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Generation mean analysis for grain yield and yield contributing traits in blackgram [*Vigna mungo* (L.) Hepper]

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Abstract

Generation mean analysis was worked out for two crosses of blackgram viz., TAU-1 × PDKV Black gold and NUL-7 × TBU-43-1. Six parameter model was utilized in this study to identify the gene actions of various grain yield and yield contributing traits. Scaling test revealed that the digenic model (additive-dominance model) was inadequate for most of the traits, confirming the existence of non-allelic interactions for all of the crosses. Duplicate type of epistasis was reported for most of the traits in both the crosses except for pod length in cross TAU-1 × PDKV Black gold and 100 seed weight in cross NUL-7 × TBU-43-1. Magnitude of dominance gene effect was reported to be higher than additive gene effect in most of the traits in both crosses. Hence, it was evident from the study that the bi-parental mating or diallel selective mating followed by selection in advanced generations should be employed for harnessing desirable recombinants. The additive component was found to be significant for the traits viz., plant height, number of clusters per plant, number of pods per cluster, pod length and number of seeds per plant in cross NUL-7 × TBU-43-1. While, additive × additive (i) gene interaction was found significant for only number of seeds per pod in cross and NUL-7 × TBU-43-1. For development of these characters, one should follow the simple selection with pedigree breeding method.

Keywords: Blackgram, generation mean analysis, gene action, scaling test, six parameter, epistasis

Introduction

Blackgram [*Vigna mungo* (L.) Hepper], is one of the nutritious pulse crop. It is a self pollinated grain legume belongs to the family Fabaceae with chromosome number $2n=2x=22$. It is considered to have evolved in India, with a secondary centre of origin in Central Asia (Pratap and Kumar, 2011) [15]. It is one of the important short duration pulse crops grown in a wide range of agro-climatic conditions in all the three seasons. It is an excellent source of easily digestible good quality vegetable protein and ability to restore the fertility of soil through symbiotic nitrogen fixation. Seeds are highly nutritious with protein (24-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins (Vadivel *et al.*, 2019) [25]. In India it was domesticated from its wild progenitor, *V. mungo* var. *silvestris* (Chandel *et al.*, 1984) [5]. India is the world's largest producer and consumer of urdbean cultivated on an area about 35.36 lakh ha with an annual production of 2.31 Mt and average yield of 856 kg/ha (Anonymous, 2024) [1]. Yield is a complex trait controlled by a various genetic and environmental factor. Identification of gene action and inheritance pattern is important to improve the particular trait. Gene action has been estimated through generation mean analysis by Hayman (1954) [6] and Jinks (1954) [9]. Generation mean analysis is a clear, concise and efficient approach for elucidating gene action since it use first degree statistics to determine allelic and non-allelic interactions. Therefore, this study was conducted to identify the gene action of yield and yield contributing traits through generation mean analysis in two crosses of blackgram. It is more suitable for obtaining unbiased estimates of additive and dominance gene effects as well as additional information on epistasis/inter-allelic interaction, cause of gene action and assisting breeders in choosing the appropriate breeding method to improve various quantitative traits along with qualitative traits in the crop through boosting the frequency of favourable genes.

Materials and Methods

The experimental material comprising of six populations viz., P₁, P₂, F₁, F₂, B₁ and B₂ of two cross combinations viz., TAU-1 × PDKV Black gold and NUL-7 × TBU-43-1. The six generations i.e. P₁, P₂, F₁, F₂, B₁ and B₂ developed during the years from 2019-2022, were evaluated in RBD in three replications during *rabi* 2022 at the Post Graduate Institute, Botany Farm, Mahatma Phule Krishi Vidyapeeth, Rahuri. The observations were recorded on 11 yield and yield contributing traits viz., days to first flowering, days to maturity, plant height (cm), number of primary branches/plant, number of clusters/plant, number of pods/cluster, number of pods/plant, pod length (cm), number of seeds/pod, 100-seed weight (g) and grain yield/plant (g). Five plants were randomly selected from each parent (P₁ and P₂) and F₁, while 10 plants from backcrosses (B₁ and B₂) and 40 from F₂ for recording the observations. To maintain a healthy crop, all necessary agronomical practices were implemented.

Statistical Analysis

The simple scaling tests 'A', 'B', 'C' and 'D' was estimated as suggested by Mather (1949)^[12] and Hayman and Mather (1955)^[8]. The significant deviation of A and B tests from zero indicate the presence of all three types of epistatic interactions viz., additive × additive [i], additive × dominance [j] and dominance × dominance [l] whereas, C scaling test reveals the presence of dominance × dominance [l] type of interaction and D indicates the significance of additive × additive [i] type of interaction. The generation mean analysis was carried out following the six parameter model proposed by Hayman (1958)^[7], which are mean effect [m], additive effect [d], dominance effect [h], additive × additive interaction [i], additive × dominance [j] and dominance × dominance interaction [l].

Results and Discussion

The significant result of scaling tests either all or A, B, C and D alone indicates the additive-dominance model was not found adequate for all traits in both of the crosses. The failure of additive-dominance model was attributed mainly due to presence of epistasis. The generation mean analysis was adopted to detect non-allelic interaction component of the mean of the phenotypic distribution. The results of scaling test and genetic parameters of the both crosses were presented in (Table 1 and 2). The parameter [m] was significant in both the crosses (TAU-1 × PDKV Black gold and NUL-7 × TBU-43-1) for all the characters which were studied for grain yield and its contributing traits in blackgram.

The gene effect of both additive [d] and dominance [h] component were estimated highly significant in both of crosses for days to first flowering. While dominance [h] effect was predominant in both of crosses. From interaction components, it was observed that all three interactions, additive × additive [i], additive × dominance [j] and dominance × dominance [l] components was significant in both of the crosses. Among these additive × additive [i] component recorded greater magnitude than other components in both crosses with duplicate type of epistasis based on opposite signs of [h] and [l] components. These results are in agreement with Bindra *et al.* (2017)^[3] who observed duplicate epistasis for inheritance of days to first

flowering. Both additive [d] and dominance [h] component was significant in both the crosses, with the preponderance of dominance [h] component for trait days to maturity. All non-allelic interactions were significant in both crosses. Among these, additive × additive [i] component recorded greater magnitude than other components in both crosses with duplicate type of epistasis for days to maturity. Similar results were found by Chand and Rao (2002)^[4], Lalitha (2003)^[11], Singh *et al.* (2007)^[23], Bharathi (2022)^[2], Panigrahi *et al.* (2020)^[13], Sateesh *et al.* (2022)^[21], Reddy *et al.* (2022)^[19] and Puspa Reni (2022)^[16] who reported duplicate epistasis. For trait, plant height, both main effects i.e. additive [d] and dominance [h] were significant in both crosses with preponderance of dominance [h] effect. Additive × additive [i] component was significant in cross I. While, in cross II, additive × additive [i] and dominance × dominance [l] components were significant with duplicate type of epistasis. These results are in harmony with the findings of Kanchana Rani (2008)^[10] for additive gene action and Thamodharan *et al.* (2017)^[24] and Vadivel *et al.* (2019)^[25] for non-additive gene action respectively.

For trait, number of primary branches per plant, significant dominance [h] effect was reported in both crosses. In case of epistasis, in cross I, additive × dominance [j] and dominance × dominance [l] components were significant. While, in cross II, additive × additive [i] and dominance × dominance [l] components were significant. Among these, dominance × dominance [l] component recorded greater magnitude than other components in both crosses with duplicate type of epistasis for number of primary branches per plant. Same results were given by Panigrahi *et al.* (2020)^[13] for additive gene action. In case of number of clusters per plant, both additive [d] and dominance [h] component in cross I and dominance [h] component in cross II were significant, with greater magnitude of additive [d] component in cross I and dominance [h] component in cross II. It was noted that, the inheritance of clusters per plant was due to additive and dominance gene effect in cross I and cross II. From interaction components, it was observed that additive × additive [i] and dominance × dominance [l] components were significant in both crosses. Among these, dominance × dominance [l] component recorded greater magnitude than other components in both crosses with duplicate type of epistasis. These results are in harmony with the findings of Vadivel *et al.* (2019)^[25] and Panigrahi *et al.* (2020)^[13] for additive and non-additive gene action respectively.

It was noted that, the inheritance of number of pods per cluster was due to additive and dominance gene effect in cross I and cross II. All non-allelic were significant in cross I. While, in cross II, additive × additive [i] and dominance × dominance [l] components were significant. Among these, dominance × dominance [l] component recorded greater magnitude than other components in both crosses with duplicate type of epistasis. Predominance of duplicate type of non allelic interaction for this trait was earlier reported by Vadivel *et al.* (2019)^[25], Sathya *et al.* (2021)^[20], Ragul *et al.* (2021)^[17] and Reddy *et al.* (2022)^[19]. The greater magnitude of dominance [h] component was recorded in both the crosses in pods per plant. Additive × additive [i] and dominance × dominance [l] components were significant in both crosses with duplicate type of epistasis in cross I and II. Kanchan rani (2008)^[10] for additive gene action and Vadivel *et al.* (2019)^[25] and Panigrahi *et al.*

(2020) ^[13] for additive and non-additive gene action respectively reported for this trait. It was observed that dominance components were significant in cross I and only additive component was significant in cross II. This indicates preponderance of dominance gene effect in cross I and additive gene effect for pod length trait. From interaction components, it was observed that additive x additive [i] and dominance x dominance [I] components were significant in cross I. Only dominance x dominance [I] component significant for cross II. Among these, additive x additive [i] component recorded greater magnitude than dominance x dominance [I] component in cross I and dominance x dominance [I] component in greater magnitude in cross II with duplicate type of epistasis in cross I based on opposite signs of dominance [h] and dominance x dominance [I] components. While, in cross II complementary type epistasis found in cross II. Vadivel *et al.* (2019) ^[25] and Sathya *et al.* (2021) ^[20] observed the additive and epistatic gene action for pod length among blackgram crosses.

It was observed that dominance [h] and additive [d] components were significant in cross I and cross II respectively for number of seeds per pod. Additive x additive [i] type epistasis was significant in both the crosses, while dominance x dominance [I] and additive x dominance [j] interaction were significant in cross I and cross II, respectively. Duplicate type of epistasis is observed. The results of gene action for number of seeds per pod (both

additive and dominance) in this study were similar to those reported by Seenaiah *et al.* (1995) ^[22], Zubair *et al.* (2010) ^[26] reported for additive gene action. For 100 seed weight, dominance [h] effect was significant in both crosses with significant additive x additive [i] type epistasis in both crosses. Complementary and duplicate type of epistasis was observed in cross I and II, respectively. Lalitha (2003) ^[11], Ramakant and Srivastava (2012) ^[18], Panigrahi *et al.* (2015) ^[14], Vadivel *et al.* (2019) ^[25], Panigrahi *et al.* (2020) ^[13], Sathya *et al.* (2021) ^[20], Ragul *et al.* (2021) ^[17], Sateesh *et al.* (2022) ^[21], Puspa Reni (2022) ^[16] and Reddy *et al.* (2022) ^[19] also obtained the alike outcomes showing existence of duplicate epistasis for the trait. The true objective of any breeding program is to improve yield, especially seed yield, where the crop's economic product is seed. Thereby, in order to be designated as a commercial variety, a novel genotype/line must outperform the yield levels of a popularly established commercial variety while also containing useful genes for number of important traits. The dominance genetic component [h] was significant in both for grain yield per plant. From interaction components, it was observed that additive x additive [i] component was significant in cross I while dominance x dominance [I] component significant for cross I and II with duplicate type of epistasis. Similarly, duplicate type of epistasis was reported by Lalitha (2003) ^[11], Bharathi (2022) ^[2], Sathya *et al.* (2021) ^[20], Ragul *et al.* (2021) ^[17], Sateesh *et al.* (2022) ^[21] and Puspa Reni (2022) ^[16].

Table 1: Estimates of individual and joint scaling test for grain yield and its components in two crosses of blackgram (Cross-I: TAU-1 × PDKV black gold and Cross-II: NUL-7 × TBU-43-1)

Sr. No.	Name of Characters	Crosses	Scaling tests				Chi square (χ^2)
			A	B	C	D	
1.	Days to first flowering	C-I	1.00	-0.33	7.00**	3.17**	202.50**
		C-II	1.00**	-0.33	4.00**	1.67**	46.50**
2.	Days to maturity	C-I	-3.33**	-2.00**	-0.67	2.33**	119.77**
		C-II	-1.00**	0.67**	2.33**	1.33**	60.69**
3.	Plant height (cm)	C-I	0.73	-3.67	-11.33**	-4.20**	23.51**
		C-II	-1.93	-4.13**	-0.47	2.80**	30.21**
4.	Number of primary branches per plant	C-I	-1.07**	-1.13**	-1.27**	0.47**	29.42**
		C-II	-1.00**	-1.53**	-0.97*	0.78**	43.97**
5.	Number of clusters per plant	C-I	-0.60	-2.00	4.13*	3.37**	15.77**
		C-II	-2.33*	-3.73**	-1.17	2.45**	32.05**
6.	Number of pods per cluster	C-I	-2.08**	-0.08	-0.45	0.85**	50.07**
		C-II	0.23	0.37	1.33**	0.74**	25.09**
7.	Number of pods per plant	C-I	1.13	-2.13	-16.83**	-7.92**	54.55**
		C-II	-4.73	-11.07**	-1.57	7.12**	18.76**
8.	Pod length (cm)	C-I	-0.24	-0.32*	-0.50*	-0.21*	15.30**
		C-II	-0.34	-1.10**	-1.17**	0.13	40.44**
9.	Number of seeds per pod	C-I	1.27**	0.89**	-1.27**	-1.72**	191.15**
		C-II	-0.88**	1.00**	0.82**	0.35**	102.02**
10.	100 seed weight (g)	C-I	-1.36**	-1.40**	-4.39**	-0.82**	58.57**
		C-II	-0.09	-0.26	-1.68**	-0.67**	20.01**
11.	Grain yield per plant (g)	C-I	-0.24	-0.11	-3.48**	-1.56**	26.17**
		C-II	-1.55**	-1.98**	1.02	2.27**	46.04**

Table 2: Estimates of genetic effects for grain yield and its component traits in two crosses of blackgram. (Cross-I: TAU-1 × PDKV black gold and Cross-II: NUL-7 × TBU-43-1)

Name of Character	Crosses	Genetic components						Type of epistasis
		m	d	h	i	j	l	
Days to first flowering	C-I	31.42**	1.67**	-5.67**	-6.33**	0.67*	5.67**	Duplicate
	C-II	32.67**	-1.00**	-3.33**	-3.33**	0.67**	2.67**	Duplicate
Days to maturity	C-I	70.83**	0.67**	-2.00**	-4.67**	-0.67*	10.00**	Duplicate
	C-II	72.83**	-2.33**	-2.50**	-2.67**	-0.83**	3.00**	Duplicate
Plant height (cm)	C-I	35.67**	4.27**	12.20**	8.40**	2.20	-5.47	Duplicate
	C-II	31.67**	-1.60**	-4.77**	-5.60**	1.10	11.67**	Duplicate
No. of primary branches per plant	C-I	2.48**	-0.17	-0.93*	-0.93	0.03**	3.13**	Duplicate
	C-II	2.64**	0.10	-1.07**	-1.57**	0.27	4.10**	Duplicate
No. of clusters per plant	C-I	13.57**	1.63**	-3.93*	-6.73**	0.70	9.33**	Duplicate
	C-II	12.26**	-0.47	-3.20*	-4.90**	0.70	10.97**	Duplicate
No. of pods per cluster	C-I	3.46**	-0.63**	-1.01*	-1.71**	-1.00**	3.87**	Duplicate
	C-II	3.98**	-0.02	-1.09**	-1.48**	0.30	1.63*	Duplicate
No. of pods per plant	C-I	31.43**	4.50**	22.17*	15.83**	1.63	-14.83**	Duplicate
	C-II	32.76**	-0.53	-9.60*	-14.23**	3.17	30.03**	Duplicate
Pod length (cm)	C-I	4.59**	0.10	0.74*	0.42*	0.28	-0.35**	Duplicate
	C-II	4.39**	0.29*	0.25	-0.27	0.38*	1.71**	Complementary
Number of seeds per pod	C-I	6.12**	-0.04	3.99**	3.43**	0.19	-5.59**	Duplicate
	C-II	5.31**	-1.37**	-0.07	-0.70**	-0.94**	0.58	Duplicate
100 seed weight (g)	C-I	4.99**	-0.12	1.88**	1.63**	0.02	1.13	Complementary
	C-II	4.65**	-0.12	1.59**	1.34**	0.08	-0.99	Duplicate
Grain yield per plant (g)	C-I	9.89**	0.52	4.21**	3.13**	-0.06	-2.77*	Duplicate
	C-II	10.31**	-0.26	-3.00**	-4.55**	0.21	8.08**	Duplicate

Conclusion

The results of this study showed that as a consequence of higher magnitude of interactions, the non-fixable gene effects were higher than the fixable indicating the major role of non-additive gene effects. In view of high magnitude of gene interactions the successful breeding methods will be the ones, which can mop-up the genes to form superior gene constellations interacting in a favourable manner. Some forms of recurrent selection namely, diallel selective mating or biparental mating and selections in later generation followed by hybridization might prove to be effective alternative approaches. Majority of the traits studied in both crosses exhibited a predominant presence of duplicate type epistasis except 100 seed weight in cross I and for pod length in cross II. Thus, selection intensity should be mild in earlier generation and intense in later generations or one/two cycle of intermating of segregating population may be useful to improve these characters. The traits showing preponderance of additive gene action could be improved through simple selection method like pedigree.

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