



## SHORT RESEARCH ARTICLE

# Unraveling genetic complexity: Identifying black gram (*Vigna mungo* L.) genotypes for rice fallow conditions

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## Abstract

A study on generation mean analysis was conducted to determine suitable genotypes of black gram (*Vigna mungo* L.) for rice fallow conditions, considering various agronomic traits controlled by quantitative inheritance. The Hayman's six-parameter model, utilizing a Random Block layout with two replications over six generations viz.,  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$ , and  $BC_2$  involving six parents viz., MDU 1, VBN (BG) 6, Mash-114 and ADT 3, PU 31 and CO 6 was followed. The filial generations derived from four crosses, along with their parents involved in the hybridization, were evaluated at TRRI, Aduthurai, during the summer of 2019 under rice fallow conditions. The focus of the evaluation was on yield and its nine component traits, including plant height, branches per plant, 50% flowering, pods per cluster, pod number, 100 seed weight, and single plant yield. The study revealed a predominant influence of the duplicate dominant gene on these yield attributes, indicating the complexity of the genetic basis. This complexity suggests that conventional selection methods may be hindered, making heterosis breeding or bulk method/recurrent selection more favorable for obtaining the desired gene combinations in genotypes suitable for rice fallow conditions.

**Keywords:** Rice fallow, generation mean analysis, gene action, black gram, yield attributes, early maturity.

Black gram [*Vigna mungo* (L.) Hepper] holds significant prominence as a crucial pulse crop, especially in Asian countries, due to its rich nutritional profile and pivotal role in sustainable agriculture. It actively contributes to maintaining soil fertility through biological nitrogen fixation. Black gram is cultivated in about 5.03 mha and produces around 3.23 mt of pulse in India (Anonymous 2018). However, the per capita availability of pulses in India has witnessed a decline and falling short of the Indian Medical Council's recommended daily pulse intake of 50 g per capita (IIPR Vision 2030). India is importing a substantial amount of pulses annually, incurring a cost exceeding 10,000 crores (Girish et al. 2012). Addressing the need for increased production, a comprehensive crop improvement program is imperative to develop high-yielding black gram varieties. Black gram's short duration and compatibility with intercropping, rice fallow, and crop rotation make it an attractive option to enhance overall agricultural output. In regions like the Cauvery Delta of Tamil Nadu and Puducherry, black gram is predominantly cultivated as a rice fallow crop, utilizing approximately one mha of rice fallow land (FAOSTAT 2012). Noteworthy black gram varieties such as ADT 3, ADT 6, and KKM 1 are currently available in Tamil Nadu, specifically tailored for the rice fallow scenario. Given this backdrop, the present investigation was focused on deciphering the inheritance

of yield traits in black gram cultivated under rice fallow conditions.

The experiment involved six parents viz., MDU 1, VBN (BG) 6, Mash-114 and ADT 3, PU 31 and CO 6 of black gram and their crosses, namely, MDU 1 x VBN (BG) 6 (Cross I), MDU 1 x Mash-114 (Cross II), ADT 3 x PU 31 (Cross III), and CO 6 x VBN (BG) 6 (Cross IV). The study utilized Hayman's (1958), six-parameter generation mean analysis model. The generations  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$  were developed in each

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cross at Agricultural College and Research Institute, Madurai, during *rabi* 2018, and subsequently evaluated alongside their parental lines, MDU 1, VBN (BG) 6, Mash - 114, ADT 3, PU 31, and CO 6 at TRRI, Aduthurai, during the *summer* of 2019 in a rice-fallow state (Fig. 1). The experimental design employed a random block layout with two replications. Within each cross, six generations were raised in rows and randomization was applied independently for each cross. The observations were recorded on 10 traits, including plant height, number of branches per plant, days to 50% flowering, number of clusters per plant, pod number, days to maturity, number of seeds per pod, 100 seed weight and single plant yield (g) on individual test materials. Forty plants were studied in each P<sub>1</sub>, P<sub>2</sub> and F<sub>1</sub> generation whereas 200 plants were studied in F<sub>2</sub> and 120 each in BC<sub>1</sub> and BC<sub>2</sub> generations.

Analysis of Variance (ANOVA) was carried out to discern significant differences among populations across six generations. Epistatic gene interactions are examined using scaling tests (A, B, C, and D) as per Hayman and Mather (1955), along with joint scaling tests by Cavalli (1952). Data inadequacy for a simple additive dominance model prompts the extension of analysis to estimate parameters for epistasis using the six-generation means. The estimates of mid parent  $m$ , additive effect ( $\hat{a}$ ), dominance effect ( $\hat{h}$ ), additive x additive ( $\hat{i}$ ), additive x dominance ( $\hat{j}$ ) and dominance x dominance ( $\hat{l}$ ) interactions were obtained using Mather and Jinks's (1971) perfect fit method.

The present investigation analyzed the underlying genetic nature of ten quantitative traits crucial for black gram yield, partitioning them into different genetic and interaction components, namely (i), (j), (l), additive (d), and dominance (h) components. Table 1 provides the inheritance patterns of various quantitative yield components *via* generation mean analysis across the four cross combinations. The genetics of inheritance governing each of the quantitative traits are described here.

### Scaling test

Scaling tests were employed to detect non-allelic interactions, revealing duplicate digenic interactions across all crosses. Genetic parameter estimates, including ( $m$ ), additive effect [d], and dominance effect [h], were derived for all ten traits in four crosses. Significance in scaling tests indicated the inadequateness of the basic additive-dominance model, as evidenced by scales A, B, C, and D. Additionally, joint scaling test analysis highlighted the significant influence of additive [d], and duplicate dominant [h] gene effects on all traits. These findings emphasize the complicated genetic nature underlying the passing down of these traits, informing future breeding strategies for crop improvement.

Analysis of gene action revealed significant contributions from the additive component (d) across all crosses. Furthermore, the dominant component (h) displayed significance in crosses II and III. In crosses II and III, significant

interaction components (i), and (l) were noted, while in cross IV, the only interaction component (j) was present, suggesting the existence of both non-additive and additive gene effects influencing plant height. Notably, crosses II, III, and IV displayed opposing signs for components (h) and (l), revealing duplicate gene action, while cross I demonstrated complementary gene action. Delayed selection until later generations to consolidate the desired short stature beneficial for rice-fallow crops is suggested.

Genotypes characterized by more branches per plant are highly desirable as they offer extensive ground coverage, mitigating soil moisture loss and boosting yield through increased pod and seed production. The gene action governing this trait was predominantly influenced by dominance, dominance x dominance, and additive x additive interactions, as evidenced by the presence of interaction components (h), (i), and (l) in cross II. The opposing effects of (h) and (l) in crosses II and IV suggests duplicate gene action. Ranjana Patial et al. (2022) also reported comparable patterns in the number of branches per plant in black gram. Based on the present results, it is suggested that early selection in segregating generations is not recommended. Instead, later-generation selection and intermating of F<sub>2</sub> segregants are advised to disrupt undesirable linkages.

The present study revealed that genetic components (d) and (h) were non-significant across all crosses for days to flowering. Notably, interaction components (j), and (l) were significant in cross II only, demonstrating the existence of both (j) and (l) interactions. Moreover, crosses II and IV exhibited opposite signs for components (h) and (l), suggesting duplicate gene action. Genetic studies confirmed that days to 50% flowering was controlled by non-additive gene action due to the prevalence of (h), (j) and (l) non-allelic interactions. Consequently, selection for early flowering genotypes with rice fallow characteristics may need to be deferred to later generations. Early maturity of genotypes is most suitable for rice fallow conditions. The genetic components (d) and (h) were insignificant for all the crosses. However, in cross II, the interaction component (j) was notable, indicating an additive x dominance interaction, but in cross II, (h) and (l) components were of the same sign, suggesting complementary gene action. The additive component outweighed the corresponding dominant gene action. To stabilize early maturing genotypes, pureline and pedigree selection methods are recommended. Similar studies carried out by Panigrahi et al. (2015) in green gram also highlighted gene action corresponding with black gram.

Clusters per plant is influenced by no. of pods per plant and seed yield. Gene action indicated the presence of an additive component (d) in crosses III and IV, while a dominant component (h) was observed solely in cross III, suggesting a higher proportion of additive gene action than dominant gene action. Additionally, interaction components (i), (l), and

**Table 1.** Inheritances of various quantitative traits of yield components by generation mean analysis of four cross combinations

Parameter /cross	Plant height				Branches per plant			
	Cross I	Cross II	Cross III	Cross IV	Cross I	Cross II	Cross III	Cross IV
A	3.52 ± 3.29	8.79* ± 3.10	8.31* ± 2.65	17.85* ± 1.88	-0.69 ± 0.57	-0.21 ± 0.61	-0.31 ± 0.65	0.52 ± 0.70
B	-1.91 ± 3.54	11.95* ± 3.03	11.97* ± 2.45	9.41* ± 1.81	0.24 ± 0.58	0.69 ± 0.56	-1.54* ± 0.64	0.59 ± 0.76
C	8.87* ± 3.21	11.03* ± 4.51	-14.73* ± 3.29	55.76* ± 2.30	-0.77 ± 0.71	-3.18* ± 0.58	-2.17* ± 0.88	3.41* ± 0.79
D	3.63 ± 2.45	-4.85* ± 1.82	-17.50* ± 1.45	14.25* ± 1.06	-0.16 ± 0.34	-1.83* ± 0.37	-0.16 ± 0.36	1.15* ± 0.47
m	31.40* ± 0.53	28.01* ± 0.48	21.01* ± 0.25	34.52* ± 0.25	1.51* ± 0.08	0.96* ± 0.07	1.40* ± 0.08	2.49* ± 0.10
(d)	5.15* ± 2.20	4.58* ± 1.54	7.45* ± 1.36	3.05* ± 0.93	0.00 ± 0.31	-0.17 ± 0.34	0.54 ± 0.32	0.00 ± 0.43
(h)	4.69 ± 5.04	21.21* ± 4.17	39.42* ± 3.29	-26.56 ± 2.35	-0.08 ± 0.76	3.03* ± 0.78	1.06 ± 0.83	-1.95 ± 1.00
(i)	-7.26 ± 4.89	9.70* ± 3.64	35.00* ± 2.90	-28.51 ± 2.11	-	3.66* ± 0.74	0.32 ± 0.72	-2.29 ± 0.94
(j)	2.71 ± 2.32	-1.58 ± 1.70	-1.83 ± 1.49	4.22* ± 1.21	-	-0.45 ± 0.40	0.61 ± 0.39	-0.04 ± 0.48
(l)	5.65 ± 9.38	-30.44* ± 7.64	-55.28* ± 6.36	1.25 ± 4.37	-	-4.14* ± 1.49	1.53 ± 1.55	1.18 ± 1.89
	Days to 50% flowering				Days to maturity			
A	-0.21 ± 1.78	0.48 ± 1.36	-0.94 ± 1.48	1.66* ± 1.12	-2.10 ± 2.91	1.52 ± 2.60	-2.48 ± 2.89	-2.09 ± 2.27
B	0.84 ± 1.70	4.33* ± 1.50	0.07 ± 1.37	1.40* ± 1.16	0.26 ± 2.91	10.14* ± 3.15	1.55 ± 3.12	-0.65 ± 2.56
C	-0.70 ± 1.94	1.42 ± 1.37	-3.39 ± 1.92	9.83* ± 1.33	0.25 ± 3.45	11.62* ± 2.56	-4.98 ± 3.48	-8.30 ± 2.89
D	-0.66 ± 1.13	-1.69 ± 0.94	-1.26 ± 0.83	3.39* ± 0.84	1.05 ± 2.03	-0.02 ± 2.08	-2.03 ± 1.91	-2.78 ± 1.58
m	35.55* ± 0.23	34.95* ± 0.17	34.35* ± 0.17	37.11* ± 0.22	76.96* ± 0.53	76.24* ± 0.44	74.18* ± 0.37	74.34* ± 0.36
(d)	0.83 ± 1.03	0.00 ± 0.87	0.71 ± 0.76	0.42 ± 0.71	0.71 ± 1.73	0.33 ± 1.89	0.63 ± 1.76	0.46 ± 1.40
(h)	0.76 ± 2.42	1.71 ± 1.97	3.62 ± 1.89	-7.33 ± 1.74	-4.51 ± 4.28	-4.00 ± 4.27	5.46 ± 4.13	3.60 ± 3.40
(i)	-	3.39 ± 1.88	-	-6.77 ± 1.67	-	0.04 ± 4.17	-	-
(j)	-	-1.93* ± 0.96	-	0.13 ± 0.74	-	-4.31* ± 1.98	-	-
(l)	-	-8.20* ± 3.76	-	3.71 ± 3.13	-	-11.70 ± 7.97	-	-
	Number of clusters per plant				Number of pods per cluster			
A	-0.07 ± 1.06	1.48 ± 1.16	-2.41* ± 1.06	-0.24 ± 0.80	-0.01 ± 0.67	-0.28 ± 0.66	0.66 ± 0.56	0.40 ± 0.57
B	-1.02 ± 0.84	1.56 ± 0.93	-2.28* ± 0.96	-2.62 ± 0.88	-0.02 ± 0.61	0.07 ± 0.64	-0.71 ± 0.62	-1.40* ± 0.51
C	1.75 ± 1.19	1.17 ± 1.28	-4.29* ± 1.62	7.98* ± 1.29	-1.31 ± 0.74	-1.90* ± 0.77	-0.83 ± 0.80	0.41 ± 0.57
D	1.42* ± 0.57	-0.94 ± 0.66	0.21 ± 0.52	5.42* ± 0.55	-0.64 ± 0.37	-0.85* ± 0.36	-0.39 ± 0.33	0.70* ± 0.32
m	5.75* ± 0.13	4.72* ± 0.14	4.79* ± 0.13	7.42* ± 0.18	3.29* ± 0.07	3.02* ± 0.08	3.08* ± 0.08	3.46* ± 0.05
(d)	0.33 ± 0.50	0.71 ± 0.59	1.29* ± 0.45	1.08* ± 0.41	0.04 ± 0.34	0.54 ± 0.33	0.54 ± 0.29	0.79* ± 0.30
(h)	-2.21 ± 1.26	2.51 ± 1.43	2.74* ± 1.29	-10.07 ± 1.22	0.43 ± 0.82	1.96* ± 0.80	0.35 ± 0.76	-2.48* ± 0.69
(i)	-2.83* ± 1.14	-	-0.41 ± 1.03	-10.85 ± 1.10	-	1.69* ± 0.72	-	-1.40* ± 0.63
(j)	0.48 ± 0.61	-	-0.07 ± 0.48	1.19* ± 0.50	-	-0.17 ± 0.44	-	0.90* ± 0.36
(l)	3.92 ± 2.34	-	5.11* ± 2.41	13.71* ± 2.09	-	-1.48 ± 1.51	-	2.40 ± 1.32
	No. of pods per plant				No. of seeds per pod			
A	1.67 ± 4.23	3.80 ± 4.26	-1.66 ± 4.25	9.01* ± 3.55	-2.58* ± 0.71	-0.60 ± 0.58	1.69* ± 0.60	-0.38 ± 0.51
B	3.68 ± 3.03	5.02 ± 3.98	-7.40* ± 3.61	-4.65 ± 2.63	-1.90* ± 0.68	-1.43* ± 0.46	0.62 ± 0.47	-1.34* ± 0.44
C	1.73 ± 4.06	-9.37 ± 4.94	-15.57* ± 5.47	30.95* ± 3.38	-3.59* ± 0.78	-3.08* ± 0.67	1.72* ± 0.65	-5.21* ± 0.61
D	-1.82 ± 2.49	-9.10* ± 2.60	-3.25 ± 2.30	13.30* ± 2.18	0.45 ± 0.46	-0.52 ± 0.33	-0.30 ± 0.34	-1.75* ± 0.30
m	17.28* ± 0.55	13.89* ± 0.53	14.42* ± 0.51	22.46* ± 0.53	6.54* ± 0.09	6.49* ± 0.08	6.69* ± 0.07	5.44* ± 0.07
(d)	1.96 ± 2.23	4.46 ± 2.37	6.58* ± 2.06	7.04* ± 1.91	-0.13 ± 0.42	1.17* ± 0.29	0.75* ± 0.30	0.63* ± 0.26
(h)	6.68 ± 5.26	24.23* ± 5.66	12.27* ± 5.25	-22.29* ± 4.56	-0.88 ± 0.99	1.77* ± 0.73	-0.04 ± 0.73	2.27* ± 0.65

(i)	-	18.19* ± 5.20	6.51 ± 4.60	-26.59* ± 4.37	-0.89 ± 0.92	1.04 ± 0.67	0.59 ± 0.67	3.50* ± 0.59
(j)	-	-0.61 ± 2.53	2.87 ± 2.21	6.83* ± 2.09	-0.34 ± 0.44	0.42 ± 0.32	0.54 ± 0.35	0.48 ± 0.29
(l)	-	-27.01* ± 10.71	2.56 ± 9.88	22.23* ± 8.36	5.37* ± 1.86	1.00 ± 1.34	-2.91* ± 1.37	-1.79 ± 1.21
		100 seed weight			Single plant yield			
A	-0.11 ± 0.26	0.07 ± 0.18	0.96* ± 0.18	0.42* ± 0.14	-1.61 ± 1.23	0.46 ± 1.55	2.97* ± 1.24	1.27 ± 0.93
B	0.05 ± 0.32	-0.92* ± 0.14	-0.08 ± 0.14	1.18* ± 0.35	-0.30 ± 0.73	-0.66 ± 1.19	-1.15 ± 0.91	-1.18 ± 0.75
C	0.51 ± 0.45	0.89* ± 0.21	-0.77* ± 0.21	1.27* ± 0.32	-1.86 ± 1.30	-4.21* ± 1.77	-2.75* ± 1.24	6.01* ± 1.30
D	0.28* ± 0.15	0.87* ± 0.12	-0.83* ± 0.09	-0.16 ± 0.14	0.02 ± 0.65	-2.01* ± 0.82	-2.28* ± 0.67	2.96* ± 0.56
m	4.05* ± 0.05	4.27* ± 0.04	3.35* ± 0.02	4.25* ± 0.03	4.41* ± 0.16	3.90* ± 0.16	3.17* ± 0.11	5.40* ± 0.17
(d)	0.23 ± 0.11	0.39* ± 0.09	0.52* ± 0.08	-0.06 ± 0.12	0.74 ± 0.57	2.34* ± 0.75	2.65* ± 0.63	1.67* ± 0.43
(h)	-0.28 ± 0.36	-2.05* ± 0.24	1.64* ± 0.20	0.59 ± 0.31	0.84 ± 1.42	5.83* ± 1.83	5.72* ± 1.45	-5.09* ± 1.24
(i)	-0.57 ± 0.30	-1.74* ± 0.23	1.65* ± 0.17	0.33 ± 0.27	-	4.01* ± 1.63	4.57* ± 1.33	-5.92* ± 1.11
(j)	-0.08 ± 0.18	0.49* ± 0.11	0.52* ± 0.09	-0.38* ± 0.19	-	0.56 ± 0.81	2.06* ± 0.68	1.22* ± 0.48
(l)	0.62 ± 0.64	2.59* ± 0.42	-2.53* ± 0.38	-1.93* ± 0.59	-	-3.81 ± 3.49	-6.39* ± 2.80	5.83* ± 2.16

\*Significant at 5% probability level

(j) were significant in various crosses, revealing the existence of additive x additive, additive x dominance, and dominance x dominance non-allelic interactions. Haque et al. (2013) also reported similar gene action in black gram. However, the set of the material was different. The opposite signs of (h) and (l) in crosses I and IV suggest duplicate interactions. Given the predominance of duplicate dominant gene action, heterosis breeding might be effective in improving cluster numbers per plant. The number of pods per cluster was governed by both additive and non-additive gene action, as evident from the presence of genetic component (h) in crosses II and IV. Additionally, in these crosses, genetic

component (i) was significant, indicating additive x additive interaction. In cross IV alone, interaction component (j) was predominant, suggesting additive x dominance gene action.



Fig. 1. Establishment of crop under rice fallow nature

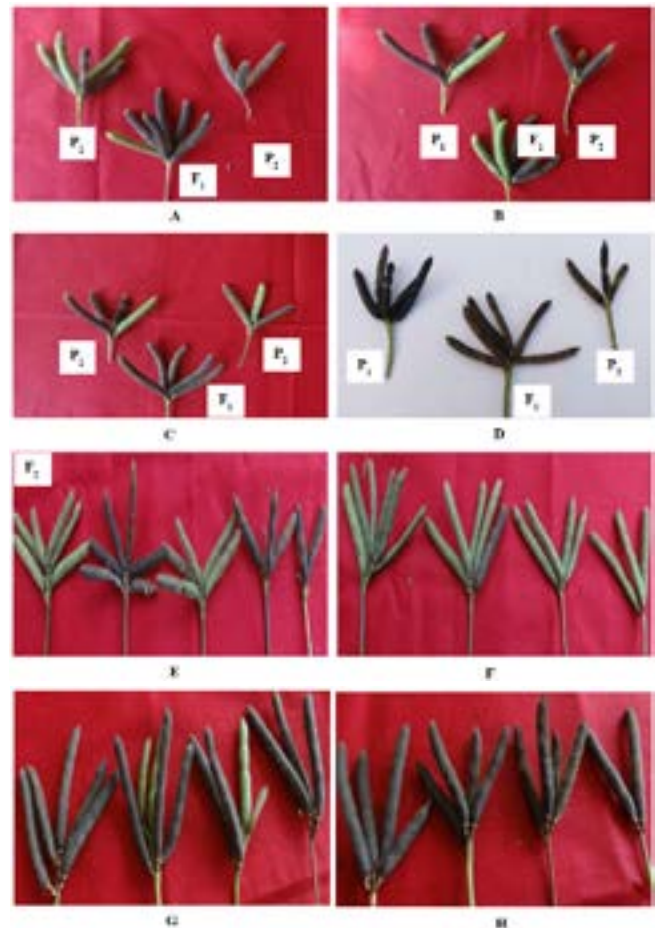


Fig. 2. Parent progeny comparison for pod characteristic under rice fallow condition (A) MDU 1 x VBN 6, (B) MDU 1 x Mash-114, (C) ADT 3 x PU 31, (D) CO 6 x VBN 6, (E) MDU 1 x VBN 6, (F) MDU 1 x Mash-114, (G) ADT 3 x PU 31, (H) CO 6 x VBN 6

The presence of additive, dominance, additive x additive, and additive x dominance components underscores their roles in governing traits. The opposite orientation of components (h) and (l) in crosses II and IV suggests duplicate gene interaction. Sathya et al. (2021) also found dominant gene action, which could be improved through conventional breeding methods.

Number of pods/plant (Fig. 2), the most significant traits for high yield is governed by additive, dominant, and epistatic interactions. Specifically, the additive component (d) was evident in crosses III and IV, while the dominance component (h) was present in crosses II, III, and IV. Interaction components (i) and (l) were significant in crosses II and IV, respectively, with component (j) significant only in cross IV. Consequently, the number of pods per plant was influenced by a combination of additive, dominance, additive x additive, dominance x dominance, and additive x dominance interactions. Opposing signs of components (h) and (l) in crosses II and IV indicated duplicate gene action. Early generation selection is ineffective due to the presence of various gene actions and the negative significance of component (i). Recurrent selection could be employed to disrupt undesirable linkages and accumulate beneficial gene components. For no. of seeds per pod, all genetic components except interaction component (j) were significant, indicating the prevalence of both additive and non-additive gene action. The additive component (d) was observed in crosses II, III, and IV, while component (h) was recorded in cross I. Interaction component (i) was significant in cross IV, and (l) was significant in crosses I and III, indicating additive x additive and dominant x dominant genetic interactions, respectively. Opposing signs of (h) and (l) in crosses I and IV, and consistent signs in crosses II and III, suggest the presence of duplicate and complementary gene action, respectively. Complementary gene action indicates additive gene action, with parents selected from diverse origins. Additive gene action magnitude was higher than dominant gene action, suggesting pureline and pedigree selection for improving seeds per pod as also suggested by Sathya et al. (2021) in black gram.

In Cross II and III, both additive (d) and dominant (h) components were notably high with respect to 100 seed weight. Interaction component (i) was significant in crosses II and III, while components (j) and (l) were present in all three crosses except for cross I, indicating additive, dominance, additive x additive, additive x dominance, and dominance x dominance gene interactions. Opposite signs of (h) and (l) across all crosses indicated duplicate gene action. Chakraborty et al. (2010), have also observed additive and non-additive components influencing the inheritance of 100-seed weight in black gram improvement potential through simple selection, thus advocating for heterosis breeding. Genotypes suitable for rice fallow conditions require early maturity and competitive yield potential. The gene action for

seed yield conducted in rice fallow conditions demonstrated the presence of additive (d), dominance (h) gene action, and interaction component (i) across all the crosses except cross I. Interaction components (j) and (l) were observed in crosses III and IV, indicating additive, dominance, additive x additive, additive x dominance, and dominance x dominance gene interactions. Opposite signs of (h) and (l) were noted in the expression of this trait. The selection in later generations for desirable genotypes is suggested. Recurrent selection is recommended to disrupt undesirable linkages and restore favorable gene combinations.

### Authors' contribution

Conceptualization of research (GT); Designing of the experiments (SG); Contribution of experimental materials (SG); Execution of field/lab experiments and data collection (GT); Analysis of data and interpretation (GT); Preparation of the manuscript (GG, SG).

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