



Genetic Variability and Association Studies on Yield and Yield Attributing Traits in Blackgram (*Vigna mungo* L. Hepper)

D. Shoba ^{a*}, J. Jecintha ^b, J. Joselen Joyci ^b, J.L. Joshi ^c,
M. Arumugam Pillai ^b and S. Juliet Hepziba ^b

^a Agricultural Research Station, Kovilpatti-628 501, Tamil Nadu Agricultural University, Tamil Nadu, India.

^b Department of Genetics and Plant Breeding, VOC Agricultural College and Research Institute, Killikulam-628 252, TNAU, Tamil Nadu, India.

^c Agricultural Research Station, Thirupathisaram-629 901, Tamil Nadu Agricultural University, Tamil Nadu, India.

Authors' contributions

This work was carried out in collaboration among all authors. Author DS designed the study, wrote the protocol and performed the statistical analysis, Authors JJ and JJJ wrote the first draft of the manuscript and managed the literature searches. Author JLJ, Author AMP and Author SJH managed the analyses of the study. All authors read and approved the final manuscript.

Article Information

DOI: <https://doi.org/10.9734/arja/2024/v17i4600>

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://www.sdiarticle5.com/review-history/126700>

Short Research Article

Received: 14/09/2024

Accepted: 19/11/2024

Published: 25/11/2024

*Corresponding author: E-mail: shoba.d@tnau.ac.in;

ABSTRACT

Aims: Low and static productivity (450–800 kg/ha) is one of the main obstacles in blackgram (*Vigna mungo* L. Hepper) crop. The low productivity is due to inadequate seed systems, a lack of access to genetic and genomic resources, and a lack of active breeding initiatives. Hence the present study was carried out to assess the variability and association among yield contributing traits for blackgram improvement programmes.

Place and Duration of Study: The field study was carried out during 2019-2020 in V.O. Chidambaranar Agricultural College and Research Institute, Killikulam, Tamil Nadu Agricultural University at Department of Genetics and Plant Breeding.

Study Design and Methodology: A total of 60 F₄ progenies developed from the cross IC 436656 x KKB14045 in blackgram for the assessment of *per se* performance, genetic variability and association studies.

Results: Based on the production of a single plant, seventeen offspring were determined to be promising. The traits viz., number of clusters per plant, number of pods per plant, and single plant yield showed high PCV and GCV, which indicated that there was a high level of genetic variability in the population. The variables of plant height, number of clusters / plant, number of pods/plant, and single plant yield showed significant heritability and high genetic advancement, indicating additive gene action. Single plant yield was positively and significantly correlated with the traits viz., plant height, number of clusters / plant, number of pods / plant, and number of seeds / pod. Therefore, choosing these characteristics is crucial to creating high yielding blackgram cultivars.

Keywords: Blackgram; F₄ progenies; *per se* performance; genetic variability; association studies.

1. INTRODUCTION

An expensive pulse, blackgram (*Vigna mungo* L. Hepper) is high in iron, copper, calcium, magnesium, zinc, potassium, phosphorus, and vitamin B complex. Presently, India is the world's top producer of black gram, contributing over 70% of the total production. India produces approximately 2.7 million tonnes from an approximately 4.4 m ha area with an average yield of 598 kg/ha (Directorate of Economics and Statistics, 2021). Due of the plants' resilience to severe weather, blackgram cultivation is comparatively simple. Poor management techniques and several physical, biochemical, and crop genetic factors, however, contribute to the low yield of blackgram (agrifarming.in). India's reliance on imports from some other black gram-producing nations has grown because of the poor rate of production expansion [1].

Estimating the variability in the plant population is crucial to the breeding program's effectiveness for blackgram. A population's level of genetic variety has a significant impact on how effective selection is. Although the genetic component alone is heritable, the observed variability is a result of both genotypic and epigenetic variables. Since more diversity expands the potential for selection, a high degree of phenotypic and genotypic variability

is necessary for the selection of good genotypes. The likelihood that a genotype may be recognized by its phenotypic expression is indicated by the heritability magnitude. The term "genetic advance" describes how the mean genotypic value of the chosen families has improved over the population. Because the trait's additive gene action is so prevalent, high heritability suggests that changes in phenotypic performance could be achieved with simple selection.

Additionally, correlation aids in comprehending how different components affect yield [2]. When it comes to creating successful and sustainable breeding programs for seed yield, when direct selection is not very effective, the relationship between seed yield and plant characteristics is crucial [3]. In order to identify ideal progenies and attributes for yield improvement, the current study concentrated on genetic variability and association studies in 60 F₄ blackgram progenies.

2. MATERIALS AND METHODS

The experimental material consisted of 60 F₄ progenies derived from the cross IC 436656 x KKB 14045. The field experiment was conducted at Department of Genetics and Plant Breeding at VOC Agricultural college and Research Institute, Killikulam during 2019-2020.

Biometrical traits viz., plant height (cm), days to fifty percent flowering, number of primary branches / plant, number of clusters / plant, number of pods / plant, number of seeds / pod and single plant yield (g) were recorded.

All the 60 F₄ progenies were raised in 3 meter row with a spacing of 30 x10 cm and proper agronomic practices were followed. The statistical methods suggested by Johnson et al. [4] for various genetic variability parameters viz., genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as percentage of mean (GAM) were worked out. Genotypic correlation coefficient was worked out using the formulae given by Al-Jibouri et al. [5]. TNAU STAT software was used for analysis of variability and correlation studies [6].

3. RESULTS AND DISCUSSION

The *per se* performance of F₄ progenies for the studied traits is given in Table 1.

The progenies viz., 2.12, 2.29, 2.32, 4.1, 4.8, 5.11, 5.14, 5.19, 5.45, 5.47, 5.48, 5.56, 5.58, 5.59, 5.61, 5.66 and 5.67 were identified as potential based on single plant yield. Thirty-seven progenies exhibited significantly superior performance for early maturity, five progenies for plant height, four progenies for number of branches / plant, thirteen progenies for number of clusters / plant, twelve progenies for number of pods/plant. The identified progenies may be forwarded to further generations in blackgram improvement programs.

Variability parameters in F₄ progenies of the cross IC 436656 x KKB 14-45 is given in Table 2. High PCV and GCV were observed for the traits viz., number of clusters / plant (43.51% and 38.16% respectively), number of pods / plant (44.61% and 40.93% respectively) and single plant yield (59.35% and 55.63% respectively) suggesting the presence of high genetic variability present in the population and selection is effective for these traits. Priya et al., [7] reported the similar results for the traits viz., single plant yield, number of clusters / plant, number of pods / plant; Pratap et al., [8] for the traits viz., number of pods / plant and grain yield / plant; Narayanan et al., [9] for the traits viz., number of pods / plant and single plant yield.

High heritability coupled with high genetic advance were observed in the traits viz., plant height (61.92% and 26.35% respectively), number of clusters / plant (76.93% and 68.94% respectively), number of pods / plant (84.16% and 77.34% respectively) and single plant yield (87.86% and 107.42% respectively). The trait number of branches per plant showed both strong genetic advancement and medium heritability (47.82% and 24.49%, respectively), indicating additive gene action for the genetic regulation of these traits. Sushmitharaj et al. [10] and Sathees et al., [11] reported similar findings for number of clusters / plant and single plant yield; Priya et al., [7] for the traits viz., plant height, number of primary branches / plant, number of clusters / plant, number of pods / plant and single plant yield. Vadivel et al., [12] for the traits viz., number of branches / plant, number of pods / plant and seed yield / plant; Gomathy et al., [13] for plant height, number of primary branches / plant, number of clusters/ plant, number of pods / plant and yield; Pratap et al., [8] for plant height; Narayanan et al., [9] for number of pods / plant and single plant yield.

The association between the yield and component traits is presented in Table 3. The trait single plant yield had significant and positive association with the traits viz., plant height (0.507), number of clusters/plant (0.588), number of pods/plant (0.749) and number of seeds/pod (0.295). Similar significant and positive association was reported in blackgram by Sohel et al., [14] for pods/plant; Sushmitharaj et al., [10] for plant height, number of clusters / plant and number of pods / plant in thirty two advanced black gram genotypes; Keerthiga et al., [15] for number of seeds / pod in 30 F₄ progenies of greengram; Priya et al., [7] for number of pods/plant and number of clusters/plant in one hundred and twenty black-gram genotypes; Blessy and Naik [16] for number of pods/plant and number of clusters / plant in fourteen blackgram genotypes. Sathees et al., [11] for plant height, number of clusters / plant, number of pods/plant and number of seeds / pod in one hundred and sixty-two F₂ plants of the cross IC 436656 x KKB 14045; Pratap et al., [8] for number of pods/plant, number of seeds/pod and plant height; Gomathy et al., [13] for number of clusters / plant and number of pods / plant in 140 F₃ progenies developed from the cross IC 436656 x KKB14045. Narayanan et al., [9] for number of clusters / plant, number of pods/plant and number of seeds / pod in F₄ black gram population.

Table 1. The *per se* performance of F₄ progenies in blackgram

SI No	F ₄ progenies	Days to 50% flowering	Plant height (cm)	Number of branches / plant	Number of clusters / plant	Number of pods / plant	Number of seeds / pod	Single plant yield (g)
1	1.11	32*	31.25	5.5	18.00	23.00	5.50	3.50
2	1.12	36*	28.40	7.5*	20.50	39.00	5.50	2.73
3	1.13	38	30.65	7.5*	24.00*	33.00	6.00	2.18
4	1.14	39	27.45	7.0	10.50	33.50	6.00	4.61
5	1.47	37*	35.05	7.5*	20.50	31.00	6.50	4.65
6	1.54	37*	31.50	6.0	10.00	24.75	5.50	4.38
7	1.55	34*	19.15	6.0	7.00	11.50	5.00	3.03
8	1.61	38	22.80	6.0	9.00	10.00	5.50	1.68
9	1.65	33*	26.45	4.0	7.00	15.00	5.50	2.50
10	1.67	37*	25.40	6.0	12.50	29.00	5.50	2.93
11	1.73	33*	27.70	6.5	12.50	27.50	6.00	3.49
12	1.75	32*	31.75	7.0	23.50*	30.00	6.00	4.84
13	2.1	45	26.60	6.0	8.00	14.00	5.50	4.02
14	2.12	41	32.50	5.0	20.00	39.50	5.50	12.36*
15	2.19	33*	27.25	6.5	11.50	23.00	6.00	6.90
16	2.2	40	34.25	8.0	26.50*	23.00	5.50	4.45
17	2.23	34*	29.25	7.0	15.50	21.00	5.00	2.43
18	2.25	43	22.10	3.5	10.00	18.50	4.50	4.84
19	2.29	46	22.65	6.0	24.00*	50.50*	5.00	12.54*
20	2.32	39	27.23	7.5*	27.00*	36.50	6.00	11.52*
21	2.33	40	27.90	4.0	14.00	26.00	5.00	4.72
22	4.1	38	30.10	4.5	14.50	33.50	6.00	13.68*
23	4.7	36*	25.90	4.0	11.00	24.00	5.50	4.92
24	4.8	38	27.25	5.5	11.50	29.50	5.50	11.91*
25	4.12	35*	28.50	4.5	10.00	24.50	5.00	3.13
26	4.17	37*	28.00	5.0	9.50	13.00	6.00	3.24
27	4.22	36*	31.15	6.0	13.50	19.50	5.00	6.49
28	4.23	46	22.70	3.0	2.50	7.50	5.00	2.72
29	5.11	35*	29.65	6.5	26.50*	62.00*	6.00	13.32*
30	5.13	39	26.60	6.0	13.50	27.00	5.50	7.30
31	5.14	40	28.75	5.0	23.50*	45.50*	6.00	15.10*
32	5.17	38	25.20	4.5	14.50	27.00	5.50	8.61
33	5.18	36*	31.75	5.0	24.00*	39.50	5.50	9.62
34	5.19	34*	37.25*	5.0	20.00	43.00*	5.50	12.01*
35	5.21	34*	26.43	5.0	16.50	27.00	5.00	8.95
36	5.22	36*	21.90	3.5	7.50	12.00	5.00	1.76
37	5.34	36*	23.00	5.0	15.50	35.50	5.00	10.19
38	5.36	39	27.35	5.0	16.50	28.50	6.00	9.91
39	5.37	39	27.15	4.5	11.50	12.00	5.00	4.65
40	5.41	37*	22.93	4.5	16.00	37.00	5.50	8.61
41	5.42	36*	30.43	6.5	13.50	24.00	6.00	5.47
42	5.45	37*	33.75	4.5	21.00	43.00*	6.00	13.63*
43	5.47	38	41.05*	4.5	30.00*	57.00*	6.00	13.57*
44	5.48	36*	39.70*	4.5	26.00*	42.00*	6.00	17.05*
45	5.51	37*	33.15	5.0	24.50*	36.00	5.50	4.30
46	5.53	34*	22.05	4.5	13.00	28.00	5.50	3.85
47	5.54	35*	22.78	5.0	15.50	25.50	6.00	4.39
48	5.55	34*	25.30	4.5	12.00	25.50	5.00	5.85
49	5.56	32*	30.90	4.5	19.00	44.00*	6.00	13.30*
50	5.57	35*	30.90	5.0	21.00	42.50*	5.50	6.84
51	5.58	34*	47.15*	5.0	37.50*	60.50*	6.00	13.88*
52	5.59	38	35.55	3.5	11.50	28.00	5.50	11.41*
53	5.61	36*	28.20	4.5	16.50	27.00	5.50	13.17*
54	5.66	36*	32.35	5.5	18.00	59.50*	5.50	12.52*
55	5.67	36*	41.55*	6.5	27.50*	59.00*	5.50	14.40*
56	6.7	36*	28.10	5.5	12.00	23.00	5.50	5.62
57	6.14	38	29.35	5.5	16.00	32.00	5.50	6.10
58	6.26	32*	27.80	4.0	14.00	24.00	5.50	6.18
59	6.27	38	22.88	5.0	14.25	22.50	5.50	7.20
60	6.28	39	21.25	5.5	13.00	17.00	5.50	3.93
MEAN		36	28.88	5.4	16.42	30.45	5.55	7.38
CD		1.83	7.37	1.92	6.87	10.82	1.05	3.06

Table 2. Variability parameters in F₄ progenies of the cross IC 436656 × KKB 14-45

Traits	GCV	PCV	Heritability (%)	GAM (%)
Days to 50% flowering	8.29	8.66	91.66	16.35
Plant height (cm)	16.26	20.66	61.92	26.35
Number of branches / plant	17.19	24.86	47.82	24.49
Number of clusters / plant	38.16	43.51	76.93	68.94
Number of pods /plant	40.93	44.61	84.16	77.34
Number of seeds / pods	2.64	9.79	7.27	1.47
Single plant yield (g)	55.63	59.35	87.86	107.42

Table 3. Correlation coefficients among yield components in F₄ progenies of the cross IC 436656 x KKB 14045

Traits	Days to 50% flowering	Plant height (cm)	Number of branches / Plant	Number of clusters / plant	Number of pods / plant	Number of seeds / pod	Single plant yield (g)
Days to 50% flowering	1	-0.208	-0.067	-0.11	-0.104	-0.223*	0.048
Plant height (cm)		1	0.143	0.700*	0.617*	0.433*	0.507*
Number of branches / Plant			1	0.322*	0.144	0.361*	-0.161
Number of clusters / Plant				1	0.809*	0.428*	0.588*
Number of pods / plant					1	0.379*	0.749*
Number of seeds / pod						1	0.295*
Single plant yield (g)							1

* Significant at 5% level

From inter correlation studies, days to 50 % flowering was significant and negative association with number of seeds / pod (-0.223); plant height had significant and positive association with number of clusters / plant (0.700), number of pods / plant (0.617) and number of seeds / pod (0.433); number of branches / plant had significant and positive association with number of clusters / plant (0.322) and number of seeds / pod (0.361); number of clusters / plant had significant and positive association with number of pods / plant (0.809) and number of seeds / pod (0.428); number of pods / plant was in significant with number of seeds / pod (0.379). Blackgram breeding programs would benefit greatly from the selection of these traits, which might be used to increase blackgram yield [17].

4. CONCLUSION

It is crucial to measure the variability in the plant population to ensure the effectiveness of the blackgram breeding program. Based on a single plant's yield, seventeen offspring were determined to be promising. A high degree of genetic variability in the population was suggested by the high PCV and GCV of the variables yield per single plant, number of clusters / plant, and number of pods / plant. Among the variables with high genetic progress and high heritability that demonstrated additive gene activity were plant height, number of clusters / plant, number of pods / plant, and single plant yield. The yield of a single plant was found to be positively and significantly correlated with plant height, number of clusters / plant, number of pods / plant, and number of seeds / pod. Thus, selecting these traits is essential to producing high yielding blackgram cultivars.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Authors hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

ACKNOWLEDGEMENT

The authors are grateful to Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India for providing the financial support to conduct the work.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Nair RM, Chaudhari S, Devi N, Shivanna A, Gowda A, Boddepalli VN, et al. Genetics, genomics and breeding of blackgram (*Vigna mungo* L. Hepper). Front Plant Sci. 2024;14: DOI: 10.3389/fpls.2023.1273363.
2. Kozak M, Kang MS. Note on modern path analysis in application to crop science. Commun Biometr Crop Sci. 2006;1:32-4.
3. Mathivathana MK, Shunmugavalli N, Muthuswamy A, Harris CV. Correlation and path analysis in black gram. Agric Sci Digest. 2015;35(2):158-60.
4. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agron J. 1955;47(7):314-8.
5. Al-Jibouri H, Miller PA, Robinson HF. Genotypic and environmental variances and covariances in an upland cotton cross of interspecific origin. Agron J. 1958;50(10):633-6.
6. Manivannan N. TNAU STAT Statistical package. Available: <https://sites.google.com/site/tnaustat>
7. Priya L, Pillai MA, Shoba D, Prem Kumari SM, Aananthi N. Genetic variability and correlation studies in black-gram (*Vigna mungo* (L.) Hepper). Electron J Plant Breed. 2018;9(4):1583-7.
8. Partap B, Kumar M, Kumar V, Kumar A. Genetic variability and correlation studies of seed yield and its components in black gram (*Vigna mungo* (L.) Hepper). J Pharmacogn Phytochem. 2019;8(3):2035-40.
9. Narayanan M, Pillai MA, Shoba D, Pushpam AK. Genetic variability, correlation, path coefficient analysis for yield and yield components in F4 progenies of KKM 1 x VBN 6 in black gram (*Vigna mungo* L. Hepper). Pharma Innov J. 2021;10(11):1248-53.
10. Sushmitharaj DV, Shoba D, Pillai MA. Genetic variability and correlation studies in black gram (*Vigna mungo* [L.] Hepper) with reference to YMV resistance. Int J Curr Microbiol Appl Sci. 2018;Special Issue 6:2849-56.

11. Sathees N, Shoba D, Saravanan S, Prem Kumari SM, Pillai MA. Studies on genetic variability, association and path coefficient analysis in blackgram (*Vigna mungo* L. Hepper). Int J Curr Microbiol Appl Sci. 2019;8(6):1892-9.
12. Vadivelu K, Manivannan N, Mahalingam A, Satya VK, Vanniarajan C, Saminathan VR. 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. 2019;10(2):732-5.
13. Gomathi D, Shoba D, Ramamoorthy V, Pillai MA. Genetic variability and association analysis in F3 progenies of IC 436656 x KKB14045 in black gram (*Vigna mungo* L. Hepper) for agro-morphological traits. Electron J Plant Breed. 2020;11(4):1211-4.
14. Sohel MH, Miah MR, Mohiuddin SJ, Islam AKMS, Rahman MM, Haque MA. Correlation and path coefficient analysis of black gram (*Vigna mungo* L.). J Biosci Agric Res. 2016;7(02):621-9.
15. Keerthiga S, Sen S, Pandya HR, Modha KG. Correlation and path analysis in F4 progenies of green gram (*Vigna radiata* (L.) R. Wilczek) for seed yield and its attributes. Int J Curr Microbiol Appl Sci. 2018;7(1):710-9.
16. Blessy V, Naik BP. Studies on correlation and path analysis in blackgram (*Vigna mungo* (L.) Hepper). Int J Curr Microbiol Appl Sci. 2018;7(8):1991-7.
17. Directorate of Economics and Statistics. Ministry of Agriculture and Farmers Welfare Department of Agriculture, Cooperation and Farmers Welfare. Third Advance Estimates of Production of Food Grains for 2020-21. Government of India; 2021.

Disclaimer/Publisher's Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of the publisher and/or the editor(s). This publisher and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.

© Copyright (2024): Author(s). The licensee is the journal publisher. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history:
The peer review history for this paper can be accessed here:
<https://www.sdiarticle5.com/review-history/126700>