the number of primary branches per plant (45.00 %) and the number of seeds per pod (37.22 %). Low values of heritability were observed for the number of pods per cluster (24.67 %). High levels of heritability were reported for plant height, pod length and hundred seed weight by Sabesan *et al.* (2018) and Soheli *et al.* (2016); days to 50 per cent flowering, single plant yield and hundred seed weight by Panda *et al.* (2017) and Kumar *et al.* (2014) in blackgram.

High heritability along with high genetic advance as per cent of mean was observed for hundred seed weight (96.99, 23.00), plant height (78.33, 22.76) and single plant yield (72.44, 28.44) (**Table 2**). The coupled action of high heritability along with high genetic advance as per cent of mean indicated the additive gene effects which would be improved by selection of these traits. High heritability along with low genetic advance as per cent of the mean was observed for days to 50 per cent flowering (72.98, 7.71) which indicates non additive gene action. Low heritability along with low genetic advance as per cent of mean was observed for the number of pods per cluster (24.67, 5.95) indicating ineffectiveness of selection if practised for this trait. High heritability along with high values of genetic advance as per cent of mean for plant height and single plant yield was observed by Ranjeet *et al.* (2018); plant height, single plant yield, the number of pods per plant and the number of branches per plant was observed by Narendrabhai *et al.* (2020) in blackgram. Hence, the traits viz., plant height, the number of primary branches per plant, the number of pods per plant, the number of seeds per pod, hundred seed weight and single plant yield are important traits and preference should be given to the above traits while performing selection because these traits will be helpful in improving yield in blackgram.

Frequency distribution of traits, skewness and kurtosis were studied for all the biometrical traits. Among all the traits, normal distribution was observed for the number of pods per plant, the number of primary branches per plant, days to 50 per cent flowering, the number of seeds per pod, pod length and hundred seed weight. Significant and positive skewness was studied for plant height,

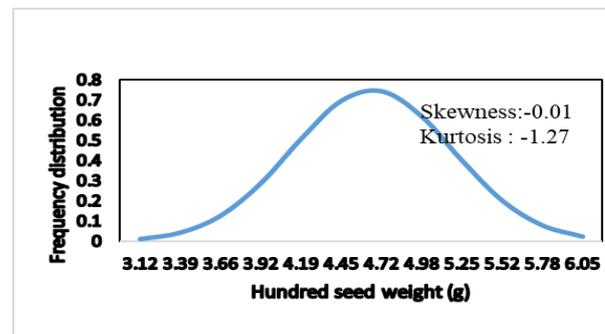
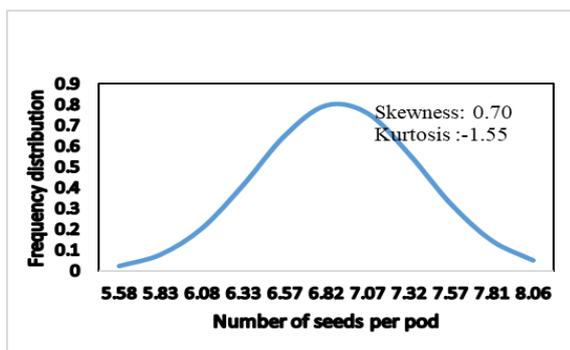
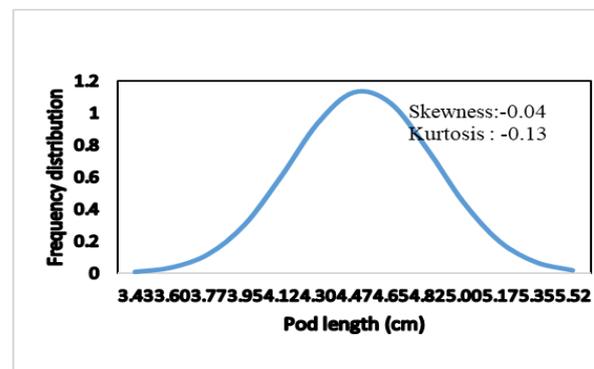
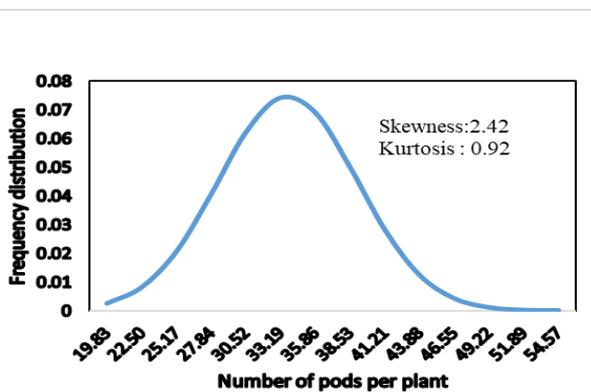
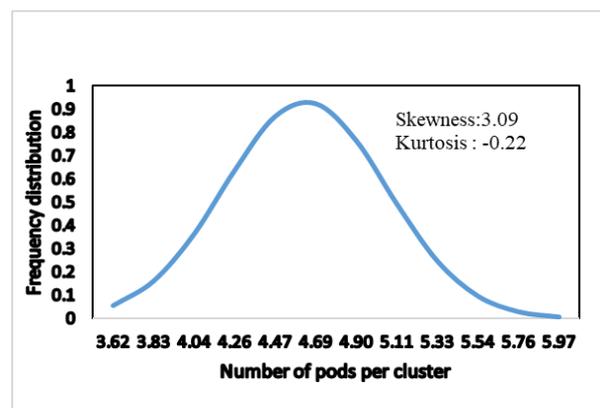
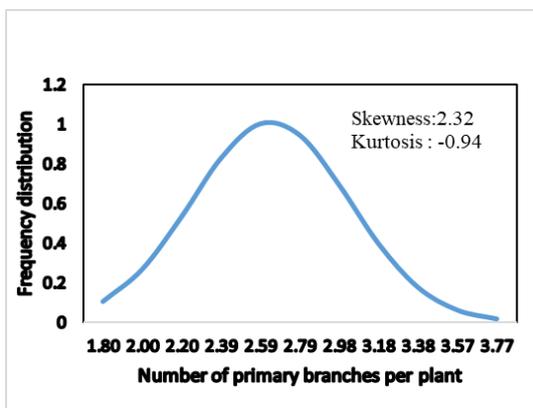
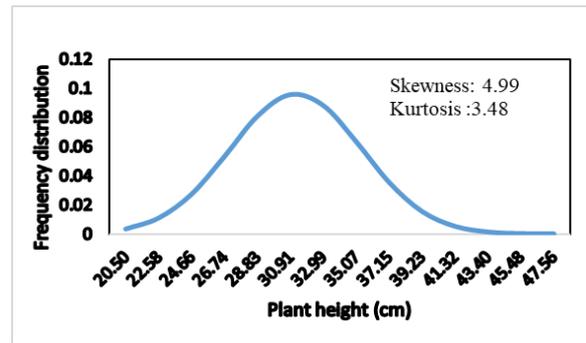
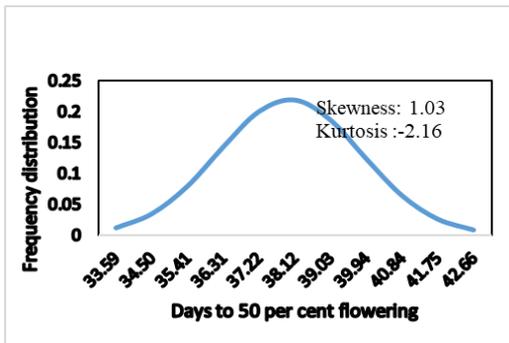
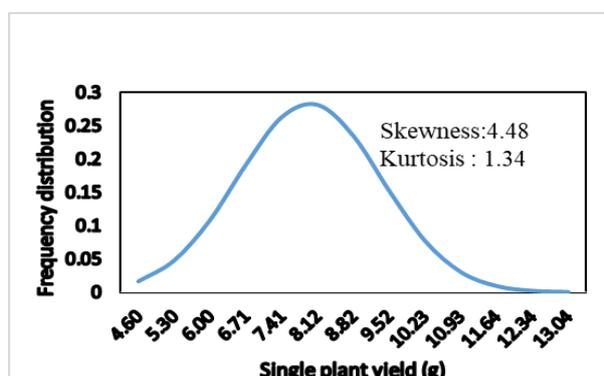


Fig. 1. Frequency distribution curve for different traits in blackgram

Fig. 1. Continued



the number of pods per cluster and single plant yield. In the case of kurtosis, all the traits were mesokurtic in nature indicating that these lines had adequate variability for these traits. The trait plant height was observed to be leptokurtic indicating the narrow level of variability (Fig. 1).

Correlation analysis is a statistical tool exploited to find out the degree of relationship between two or more variables. The values of genotypic correlation coefficients among the yield and yield attributing traits are indicated in Table 3. In the present study, out of 45 total associations, 24 associations were positively significant which highlights the additive genetic effect. The traits viz., the number of pods per plant, plant height, the number of seeds per pod, the number of primary branches per plant, the number of pods per cluster, pod length and hundred seed weight were positively correlated with single plant yield.

Sathees *et al.* (2019) observed the number of pods per plant, plant height, the number of seeds per pod, the number of primary branches per plant, pod length and hundred seed weight had a positive correlation with single plant yield in blackgram. Ranjeet *et al.* (2018) observed that the number of seeds per pod, the number of pods per plant and day to 50 per cent flowering had a positive correlation with seed yield in blackgram.

The correlation coefficient describes only the relationship between the yield and other yield attributing traits but it fails to show the direct as well as indirect effects for various traits on yield because the characters that are in association do not exert effects by themselves but are linked to other component traits. So, in order to get direct as well as the indirect contribution of yield over other traits, path coefficient analysis need be taken into consideration (Table 4).

In this study, a number of pods per plant and pod length had a high positive direct effect on single plant yield. Manish *et al.* (2017) studied the number of branches per plant, plant height and number of pods per plant had a high positive direct effect on single plant yield in blackgram. Kiran *et al.* (2021) observed that number of branches per plant, plant height, number of pods per plant and hundred seed weight had a high positive direct effect on single plant yield in blackgram.

Plant height, the number of primary branches per plant, the number of pods per cluster and the number of seeds per pod had a high indirect effect on seed yield through the number of pods per plant. Hence, the characters viz., plant height, the number of primary branches per plant, the number of pods per cluster, the number of pods per

Table 3. Genotypic correlation coefficients among the nine characters of pre breeding lines of blackgram.

	Days to 50 per cent flowering	Plant height	Number of primary branches per plant	Number of pods per cluster	Number of pods per plant	Pod length	Number of seeds per pod	Hundred seed weight	Single plant yield
Days to 50 per cent flowering	1.000	0.133	0.141	-0.252**	-0.079	0.019	0.084	0.025	-0.089
Plant height		1.000	0.856**	0.182*	0.592**	0.477**	0.553**	0.309**	0.631**
Number of primary branches per plant			1.000	0.210*	0.589**	0.490**	0.509**	0.236**	0.575**
Number of pods per cluster				1.000	0.517**	-0.058	0.430**	-0.063	0.541**
Number of pods per plant					1.000	0.179*	0.477**	0.064	0.864**
Pod length						1.000	0.543**	0.491**	0.436**
Number of seeds per pod							1.000	0.064	0.577**
Hundred seed weight								1.000	0.261**
Single plant yield									1.000

* Significant at 5 per cent level** Significant at 1 per cent level

Table 4. Direct and indirect effect of nine characters on single plant yield in pre breeding lines of blackgram

	Days to 50 per cent flowering	Plant height	Number of primary branches per plant	Number of pods per cluster	Number of pods per plant	Pod length	Number of seeds per pod	Hundred seed weight	Single plant yield
Days to 50 per cent flowering	0.027	0.027	-0.032	-0.058	-0.057	0.006	-0.004	0.001	-0.089
Plant height	0.004	0.204	-0.194	0.042	0.427	0.158	-0.027	0.019	0.631**
Number of primary branches per plant	0.004	0.174	-0.227	0.048	0.424	0.162	-0.025	0.014	0.575**
Number of pods per cluster	-0.007	0.037	-0.048	0.229	0.373	-0.019	-0.021	-0.004	0.541**
Number of pods per plant	-0.002	0.121	-0.133	0.119	0.721	0.059	-0.023	0.004	0.864**
Pod length	0.001	0.097	-0.111	-0.013	0.129	0.331	-0.027	0.029	0.436**
Number of seeds per pod	0.002	0.113	-0.115	0.099	0.344	0.180	-0.049	0.004	0.577**
Hundred seed weight	0.001	0.063	-0.054	-0.015	0.046	0.163	-0.003	0.060	0.261**

Residual effect: 0.354

plant, pod length, the number of seeds per pod and hundred seed weight turns out to be the yield attributing traits. Whereas, to hinge on direct effect, the number of pods per plant should be given more emphasis while executing the selection for genetic enhancement of seed yield in blackgram. The residual effect in the present study was 0.354, which implies that the characters in the path analysis contribute 65 per cent to the variability in single plant yield.

Based on the present study, the pre breeding lines performing with better mean values for yield attributing traits could be further used in the breeding program for the development of high yielding varieties and to enhance the genetic base in crop improvement.

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