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RESEARCH ARTICLE

Genetic Analysis on Yield and Yield Components Traits in the Segregating Populations of Blackgram[*Vigna mungo* (L.) Hepper]

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ABSTRACT

The magnitude of variability and association among various traits in F_2 populations of three crosses *viz.,* MDU 1 x TU68, VBN6 x TU68, and VBN8 x TU68 of blackgram were studied. The experiment was conducted at the National Pulses Research Centre, Vamban, during *Rabi* 2019. The genotypic coefficient of variability was lower than the values of phenotypic coefficient of variability, which revealed the influence of the environment in deciding the expression of these populations.The traits *viz.*, plant height, number of branches per plant, number of clusters per plant, number of pods per plant, and seed yield per plant has recorded high heritability and high genetic advance as per cent of mean for the majority of the crosses. It indicated that these traits were less influenced by the environment and possessed with high magnitude of genetic variability. Association studies revealed that the traits *viz.*, number of clusters per plant, and number of pods per plant in all the three crosses recorded significant and positive association with seed yield per plant. Hence, based on the present investigation, it can be concluded that the number of clusters per plant and number of pods per plant should be given due importance in framing the selection indices for seed yield improvement in blackgram. However, separate selection indices are required for each population as the association of traits differs among populations.

Keywords: *Blackgram; Segregating populations; Variability; Correlation; Yield traits.*

INTRODUCTION

Pulses are the principal source of dietary protein among vegetarians. It is an integral part of the daily diet because of itshigh protein content and good amino-acid balance. On account of the balanced aminoacid composition of cereals and protein blend, which matches with the milk protein, pulses are often called the life line of human beings. Among the pulses,blackgram[*Vigna mungo* (L.) Hepper] is an important food legume crop of the Indian sub-continent. It is an important short-duration crop and is widely cultivated in India. It gives us an excellent source of easily digestible good quality protein and the ability to restore soil fertility through symbiotic nitrogen fixation. Seeds are highly nutritious with protein (24-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids, and vitamins.In India, the area that comes under blackgram is about 4.50 million hectares with a production of 2.83 million tonnes (Project coordinator's report, 2019). However, the global productivity of pulses in general and blackgram in particular is very low as compared to cereals. One amongst many reasons for the low productivity of blackgram is the low yield potential of the present-day cultivars. Lesser variability is one factors responsible for the poor progress made in the breeding programme of pulse crops.Crop improvement programmes can improve productivity in various aspects. The basic need for any crop improvement programme is variation in a population. The knowledge on inheritance can be understood by the variability studies of various quantitative and yield traits through the estimation of variances namely, genotypic coefficients of variations, phenotypic coefficients of variations, heritability in per cent, and genetic advance as per cent of mean, which help to frame the effective crop improvement programme (Reni *et al.,* 2013).

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Association of yield components is very important for an efficient selection programme. The association analysis provides information on the correlation of various traits towards yield and its components, respectively. With this background, the present study was carried out to assess variability and association studies in three F_2 populations of blackgram.

MATERIALS AND METHOD

The experiment was performed at the National Pulses Research center (NPRC), Tamil Nadu Agricultural University, Vamban during *Rabi* 2019. The experimental material consists of F_2 generation obtained from three crosses of blackgram,*i.e.,* MDU 1 x TU68 (cross 1), VBN6 x TU68 (cross 2), and VBN8 x TU68 (cross 3). The variety, MDU 1 is a high yielder but susceptible to MYMV was released from Agriculture College and Research Institute, Tamil Nadu Agricultural University, Madurai for commercial cultivation. VBN 6 and VBN 8 were released from National Pulses Research Centre, Tamil Nadu Agricultural University, Vamban. The genotype TU 68 was developed from the cross TU 94-2 x *Vigna mungo* var. *silvestris* by Bhabha Atomic Research Centre, Trombay. TU 68 is a donor for bruchid resistance. All three parents, viz., VBN 6, VBN 8, and TU 68 have MYMV disease resistance. Observations were recorded for days to flowering, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight (g) and seed yield per plant (g). Observations were recorded on all the single plants of F_2 generation of three cross combinations along with their parents. Various genetic parameters like PCV, GCV, heritability and genetic advance as per cent of mean were worked out by adopting the methods given by Johnson *et al.* (1955). In addition, skewness and kurtosis were also worked out as per the standard method. A simple correlation between seed yield and its component traits and among themselves wasworked out as per the method suggested by Johnson *et al.* (1955).The data were analyzed using the statistical software TNAUSTAT statistical package (Manivannan, 2014).

RESULTS AND DISCUSSION

PCV and GCV are essential in understanding the nature and magnitude of variability present in the population due to the genetic and non-genetic causes. As GCV provides the total amount of heritable portion in the total variability, PCV also includes the environmental variability.The mean and the variability parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2), and genetic advance as per cent of mean (GAM) for the F_2 populations of three crosses viz., MDU 1 x TU 68 (C1), VBN 6 X TU 68 (C2) and VBN 8 x TU 68 (C3) are presented in the Table. 1. Mean performances among the crosses of blackgram for various traits showed that majority of the traits has shown average performances in the F_2 population of the various crosses within the parental range except fora number of pods per plant, which recorded higher performances than the parent, i.e., P_1 and P_2 among the crosses. The traits number of clusters per plant and pod length in the F_2 generation of MDU1 x TU68 cross has shown higher mean comparing the parental generations. In VBN6 x TU68 cross, the traits number of pods per cluster and seed yield per plant haverecorded higher mean effects than the parents. The trait number of branches per plant and seed yield per plant have recorded higher mean effects in the F_2 population over the parents in the cross VBN8 x TU68.

The variability results indicated that the estimates of the phenotypic coefficient of variation were higher than the genotypic coefficient of variation for all the characters studied indicating the environmental influence over the traits.The trait seed yield per plant recorded high PCV and GCV for all the crosses involved in the study.Similarly, Thirumalai and Murugan (2020) and Sathees *et al*. (2019) recorded higher PCV and GCV for seed yield per plant in their study. Days to flowering recorded low PCV and GCV for all the crosses. Plant height recorded high PCV with moderate GCV for all the crosses except VBN6 x TU68 cross which recorded moderate PCV and GCV for the trait. Similar results were given by Punia *et al.* (2014). High PCV and GCV were observed for the traits viz., number of branches per plant, number of clusters per plant, and number of pods per plant in the crosses VBN 6 x TU 68 and VBN 8 x TU 68. Similar results were given by Ramya *et al.,* (2014), Gowsalya *et al.*(2017) and Sushmitharaj *et al.*(2018). However, these traits recorded high PCV with moderate GCV in the cross MDU 1 x TU 68. Similar results were reported by Bishnoi *et al.*(2017). Similarly,Usharani and Kumar (2016) reported moderate GCV for these traits in their study. High to moderate PCV and GCV ve recorded the traits number of pods per cluster, pod length, a number of seeds per pod and 100-seed weight among all the crosses. Similar results were also given by Neelavathi and Govindarasu (2010), Kumar *et al.*(2015), Singh *et al.*(2014) and Sushmitharaj *et al.* (2018).

Heritability and genetic advance as per cent of the mean isessential for any population to know the magnitude of inheritance of traits and helpful in formulating the selection procedure. High heritability coupled with low genetic advance indicates the presence of non -additive gene action and selection for such traits may not be rewarding.

Table 1 .Variability parametersin F_2 population among various crosses of blackgramfor yield and yield components traits.

Characters	Cross	MEAN			PCV (%)	GCV (%)	h^2 (%)	GAM (%)	Skewness	Kurtosis
		P_1	P_2	F_2						
Days to flowering	C1	36.15	26.00	32.26	9.37	8.39	80.15	16.30	0.28	-0.65
	C2	34.20	26.05	31.17	9.88	9.05	83.86	17.98	-0.43	-0.53
	C3	34.30	25.46	30.93	10.25	9.38	83.89	18.65	-0.29	-0.68
Plant height (cm)	C1	39.00	21.61	24.39	20.13	11.66	33.54	14.65	0.85**	0.81
	C2	28.80	24.70	25.09	19.70	15.77	64.07	27.38	-0.15	0.77
	C3	24.20	21.62	19.84	25.18	14.03	31.04	16.96	0.40	-0.57
No. of branches per plant	C1	2.00	3.50	2.19	33.19	11.73	12.50	9.00	0.48*	0.35
	C2	2.25	3.85	2.47	43.69	30.75	49.54	46.97	1.19**	2.3**
	C3	2.25	2.77	3.02	45.07	38.99	74.86	73.21	0.80**	0.21
No. of clusters per plant	C1	6.20	6.67	8.29	28.77	16.45	32.71	20.42	1.23**	4.06**
	C2	7.35	12.45	10.72	38.76	33.39	74.18	62.40	1.28**	1.96**
	C3	7.80	10.15	10.05	35.29	25.15	50.79	38.89	0.66*	-0.22
No. of pods per cluster	C1	3.40	3.11	3.20	19.09	8.69	20.72	8.58	0.51*	0.85
	C2	2.75	2.35	3.02	23.83	18.14	57.95	29.97	-0.17	-0.66
	C3	2.70	2.38	2.29	30.69	22.10	51.85	34.53	-0.28	-0.61
No. of pods per plant	C1	20.75	20.11	26.11	31.49	13.95	19.64	13.42	0.57*	0.44
	C2	23.70	28.35	31.12	45.91	29.11	40.19	40.04	1.57**	2.91
	C3	19.65	21.92	22.72	47.66	27.42	33.09	34.23	0.61*	-0.19
Pod length (cm)	C1	4.72	4.23	5.09	11.68	8.57	53.74	13.63	0.25	-0.32
	C2	5.54	4.92	4.86	19.55	17.40	79.18	33.60	-0.43	-1.04
	C3	5.52	4.91	5.34	8.19	3.84	21.99	3.91	-0.39	1.55**
No. of seeds per pod	C1	6.95	5.44	6.36	15.82	8.62	29.66	10.18	-0.73**	0.65
	C2	6.55	5.45	6.81	10.62	7.53	50.23	11.58	0.18	-0.81
	C3	6.55	5.85	6.06	10.30	3.79	13.51	3.02	-0.34	0.76
100- seed weight (g)	C1	3.94	2.56	2.85	14.96	8.29	30.74	9.98	0.61**	0.03
	C2	3.45	2.77	2.78	12.68	5.93	21.86	6.01	1.43**	3.00**
	C3	3.80	2.56	3.11	28.35	26.50	87.37	53.74	4.21**	26.59**
Seed yield per plant (g)	C1	5.17	3.65	4.48	41.64	36.82	78.17	70.64	3.36**	15.84**
	C2	5.02	4.46	5.19	45.84	38.07	68.96	68.60	1.52**	2.10**
	C3	4.94	3.44	5.16	43.78	34.46	61.97	58.87	1.27**	1.55**

*,** Significant at 5%and 1% respectively. C1=MDU 1 x TU 68; C2=VBN 6 x TU 68; C3=VBN 8 x TU 68.

Note: PCV= Phenotypic coefficient of variation; GCV = Genotypic coefficient of Variation; h^2=Heritability (%); GAM = Genetic advance as per cent of mean

High heritability along with high genetic advance and low heritability accompanied with high genetic advance indicate the presence of additive gene effect. Selection based on the high heritability with high genetic advance rewards good results in the improvement for such traits due to the presence of an additive type of gene action. Low heritability with low genetic advance suggests that the environment highly affects the trait. In such instances, selection may be ineffective. Days to flowering recorded high heritability with moderate GAM for all four crosses. Plant height recorded high heritability with high GAM for the cross VBN 6 x TU 68. Crosses MDU1x TU 68 and VBN 8 x TU 68 recorded moderate heritability and moderate GAM for plant height. Similar results were recorded by Panigrahi *et al.*(2014) and

Sushmitharaj *et al*. (2018) for plant height. High heritability with high GAM was observed for the trait number of branches per plant for the cross VBN 8 x TU 68. Whereasthe remaining crosses recorded moderate to low heritability and GAM for a number of branches per plant (Punia *et al.,* 2014; Kumar *et al.,* 2015).The number of clusters per plant recorded high heritability along with high GAM for the cross VBN6 x TU 68 (Gowsalya *et al.,* 2017). The remaining crosses recorded moderate heritability and high GAM fora number of clusters per plant. Similar results were given by Kumar *et al.*(2015) and Arulbalachandran *et al.* (2010). The trait number of pods per cluster had moderate heritability and high GAM among the crosses of VBN6 x TU 68 and VBN 8x TU 68.Cross MDU 1 x TU 68 recorded low heritability with low GAM for this trait. A number of pods per plant recorded moderate heritability and high GAM in the crosses VBN6 x TU 68 and VBN 8x TU 68. However, MDU 1 x TU 68 recorded low heritability with moderate GAM for the trait. Similar results were also observed by Sushmitharaj *et al.*(2018) and Bishnoi *et al.*(2017). Pod length, number of seeds per pod, and 100 – seed weight recorded high to low ranges of heritability and GAM for all crosses. The trait seed yield per plant recorded high heritability and high GAM for all the crosses. Similar results were also recorded by Gowsalya *et al.*(2017), Hemalatha *et al.*(2017), Sushmitharaj *et al.*(2018) and Anuradha *et al*. (2020).

Table 2.Simple correlation between single plant yield and yield component traits among F$_2$ generations of various crosses in blackgram

Characters	Cross	Plant height (cm)	No. of Branches per plant	No. of Clusters per plant	No. of Pods per cluster	No. of Pods per plant	Pod Length (cm)	No. of seeds per pod	100- seed weight(g)	Seed yield per Plant (g)
Days to Flowering	C1	-0.01	-0.09	-0.04	0.00	-0.05	0.03	0.14*	0.23**	0.15
	C2	0.06	0.02	0.01	-0.14	0.02	0.12	-0.01	0.06	0.09
	C3	0.10	-0.03	0.02	-0.04	0.04	0.17	0.08	0.19	0.01
Plant height (cm)	C1		0.23*	0.23**	0.09	0.14	0.07	0.10	0.11	0.05
	C2		0.41**	0.48**	0.15	0.54**	0.15	0.23**	-0.03	0.50**
	C3		0.24*	0.22*	0.11	0.32**	0.17	0.22*	0.01	0.25*
No. of Branches per plant	C1			0.36**	0.08	0.24**	0.11	0.06	0.16	0.12
	C2			0.67**	0.07	0.61**	0.04	0.16*	-0.07	0.61**
	C3			0.55**	0.09	0.31**	-0.03	0.00	0.21	0.35**
No. of Clusters per plant	C1				0.03	0.74**	-0.05	0.04	-0.17	0.37**
	C2				0.05	0.86**	0.17	0.18*	-0.07	0.73**
	C3				0.44**	0.79**	0.13	0.19	-0.05	0.55**
No. of Pods per cluster	C1					0.32**	-0.04	-0.04	-0.05	0.11
	C2					0.33**	-0.32**	0.18*	-0.15	0.15
	C3					0.75**	0.10	0.10	-0.10	0.39**
No. of Pods per plant	C1						-0.10	0.01	-0.22*	0.47**
	C2						0.03	0.25**	-0.04	0.76**
	C3						0.16	0.18	-0.13	0.61**
Pod Length (cm)	C1							0.61**	0.18*	0.02
	C2							0.23**	0.08	0.23**
	C3							0.70**	0.16	0.19
No. of seeds per pod	C1								0.01	0.17
	C2								-0.11	0.20*
	C3								0.08	0.17
100- seed weight(g)	C1									0.22*
	C2									0.15
	C3									0.28**

*,** Significant at 5%and 1% respectively.C1=MDU 1 x TU 68; C2=VBN 6 x TU 68; C3=VBN 8 x TU 68

Among the F_2 populations, noskewness / normal distribution was observed for days to flowering and pod length in all three crosses. The traits *viz*., number of branches per plant, number of clusters per plant, number of pods per plant, 100- seed weight and seed yield per plant recorded significant and positive skewness in all the three crosses indicates the lesser proportion of segregants with higher values for these traits. The remaining traits recorded positive to no skewness for all the three crosses involved. The traits days to flowering, plant height, number of pods per cluster, number of pods per plant, and number of seeds per pod had mesokurtic nature of distribution indicates the existence of moderate variability for these traits in all three crosses. The remaining traits recorded leptokurtic to mesokurtic nature of distribution among the three crosses indicated the narrow to moderate level of variability for these traits in all the crosses.

Simple correlations coefficients between seed yield per plant and its component characters and inter relationships among the different traits are presented in Table. 2. Seed yield per plant expressed significant and positive association with the traits studied *viz*., number of clusters per plant and number of pods per plant in all the three crosses. This result was in accordance with the findings of Kumar *et al.* (2013), Keerthiga *et al.*(2018) and Sushmitharaj *et al.*(2018). Plant height and a number of branches per plant have significant and positive association with seed yield per plant in all the cross except MDU 1 x TU 68 cross. The trait number of pods per cluster had a significant and positive association with seed yield per plant in the VBN 8 x TU 68 cross combination only. The trait 100- seed weight recorded a significant and positive association with seed yield per plant in the crosses MDU1 x TU 68 and VBN 8 x TU 68. Similar results were also given by Mehra *et al.* (2016), Singh *et al.* (2016), Rajasekhar *et al.*(2017) and Keerthiga *et al.*(2018).

CONCLUSION

Based on the results of the present investigation, 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 branches per plant, number of clusters per plant, number of pods per plant and seed yield per plant recorded high heritability along with high genetic advance as per cent of mean. Hence, these traits were less influenced by the environment and possess an additive type of gene action with high genetic variability. Hence, selection can be practiced for these traits in these populations. Based on association studies it can be concluded that a number of clusters per plant and number of pods per plant recorded significant and positive association with seed yield per plant. These traits also hadsignificant and positive correlation among them. Hence, these traits can be used as a selection index for the seed yield improvement programme in blackgram. However, separate selection indices are required for each population as the association of traits differs among populations.

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Ethics statement:

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

Originality and plagiarism

The author declares that the stud has written based on the original works. The methods utilized were properly cited and acknowledged.

Consent for publication

All the authors agreed to publish the content.

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.

Author contribution:

Experiments- SR,Guidance –NM, KI, NG and GK Writing original draft - SR, NM, KI, NG and GK Writing- reviewing & editing - SR, NM

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