

International Journal of Agriculture Extension and Social Development

Volume 9; Issue 9; September 2026; Page No. 33-38

Received: 22-06-2026
Accepted: 27-07-2026

Indexed Journal
Peer Reviewed Journal

Variability analysis in F_2 populations of blackgram (*Vigna Mungo* (L.) Hepper) for yield and its attributing traits

¹Gabriel Darlong, ²Dr. RK Patel, ³Titus Dalang K Momin, ⁴Aslangti Reang, ⁵Larimon Shylla, ⁶MK Maqbool Qutub, ⁷Yoodarimiki Shylla and ⁸Tara Man Rai

¹Agriculture Officer, Department of Agriculture and Farmers Welfare, Government of Tripura, Agartala, Tripura, India

²Associate Professor, Department of Genetics and Plant Breeding, N.M. College of Agriculture, Navsari Agricultural University, Navsari, Gujarat, India

³State Coordinator (Extension Reforms), ATMA, Directorate of Agriculture, Department of Agriculture and Farmers Welfare, Shillong, Meghalaya, India

⁴Agriculture Officer, Government of Tripura, Agartala, Tripura, India

⁵Animal Husbandry and Veterinary Officer, Sutnga Veterinary Dispensary, Sutnga, Meghalaya, India

⁶Research Scholar, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

⁷Quality Manager, Meghalaya State Organic Certification Body (MSOCB), Upper Shillong, Meghalaya, India

⁸Research Scholar, Rajiv Gandhi University, Rono Hills, Arunachal Pradesh, India

DOI: <https://www.doi.org/10.33545/26180723.2026.v9.i9a.4167>

Corresponding Author: Gabriel Darlong

Abstract

In the present investigation, an attempt was made to assess the extent of genetic variability generated through hybridization by estimating important genetic parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, and genetic advance. In addition, the interrelationships among seed yield and its component traits were studied through correlation analysis to identify suitable selection criteria for yield improvement. The experimental material was developed by carefully selecting diverse parental genotypes with the objective of improving important yield-contributing traits such as branches per plant, clusters per plant, pods per plant, and harvest index. The study comprised four diverse parental genotypes and three F_2 populations, and was conducted during the late *khari* season of 2020 at the Pulses and Castor Research Station, Navsari Agricultural University, Navsari, Gujarat. Observations were recorded on 12 quantitative traits in the parental lines and their corresponding F_2 populations. The higher variances observed for most of the traits in the F_2 populations indicated the presence of substantial genetic variability among the segregating populations, providing ample scope for effective selection. The close correspondence between GCV and PCV values for most traits suggested that their expression was predominantly governed by genetic factors with comparatively less environmental influence. Furthermore, high heritability coupled with high genetic advance as a percentage of the mean was recorded for plant height, branches per plant, clusters per plant, pods per plant, 100-seed weight, seed yield per plant, and chlorophyll content, indicating the predominance of additive gene action. These findings suggest that direct phenotypic selection and pure-line breeding would be effective strategies for improving these traits and developing superior high-yielding black gram genotypes.

Keywords: Variability, Hybridization, GCV, PCV, Segregation, Quantitative character, genetic advance

Introduction

Pulses are an indispensable source of dietary protein, particularly for the predominantly vegetarian population of India. Besides their nutritional importance, they improve soil fertility through biological nitrogen fixation, thereby enhancing the productivity of succeeding crops. Among the pulse crops, black gram (*Vigna mungo* (L.) Hepper; $2n = 22$) is one of the most important grain legumes cultivated in tropical and subtropical regions, especially in India. Commonly known as urdbean, urid, or mash, it is a self-pollinated crop belonging to the family Fabaceae and subfamily Papilionoideae. India is recognized as the primary

centre of genetic diversity for black gram (Zeven *et al.*, 1982) [13], highlighting its significance in the origin and diversification of this crop.

Black gram is popularly referred to as the "King of Pulses" because of its excellent culinary qualities, wide adaptability, and high nutritional value. It is an erect, semi-erect, or trailing annual herb with a well-developed tap root system bearing numerous root nodules that facilitate atmospheric nitrogen fixation. The crop produces narrow, cylindrical pods and is valued for its seeds, which are rich in protein, carbohydrates, vitamins, and essential minerals while being naturally free from cholesterol. The seeds contain approximately 24%

protein, 1.4% fat, 3.2% minerals, and 57.3% carbohydrates (Aykroyd and Doughty, 1964)^[13]. In addition, black gram is an excellent source of essential amino acids such as lysine and tryptophan, which are deficient in cereal grains, thereby improving the biological value of cereal-based diets. It is also rich in potassium, calcium, magnesium, iron, copper, and manganese, making it an important component of a balanced human diet (Goyal *et al.*, 2010)^[13].

Black gram can be cultivated successfully under a wide range of agro-climatic conditions and soil types, although sandy and sandy loam soils are considered most suitable for its cultivation. Owing to its heat-loving nature, photo-insensitivity, and short duration, the crop can be grown throughout the year under suitable conditions. It is widely cultivated in arid, semi-arid, and subtropical regions and plays an important role in sustainable agriculture by improving soil organic matter and contributing biologically fixed nitrogen to the soil.

Despite the availability of improved varieties, the productivity of black gram in India remains relatively low compared with its genetic potential. The crop is often grown under rainfed conditions on marginal lands with poor soil fertility, inadequate irrigation, suboptimal nutrient management, and limited plant protection measures. Furthermore, the availability of quality seed of improved cultivars is often inadequate, compelling farmers to rely on local landraces that are generally low yielding and susceptible to major diseases such as Mungbean Yellow Mosaic Virus (MYMV), powdery mildew, and leaf crinkle disease. These constraints substantially reduce productivity and profitability.

Genetic improvement through the development of high-yielding, disease-resistant, and widely adaptable cultivars remains one of the most effective strategies for enhancing black gram productivity. Successful crop improvement depends on the availability of sufficient genetic variability and a thorough understanding of the inheritance of economically important traits. Estimation of genetic parameters such as variability, heritability, genetic advance, correlation, and path coefficient provides valuable information for identifying superior genotypes and formulating efficient selection strategies. Therefore, the present investigation was undertaken to assess the genetic variability and character association in segregating F_2 populations of black gram, with the objective of identifying promising traits and genotypes for effective yield improvement through selection.

Technology in our country. The real yield potential of the crop can be exploited through varietal improvement programme which needs the information pertaining to range of existing genetic variability and its relationship with various economically important characters present in the promising available genetic stocks. Keeping these important points in consideration, the present study targeted on the genetic variability, heritability and genetic advance studies, genotypic and phenotypic correlation between seed yield and its related characters and to analyze path coefficient for assessing the direct and indirect effects of individual characters on seed yield.

Materials and Methods

The present investigation was conducted at the Pulses and

Castor Research Station, Navsari Agricultural University (NAU), Navsari, Gujarat, during the late *kharif* season of 2020 to assess the genetic variability, heritability, correlation, and path coefficient among segregating populations of black gram (*Vigna mungo* L. Hepper). The experimental field consisted of medium black soil with medium to poor drainage, good water-holding capacity, and a soil pH ranging from 7.5 to 7.8. The prevailing weather conditions during the crop growth period were normal and favourable for successful crop establishment and development.

The experimental material comprised three F_2 populations developed from the crosses NUK-15-02 $\times$ NUK-15-07, NUK-15-02 $\times$ NUK-15-09, and NUK-15-02 $\times$ GU-1, which were maintained at the Pulses and Castor Research Station, Navsari Agricultural University, Navsari. The important characteristics of the parental lines used in the study are presented in Table 1.1. Parent NUK-15-02 is resistant to Mungbean Yellow Mosaic Virus (MYMV); NUK-15-07 is a high-yielding genotype resistant to MYMV, powdery mildew, and leaf crinkle disease; NUK-15-09 possesses moderate resistance to MYMV, leaf crinkle virus, leaf curl virus, and powdery mildew; while GU-1 is a late-maturing genotype with moderate resistance to powdery mildew.

The three F_2 populations, along with their respective parents and F_1 s, were grown in a non-replicated trial during late *kharif* 2020. Each parent and F_1 was sown in two rows comprising approximately 40 plants, whereas each F_2 population was planted in ten rows consisting of about 200 plants at a spacing of 45 cm between rows and 30 cm between plants. All recommended agronomic and plant protection practices were followed uniformly throughout the crop season to ensure healthy crop growth.

Random sampling was employed for recording observations on the experimental material. Ten competitive plants were randomly selected from each parent and F_1 generation, whereas 100 plants were selected from each F_2 population after excluding three border plants from both ends of each row to eliminate border effects. Observations were recorded on twelve quantitative characters, namely days to flowering, plant height (cm), branches per plant, clusters per plant, pods per plant, pod length (cm), seeds per pod, 100-seed weight (g), seed yield per plant (g), days to maturity, chlorophyll content, and harvest index. These observations were subjected to statistical analyses for estimating genetic parameters and determining the association among yield and its component traits.

Results and Discussion

The segregating populations exhibited improved mean performance over the parental means for several economically important traits, indicating the effectiveness of hybridization in generating useful variability. The cross NUK-15-02 $\times$ NUK-15-09 recorded higher mean values for pods per plant, 100-seed weight, days to maturity, and chlorophyll content, while NUK-15-02 $\times$ GU-1 showed superiority for pods per plant and chlorophyll content. In contrast, NUK-15-02 $\times$ NUK-15-07 exhibited a desirable reduction in days to flowering, suggesting its potential for developing early-maturing genotypes.

Considerable variation was observed among the F_2 populations for most of the characters studied. The cross

NUK-15-02 $\times$ NUK-15-07 exhibited higher variance for days to flowering, plant height, branches per plant, clusters per plant, pods per plant, pod length, 100-seed weight, seed yield per plant, days to maturity, and chlorophyll content. Similarly, NUK-15-02 $\times$ NUK-15-09 showed high variance for days to flowering, plant height, branches per plant, clusters per plant, pods per plant, seed yield per plant, chlorophyll content, and harvest index, whereas NUK-15-02 $\times$ GU-1 recorded higher variance for days to flowering, plant height, clusters per plant, pods per plant, seed yield per plant, chlorophyll content, and harvest index. The high variance observed for these traits indicates the presence of substantial genetic variability, providing ample opportunity for effective selection in subsequent generations.

The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) showed wide variation across the studied traits. In all populations, GCV values were generally close to the corresponding PCV values, indicating that the expression of these traits was largely controlled by genetic factors with comparatively lower environmental influence. High GCV and PCV values were recorded for branches per plant, clusters per plant, pods per plant, seed yield per plant, and chlorophyll content, suggesting greater scope for improvement through selection. Moderate GCV and PCV values were observed for plant height and 100-seed weight, whereas days to flowering and days to maturity exhibited low variability. Moderate GCV was also observed for pods per plant, harvest index, and pod length in most crosses, although exceptions were noted in specific populations. The low to moderate variability for these traits indicates comparatively limited scope for improvement through direct selection.

Broad-sense heritability estimates were generally high for most of the traits across the three F_2 populations. High heritability was observed for days to flowering, plant height, branches per plant, clusters per plant, pods per plant, pod length, seeds per pod, and seed yield per plant, indicating that these traits were predominantly governed by genetic factors. However, broad-sense heritability includes both additive and non-additive genetic effects; therefore, high heritability alone may not guarantee effective selection. The cross NUK-15-02 $\times$ NUK-15-07 and NUK-15-02 $\times$ GU-1 exhibited high heritability for 100-seed weight, while NUK-15-02 $\times$ NUK-15-09 showed moderate heritability. Days to maturity exhibited low, moderate, and high heritability in NUK-15-02 $\times$ NUK-15-09, NUK-15-02 $\times$ GU-1, and NUK-15-02 $\times$ NUK-15-07, respectively. Chlorophyll content and harvest index also showed varying levels of heritability among the populations. Traits with low to moderate heritability were more susceptible to environmental influence, making genetic improvement through selection comparatively difficult.

Genetic advance expressed as a percentage of the mean was high for plant height, branches per plant, clusters per plant, pods per plant, 100-seed weight, seed yield per plant, and chlorophyll content across the populations. High genetic advance coupled with high heritability suggests the predominance of additive gene action and indicates that selection for these traits would be highly effective. Moderate genetic advance was observed for pod length, seeds per pod, and harvest index in some populations, whereas days to flowering and days to maturity generally exhibited low genetic advance. These results suggest that non-additive gene action predominates for these traits, thereby reducing the effectiveness of simple phenotypic selection.

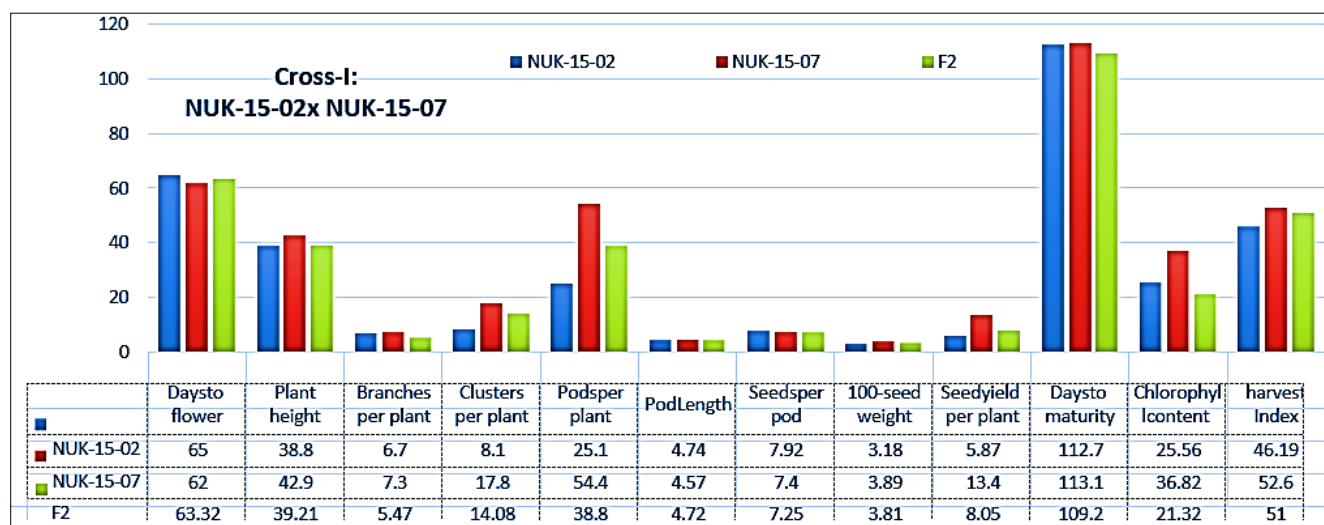
The combined assessment of heritability and genetic advance provides a more reliable estimate of the expected response to selection than heritability alone. In the present investigation, plant height, branches per plant, clusters per plant, pods per plant, 100-seed weight, seed yield per plant, and chlorophyll content exhibited high heritability coupled with high genetic advance in all three populations, confirming the predominance of additive gene action and indicating good prospects for improvement through pure-line selection. Conversely, high heritability associated with moderate or low genetic advance for days to flowering, pod length, and seeds per pod suggested a greater contribution of non-additive gene effects or environmental influence. Low heritability coupled with low genetic advance for days to maturity in NUK-15-02 $\times$ NUK-15-09 and NUK-15-02 $\times$ GU-1 further indicated the importance of non-additive gene action in controlling this trait.

Since seed yield is a complex quantitative trait influenced by several component characters, correlation and path coefficient analyses were undertaken to identify the most important yield determinants. In all three F_2 populations, seed yield per plant showed strong and positive associations with plant height, clusters per plant, and pods per plant, indicating that simultaneous improvement in these traits would result in enhanced seed yield. Positive and significant correlations were also observed between seed yield and branches per plant in NUK-15-02 $\times$ NUK-15-09 and NUK-15-02 $\times$ GU-1, and between seed yield and harvest index in NUK-15-02 $\times$ NUK-15-07 and NUK-15-02 $\times$ GU-1. Among all the component traits, pods per plant exhibited the highest positive correlation with seed yield, followed by clusters per plant and plant height. Path coefficient analysis further revealed that pods per plant exerted the highest positive direct effect on seed yield in all three populations, followed by clusters per plant and plant height. These findings clearly indicate that emphasis on these characters during selection would be highly effective in improving seed yield in greengram breeding programme.

Table 1: Estimation of Genetic Variability Parameters for Different Quantitative Characters in F₂ Generations of Three Crosses

Characters	Cross	Mean	σ^2_p	σ^2_e	σ^2_g	GCV	PCV	$h^2(bs)$	GA	GAM
Days to Flower	I	63.32	19.76	1.56	18.20	6.74	7.02	92.11	8.43	13.32
	II	63.72	10.99	2.74	8.25	4.51	5.20	75.06	5.13	8.05
	III	61.15	9.66	2.40	7.27	4.41	5.08	75.20	4.82	7.88
Plant height(cm)	I	39.21	36.19	3.14	33.04	14.66	15.34	91.31	11.32	28.86
	II	63.29	83.08	20.05	63.02	12.54	14.40	75.86	14.24	22.51
	III	46.32	45.11	10.57	34.54	12.69	14.50	76.57	10.59	22.87
Branches per Plant	I	5.47	7.93	0.90	7.03	48.47	51.48	88.65	5.14	94.00
	II	4.46	5.50	0.77	4.73	48.76	52.60	85.93	4.15	93.11
	III	3.20	1.56	0.36	1.20	34.18	38.98	76.90	1.98	61.75
Clusters per Plant	I	14.08	24.74	1.50	23.24	34.24	35.33	93.94	9.63	68.36
	II	24.57	108.57	7.37	101.20	40.94	42.41	93.21	20.01	81.43
	III	21.77	75.41	7.88	67.53	37.75	39.89	89.55	16.02	73.58
Pods per plant	I	38.80	228.59	12.94	215.65	37.85	38.97	94.34	29.38	75.73
	II	64.98	952.00	56.57	895.43	46.05	47.48	94.06	59.78	92.00
	III	66.17	647.88	72.46	575.42	36.25	38.47	88.82	46.57	70.38
Pod length (cm)	I	4.72	0.43	0.08	0.34	12.40	13.85	80.20	1.08	22.88
	II	4.81	0.21	0.05	0.16	8.23	9.54	74.50	0.70	14.63
	III	4.76	0.24	0.06	0.17	8.77	10.19	74.06	0.74	15.54
Seeds per pod	I	7.25	1.04	0.24	0.80	12.32	14.05	76.82	1.61	22.24
	II	7.39	0.89	0.23	0.66	11.00	12.74	74.52	1.45	19.56
	III	7.39	0.73	0.27	0.45	9.13	11.52	62.72	1.10	14.89
100 Seed weight (g)	I	3.81	0.56	0.13	0.43	17.21	19.66	76.61	1.18	31.03
	II	4.13	0.55	0.23	0.32	13.65	18.00	57.53	0.88	21.33
	III	3.97	0.52	0.12	0.39	15.78	18.11	76.00	1.12	28.35
Seed yield per plant (g)	I	8.05	15.54	2.72	12.82	44.46	48.94	82.51	6.70	83.19
	II	14.05	46.90	3.38	43.52	46.94	48.73	92.79	13.09	93.14
	III	15.17	53.09	6.31	46.78	45.08	48.03	88.11	13.22	87.18
Days to maturity	I	109.20	32.51	8.96	23.55	4.44	5.22	72.44	8.51	7.79
	II	113.40	11.72	10.70	1.02	0.89	3.02	8.68	0.61	0.54
	III	111.07	10.13	4.79	5.33	2.08	2.87	52.67	3.45	3.11
Chlorophyll Content	I	21.32	134.93	16.42	118.51	51.06	54.48	87.83	21.02	98.57
	II	25.14	99.37	40.77	58.60	30.45	39.66	58.97	12.11	48.18
	III	31.59	135.21	28.16	107.05	32.75	36.80	79.18	18.97	60.03
Harvest Index (%)	I	51.00	44.91	19.27	25.64	9.93	13.14	57.08	7.88	15.45
	II	50.51	61.40	16.20	45.20	13.31	15.51	73.62	11.88	23.53
	III	54.14	68.65	11.79	56.86	13.93	15.30	82.82	14.14	26.11

Cross-I:	NUK-15-02xNUK-15-07	Cross-II:	NUK-15-02xNUK-15-09	Cross-III:	NUK-15-02xGU-1
----------	---------------------	-----------	---------------------	------------	----------------

**Fig 1:** Mean value of parents and F₂ segregating population in NUK-15-02 × NUK-15-07 for different characters in blackgram.

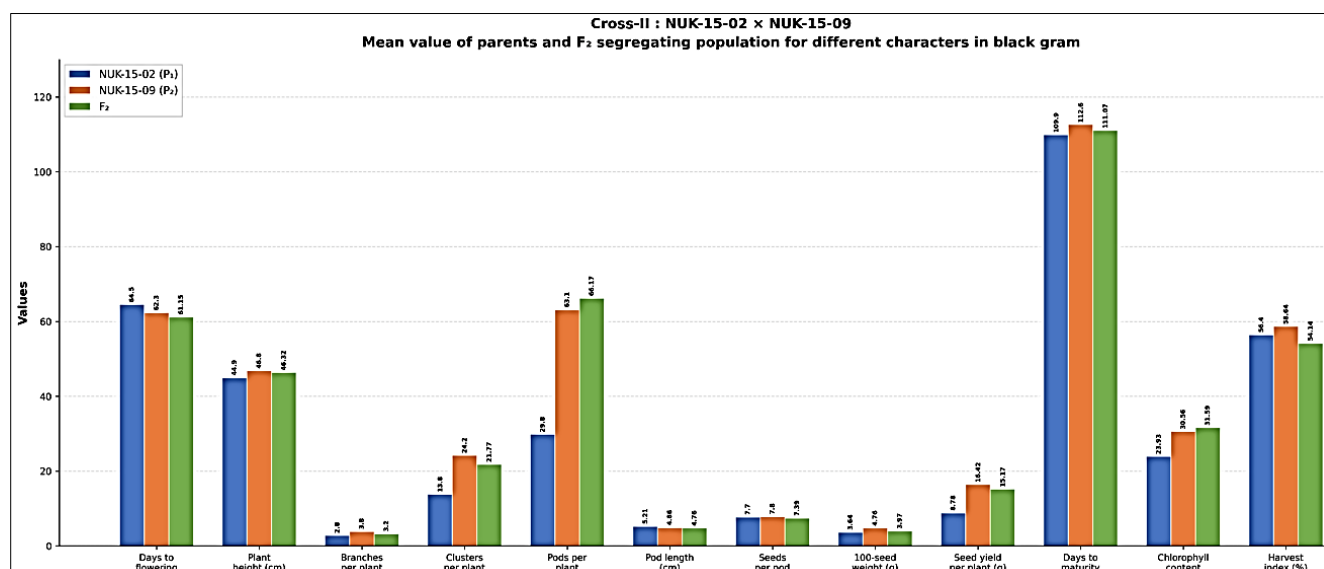


Fig 2: Mean value of parents and F₂ segregating population in NUK-15-02 × GUI for different character in black gram

Conclusion

The findings of the present investigation demonstrated that hybridization among the four black gram genotypes, namely NUK-15-02, NUK-15-07, NUK-15-09, and GU-1, successfully generated substantial genetic variability for important quantitative traits. Among the three F₂ populations, the cross NUK-15-02 × GU-1 exhibited high genotypic and phenotypic coefficients of variation, high heritability, and high genetic advance as a percentage of the mean for most of the yield-contributing traits, indicating the predominance of additive gene action and the effectiveness of simple phenotypic selection. Correlation and path coefficient analyses further revealed that plant height, branches per plant, clusters per plant, pods per plant, pod length, and harvest index were important yield-contributing characters and should receive due emphasis during selection for improving seed yield. The high positive direct effect of pods per plant on seed yield highlights its importance as a reliable selection criterion in black gram improvement programmes. Furthermore, the segregating populations derived from NUK-15-02 × NUK-15-07, NUK-15-02 × NUK-15-09, and NUK-15-02 × GU-1 possess sufficient variability for further genetic improvement. Advancement of these populations through pedigree selection, intermating within and between superior segregants, or biparental mating may help break undesirable linkage blocks, generate additional recombination, and facilitate the development of high-yielding, disease-resistant black gram cultivars.

Acknowledgement

The authors sincerely express their gratitude to the Department of Plant Breeding and Genetics, N.M. College of Agriculture, Navsari Agricultural University, Navsari, Gujarat, for providing the necessary research facilities, experimental materials, and technical support for conducting this study. The authors also acknowledge the staff of the Pulses and Castor Research Station for their assistance during the field experimentation and data collection.

References

- Allard RW. Principles of Plant Breeding. 2nd ed. New York: John Wiley & Sons; 1999.
- Anonymous. Agricultural Statistics at a Glance 2017. New Delhi: Government of India, Ministry of Agriculture and Farmers Welfare; 2017.
- Aykroyd WR, Doughty J. Legumes in Human Nutrition. FAO Nutritional Studies No. 19. Rome: Food and Agriculture Organization; 1964.
- Bishnoi A, Gupta P, Lal GM. Evaluation of genetic variability and heritability in black gram (*Vigna mungo* (L.) Hepper) genotypes. Journal of Pharmacognosy and Phytochemistry. 2017;6(4):493-496.
- Chauhan S, Mittal RK, Sood VK, Patial R. Evaluation of genetic variability, heritability and genetic advance in black gram (*Vigna mungo* (L.) Hepper). Legume Research. 2020; 43:488-494.
- Cockerham CC. Estimation of genetic variances. In: Hanson WD, Robinson HF, editors. Statistical Genetics and Plant Breeding. NAS-NRC Publication No. 982. Washington, DC: National Academy of Sciences-National Research Council; 1963. p. 53-94.
- Gupta S, Gupta SR, Dikshit HK, Singh RA. Variability and its characterization in Indian collections of black gram (*Vigna mungo* (L.) Hepper). Plant Genetic Resources Newsletter. 2001; 127:20-24.
- Konda CR, Salimath PM, Mishra MN. Genotype × environment interaction for yield and its component traits in black gram (*Vigna mungo* (L.) Hepper). Legume Research. 2014; 37:195-198.
- Kumar GV, Vanaja M, Jyothi LN, Maheshwari M. Studies on variability, heritability and genetic advance for quantitative traits in black gram (*Vigna mungo* (L.) Hepper). Agricultural Research Journal. 2015;52(4):28-31.
- Miah MA, Rob MM, Habiba U, Das K, Islam M. Correlation and path coefficient analysis in black gram (*Vigna mungo* L.). European Academic Research. 2016; 3:10906-10917.
- Patel RV, Patil SS, Patel SR, Jadhav BD. Genetic variability and character association in black gram (*Vigna mungo* (L.) Hepper). Trends in Biosciences.

- 2014;7(23):3795-3798.
12. Patro TSSK, Neeraja B, Ashok S, Sandhya Rani Y, Jyothsna S. Character association and path coefficient analysis for seed yield and its component traits in black gram (*Vigna mungo* (L.) Hepper). International Journal of Agriculture Sciences. 2016.
 13. Zeven AC, Wet JD. Dictionary of cultivated plants and their regions of diversity. 1982.
 14. Goyal A, Bonchi F, Lakshmanan LV. Learning influence probabilities in social networks. In Proceedings of the third ACM international conference on Web search and data mining 2010 Feb 4 (pp. 241-250).