RESEARCH ARTICLE Agricultural Science Digest, Volume 44 Issue 1: 100-105 (February 2024)

Genetic Analysis of F_2 Populations for Quantitative Traits in Blackgram [*Vigna mungo* (L.) Hepper]

A. Surendhar[1], P. Jayamani[2], K. Iyanar[3], G. Senthilraja[2], P.S. Shanmugam[2]

10.18805/ag.D-5804

ABSTRACT

Background: Blackgram is an important pulse crop grown in India. The creation of new variability through hybridization or mutation breeding will produce novel segregants for important yield attributing traits. The selection from the population will be effective if the traits have good genetic variability estimates.

Methods: The present investigation was conducted on analysing genetic variability parameters in F_2 populations of the blackgram crosses CO 5 × VBN 9 and CO 6 × VBN 11 which were evaluated during *rabi,* 2022.

Result: Based on the coefficient of variations, it was found that sufficient amount of genetic variability and high to moderate heritability with high genetic advance were present in the populations for the traits *viz*., 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 indicates the presence of additive gene action which can be improved by simple selection in the earlier generations. The positive skewness was observed for the traits *viz*., number of branches per plant, number of pods per cluster, number of pods per plant, hundred seed weight and seed yield per plant in F_2 population of CO 5 × VBN 9 and number of clusters per plant, number of pods per cluster, number of pods per plant and seed yield per plant in the F_2 population of CO 6 × VBN 11. The above traits could be improved by intensive selection for rapid improvement. The leptokurtic nature of the distribution for the trait hundred seed weight in CO 5 × VBN 9 population and the traits *viz*., number of clusters per plant, number of pods per plant, pod length, number of seeds per pod and seed yield per plant in CO 6 × VBN 11 population indicates that these traits are controlled by few minor genes. Hence, the good segregants could be selected from these two populations for yield improvement.

Key words: Blackgram, GCV, PCV, Skewness and kurtosis, Variability, *Vigna mungo*.

INTRODUCTION

Pulses are the leguminous crops rich in dietary protein which is essential for the human growth and developmental process. Among the pulses, blackgram is the important crop that is majorly grown in India. It is cultivated in Indian subcontinent as intercrop with cereals, rice fallow and rainfed crop. It is consumed in a variety of forms in the Indian cuisine due to its nutritive qualities and is having high protein content (25%), carbohydrate (60%), fat (1.5%), minerals and vitamins (Mehra *et al*., 2016). The production of blackgram needs to be raised either through extensive cultivation or by enhancing productivity through developing high yielding cultivars to meet the growing demand. Every year, the area of arable land decreases as a result of urbanisation and industrialization. Thus, new high yielding cultivars are primarily responsible for making production enhancement. The creation of new variability through hybridization or mutation breeding will produce novel segregants for important yield attributing traits. The selection from the population will be effective if the traits have good genetic variability estimates (Reni *et al*., 2013). In this study, variability was created through hybridization and F_2 segregating populations were developed. In order to determine the proper selection criteria, the F_2 populations were investigated for the variability parameters and frequency distribution such as skewness and kurtosis to identify superior segregants (Rani *et al*., 2016).

[1]Department of Genetics and Plant Breeding, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore-641 003, Tamil Nadu, India.
[2]Department of Pulses, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore-641 003, Tamil Nadu, India.
[3]Department of Millets, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore-641 003, Tamil Nadu, India.

Corresponding Author: P. Jayamani, Department of Pulses, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore-641 003, Tamil Nadu, India.
Email: jayamani1108@gmail.com

How to cite this article: Surendhar, A., Jayamani, P., Iyanar, K., Senthilraja, G. and Shanmugam, P.S. (2024). Genetic Analysis of F_2 Populations for Quantitative Traits in Blackgram [*Vigna mungo* (L.) Hepper]. Agricultural Science Digest. 44(1): 100-105. doi: 10.18805/ag.D-5804.

Submitted: 31-05-2023 **Accepted:** 16-08-2023 **Online:** 05-09-2023

MATERIALS AND METHODS

The present study on blackgram was conducted in the Department of Pulses, Tamil Nadu Agricultural University, Coimbatore. The crosses CO 5 × VBN 9 and CO 6 × VBN 11 were made during summer, 2022 and the F_1 plants were raised along with parents during *kharif*, 2022. The true hybrid

plants were identified based on the contrasting morphological traits of the respective parents and the individual plants were forwarded to F_2 generation. The F_2 populations of two crosses were raised during *rabi*, 2022 with the spacing of 30 × 10 cm. The good crop stand was established with recommended package of practices and plant protection measures on need basis. Nine quantitative traits *viz*., 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, number of seeds per pod, hundred seed weight (g) and seed yield per plant (g) were recorded from 62 and 71 plants in the F_2 populations of CO 5 × VBN 9 and CO 6 × VBN 11 crosses, respectively.

The F_2 data was subjected for estimation of second order statistics (genetic variability parameters). The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for nine characters were calculated as per the formulae given by Burton (1952). These estimates were categorized by Sivasubramanian and Madhavamenon (1973) as low (<10%), moderate (10-20%) and high (>20%). To know the heritable portion of variability, broad sense heritability (h^2) was estimated as the ratio of genotypic variance to the phenotypic variance (Lush *et al*., 1940) and categorized as low (<30%), moderate (30-60%) and high (>60%). The genetic advance was calculated (Johnson *et al*., 1955) and expressed as a per cent of mean (GAM). The GAM values were categorized into low (<10%), moderate (10-20%) and high (>20%). The third and fourth order statistics *viz*., skewness and kurtosis were estimated to analyse the nature of the frequency distribution (Snedecor and Cochran, 1989). The significance for these two estimates were examined by 't' test. These analyses were performed using the statistical package SPSS 16.0 version.

RESULTS AND DISCUSSION

Confirmation of F_1 hybridity

The two crosses were subjected for the hybrid confirmation through morphological traits contrasting between the parents. In the cross I (CO 5 × VBN 9), the parents were contrasting for leaf vein colour and immature pod colour (green in CO 5 and purple in VBN 9 for both the traits). The true F_1 plants were identified with the expression dominant trait purple leaf vein colour (Plate 1a) and purple pigmentation on immature pod (Plate 1b) which are the characteristics of male parent, VBN 9. In the cross II (CO 6 × VBN 11), for pod pubescence trait, the female parent is having glabrous pods and in case of male parent, it is hairy. Hence, the F_1 plants were identified with the presence of dominant trait, hairy pods (Plate 2).

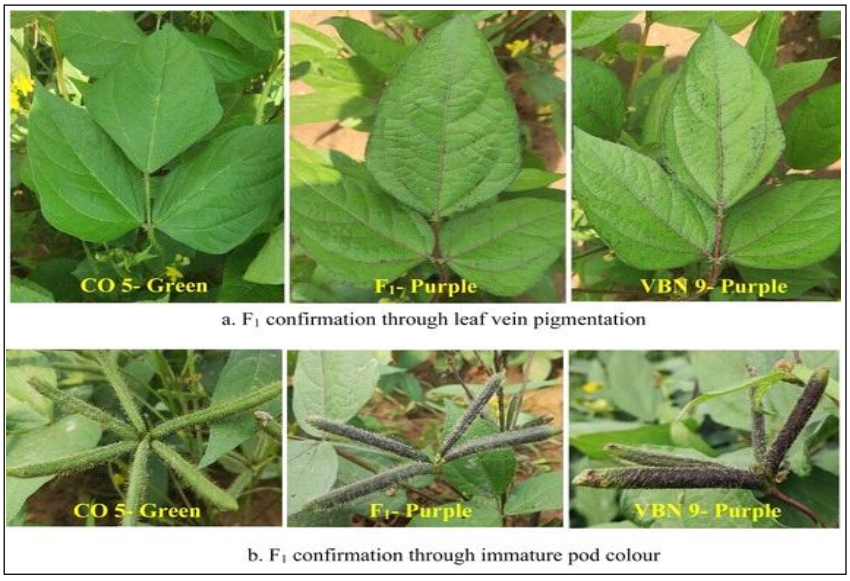


Plate 1: Confirmation of CO 5 × VBN 9 hybrid through morphological traits.



Plate 2: Confirmation of CO 6 × VBN 11 hybrid through pod pubescence.

Mean and range for seed yield per plant

The wide range of variations were observed in all the traits of F_2 populations which can be further analysed for genetic variability parameters for deciding the selection criteria. Among the traits, number of pods per plant and seed yield per plant were recorded with wider variations. The number of pods per plant ranged from 26.00 to 72.00 with the mean of 42.19 in cross I and it ranged between 29.00 and 86.00 with 45.89 mean value in cross II. A total of 25 plants in cross I and 30 plants in cross II excelled the F_2 mean value for number of pods per plant. In the cross I, the seed yield per plant ranged from 10.15 to 27.67 g with the mean value of 14.72 g (Table 1). Whereas, in cross II, it ranged between 10.32 g and 29.25 g with the average yield of 14.43 g. The number of plants outperformed for seed yield per plant over the F_2 mean were 24 and 23 in the cross I and II, respectively. This kind of wide variation and good segregants give scope for the yield improvement through selection process.

Coefficient of variations

In any breeding programme, selection is the important process for the effective improvement of the traits. To make the selection, presence of variation is the prerequisite from which the plants can be selected and forwarded. Hence, to analyse the extent of variation, phenotypic and genotypic coefficient of variations were calculated. Phenotypic coefficient of variation in both F_2 populations was higher than the genotypic coefficient of variations (Table 1) with small range of difference between them. This suggests that genetic components contributed more towards population variability than environmental influences. The PCV values ranged from 6.38 to 41.60% in cross I and from 6.09 to 37.52% in cross II for the traits pod length and number of branches per plant, respectively. The GCV values ranged from 2.52 (hundred seed weight) to 28.07% (number of branches per plant) in cross I and from 1.69 (hundred seed weight) to 23.00% (seed yield per plant) in cross II. The high GCV values were observed for the traits *viz*., number of branches per plant (28.07%) and seed yield per plant (24.96%) in cross I. In cross II, plant height (22.10%), number of pods per plant (20.51%) and seed yield per plant (23.00%) were observed with high GCV. The straightforward selection process could enhance these traits in the respective populations. Similar findings of high GCV for number of branches per plant, number of pods per plant and seed yield per plant were also reported by Sowmini *et al.* (2013) and Vinoth *et al.* (2014) in RIL population of blackgram and Susmitha *et al*. (2018) in greengram. The values of GCV for the traits *viz*., plant height (16.55%), number of clusters per plant (13.28%) and number of pods per plant (17.47%) in cross I and number of branches per plant (15.96%), number of clusters per plant (16.14%) and number of pods per cluster (10.59%) in the cross II were found to be moderate which directs that the selection can be made in the later generations for these traits. Moderate GCV were also found in the reports of Vadivel *et al.* (2019), Sathya *et al.* (2021)

Table 1: Variability parameters for nine quantitative characters in F_2 populations of two crosses.

Characters	Mean		Range		PCV %		GCV %		h^2 %		GAM %		Skewness		Kurtosis	
	C I	C II	C I	C II	C I	C II	C I	C II	C I	C II	C I	C II	C I	C II	C I	C II
PH	43.40	35.97	24.5-57.00	21.00-56.50	17.83	23.34	16.55	22.10	86.13	90.47	31.64	43.31	-0.49	0.57	-0.25	-0.07
NBP	1.63	1.61	1.00-3.00	1.00-3.00	41.60	37.52	28.07	15.96	45.55	18.10	39.03	13.99	0.63*	0.45	-0.67	-0.62
NCP	13.81	13.90	8.00-24.00	9.00-27.00	23.01	21.68	13.28	16.14	33.33	55.43	15.80	24.76	0.54	1.72**	0.75	5.01**
NPC	3.58	3.89	3.00-5.33	3.00-5.67	15.17	13.68	3.54	10.59	5.45	59.94	1.70	16.89	1.10**	0.65*	1.00	0.80
NPP	42.19	45.89	26.00-72.00	29.00-86.00	24.69	24.69	17.47	20.51	50.07	69.02	25.46	35.10	0.74*	1.45**	0.09	2.71**
PL	5.39	5.10	4.53-6.03	4.03-5.83	6.38	6.09	3.78	5.27	35.17	74.91	4.62	9.39	-0.17	-0.27	-0.23	1.35*
NSP	7.58	6.95	5.67-8.67	5.00-8.33	8.26	8.61	6.65	8.19	64.86	90.69	11.03	16.08	-0.61	-0.93**	0.85	1.22*
HSW	5.07	5.02	4.00-6.70	4.00-6.40	8.99	12.43	2.52	1.69	7.89	1.84	1.46	0.47	0.87**	0.42	2.70**	-0.67
SYP	14.72	14.43	10.15-27.67	10.32-29.25	28.67	27.37	24.96	23.00	75.80	70.63	44.76	39.82	1.10**	1.90**	0.62	3.59**

PH- Plant height (cm); NBP- Number of branches per plant; NCP- Number of clusters per plant; NPC- Number of pods per cluster; NPP- Number of pods per plant; PL- Pod length (cm); NSP- Number of seeds per pod; HSW- Hundred seed weight (g); SYP- Seed yield per plant (g). C I: F_2 population of the cross CO 5 × VBN 9; C II: F_2 population of the cross CO 6 × VBN 11. * and ** : Significance at 0.05 and 0.01 probability levels, respectively.

and Ragul *et al.* (2021) for plant height and number of pods per cluster in blackgram.

Heritability and genetic advance

The selection for the improvement of particular trait will be effective when the variation present in population is more due to genetic cause. Hence, the heritability and genetic advance of the traits were analysed in both the populations and the values were given in the Table 1. In cross I, heritability ranged from 5.45 (number of pods per cluster) to 86.13% (plant height) and genetic advance ranged from 1.46 (hundred seed weight) to 44.76% (seed yield per plant). In cross II, heritability was observed between 1.84% (hundred seed weight) and 90.69% (number of seeds per pod). The genetic advance parameter ranged between 0.47% (hundred seed weight) and 43.31% (plant height) in cross II. The high heritability (>60.00%) accompanied with high genetic advance (>20%) were observed for the traits plant height and seed yield per plant in both the crosses. In addition to this, number of pods per plant also showed the high values of these parameters in the cross II. It suggests that selection of these traits may be advantageous and the heritability is most likely caused by additive gene effects (Nadarajan *et al*., 2018). These higher estimates were also reported by Priya *et al.* (2019) for number of pods per plant and seed yield per plant in blackgram and Susmitha *et al.* (2018) for plant height in greengram. The moderate heritability (30-60%) together with substantial genetic advance (>20%) were found for the traits *viz*., number of branches per plant and number of pods per plant of cross I and number of clusters per plant of cross II. The moderate heritability is due to the environmental influences on these traits. This kind of variability for these three traits were also reported by Sathya *et al.* (2021) in F_2 population of blackgram. In certain circumstances, the selection might be successful for the improvement.

Skewness and kurtosis

The skewness was examined to analyse the surface nature of the distribution curve. These parameters were analysed to find out the presence of gene interaction and to decide the kind of selection intensity to be followed. Cross I was observed with significant positive skewness (Table 1; Fig 1)

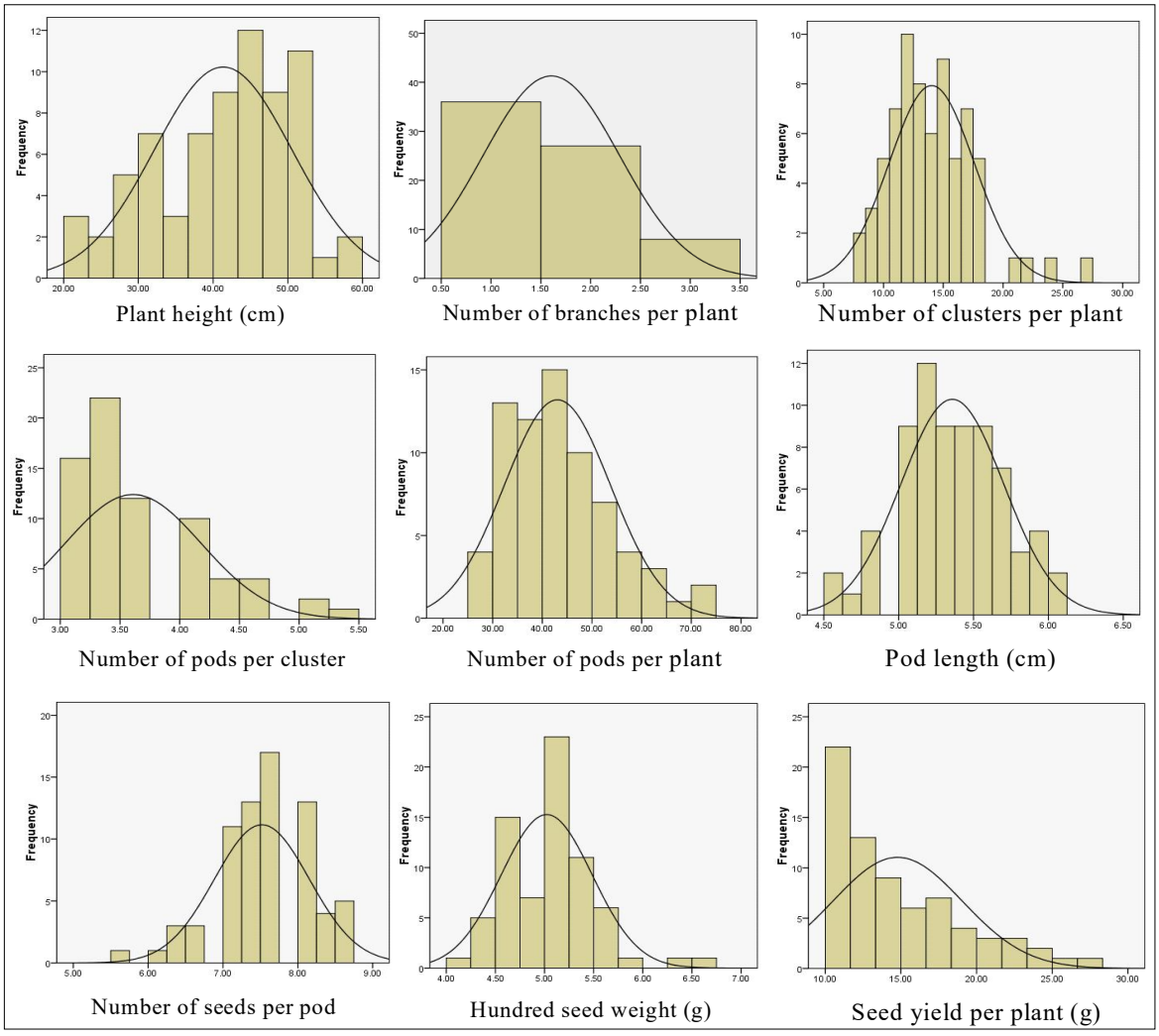


Fig 1: Frequency distribution of nine characters in the F_2 population of the cross CO 5 × VBN 9.

for the traits *viz*., number of branches per plant (0.63), number of pods per cluster (1.10), number of pods per plant (0.74), hundred seed weight (0.87) and seed yield per plant (1.10). Similarly, cross II also had significant positive skewness (Table 1; Fig 2) for the traits, number of clusters per plant (1.72), number of pods per cluster (0.65), number of pods per plant (1.45) and seed yield per plant (1.90). This kind of positive skewness in the population indicates the presence of dominant and complementary gene interaction. The genetic gain for these traits could be rapidly increased through intensive selection from the higher tail end of the distribution curve (Snape and Riggs, 1975; Bassuony *et al*., 2022). Similar findings of positive skewness were reported by Vadivel *et al.* (2019) for number of clusters per plant and seed yield per plant in blackgram, Devi *et al.* (2021) for hundred seed weight and seed yield per plant in RIL population of blackgram, Harshita *et al.* (2020) for number of branches per plant and number of pods per plant and Hema *et al*. (2022) for number of branches per plant and seed yield per plant in interspecific lines of greengram. Contrastingly, in cross II, number of seed per pod (-0.93) was negatively skewed which indicates the dominant and duplicate gene interaction controlling them and mild selection can be done from the higher end of the distribution curve for rapid improvement of these traits. The negative skewness for number of seeds per pod also reported by Vadivel *et al.* (2019) in blackgram. The normal distribution was noticed in the trait *viz*., plant height, number of clusters per plant, pod length and number seeds per pod of cross I and plant height, number of clusters per plant, pod length and hundred seed weight of cross II.

The kurtosis is peakness of the distribution curve. A distribution with positive kurtosis (excess) is called leptokurtic and negative kurtosis is called platykurtic which means the trait is controlled by large and fewer number of genes, respectively (Bassuony *et al*., 2022). The kurtosis value (Table 1; Fig 1) of hundred seed weight (2.70) in cross I and the traits *viz*., number of clusters per plant (5.01), number of pods per plant (2.71), pod length (1.35), number of seeds per pod (1.22) and seed yield per plant (3.59) in

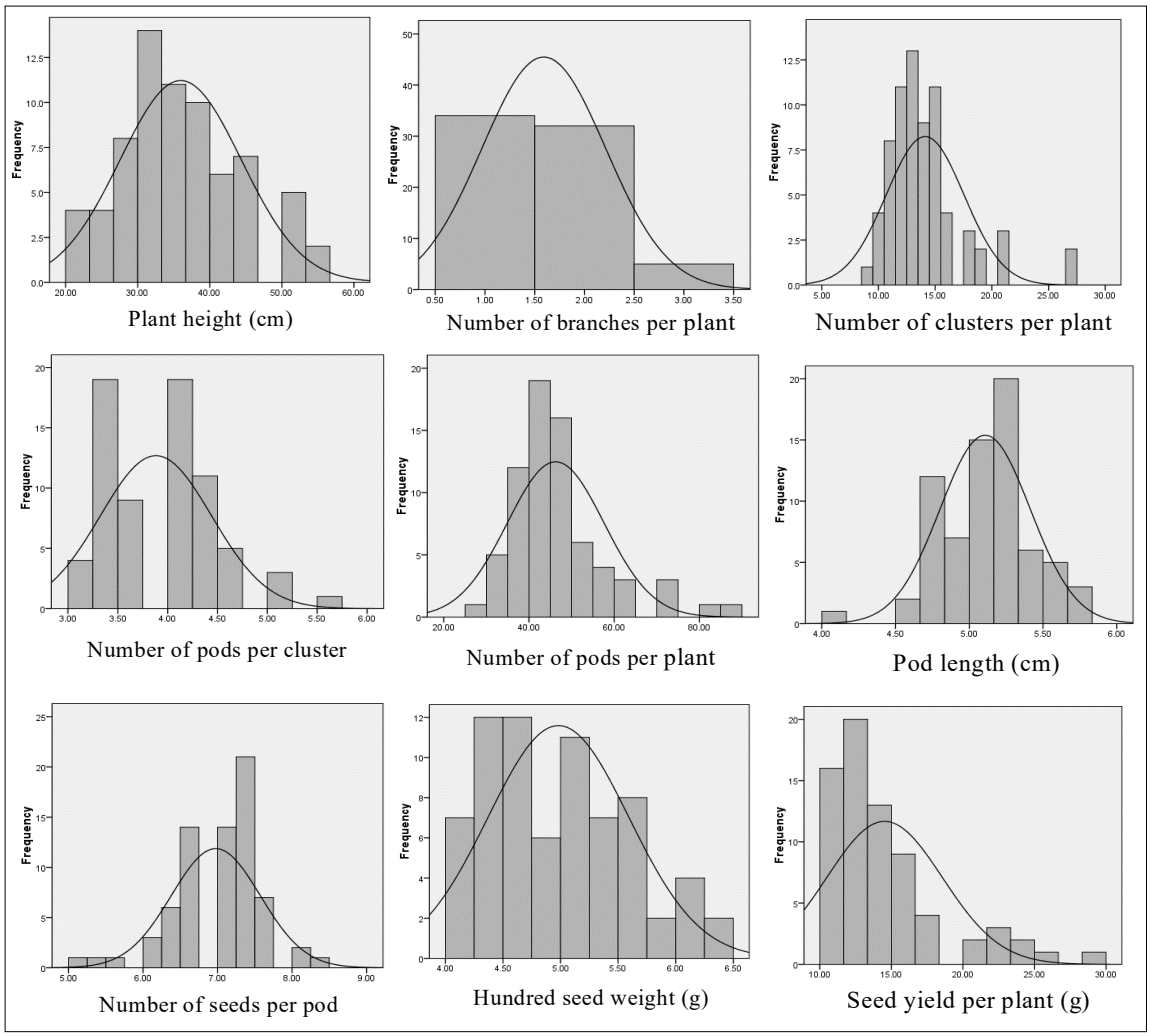


Fig 2: Frequency distribution of nine characters in the F_2 population of the cross CO 6 × VBN 11.

cross II were significant positive with leptokurtic nature (Table 1; Fig 2) which implies that fewer number of genes controlling them. Similar leptokurtic nature in RIL population for pod length and number of seeds per pod were found in the earlier reports (Devi *et al*., 2021; Vadivel *et al*., 2019).

CONCLUSION

Based on the above discussion, it was concluded that the improvement of the traits *viz*., 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 will be effective through simple selection process. The positive skewness and leptokurtic nature of the traits could be improved by stringent selection from higher end of the distribution for rapid improvement of the traits. Hence, the selection can be made from the segregating populations of the present study for the development of high yielding blackgram varieties.

ACKNOWLEDGEMENT

The first author is grateful to the Council for Scientific and Industrial Research (CSIR), Ministry of Science and Technology, Government of India for offering a Senior Research Fellowship.

Conflict of interest

All authors declare that they have no conflict of interest.

REFERENCES

Bassuony, N.N., Zsembeli, J., Juhász, C. and Elshenawy, M.M. (2022). Estimation of genetic variability and frequency distribution in F_2 generation of rice under normal and deficit water supply. Cereal Research Communications. 50: 489-500.

Burton, G.W. (1952). Quantitative inheritance in grasses. Pro VI The International Grassland Congress. 1952: 277-283.

Devi, M., Jayamani, P. and Kumar, M. (2021). Genetic Analysis and Seed Polymorphism in Inter sub-specific cross of blackgram [*Vigna mungo* (L.) Hepper]. Madras Agricultural Journal. 108(1): 10-12. doi: 10.29321/MAJ.10.000563.

Harshitha, G.P. and Jayamani, P. (2020). Genetic analysis in pre-breeding lines of greengram [*Vigna radiata* (L.) Wilczek.]. International Journal of Current Microbiology and Applied Sciences. 9(7): 2791-2798.

Hema, T., Jayamani, P., Gnanamalar, R.P., Rajeswari, E. and Vishnupriya, R. (2022). Genetic analysis in pre-breeding lines of greengram [*Vigna radiata* (L.) Wilczek]. Legume Research-An International Journal. 14(3): doi: 10.18805/LR-4867.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybeans. Agronomy Journal. 47(7): 314-318.

Lush, J.L. (1940). Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics. Journal of Animal Science. 33(1): 293-301.

Mehra, R., Tikle, A.N., Saxena, A., Munjal, A., Khandia, R. and Singh, M. (2016). Correlation, path-coefficient and genetic diversity in blackgram [*Vigna mungo* (L) Hepper]. International Journal of Plant Sciences. 7(1): 1-11.

Nadarajan, N., Manivannan, N. and Gunasekaran, M. (2018). Quantitative Genetics and Biometrical Techniques in Plant Breeding. Kalyani Publishers, New Delhi. pp: 75-78.

Priya, L., Pillai, M.A. and Shoba, D. (2019). Genetic divergence, variability and correlation studies in black gram [*Vigna mungo* (L.) Hepper]. Legume Research-An International Journal. 44(1): 36-40. doi: 10.18805/LR-4065.

Ragul, S., Manivannan, N., Iyanar, K., Ganapathy, N. and Karthikeyan, G. (2021). Genetic analysis on yield and yield components traits in the segregating populations of blackgram [*Vigna mungo* (L.) Hepper]. Madras Agricultural Journal. 107 (10-12): 1-6. https://doi.org/10.29321/MAJ.10.000553.

Rani, C.S., Anandakumar, C.R., Raveendran, M., Subramanian, K.S. and Robin, S. (2016). Genetic variability studies and multivariate analysis in F_2 segregating populations involving medicinal rice (*Oryza sativa* L.) cultivar Kavuni. International Journal of Agriculture Sciences. 8(35): 1733-1735.

Reni, Pushpa, Y., Rao, Y.K., Satish, Y. and Babu, J.S. (2013). Estimates of genetic parameters and path analysis in blackgram [*Vigna mungo* (L.) Hepper]. International Journal of Plant, Animal and Environmental Sciences. 3(4): 231-234.

Sathya, P., Manivannan, N., Viswanathan, P.L., Ganapathy, N. and Karthikeyan, G. (2021). Genetic variability, association and path coefficient analyses in segregating populations of black gram [*Vigna mungo* (L.) Hepper]. Madras Agricultural Journal. 107(10-12): 1-6. https://doi.org/10.29321/MAJ.10.000554.

Sivasubramanian, S. and Madhavamenon, P. (1973). Genotypic and phenotypic variability in rice. Madras Agricultural Journal. 60: 1093-1096.

Snape, J.W. and Riggs, T.J. (1975). Genetical consequences of single seed descent in the breeding of self-pollinated crops. Heredity. 35(2): 211-219.

Snedecor, G.W. and Cochran, W.G. (1989). Statistical Methods, 8th Edn. Ames Iowa State University Press. 54: 71-82.

Sowmini, K. and Jayamani, P. (2013). Genetic variability studies for yield and its component traits in RIL population of blackgram [*Vigna mungo* (L.) Hepper]. Electronic Journal of Plant Breeding. 4(1): 1050-1055.

Susmitha, D. and Jayamani, P. (2018). Genetic variability studies for yield and its contributing traits in greengram [*Vigna radiata* (L.) Wilczek]. Electronic Journal of Plant Breeding. 9(2): 716-722.

Vadivel, 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 blackgram [*Vigna mungo* (L.) Hepper]. Electronic Journal of Plant Breeding. 10(2): 732-735.

Vinoth, R. and Jayamani, P. (2014). Genetic variability studies for yield and its component traits in inter sub specific RIL population of blackgram [*Vigna mungo* (L.) Hepper]. Trends in Biosciences. 7(4): 243-245.