



RESEARCH ARTICLE

Analysis of yield and its components in black gram through generation mean analysis

Dhamotharan Palanisamy¹, Manivannan Narayana^{1*}, Ganesan Kalipatty Nalliappan¹, Janaki Ponnusamy², Harish Sankarasubramanian³ & Babu Rajendra Prasad Venugopal⁴

¹Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore 641 003, India

²Department of Soil Science and Agricultural Chemistry, Tamil Nadu Agricultural University, Coimbatore 641 003, India

³Department of Plant Pathology, Tamil Nadu Agricultural University, Coimbatore 641 003, India

⁴Department of Crop Physiology, Tamil Nadu Agricultural University, Coimbatore 641 003, India

*Email: nm68@tnau.ac.in

OPEN ACCESS

ARTICLE HISTORY

Received: 25 September 2024

Accepted: 21 November 2024

Available online

Version 1.0 : 21 February 2025

Version 2.0 : 25 February 2025



Check for updates

Additional information

Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

Reprints & permissions information is available at https://horizonepublishing.com/journals/index.php/PST/open_access_policy

Publisher's Note: Horizon e-Publishing Group remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Indexing: Plant Science Today, published by Horizon e-Publishing Group, is covered by Scopus, Web of Science, BIOSIS Previews, Clarivate Analytics, NAAS, UGC Care, etc See https://horizonepublishing.com/journals/index.php/PST/indexing_abstracting

Copyright: © The Author(s). This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution and reproduction in any medium, provided the original author and source are credited (<https://creativecommons.org/licenses/by/4.0/>)

CITE THIS ARTICLE

Palanisamy D, Narayana M, Nalliappan GK, Ponnusamy J, Sankarasubramanian H, Venugopal BRP. Analysis of yield and its components in black gram through generation mean analysis. *Plant Science Today*. 2025; 12(1): 1-6. <https://doi.org/10.14719/pst.5289>

Abstract

Understanding the gene action governing yield and its component traits is crucial for developing an effective breeding strategy. In the present study, generation mean analysis was employed to unravel the genetic architecture of yield and its component traits in three crosses of black gram. The crosses, namely ADT 3 × VBG 17007 (cross 1: C1), ADT 3 × VBG 19010 (cross 2: C2) and VBG 13003 × VBG 17007 (Cross 3: C3), were developed using four parents contrasting in salt tolerance. The analysis of variance revealed significant differences among the five generations-P₁, P₂, F₁, F₂ and F₃-for most of the traits. All studied traits showed significance in either one or both the C and D scales, indicating the inadequacy of the additive-dominance model in explaining the genetic variation. Most traits, except for clusters per plant in Cross 1 (ADT 3 × VBG 17007) and seeds per pod across all crosses, exhibited significant additive genetic components. Furthermore, non-additive components, including dominance, additive × additive and dominance × dominance interactions, were significant for all traits across the three crosses. This suggests the presence of epistasis, emphasizing the need to delay selection to later generations in these crosses for effective genetic improvement.

Keywords

additive-dominance; black gram; component traits; epistasis; generation mean analysis; seed yield

Introduction

Pulses are often referred to as the "poor man's meat" due to their significant dietary value. They have played a crucial role in Indian agriculture, particularly in maintaining soil health by fixing atmospheric nitrogen through symbiotic bacteria in the root nodules (1). However, during the Green Revolution, insufficient attention was given to pulses, leading to low productivity in India (2). The total cultivation area of pulses in India is approximately 4.63 million ha, with a productivity of 987 kg ha⁻¹. In Tamil Nadu, the area under cultivation is 0.41 million hectares, with a productivity of 660 kg ha⁻¹ (3). The Indian Council of Medical Research (ICMR) recommends a daily intake of 84g of pulses. However, the per capita availability of pulses in 2021-22 was 53.8g, a decline from 70g in 1959 (4). Pulses are a vital source of protein and the decreasing production and productivity are major contributors to malnutrition, especially with the rapidly growing population. This highlights the urgent need to increase pulse productivity to meet both national and local requirements (5, 6).

Black gram [*Vigna mungo* (L.) Hepper; $2n = 22$] is a short-duration, multifunctional and nutritious legume predominantly grown in South and Southeast Asia (7, 8). It serves as an essential protein source for the growing population, provides feed for livestock and contributes to improving soil health and fertility. Believed to have originated in India 3,500 years ago from the wild progenitor *V. mungo* var. *silvestris*, it later spread to Thailand (9, 10). Black gram is renowned for its nutritional composition, containing 26.2% protein, 1.2% fat, 56.6% carbohydrates and essential minerals such as calcium (185 mg/100g) and iron (8.7 mg/100g), in addition to a substantial calorie content of 350 cal/100g (11, 12). Given its nutritional value, black gram plays a vital role in addressing global nutritional security, particularly in developing countries facing malnutrition challenges. Among legumes, black gram is highly sensitive to salt (13), a factor that exacerbates the situation in the coastal regions of Tamil Nadu, where rice-pulse cropping systems are typically followed (14). Enhancing the productivity of black gram requires a deeper understanding of the genetic basis of traits that influence yield, which will facilitate targeted improvements.

Generally, quantitative traits are influenced by multiple genes interacting in complex ways. A comprehensive understanding of the gene action and genetic variances of these traits is essential for plant breeders aiming to improve them. Knowledge of the genetic architecture of a trait is closely linked to the breeding methods used for improving the breeding population (15). The additive and dominant nature of a trait is directly related to its breeding value and the genetic gain achieved during improvement. Over the last century, several genetic models have been developed to decipher different genetic aspects, such as additive and dominance effects, using various mating designs such as diallel, Line \times Tester and North Carolina designs. However, these models often fail to account for epistatic interactions (15), which can lead to overestimation or underestimation of genetic components. To address non-allelic interactions, Hayman in 1958 proposed an assumption-free genetic model using generation mean analysis (GMA). GMA provides insights into the relative importance of average additive

gene effects, dominance deviations and effects arising from non-allelic genetic interactions (16). This analysis helps determine the reliable genotypic values of individuals, which is crucial for formulating appropriate breeding strategies. In this context, four salt-tolerance-responsive genotypes were utilized to study the genetics of yield and its component traits using generation mean analysis.

Materials and Methods

Experiment materials

The experiment was conducted at the Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, located at a latitude of 11.012890°N and longitude of 76.936805° W. Three crosses of black gram, namely ADT 3 \times VBG 17007 (C1), ADT 3 \times VBG 19010 (C2) and VBG 13003 \times VBG 17007 (C3), were obtained from two salt-sensitive and two salt-tolerant lines for the seedling stage, i.e., ADT 3, VBG 13003, VBG 17007 and VBG 19010. All four parent materials were sourced from the National Pulses Research Centre, Tamil Nadu Agricultural University, Vamban. F_1 hybrids of the three crosses were selfed to produce F_2 and a portion of the F_1 seeds was used to raise the F_2 generation. Similarly, part of the F_2 seeds were raised to produce seeds for the F_3 generation. Each F_3 family was raised separately and evaluated. Five breeding populations, namely P_1 , P_2 , F_1 , F_2 and F_3 , were used in the study. All populations of the three crosses were evaluated from February to April 2024, with a planting spacing of 30 \times 10 cm (Fig. 1). The recommended agronomic practices for Tamil Nadu were followed (17).

Observations were recorded for nine quantitative traits on an individual plant basis, including plant height (cm) (PH), number of branches per plant (BPP), number of clusters per plant (CPP), number of pods per cluster (PPC), number of pods per plant (PPP), pod length (cm) (PL), number of seeds per pod (SPP), 100-seed weight (g) (HSW) and seed yield per plant (g) (SYPP). The means and variances of the five generations (P_1 , P_2 , F_1 , F_2 and F_3) were used to evaluate genetic parameters. The details of the plant populations studied are presented in Table 1.

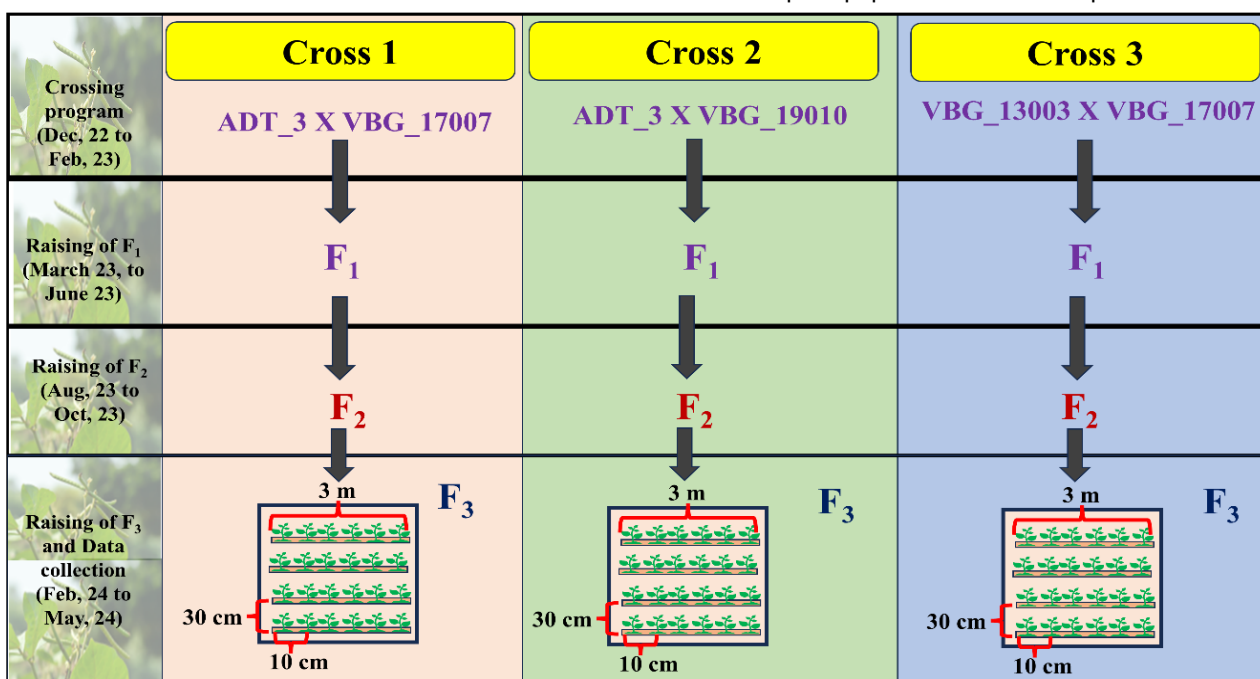


Fig. 1. Schematic workflow of generation mean analysis of three crosses.

Table 1. Total number of plants studied in each generation of three crosses

S No	Generations	C1	C2	C3
1	P ₁	10	10	10
2	P ₂	10	10	10
3	F ₁	10	10	10
4	F ₂	106	102	113
5	F ₃	396	331	311

Note: C1 - ADT 3 X VBG 17007, C2 - ADT 3 X VBG 19010, C3 - VBG 13003 X VBG 17007

Statistical analysis

A scaling test was used to examine the occurrence of non-allelic interaction components (18, 19). The scales C and D were computed (19) and the significance of any scale indicates the inefficacy of the additive-dominance model.

$$C = 4\bar{F}_2 - 2\bar{F}_1 - \bar{P}_1 - \bar{P}_2$$

$$D = 4_3\bar{F}_+ - 2\bar{F}_2 - \bar{P}_1 - \bar{P}_2$$

Where, \bar{P}_1 , \bar{P}_2 , \bar{F}_1 , \bar{F}_2 , \bar{F}_3 represents the mean values of the respective breeding population for the respective trait. The genetic components for m, d, h, i and l were estimated using TNAUSTAT software (20).

Results and Discussion

Mean comparison

The mean values and standard errors for the various generations of each cross are summarized in Table 2. Table 3 presents the scaling test results and genetic parameters for various yield-related traits. GMA is a promising tool for dissecting the genetic components into fixable and non-fixable effects. It provides

valuable insights into the genetic components and mechanisms involved in the expression of yield and other biometric traits, thereby facilitating the identification of suitable breeding strategies (15).

The mean performance of the hybrid and segregating generations of the three crosses showed varying results compared to their parents. In the C1 cross, the F₁ generation exhibited variable performance for six traits, with 100-seed weight (HSW) and plant height (PH) showing better performance than the parents. In the F₂ generation, all traits, except for seeds per pod (SPP) and HSW, underperformed compared to both parents. In the F₃ generation, most traits showed improved performance over the parents, except for pods per cluster (PPC), PH, clusters per plant (CPP) and pods per plant (PPP). The trait PPC exhibited variable performance, while the other three traits showed poor performance.

In the C2 cross, the F₁ generation showed poor performance for most traits, although pod length (PL) and SPP outperformed the parents. In the F₂ generation, all traits, except for PL and HSW, underperformed, with PL and HSW exhibiting intermediate responses. Similar trends were observed in the F₃ generation.

In the C3 cross, the majority of traits in the F₁ generation showed superior performance compared to the parents. However, in both the F₂ and F₃ generations, all traits underperformed relative to the parents. Similar results were observed in earlier studies on black gram (11, 21).

Gene action

The gene effects and scaling tests (C and D) for each cross are summarized in Table 3. The results of the scaling tests were used

Table 2. Mean and standard error for yield and yield contributing traits in various generations of three crosses

Characters	Cross	P ₁	P ₂	F ₁	F ₂	F ₃
Plant height (cm)	C1	48.00 ± 1.81	48.40 ± 1.66	49.90 ± 1.32	41.90 ± 1.27	32.10 ± 0.56
	C2	48.50 ± 3.53	39.80 ± 2.41	34.80 ± 1.34	35.78 ± 1.16	38.47 ± 0.50
	C3	48.60 ± 1.23	49.60 ± 1.18	49.50 ± 1.17	44.01 ± 1.20	29.08 ± 0.56
Branches per plant	C1	2.70 ± 0.15	2.90 ± 0.23	2.80 ± 0.13	2.47 ± 0.07	2.95 ± 0.05
	C2	3.80 ± 0.25	3.50 ± 0.22	3.10 ± 0.18	2.88 ± 0.07	2.53 ± 0.05
	C3	2.70 ± 0.15	2.80 ± 0.20	3.10 ± 0.28	2.53 ± 0.08	1.90 ± 0.06
Clusters per plant	C1	20.60 ± 1.61	22.60 ± 1.63	21.30 ± 1.15	19.66 ± 0.87	14.50 ± 0.27
	C2	17.40 ± 0.82	19.50 ± 1.21	19.10 ± 1.08	16.41 ± 0.78	15.47 ± 0.38
	C3	22.00 ± 0.93	26.40 ± 1.23	26.00 ± 1.09	17.45 ± 0.68	10.70 ± 0.27
Pods per cluster	C1	2.80 ± 0.20	3.60 ± 0.27	3.00 ± 0.21	2.26 ± 0.07	2.97 ± 0.06
	C2	3.20 ± 0.13	3.60 ± 0.16	3.20 ± 0.20	2.08 ± 0.07	3.31 ± 0.25
	C3	3.30 ± 0.26	3.50 ± 0.27	2.70 ± 0.21	2.71 ± 0.09	2.88 ± 0.06
Pods per plant	C1	56.40 ± 3.57	58.50 ± 2.20	53.20 ± 2.53	35.09 ± 1.83	30.90 ± 0.86
	C2	42.50 ± 3.80	48.60 ± 3.43	41.70 ± 4.55	22.04 ± 1.61	39.24 ± 1.36
	C3	51.90 ± 3.21	54.50 ± 2.89	55.30 ± 2.03	35.01 ± 1.77	29.51 ± 1.16
Pod length (cm)	C1	4.41 ± 0.09	4.26 ± 0.11	4.29 ± 0.08	4.12 ± 0.03	4.76 ± 0.21
	C2	4.31 ± 0.08	4.03 ± 0.08	4.54 ± 0.09	4.12 ± 0.03	4.30 ± 0.02
	C3	4.39 ± 0.09	4.38 ± 0.11	4.4 ± 0.01	4.00 ± 0.03	4.18 ± 0.02
Seeds per pod	C1	5.60 ± 0.31	5.30 ± 0.42	5.50 ± 0.31	5.37 ± 0.10	6.21 ± 0.13
	C2	5.50 ± 0.27	5.50 ± 0.37	6.20 ± 0.25	5.19 ± 0.10	5.70 ± 0.05
	C3	2.60 ± 0.16	3.10 ± 0.18	5.00 ± 0.30	5.19 ± 0.09	5.27 ± 0.05
100-seed weight (g)	C1	4.34 ± 0.14	3.81 ± 0.19	4.52 ± 0.10	4.01 ± 0.05	6.91 ± 1.72
	C2	4.38 ± 0.24	4.06 ± 0.12	3.97 ± 0.14	4.25 ± 0.08	3.70 ± 0.04
	C3	4.75 ± 0.20	4.11 ± 0.12	4.30 ± 0.14	3.96 ± 0.06	3.85 ± 0.06
Seed yield per plant (g)	C1	5.61 ± 0.63	4.90 ± 0.53	5.60 ± 0.22	4.29 ± 0.33	6.79 ± 0.21
	C2	7.54 ± 0.70	7.67 ± 0.71	7.50 ± 0.54	3.79 ± 0.31	7.22 ± 0.28
	C3	6.82 ± 0.95	7.15 ± 0.69	9.81 ± 0.81	3.91 ± 0.28	5.47 ± 0.23

Note: C1 - ADT 3 X VBG 17007, C2 - ADT 3 X VBG 19010, C3 - VBG 13003 X VBG 17007

Table 3. Scaling test and estimates of genetic parameters for various yield and yield contributing traits in black gram

Character	Cross	Scales		Genetic parameters					Type of epistasis
		C	D	Main effect (m)	Additive effect (d)	Dominance effect (h)	Additive X Additive (i)	Dominance X Dominance (l)	
Plant height (cm)	C1	-17.5**	-8.71**	35.78**	3.65**	-7.83**	10.18**	11.72**	Duplicate
	C2	-14.76**	-5.97**	35.78**	4.35**	-7.83**	10.22**	11.72**	Duplicate
	C3	-21.16**	-69.91**	44.01**	-0.50**	43.48**	42.08**	-64.99**	Duplicate
Branches per plant	C1	-1.31 ^{ns}	1.24**	2.47**	-0.10**	-1.05**	-1.25**	3.41**	Duplicate
	C2	-1.97 ^{ns}	-2.93**	2.88**	0.15**	1.07**	1.92**	-1.27**	Duplicate
	C3	-1.58 ^{ns}	-2.96**	2.53**	-0.05**	2.06**	1.61**	-1.85**	Duplicate
Clusters per plant	C1	-8.48**	-6.86**	16.41**	-0.59 ^{ns}	4.29**	1.98*	2.17*	Complementary
	C2	-9.45**	-7.83**	16.41**	-1.05**	4.29**	1.54**	2.17**	Complementary
	C3	-30.59**	-40.5**	17.45**	-2.20**	23.7**	17.50**	-13.21**	Duplicate
Pods per cluster	C1	-3.34**	0.96**	2.26**	-0.40**	-1.40**	-2.00**	5.74**	Duplicate
	C2	-4.89**	2.30**	2.08**	-0.20**	-2.55**	-2.75**	9.58**	Duplicate
	C3	-1.37**	-0.68**	2.71**	-0.10**	-0.48**	0.02**	0.92**	Duplicate
Pods per plant	C1	-80.92**	-61.50**	35.09**	-1.05*	23.26**	25.41**	25.90**	Complementary
	C2	-86.34**	21.78**	22.04**	-3.05*	-32.76**	-35.01**	144.16**	Duplicate
	C3	-76.96**	-58.36**	35.01**	-1.30*	28.18**	23.48**	24.81**	Complementary
Pod length (cm)	C1	-0.76 ^{ns}	2.12**	4.12**	0.08**	-1.59**	-1.39**	3.84**	Duplicate
	C2	-0.92 ^{ns}	0.61**	4.12**	0.14**	-0.19**	-0.28**	2.04**	Duplicate
	C3	6.37 ^{ns}	-0.08**	4.00**	0.01**	-2.84**	1.12**	-8.60**	Complementary
Seeds per pod	C1	-0.43**	3.22**	5.37**	0.15 ^{ns}	-2.17**	-1.92**	4.87**	Duplicate
	C2	-2.65**	1.44**	5.19**	0.00 ^{ns}	-0.70**	-1.40**	5.46**	Duplicate
	C3	5.04**	5.00**	5.19**	-0.25 ^{ns}	-0.34**	-2.99**	-0.06**	Complementary
100-seed weight (g)	C1	-1.14 ^{ns}	11.46**	4.01**	0.27**	-7.38**	-7.30**	16.80**	Duplicate
	C2	0.62 ^{ns}	-2.14**	4.25**	0.16**	1.28**	1.85**	-3.68**	Duplicate
	C3	-1.6 ^{ns}	-1.40**	3.96**	0.32**	0.54**	1.31**	0.27**	Complementary
Seed yield per plant (g)	C1	-4.58**	8.06**	4.29**	0.36**	-5.79**	-5.42**	16.85**	Duplicate
	C2	-15.04**	6.10**	3.79**	-0.06**	-6.68**	-6.70**	28.20**	Duplicate
	C3	-17.96**	0.11**	3.91**	-0.16**	-0.25**	-3.40**	24.10**	Duplicate

*, ** - significant at 1 and 5% probability

Note: C1 - ADT 3 X VBG 17007, C2 - ADT 3 X VBG 19010, C3 - VBG 13003 X VBG 17007

to assess the applicability of the additive-dominance model. All traits in the three crosses showed significance for one or both scales, indicating that the additive-dominance model is insufficient to explain the genetic control of these traits. Epistatic interactions were classified based on the directionality of the h and l parameters, as either complementary gene action (when the direction is the same) or duplicated gene action (when the direction is opposite) (22). In the cross ADT 3 x VBG 17007 (C1), complementary gene action was observed for clusters per plant (CPP) and pods per plant (PPP) (23-25), while all other traits exhibited duplicated epistatic interactions. In the cross ADT 3 x VBG 19010 (C2), complementary gene action was observed for CPP and duplicated epistasis was found for the remaining traits. In the cross VBG 13003 x VBG 17007 (C3), traits such as PPP, pod length (PL), seeds per pod (SPP) and 100-seed weight (HSW) showed complementary epistasis, while the other traits exhibited duplicated epistasis.

For the cross ADT 3 x VBG 17007 (C1), significant additive gene effects were observed for all traits except CPP and SPP. Non-significant additive components were observed for CPP in C1 and for SPP in all three crosses. Non-additive components, such as dominance, additive x additive and dominance x dominance interactions, were significant for all traits across all crosses (26).

The genetic control of traits as dominant or recessive is determined based on the direction of dominance effects (d). A positive direction indicates a dominant nature, while a negative direction suggests a recessive nature (27, 28). Dominant effects were observed for CPP in all crosses (29), while recessive effects

were noted for pods per cluster (PPC), PL, SPP and seed yield per plant (SYPP). For various traits, either dominant or recessive gene action was observed across the crosses (26). The signs of gene action reflect the mean performance of the F₁ generation (30). Similarly, the opposite directions of additive and dominance effects indicate genetic divergence between parents, emphasizing the importance of selecting appropriate parents for hybridization (31). Positive and negative signs of additive x additive interactions reveal the association and dispersion of alleles for the concerned trait, respectively (31).

Previous studies have reported a preponderance of dominance gene action for the number of branches in black gram (32) and similar trends of dominant and additive effects for pods per plant (33). Epistatic interactions for the number of pods have also been reported in similar studies (34). In contrast, some studies have suggested an additive-dominance model for seeds per pod and recommended the improvement of this trait through simple plant selection procedures (33).

Conclusion

In conclusion, the present study found that all the traits studied in the three crosses did not conform to the additive-dominance model, indicating the presence of non-allelic interactions. Significant additive components were observed for all traits, except for clusters per plant (CPP) in cross C1 and seeds per pod (SPP) in all crosses. Additionally, all traits exhibited significant non-additive components. Therefore, considering the presence

of epistatic interactions, it is recommended that selection be postponed until later generations to achieve homozygosity.

Acknowledgements

Authors wish to thank Council of Scientific and Industrial Research, Ministry of Science and Technology, Govt. of India, New Delhi to provide the fellowship to the first author [CSIR-JRF-File No: 09/641(14045)/2022-EMR-I].

Authors' Contributions

DP carried out field experiments, data curation, visualization, statistical analysis and manuscript preparation. MN carried out conceptualization, methodology and supervision. BRPV, GKN, JP and HS were involved in conceptualization and manuscript preparation.

Compliance with Ethical Standards

Conflict of interest: Authors do not have any conflict of interest to declare.

Ethical issues: None

References

- Nair RM, Chaudhari S, Devi N, Shivanna A, Gowda A, Boddepalli VN, et al. Genetics, genomics and breeding of black gram [*Vigna mungo* (L.) Hepper]. *Front Plant Sci* 2024;14:1273363. <https://www.frontiersin.org/articles/10.3389/fpls.2023.1273363/full>
- Marimuthu S, Navamaniraj KN, Kathiravan M, Balasubramanian P, Surendran U, El-Hendawy S, et al. Response of blackgram (*Vigna mungo* L.) cultivars for nipping and graded levels of nitrogen for higher productivity under irrigated conditions. *Agronomy* 2024;14(7):1474. <https://www.mdpi.com/2073-4395/14/7/1474>
- Marimuthu S, Kannan SV, Pazhanivelan S, Geethalakshmi V, Raju M, Sivamurugan AP, et al. Harnessing rain hose technology for water-saving sustainable irrigation and enhancing blackgram productivity in garden land. *Sci Rep*. 2024;14(1):18692. <https://www.nature.com/articles/s41598-024-69655-2>
- Surendran U, Jayakumar M, Marimuthu S. Low-cost drip irrigation: Impact on sugarcane yield, water and energy saving in semiarid tropical agro ecosystem in India. *Science of The Total Environment*. 2016;573:1430-40. <https://linkinghub.elsevier.com/retrieve/pii/S0048969716315960>
- Gurusamy S, Vidhya CS, Khasherao BY, Shanmugam A. Pulses for health and their varied ways of processing and consumption in India - A review. *Applied Food Research*. 2022;2(2):100171. <https://linkinghub.elsevier.com/retrieve/pii/S2772502222001317>
- Gomathi D, Shoba D, Ramamoorthy V, Pillai MA. Studies on variability, heritability, correlation and path analysis in segregating population of black gram [*Vigna mungo* (L.) Hepper]. *Legume Research - An International Journal*. 2021;46(6):690-94. <http://arccjournals.com/journal/legume-research-an-international-journal/LR-4411>
- Sankaran D, Adhimoalam K, Jayakodi M, Manickam S, Mannu J, Natesan S. Progress in genomic-driven breeding for improving the disease and insect pest resistance in black gram (*Vigna mungo*). *Physiol Mol Plant Pathol*. 2024;133:102368. <https://linkinghub.elsevier.com/retrieve/pii/S0885576524001528>
- Nainu AJ, Vadivel K, Murugan S, Kumar NS. Generation mean analysis for yield, its components and MYMV disease resistance in greengram [*Vigna radiata* (L.) Wilczek]. *Legume Research - An International Journal*. 2022;46(11):1541-46. <http://arccjournals.com/journal/legume-research-an-international-journal/LR-4829>
- Chandel KPS, Lester RN, Starling RJ. The wild ancestors of urid and mung beans (*Vigna mungo* (L.) Hepper and *V. radiata* (L.) Wilczek). *Botanical Journal of the Linnean Society*. 1984;89(1):85-96. <https://academic.oup.com/botlinnean/article-lookup/doi/10.1111/j.1095-8339.1984.tb01002.x>
- Fuller DQ, Harvey EL. The archaeobotany of Indian pulses: Identification, processing and evidence for cultivation. *Environmental Archaeology*. 2006;11(2):219-46. <http://www.tandfonline.com/doi/full/10.1179/174963106x123232>
- Ragul S, Manivannan N, Iyanar K, Ganapathy N, Karthikeyan G. Estimation of genetic parameters and gene action among crosses of blackgram (*Vigna mungo* (L.) Hepper) for seed yield and its component traits. *Electronic Journal of Plant Breeding*. 2021;12(4):1244-48. <http://www.ejplantbreeding.org/index.php/EJPB/article/view/4069>
- Mehra R, Tikle AN, Saxena A, Munjal A, Rekhakhandia, Singh M. Correlation, path coefficient and genetic diversity in blackgram (*Vigna mungo* (L.) Hepper). *International Research Journal of Plant Science*. 2016;1(7):1-11.
- Win KT, Oo AZ, Ookawa T, Kanekatsu M, Hirasawa T. Changes in hydraulic conductance cause the difference in growth response to short-term salt stress between salt-tolerant and -sensitive black gram (*Vigna mungo*) varieties. *J Plant Physiol*. 2016;193:71-78. <https://linkinghub.elsevier.com/retrieve/pii/S0176161716000456>
- Dhandapani M, Chitra S, Sangeetha M, Geethanjali S, Shanmugam A, Navamaniraj KN, et al. Source-sink alterations in rice fallow adaptive blackgram variety ADT3 for enhancement of yield and quality of seed. *International Journal of Environment and Climate Change*. 2023;13(6):194-202. <https://journalijecc.com/index.php/IJECC/article/view/1815>
- Pujar M, Govindaraj M, Gangaprasad S, Kanatti A, Gowda TH, Dushyantha Kumar BM, et al. Generation mean analysis reveals the predominant gene effects for grain iron and zinc contents in pearl millet. *Front Plant Sci* [Internet]. 2022;12:693680. <https://www.frontiersin.org/articles/10.3389/fpls.2021.693680/full>
- Hayman BI. The separation of epistatic from additive and dominance variation in generation means. *Heredity* (Edinb). 1958;12(3):371-90. <https://www.nature.com/articles/hdy195836>
- Crop production guide agriculture. Directorate of Agriculture, Tamil Nadu. 2020. p. 134-44.
- Hayman BI, Mather K. The description of genic interactions in continuous variation. *Biometrics*. 1955;11(1):69. <https://www.jstor.org/stable/3001481?origin=crossref>
- Mather K, Jinks JL. *Biometrical genetics* [Internet]. 2nd ed. Boston, MA: Springer US; 1971. p. 382. Available from: <http://link.springer.com/10.1007/978-1-4899-3404-8>
- Manivannan N. TNAUSTAT [Internet]. TNAU, Coimbatore; 2014 [cited 2024 Aug 14]. <https://sites.google.com/site/tnaustat>
- Haque A, Samad MA, Sarker N, Sarker JK, Azad AK, Deb AC. Gene effects of some agronomic traits through single cross analysis in blackgram (*Vigna mungo* L. Hepper). 2013;3:220-25. <https://doi.org/10.12692/ijb/3.6.220-225>
- Kearsey MJ, Pooni HS. *The genetical analysis of quantitative traits* [Internet]. Boston, MA: Springer US; 1996. <http://link.springer.com/10.1007/978-1-4899-4441-2>
- Prasad AVSD, Murugan E. Generation mean analysis for metric traits in urdbean (*Vigna mungo* [L.] Hepper). *Int J Curr Microbiol Appl Sci*. 2021;10(01):3104-13. <https://www.ijcmas.com/abstractview.php?ID=21206&vol=10-1-2021&SNo=361>
- Akhshi N, Cheghamirza K, Nazarian-Firouzabadi F, Ahmadi H. Generation mean analysis for yield components in common bean. *Iranian Journal of Plant Physiology*. 2014;4(3):1079-85.

25. Sathya P, Manivannan N, Viswanathan PL, Ganapathy N, Karthikeyan G. Gene action for yield and yield contributing traits in blackgram through generation mean analysis. *Electronic Journal of Plant Breeding*. 2021;12(4):1331-36. <http://www.ejplantbreeding.org/index.php/EJPB/article/view/4086>
26. Murugesan T, Dharmalingam K, Venkatesan T, Jegadeesan S, Palaniappan J. Generation mean analysis for seed yield and its contributing traits in the inter-varietal cross of blackgram [*Vigna mungo* (L.) Hepper]. *Agricultural Science Digest*. 2021;44(4):720-24. <http://arccjournals.com/journal/agricultural-science-digest/D-5358>
27. Mak C, Yap TC. Inheritance of seed protein content and other agronomic characters in long bean (*Vigna sesquipedalis* Fruw.). *Theoretical and Applied Genetics*. 1980;56(5):233-39. <http://link.springer.com/10.1007/BF00295454>
28. Owusu EY, Akromah R, Denwar NN, Adjebeng-Danquah J, Kusi F, Haruna M. Inheritance of early maturity in some cowpea (*Vigna unguiculata* (L.) Walp.) genotypes under rain fed conditions in Northern Ghana. *Advances in Agriculture*. 2018;2018(1):1-10. <https://www.hindawi.com/journals/aag/2018/8930259/>
29. Panigrahi KK, Mohanty A, Panigrahi P, Mandal P, Pradhan R, Baisakh B. Generation mean analysis using five parameters genetic model for quantitative traits in black gram (*Vigna mungo* L. Hepper). *The Pharma Innovation Journal*. 2020;9(7):368-71.
30. Cukadar-Olmedo B, Miller JF. Inheritance of the stay green trait in sunflower. *Crop Sci*. 1997;37(1):150-53. <https://access.onlinelibrary.wiley.com/doi/10.2135/cropsci1997.0011183X003700010026x>
31. Owusu EY, Kusi F, Kena AW, Akromah R, Awuku FJ, Attamah P, et al. Generation mean analysis of the key earliness related traits in cowpea (*Vigna unguiculata* (L.) Walp). *Sci Afr*. 2022;17:e01289. <https://linkinghub.elsevier.com/retrieve/pii/S246822762200196X>
32. Prasad AVSD, Murugan E. Combining ability analysis for yield and its attributes in blackgram (*Vigna mungo* (L.) Hepper). *Electronic Journal of Plant Breeding*. 2015;6(2):417-23.
33. Singh A, Singh YV, Sharma A, Visen A, Singh MK, Singh S. Genetic analysis of quantitative traits in cowpea [*Vigna unguiculata* (L.) walp.] using six parameter genetic model. *Legume Research - An International Journal*. 2016;39:502-09. <http://arccjournals.com/journal/legume-research-an-international-journal/LR-3393>
34. Rashwan AMA. Estimation of some genetic parameters using six populations of two cowpea hybrids. *Asian Journal of Crop Science*. 2010;2(4):261-67. <https://www.scialert.net/abstract/?doi=ajcs.2010.261.267>