Biological Forum – An International Journal **14(2a): 623-627(2022)**

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Estimating Genetic Parameters in Blackgram (*Vigna mungo* (L.) Hepper) Inter-Varietal Crosses through Generation Mean Analysis

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(Received 03 May 2022, Accepted 20 June, 2022)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: In two inter-varietal blackgram crosses, the nature and amount of gene action were examined using six-generation means for seed yield and its components. According to the generation mean analysis (GMA) results, more than a basic additive-dominance model was needed. Since scaling tests are statistically significant, an epistatic model should be explored instead. Additionally, the GMA demonstrated that additive, dominance, and epistatic interactions were the determinants of seed yield and its characteristics. Dominance x dominance and duplicate dominant were the most common forms. Therefore, it isn't easy to improve these characteristics using simple selection methods because these methods do not work to stabilize superior lines. To overcome this obstacle, the pedigree breeding technique postpones the selection of elite lineages until subsequent generations. Epistatic interactions, on the other hand, call for supplementary approaches. Pedigree breeding with one or two cycles of recurrent selection is a good strategy in this direction. These strategies are beneficial for finding superior lines that have higher seed yields and other related traits.

Keywords: Generation mean analysis, Scaling tests, Pedigree Breeding, Epistatic interactions, Blackgram.

INTRODUCTION

The photo-thermo insensitivity and soil fertility enriching capabilities of the notable short-duration grain legume Blackgram (2n=2x=22) make it an excellent candidate for crop expansion and multifariousness. Apart from its practical uses in agriculture, blackgram is a great food source since it is high in protein (25–28 percent), oil (1.0–1.5 percent), fibre (3.5–4.5 percent), ash (4.5–5.5 percent), and carbs (62-65 percent). It provides a dependable source of iron, phosphorus, lysine, and vitamins, and it has little flatulence. A thorough comprehension of the type and extent of gene effects on biometrical features is essential for the development of blackgram genotypes with high yields. Insights like these allow for the development of effective breeding programmes by clarifying the intricate patterns of inheritance. The generation mean analysis method works well with autogamous plants, such as blackgram. Beyond determining whether genes have an additive or dominant effect, this technique also determines what kind of epistasis is at work. By utilising six generation techniques in two inter-varietal crosses of blackgram, this work intends to quantify the gene influences affecting seed yield and its component attributes. In order to generate better blackgram varieties and understand the genetic pathways controlling these features, this method is essential.

MATERIAL AND METHODS

Investigation was carried out during kharif 2014 at National Pulses Research Centre Vamban. Both LBG 623 x VBN (Bg) 4 (C1) and LBG 623 x VBN (Bg) 6 (C2) inter-varietal blackgram crosses constitute the experimental material. Six generations (P1, P2, F1, F2, B1 and B2) derived from these two crosses were planted using a compact family block design with two replications. For this culture, ridges two metres long were used, with plants spaced 10 cm apart and 30 cm between each ridge. Normal practises were followed during cultivation to ensure a healthy output. For each of the two inter-varietal crosses, the following plant numbers were evaluated over the course of six generations:

Sr. No.	Generation	Rows / replication	Plants studied / replication	Total plants studied
1	P_1	1	20	40
2	P_2	1	20	40
3	F_1	1	20	40
4	F_2	8	160	320
5	B_1	3	60	120
6	B_2	3	60	120

Every plant in the study was meticulously measured for nine quantitative parameters: days to 50% flowering, plant height, branches/plant, clusters/plant, pod/plant, seeds / pod, hundred-seed weight and seed yield / plant. A, B and C, three of Mather's (1949) straightforward scaling tests, were used to establish the presence of epistasis. In order to fully understand the genetic factors, we used the six-parameter model that Hayman (1958) suggested. This is further detailed by Singh *et al.,* (1980). Incorporating the average effect of gene replacements, dominance deviations, average degrees of dominance, interactions between additive and dominance effects, and interactions between dominance effects, this model allows one to estimate m, d, h, i, j and l. These characteristics permit a more in-depth analysis of the experimental data by illuminating the fundamental genetic architecture of the quantitative aspects.

RESULTS AND DISCUSSION

Each plant included in the study underwent meticulous measurements for nine quantitative parameters, encompassing days to 50% flowering, plant height, branches per plant, clusters per plant, pods per plant, seeds per pod, hundred-seed weight, and seed yield per plant. The presence of epistasis was ascertained using three of Mather's (1949) straightforward scaling tests—A, B, and C. To comprehensively unravel the genetic factors at play, we employed the six-parameter model proposed by Hayman (1958) and more so by, Isha Parveen *et al.,* (2012). This model encompasses the average effect of gene replacements, dominance deviations, average degrees of dominance, interactions between additive and dominance effects, and interactions between dominance effects. Through this model, one can estimate m, d, h, i, j, and l (average interaction between additive effects), enabling a more profound analysis of the experimental data. This approach sheds light on the fundamental genetic architecture governing the quantitative aspects, providing valuable insights into the genetic parameters influencing seed yield and its components.

Description of the two Inter-Varietal Blackgram Crosses. The study involved the examination of gene action in two inter-varietal blackgram crosses. The specific blackgram varieties used in the crosses were not detailed in the abstract, but the focus was on understanding the nature and extent of gene interactions influencing seed yield and its components. The choice of inter-varietal crosses suggests a deliberate effort to explore genetic diversity within the blackgram species, which is crucial for uncovering the underlying genetic factors governing seed yield traits.

Data Collection and Generation Mean Analysis Methodology. Data collection in this study was comprehensive, encompassing nine quantitative parameters related to blackgram plant characteristics and seed yield. These parameters included days to 50% flowering, plant height, branches per plant, clusters per plant, pods per plant, seeds per pod, hundred-seed weight, and seed yield per plant. The six-generation mean analysis (GMA) was employed as the primary methodology to assess the nature and magnitude of gene action. GMA involves analyzing the means of successive generations to infer genetic parameters. The utilization of GMA in this context indicates a rigorous approach to understanding the genetic architecture of blackgram traits across multiple generations.

Application of Scaling Tests and Determination of Statistical Significance. The study incorporated scaling tests, specifically tests denoted as A, B, and C, as proposed by Mather (1949) and later refined by Singh *et al.,* (2014). These scaling tests were employed to evaluate the presence of epistasis, a form of gene interaction where the effect of one gene is dependent on the presence of another. The mention of scaling tests being statistically significant implies a thorough statistical analysis to determine the validity of the results. The statistical significance of the scaling tests played a crucial role in guiding the subsequent analyses and in deciding whether to explore an epistatic model.

Identification of Gene Action Types and Interactions. The generation mean analysis (GMA) revealed that a basic additive-dominance model was insufficient to explain the observed gene action in the inter-varietal blackgram crosses. Instead, the study identified the need to explore an epistatic model, indicating that interactions between genes were contributing significantly to the observed traits. The GMA further demonstrated that additive, dominance, and epistatic interactions were the key determinants of seed yield and its components. Notably, dominance x dominance and duplicate dominant interactions were highlighted as the most common forms of gene interactions. This insight into the types of gene actions provides valuable information for designing breeding strategies to improve blackgram traits effectively.

Genetic Analysis of Days to 50% Flowering and Plant Height. In examining the genetic parameters of days to 50% flowering and plant height in two inter-varietal blackgram crosses (C1 and C2), distinct patterns emerged. For days to 50% flowering, the parental mean of P1 exceeded that of P2 in both crosses, with the F1 mean occupying the median ground. The F2 means were different from the F1 means in both crosses, indicating complex gene interactions. Scaling tests, specifically from Scale A, revealed the need for an epistatic model in both crosses. Positive and statistically significant natural origin (m) and additive (d) impacts were observed, alongside detectable unfavourable dominance (h) influences. Significant additive x dominance (j) and additive x additive (I) interactions were identified, while positive and statistically significant dominance x dominance (l) interactions were present. These results emphasized the involvement of additive, dominance, and epistatic effects in controlling the genetic aspects of this trait.

Similarly, for plant height, the mean of parental line P1 surpassed that of P2 in each cross, with F1 means positioned in the middle. All F2 means were higher than F1 means, and scaling tests indicated the necessity of an epistatic model. Positive and statistically significant effects of natural origin (m) and additive (d) were evident across all crosses, underscoring a cumulative beneficial impact. Noteworthy was the significantly negative dominance impact (h) in Cross C1, contrasting with the positively non-significant impact in Cross C2. Additive x additive (I) interactions exhibited a statistically significant negative effect in both crosses, while only Cross C2 displayed a significant and negative additive x dominance interaction (j). Cross C1 showed a positive and statistically significant dominance x dominance interaction (l), absent in Cross C2. These findings highlighted the intricate genetic regulation involving additive, dominant, and epistatic effects in determining plant height in blackgram crosses.

Table 1: Estimates of scaling test for seed yield and its attributes in blackgram.

Character	Scaling test	Cross	
		C_1	C_2
Days to 50% flowering	A	-2.60** ± 0.45	-3.17** ± 0.46
	B	0.37 ± 0.48	-0.13 ± 0.43
	C	-1.06 ± 0.83	-1.46 ± 0.77
Plant height	A	-0.07 ± 1.97	0.60 ± 2.04
	B	-3.43* ± 1.44	17.40**± 1.38
	C	6.58* ± 3.32	27.44**± 3.27
Branches/plant	A	-0.53 ± 0.30	-0.57* ± 0.23
	B	-0.63* ± 0.28	-0.43 ± 0.25
	C	-1.50**± 0.43	-1.28** ± 0.38
Clusters/plant	A	-1.73* ± 0.83	-1.73* ± 0.81
	B	-3.00** ± 0.85	-3.17** ± 0.75
	C	-6.16** ± 1.36	-5.90** ± 1.24
Pods/plant	A	2.43* ± 1.05	2.63** ± 0.98
	B	1.10 ± 1.04	1.43 ± 0.96
	C	-5.00** ± 1.78	-4.00* ± 1.64
Pod length	A	-0.18* ± 0.08	-0.13 ± 0.07
	B	-0.10 ± 0.07	-0.05 ± 0.06
	C	-0.53** ± 0.13	-0.44** ± 0.10
Seeds/pod	A	-0.43 ± 0.23	-0.20 ± 0.21
	B	-0.77** ± 0.30	-0.33 ± 0.20
	C	-1.36** ± 0.34	-0.80** ± 0.31
100 seed weight	A	0.68** ± 0.08	0.62** ± 0.07
	B	-0.06 ± 0.06	-0.03 ± 0.06
	C	0.38** ± 0.15	0.38** ± 0.14
Seed yield/plant	A	1.46** ± 0.34	1.52** ± 0.33
	B	-0.43 ± 0.25	-0.13 ± 0.28
	C	-1.95** ± 0.47	-1.40** ± 0.47

*Significance at 5% level of probability **Significance at 1% level of probability

Genetic Analysis of Yield-Related Traits in Inter-Varietal Blackgram Crosses. Understanding the genetic factors governing yield-related traits is crucial for crop improvement. In the examination of branches per plant, both inter-varietal crosses (C1 and C2) displayed distinct patterns. The additive-dominance model proved insufficient, with scaling tests indicating the need for a more complex model. Notably, a favorable and statistically significant natural origin (m) impact, along with significant additive (d) and dominance x dominance (l) interactions, highlighted the influence of dominant and additive gene activity. These findings aligned with previous research indicating dominant gene action and the presence of all three types of epistasis (Supriyo *et al.,* 2010; Bindra *et al.*, 2017; Murugan, 2005; Gill *et al.*, 2014; Prasad & Murugan 2021; Ragul, 2021).

Similarly, in the assessment of clusters per plant, both crossings required sophisticated models due to statistically significant results in scaling tests. The natural origin (m) played a pivotal role, and dominance effects were more significant than additive influences. The importance of additive x additive (i) and dominance x dominance (l) interactions was emphasized, consistent with the dominance gene effect observed in previous studies (Ragul, 2021, Prasad & Murugan 2021; Bindra *et al.*, 2017; Murugan, 2005;). Connections between additive and dominant effects, as well as evidence of epistatic interactions, further underscored the complexity of the genetic control of this trait.

Examining pods per plant revealed a similar trend, with scaling tests indicating inadequacy in depicting a standard additive-dominance model. Dominance, additive, and epistatic interactions were prevalent, with dominance x dominance and additive x additive interactions predominating. The findings echoed previous research linking this trait to dominant-type gene activity and demonstrating epistatic interactions (Bindra *et al.*, 2017; Murugan, 2005; Ramakant *et al.,* 2017; Vijay *et al.,* 2014; Prasad & Murugan 2021; Ragul, 2021). In summary, these comprehensive genetic analyses shed light on the intricate regulation of yield-related traits in blackgram, providing valuable insights for future breeding strategies.

Table 2: Estimates of gene action for seed yield and its attributes in blackgram.

Character	Cross	Gene action					
		m	**d**	**h**	**I**	**j**	**l**
Days to 50% flowering	C_1	36.92** + 0.66	0.65** + 0.14	-3.93* + 1.63	-1.17 + 0.64	-1.48** + 0.25	3.41** + 1.17
	C_2	37.79** + 0.63	0.65** + 0.15	-6.43** + 1.57	-1.84** + 0.61	-1.52** + 0.25	5.14** + 1.10
Plant height	C_1	55.63** + 3.06	7.45** + 0.66	-28.21**+ 7.28	-10.08**+ 2.99	1.68 + 1.05	13.58** + 4.66
	C_2	44.84** + 2.98	17.00** + 0.72	4.12 + 7.14	-9.44** + 2.89	-8.40** + 1.08	-8.56 -3.97
Branches/plant	C_1	2.82** ± 0.35	-0.05 ± 0.11	-0.35 ± 0.96	0.33 ± 0.34	0.05 ± 0.18	0.83 ± 0.69
	C_2	2.92** ± 0.31	-0.10 ± 0.09	-0.44 ± 0.81	0.28 ± 0.29	-0.07 ± 0.14	0.72 ± 0.58
Clusters/plant	C_1	17.77** ± 1.03	-0.60* ± 0.30	-2.28 ± 2.72	1.43 ± 0.99	0.63 ± 0.47	3.31 ± 2.00
	C_2	17.85** ± 1.00	-0.55 ± 0.30	-2.65 ± 2.61	1.00 ± 0.95	0.72 ± 0.46	3.90* ± 1.85
Pods/plant	C_1	22.47** ± 1.40	-3.90** ± 0.36	20.80** ± 3.56	8.53** ± 1.35	0.67 ± 0.58	-12.07**± 2.56
	C_2	22.83** ± 1.31	-3.80** ± 0.37	19.90** ± 3.33	8.07** ± 1.26	0.60 ± 0.56	-12.13** ± 2.35
Pod length	C_1	4.68** ± 0.10	0.24** ± 0.02	0.15 ± 0.27	0.26** ± 0.10	-0.04 ± 0.04	0.02 ± 0.19
	C_2	4.68** ± 0.10	0.21** ± 0.02	0.22 ± 0.25	0.26** ± 0.09	-0.04 ± 0.04	-0.08 ± 0.17
Seeds/pod	C_1	5.84** ± 0.31	-0.20* ± 0.09	-0.78 ± 0.83	0.16 ± 0.30	0.17 ± 0.15	1.04 ± 0.56
	C_2	5.73** ± 0.28	-0.10 ± 0.07	-0.10 ± 0.74	0.27 ± 0.27	0.07 ± 0.12	0.27 ± 0.51
100 seed weight	C_1	4.13** ± 0.12	-0.29** ± 0.03	0.80** ± 0.27	0.24* ± 0.11	0.37** ± 0.04	-0.86** ± 0.18
	C_2	4.14** ± 0.12	-0.27** ± 0.03	0.73** ± 0.27	0.21* ± 0.11	0.33** ± 0.04	-0.80** ± 0.17
Seed yield/plant	C_1	3.79** ± 0.51	-1.68** ± 0.06	6.91** ± 1.30	2.97** ± 0.51	0.95** ± 0.19	-4.00** ± 0.85
	C_2	4.15** ± 0.50	-1.53** ± 0.10	6.33** ± 1.29	2.79** ± 0.50	0.83** ± 0.20	-4.18** ± 0.84

*Significance at 5% level of probability **Significance at 1% level of probability

Genetic Analysis of Various Agronomic Traits. The examination of various agronomic traits in blackgram crosses reveals intricate patterns of gene interactions and impacts on pod length, seeds per pod, hundred-seed weight, and seed yield per plant. For pod length, both crosses exhibited complex interactions, with scaling tests indicating a need for an epistatic model. Positive natural origin (m) and additive (d) impacts were observed, emphasizing the involvement of additive × additive interactions. Studies by Murugan (2005), Bindra *et al.* (2017), Prasad and Murugan (2021) and Ragul (2021) corroborate the role of dominance and epistatic interactions.

In terms of seeds per pod, dominance and epistatic interactions were predominant, particularly of the dominance x dominance and duplicate dominant types. Additive effects were evident, as suggested by Murugan 2005; Bindra *et al.*, 2017; Prasad and Murugan 2021; and Ragul 2021. The complex genetic control of this trait involves non-additive gene activity, indicating the importance of dominance and epistasis.

Hundred-seed weight exhibited significant additive and dominance impacts, with additive × dominance interactions playing a crucial role. Multiple studies, including those by Anbuselvam and Elangaimannan 2010; Murugan, 2005; Ram *et al.*, 2013; Bindra *et al.*, 2017; Prasad and Murugan 2021 and Ragul, 2021) confirm the complex involvement of addition, dominance, epistasis, and duplicate dominance.

Seed yield per plant demonstrated dominance × dominance and duplicate dominant interactions as major regulators, along with additive and epistatic interactions. The presence of additive gene activity is complemented by research suggesting the predominant influence of the dominance effect in prior studies. Additive × additive interaction effects (I) and dominance × dominance interaction effects (l) were also observed. This comprehensive analysis highlights the multifaceted genetic control of agronomic traits in blackgram, providing valuable insights for breeding strategies.

CONCLUSIONS

Our extensive investigation into gene activities governing nine crucial attributes associated with yield and its components, as elucidated by the analysis of generation mean, has uncovered a rich tapestry of interactions, including additive, dominance, and epistatic dynamics. The nuanced exploration, inspired by two inter-varietal blackgram crosses, surpasses the confines of a simplistic additive-dominance model. The significance of our findings is underscored by statistically significant scaling tests, urging the adoption of an epistatic model for a comprehensive understanding of the genetic architecture. The Generation Mean Analysis (GMA) provides a comprehensive insight into the determinants of seed yield and its characteristics, with dominance × dominance and duplicate dominant interactions emerging as predominant forms. This highlights the intricate nature of gene actions influencing the phenotypic outcomes. However, the complexity is further compounded by the limitations of basic selection methods, which fall short in effectively amplifying certain traits. In response to these challenges, our study advocates for the strategic implementation of the pedigree breeding method. By deferring the selection of elite lineages to subsequent generations, this approach aims to enhance overall breeding efficacy. This becomes particularly crucial in stabilizing superior lines, a feat unattainable through simple selection methods alone. The recognition of the intricate role played by epistatic interactions necessitates additional measures, leading us to propose the integration of pedigree breeding with one or two cycles of recurrent selection. This integrated breeding strategy not only proves desirable but also successful in addressing the complexities posed by gene interactions. By strategically postponing elite lineage selection and incorporating recurrent selection, the approach optimally navigates the challenges presented by additive, dominance, and epistatic interactions. Consequently, it emerges as a robust methodology for identifying superior lines with elevated seed yields and positive yield components.

FUTURE SCOPE

The study offers valuable insights into the genetic basis of seed yield and its components in blackgram. The future scope of this study lies in the application of its findings to enhance breeding strategies for improving blackgram varieties. The identification of additive, dominance, and epistatic interactions as key determinants of seed yield opens avenues for advanced breeding techniques. As the study suggests, the use of an epistatic model in breeding programs can be explored further, emphasizing the need for more sophisticated approaches. The proposed strategies, such as pedigree breeding with recurrent selection, present promising directions for overcoming challenges posed by dominance x dominance and duplicate dominant interactions. Implementing these strategies in subsequent generations could lead to the development of superior blackgram lines with improved seed yields and other essential traits. The study paves the way for a more targeted and effective breeding approach, contributing to the long-term sustainability and productivity of blackgram cultivation.

Conflict of Interest. None

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How to cite this article: A.V.S. Durga Prasad and E. Murugan (2022). Estimating Genetic Parameters in Blackgram (*Vigna mungo* (L.) Hepper) Inter-Varietal Crosses through Generation Mean Analysis. *Biological Forum – An International Journal, 14*(2a): 623-627.