Plant Archives Vol. 26, No. 1, 2026 pp. 397-404 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2026.v26.no.1.055

STUDIES ON THE GENETIC BASIS OF GRAIN QUALITY TRAITS IN RICE (*ORYZA SATIVA* L.) THROUGH GENERATION MEAN ANALYSIS

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(Date of Receiving : 06-12-2025; Date of Revision : 22-01-2026; Date of Acceptance : 18-02-2026)

ABSTRACT

Rice is a major staple food crop of global economic and social importance. Understanding the inheritance patterns of genes governing grain quality traits is essential for identifying appropriate breeding strategies for their improvement. In the present investigation, the genetic effects controlling these traits and their interactions were elucidated using generation mean analysis based on quantitative genetic principles. Five genetically diverse crosses along with their six generations (P_1, P_2, F_1, F_2, B_1 and B_2) were evaluated separately in a Compact Family Block Design with three replications during *kharif* 2023. Analysis of variance revealed significant generation mean squares for most characters across the majority of crosses. The six-parameter generation mean analysis further highlighted the predominance of both additive and non-additive gene actions in governing grain quality traits in most of the crosses studied.

***Keywords* :** Generation mean analysis, Additive, Non-additive.

Introduction

Rice is premium food grain crop and is often the main source of calories and principal food of millions of people. Rice has been referred as “Global Grain” because of its use as leading staple food in about 100 countries of the world and provides staple food to more than half of the world’s population. Rice plays a pivotal role in Indian agriculture and it is the staple food for more than 70 % Indians. It is grown in all states and in all ecologies. India is very rich in rice genetic resources.

“Rice is life” was the famous theme of International Year of Rice, 2004 denoting its overwhelming importance as an item of food and commerce. Today rice is grown and harvested on every continent except Antarctica. Rice remains a staple food for the majority of the world population. More than two thirds of the world relies of the nutritional benefit of rice. It provides more than one fifth of the calories consumed worldwide by humans. It is one of the oldest and second most intensively grown cereal crop and ranks third in grain production. Asia is considered to be rice bowl of the world and it produces and consumes more than 90 per cent of world rice (Tyagi *et al*., 2004). Chhattisgarh state is known as rice bowl of India.

India is the largest rice growing country, while China is the largest producer of rice. The world population is expected to reach 8.27 billion by 2030 demanding an increased rice product ion of 771 million tonnes (Badawi, 2004). According to 2016 world population data sheet, India’s population would increase day by day and would surpass the population of China in 2050 (Anon., 2016). Thus, it is a challenging task to ensure food and nutritional security of India’s ever increasing population and therefore, rice production must be increased by 50% in order to meet the growing demand (Miah *et al*., 2013). However, with an increasing world population and gradually deteriorating environment, food security has become a major challenge, especially in Asia and Africa (Sasson, 2012). In India, during the year 2024-

25, rice is cultivated in 43.47 million hectares with production of 122.77 million tonnes and productivity of 2825 kg per hectare (Anon., 2025a). While, in Gujarat, during the year 2024-25, rice is cultivated in 10.14 lakh hectares with production of 24.45 lakh tonnes and productivity of 2411 kg per hectare (Anon., 2025b).

The selection of a plant breeding technique to improve a given characteristic is primarily contingent upon the availability of dependable data regarding the type and extent of gene effects within the population. Various techniques in quantitative genetics can be employed to calculate distinct genetic components, such as additive, dominance, and epistatic interactions. The measurements of additive and dominant components may be inflated by the non-allelic gene interactions. In addition to additive and dominance, Hayman (1958), Brim and Cockerham (1961), Gamble (1962), Matzinger (1968), and Stuber and Moll (1974) were among the first to recognize the importance of non-allelic interaction. Jinks (1955) attributed the epistatic interaction as the primary cause of heterosis expression. Therefore, in addition to additive and dominant components, it is crucial to identify and quantify the epistasis components.

Materials and Methods

Eight genetically diverse rice parental lines (Table 1) were obtained from the Main Rice Research Station, Anand Agricultural University, Nawagam and used to generate experimental material for generation mean analysis. Five single crosses were developed during *kharif* 2021. In *kharif* 2022, the segregating generations F_2 and two backcrosses (B_1 and B_2) were produced by selfing the F_{1s} and backcrossing them with their respective parents.

Table 1: Details of parental genotypes used in hybridization program

Sr. No.	Parent	Pedigree
1.	Gurjari	Asha × Kranti
2.	GAR-13	GR-11 × IET-14726
3.	GAR-14	GR-7 × Mahisugandha
4.	Jaya	TN-1 × T-141
5.	Mahisagar	CN-540 × IR-50
6.	NWGR-19239	GR-3 × Basmati-370
7.	GR-7	GAR-13 × Pusa-1121
8.	NVSR-796	NVSR-303-14 × GAR-1

Hybridization was carried out using standard emasculation and hand-pollination techniques. Selected panicles were emasculated in the evening, pollinated the following morning and carefully bagged and tagged to ensure genetic purity. Seeds from each generation were harvested separately and properly labeled.

All six generations (P_1, P_2, F_1, F_2, B_1 and B_2) of five crosses of rice were evaluated during *kharif* 2023 at the Main Cotton Research Station, Anand Agricultural University, Nawagam. The experiment was laid out in a compact family block design (CFBD) with three replications. Each block consisted of single rows for the parents and F_1, two rows for each backcross, and four rows for the F_2 generation. Transplanting was done at a spacing of 20 × 15 cm, and recommended agronomic practices were followed. Observations on quality parameters were recorded on a per-plant basis.

Statistical analysis was performed using analysis of variance appropriate for the compact family block design as described by Panse and Sukhatme (1985). Scaling tests were employed to examine the adequacy of the additive-dominance genetic model and to detect the presence of non-allelic interactions as suggested by Hayman and Mather (1955). When the additive-dominance model was found inadequate, epistatic gene effects were inferred.

A joint scaling test outlined by Cavalli (1952) was further applied to confirm the goodness of fit of the additive-dominance model by comparing observed and expected generation means. In cases where epistasis was detected, a six-parameter generation mean analysis as suggested by Hayman (1958) was conducted to estimate the nature and magnitude of genetic effects, including additive, dominance, and different types of gene interactions. The significance of these genetic effects was assessed using standard statistical tests.

Results and Discussions

(A) Analysis of variance (ANOVA)

The analysis of variance (ANOVA) between generations within cross (Table 2) for different eight characters revealed significant difference for mean sum of square for all of the characters in most of the crosses, thereby indicating presence of ample amount of genetic variation in experimental materials used.

Table 2: Analysis of variance (ANOVA) between generations within cross

Cross	Rep.	Gen.	Error	Cross	Rep.	Gen.	Error
	df = 2	df = 5	df = 10		df = 2	df = 5	df = 10
Hulling				**Milling**			
Cross I	2.047	18.546**	0.826	Cross I	6.359	56.706**	4.827
Cross II	2.392	8.318**	0.729	Cross II	3.648	8.773**	1.729
Cross III	2.676	6.390*	1.715	Cross III	1.672	11.929**	2.739
Cross IV	0.660	4.468**	0.447	Cross IV	0.300	5.591**	0.161
Cross V	2.724	5.550^{NS}	2.177	Cross V	5.669	24.260**	3.711
Head rice recovery				**Grain length**			
Cross I	0.490	46.928**	7.476	Cross I	0.003	2.717**	0.027
Cross II	2.294	7.538**	1.256	Cross II	0.061	0.884**	0.035
Cross III	0.929	6.318^{NS}	3.306	Cross III	0.034	0.386**	0.058
Cross IV	1.179	4.174**	0.697	Cross IV	0.124	0.576*	0.122
Cross V	1.608	11.422^{NS}	3.457	Cross V	0.003	1.474**	0.018
Grain breadth				**L/B ratio**			
Cross I	0.003	0.273**	0.004	Cross I	0.010	0.223**	0.013
Cross II	0.001	0.046**	0.002	Cross II	0.007	0.056**	0.007
Cross III	0.006	0.521**	0.003	Cross III	0.012	0.826**	0.014
Cross IV	0.001	0.001^{NS}	0.008	Cross IV	0.010	0.105**	0.006
Cross V	0.005	0.243**	0.007	Cross V	0.012	0.120**	0.008
Amylose content				**Alkali spreading value**			
Cross I	0.140	2.025*	0.397	Cross I	0.004	0.396**	0.051
Cross II	3.374	1.163^{NS}	0.919	Cross II	0.014	0.502**	0.058
Cross III	0.746	0.963*	0.230	Cross III	0.013	1.763**	0.138
Cross IV	0.211	0.229^{NS}	0.171	Cross IV	0.013	2.293**	0.019
Cross V	0.259	0.813**	0.074	Cross V	0.194	0.417*	0.111

Table 3: Estimation of scaling tests for various characters in five crosses of rice

Cross	Scaling tests				χ^2	Cross	Scaling tests				χ^2
	A	B	C	D			A	B	C	D	
Hulling						**Milling**					
Cross I	-6.83**	-7.03**	-20.42**	-3.28	**	Cross I	-22.56**	-9.70**	-22.07**	5.10	**
Cross II	-3.25*	-4.38**	-15.21**	-3.79**	**	Cross II	-3.10	-6.33**	-15.72**	-3.14*	**
Cross III	-0.89	-6.65**	-10.08*	-1.27	**	Cross III	-1.24	-8.82**	-13.43**	-1.68	**
Cross IV	-2.48	-3.45**	-11.02**	-2.54	**	Cross IV	-0.55	-0.33	-13.75**	-6.44**	**
Cross V	--	--	--	--	--	Cross V	-11.90**	-6.28*	-21.77**	-1.79	**
Head rice recovery						**Grain length**					
Cross I	-19.73**	-11.64**	-17.32**	7.02**	**	Cross I	-2.80**	-0.53	-3.73**	-0.20	**
Cross II	0.64	0.18	-9.57**	-5.19**	*	Cross II	0.55	0.33*	-0.72	-0.80**	**
Cross III	--	--	--	--	--	Cross III	0.15	0.23	0.78*	0.20	NS
Cross IV	-1.59	-2.03	-11.75**	-4.06**	**	Cross IV	-0.47	0.71	-1.36	-0.80*	*
Cross V	--	--	--	--	--	Cross V	2.51**	-0.70**	2.03**	0.11	**
Grain breadth						**L/B ratio**					
Cross I	0.08	0.56**	0.29	-0.18	**	Cross I	-1.17**	-0.68**	-1.53**	0.16	**
Cross II	0.10	0.31**	-0.14	-0.28**	**	Cross II	0.12	-0.38**	-0.05	0.10	**
Cross III	-1.12**	-0.01	-1.55**	-0.21*	**	Cross III	1.23**	-0.13	1.88**	0.38*	**
Cross IV	--	--	--	--	--	Cross IV	-0.19	0.32*	-0.31	-0.22	**
Cross V	1.14**	-0.42**	1.63**	0.45**	**	Cross V	-0.48**	0.35**	-1.31**	-0.59**	**
Amylose content						**Alkali spreading value**					
Cross I	-1.56*	-1.76*	-3.70**	-0.19	**	Cross I	-0.47	-1.60**	-1.93**	0.07	**
Cross II	--	--	--	--	--	Cross II	-1.47**	-0.87*	-1.67**	0.33	**
Cross III	-1.51*	-0.46	-1.23	0.37	*	Cross III	-2.27**	-2.60**	-4.93**	-0.03	**
Cross IV	--	--	--	--	--	Cross IV	-1.53**	-3.33**	-0.47	2.20**	**
Cross V	-1.13	-1.10	-3.40**	-0.58	*	Cross V	-1.00**	-0.87*	-1.87**	0.00	**

* and ** indicate significance at 5 % and 1 % level of significance, respectively

(B) Scaling Tests

Based on the individual scaling test 'A', 'B', 'C' and 'D', the additive-dominance model was found inadequate for description of variation in generation mean for all the eight characters in most of the crosses. Either the entire four or any three, two or one individual scaling test (out of 'A', 'B', 'C' and 'D') were found significant (Table 3) which indicated the presence of digenic interactions which implies that the additive-dominance model is inadequate. These results were supported by the significant value of χ^2 joint scaling test (Cavali, 1952) for all the eight characters in most of the crosses. Therefore, six parameter model (Hayman, 1958) was used for estimation of genetic components.

(C) Genetic Effects

For the crosses and characters, where any of the simple scaling test was significant, six parameter(m, d, h, i, j and l) model as suggested by Hayman (1958) was applied to partition gene effect into epistatic components including principal gene effects.

1. **Hulling:** With respect to this trait, mean (m) was found to be highly significant in all of the crosses except cross V. The value of mean (m) was also higher than other genetic effect. The results (Table 4) also showed that dominance (h) was highly significant cross I and cross IV; dominance (h) and additive × additive (i) were highly significant in cross II. Both, additive and non-additive types of gene actions appeared to play a vital role in the inheritance of this trait. Rani *et al.* (2015) and Subbulakshmi *et al.* (2016) reported similar type of findings while working with rice.

2. **Milling:** For this trait, mean (m) was found highly significant and higher than other estimated parameters of generation mean analysis (Table 5). Apart from the mean (m), other gene effects were also found highly significant in different crosses *viz.*, additive (d), additive × dominance (j) and dominance × dominance (l) in cross I; dominance (h) and additive × additive (i) in cross II; additive (d) and additive × dominance (j) in cross III; dominance (h), additive × additive (i) and dominance × dominance (l) in cross VI; dominance × dominance (l) in cross V. These results revealed the importance of both additive and non-additive types of gene actions in the inheritance of this trait. The results of present study are akin with findings of Rani *et al.* (2015) and Subbulakshmi *et al.* (2016).

3. **Head rice recovery:** The highly significant and higher mean (m) as compared to other gene effects was observed for head rice recovery (**Table 6**) in three out of five crosses of present investigation. Among all the five crosses evaluated, in cross I, highly significance gene effects were dominance (h), additive × additive (i), additive × dominance (j) and dominance × dominance (l); in cross II, highly significance gene effects were dominance (h) and additive × additive (i); in cross IV, highly significance gene effects were dominance (h) and additive × additive (i). Thus, it revealed that the additive and non-additive types of gene actions appeared to play a vital role in the inheritance of this trait. Rani *et al.* (2015) also reported similar type of finding while working with rice.

4. **Grain length**: With respect to six parameter model, the highly significant mean (m) was observed for all of the five crosses. Besides these, it was higher than other gene effects in respective cross (Table 7). The results indicated that cross I exhibited highly significant estimates of dominance (h), additive × dominance (j) and dominance × dominance (l); cross II exhibited highly significant estimates of dominance (h), additive × additive (i) and dominance × dominance (l); cross IV exhibited highly significant estimates of dominance (h), additive × additive (i) and additive × dominance (j) and cross V exhibited highly significant estimates of additive (d), additive × dominance (j) and dominance × dominance (l). Thus, the additive and non-additive types of gene actions was found to play a vital role in the inheritance of this trait. Similar results for grain length in rice were also reported by other workers *viz.*, Rani *et al.* (2015), Subbulakshmi *et al.* (2016), Kumar *et al.* (2017), Panchal *et al.* (2019), Singh and Patel (2020), Sharma *et al.* (2024), Patel *et al*. (2025).

5. **Grain breadth**: The highly significant mean (m) was observed for all the crosses except cross IV. Besides these, it was higher than other gene effects in respective cross (Table 8). The results indicated that highly significant estimates of dominance (h), additive × dominance (j) and dominance × dominance (l) was observed in cross I; significant estimates of dominance (h), additive × additive (i), additive × dominance (j) and dominance × dominance (l) was observed in cross II; significant estimates of dominance (h), additive × dominance (j) and dominance × dominance (l) was observed in cross III; significant estimates of additive (d), dominance (h), additive × additive (i) and additive

× dominance (j) was observed in cross IV. The all over result indicated additive and non-additive types of gene actions to play a vital role in the inheritance of this trait. Similar results were reported by Rani *et al.* (2015), Subbulakshmi *et al.* (2016), Kumar *et al.* (2017), Panchal *et al.* (2019), Sharma *et al.* (2024) and Patel *et al*. (2025).

6. **L/B ratio:** With respect to this trait, mean (m) was found to be highly significant in all of the crosses. The value of mean (m) was also higher than other genetic effect. The results (Table 9) also showed that additive × dominance (j) and dominance × dominance (l) was significant cross I; additive × dominance (j) was significant cross II; dominance (h), additive × additive (i) and additive × dominance (j) was significant in cross III; dominance (h) and additive × dominance (j) was significant in cross IV; additive (d), dominance (h), additive × additive (i), additive × dominance (j) and dominance × dominance (l) was significant in cross IV. So, revealing the importance of additive and non-additive types of gene actions for the inheritance of this trait. Rani *et al.* (2015), Subbulakshmi *et al.* (2016), Kumar *et al.* (2017), Panchal *et al.* (2019), Singh and Patel (2020), Sharma *et al.* (2024) and Patel *et al*. (2025) had reported similar results.

7. **Amylose content:** For this trait, mean (m) was only found highly significant and higher than other estimated parameters of generation mean analysis (Table 10). Apart from the mean (m), other gene effects were found non-significant. Significant estimate of mean (m) was also quoted by Rani *et al.* (2015), Subbulakshmi *et al.* (2016), Bano *et al.* (2017) and Rao *et al.* (2017), Patel *et al.* (2020), Singh and Patel (2020), Sharma *et al.* (2024) and Patel *et al*. (2025).

8. **Alkali spreading value:** The highly significant and higher mean (m) as compared to other gene effects was observed for alkali spreading value (Table 11) in all the five crosses of present investigation. Among all the five crosses evaluated, additive (d), additive × dominance (j) and dominance × dominance (l) was significant in cross I; dominance × dominance (l) was significant in cross II; additive (d), dominance (h) and dominance × dominance (l) was significant in cross III; dominance (h), additive × additive (i), additive × dominance (j) and dominance × dominance (l) was significant in cross IV; dominance × dominance (l) was significant in cross V. This result indicated the importance of both additive and non-additive types of gene actions for the inheritance of this trait. Rani *et al.* (2015), Santhiya *et al.* (2024) and Sharma *et al.* (2024) also reported similar results.

Table 4: Estimation of gene effects for hulling in five crosses of rice

Gene effects	Cross I		Cross II		Cross III		Cross IV		Cross V	
	Value	SE (±)	Value	SE (±)	Value	SE (±)	Value	SE (±)	Value	SE (±)
(m)	71.27**	0.66	72.46**	0.53	71.52**	0.89	73.82**	0.55	--	--
(d)	0.49	1.18	0.25	0.87	2.85	1.51	-0.07	0.90	--	--
(h)	10.88**	3.57	10.21**	2.80	2.89	4.77	6.69*	2.90	--	--
(i)	6.56	3.54	7.58**	2.75	2.54	4.66	5.08	2.85	--	--
(j)	0.10	1.25	0.57	0.93	2.88	1.58	0.49	0.94	--	--
(l)	7.30	5.50	0.05	4.21	5.00	7.31	0.85	4.37	--	--

Table 5: Estimation of gene effects for milling in five crosses of rice

Gene effects	Cross I		Cross II		Cross III		Cross IV		Cross V	
	Value	SE (±)	Value	SE (±)	Value	SE (±)	Value	SE (±)	Value	SE (±)
(m)	64.00**	1.02	65.94**	0.55	65.86**	1.00	67.57**	0.54	65.34**	0.81
(d)	-5.34**	1.90	1.14	0.86	4.00**	1.50	-0.08	0.80	-2.55	1.55
(h)	-7.86	5.63	7.76*	3.29	5.00	5.16	13.06**	2.79	3.12	4.60
(i)	-10.19	5.59	6.28*	2.78	3.36	5.01	12.87**	2.68	3.59	4.47
(j)	-6.43**	1.94	1.62	0.96	3.79*	1.60	-0.11	0.82	-2.81	1.59
(l)	42.45**	8.75	3.15	5.37	6.70	7.64	-11.99**	4.17	14.60*	7.32

Table 6: Estimation of gene effects for head rice recovery in five crosses of rice

Gene effects	Cross I		Cross II		Cross III		Cross IV		Cross V	
	Value	SE (±)	Value	SE (±)	Value	SE (±)	Value	SE (±)	Value	SE (±)
(m)	57.95**	0.96	58.50**	0.70	--	--	60.26**	0.54	--	--
(d)	-2.88	1.78	-1.30	1.12	--	--	0.07	0.81	--	--
(h)	-12.36*	5.33	8.97*	3.78	--	--	9.62**	2.84	--	--
(i)	-14.04**	5.24	10.39**	3.60	--	--	8.12**	2.71	--	--
(j)	-4.05*	1.89	0.23	1.22	--	--	0.22	0.91	--	--
(l)	45.40**	8.32	-11.20	5.78	--	--	-4.50	4.27	--	--

Table 7: Estimation of gene effects for grain length in five crosses of rice

Gene effects	Cross I		Cross II		Cross III		Cross IV		Cross V	
	Value	SE (±)	Value	SE (±)	Value	SE (±)	Value	SE (±)	Value	SE (±)
(m)	7.06**	0.13	6.96**	0.07	8.14**	0.08	7.42**	0.13	8.05**	0.04
(d)	0.07	0.21	-0.01	0.12	-0.30	0.14	0.03	0.21	0.72**	0.06
(h)	1.57*	0.69	2.94**	0.39	0.34	0.42	1.96**	0.72	0.27	0.24
(i)	0.41	0.67	1.60**	0.38	-0.40	0.42	1.61*	0.67	-0.22	0.21
(j)	-1.14**	0.21	0.11	0.16	-0.04	0.15	-0.59**	0.23	1.61**	0.09
(l)	2.92**	1.03	-2.49**	0.62	0.01	0.65	-1.85	1.09	-1.59**	0.37

Table 8: Estimation of gene effects for grain breadth in five crosses of rice

Gene effects	Cross I		Cross II		Cross III		Cross IV		Cross V	
	Value	SE (±)	Value	SE (±)	Value	SE (±)	Value	SE (±)	Value	SE (±)
(m)	2.40**	0.03	1.93**	0.02	2.47**	0.04	--	--	2.57**	0.03
(d)	0.09	0.07	-0.05	0.03	-0.04	0.07	--	--	0.55**	0.06
(h)	0.84**	0.19	0.81**	0.10	1.02**	0.21	--	--	-0.82**	0.18
(i)	0.35	0.19	0.55**	0.10	0.41	0.21	--	--	-0.91**	0.17
(j)	-0.24**	0.07	-0.10*	0.04	-0.56**	0.07	--	--	0.78**	0.07
(l)	-1.00**	0.30	-0.97**	0.16	0.72*	0.31	--	--	0.19	0.28

Table 9: Estimation of gene effects for L/B ratio in five crosses of rice

Gene effects	Cross I		Cross II		Cross III		Cross IV		Cross V	
	Value	SE (±)	Value	SE (±)	Value	SE (±)	Value	SE (±)	Value	SE (±)
(m)	2.98**	0.07	3.62**	0.04	3.35**	0.06	3.55**	0.05	3.17**	0.05
(d)	-0.06	0.11	0.08	0.06	-0.06	0.09	0.03	0.07	-0.47**	0.07
(h)	-0.36	0.37	0.01	0.20	-1.26**	0.30	0.58*	0.26	1.27**	0.24
(i)	-0.31	0.36	-0.21	0.19	-0.77*	0.30	0.44	0.25	1.19**	0.24
(j)	-0.24*	0.11	0.25**	0.08	0.68**	0.09	-0.25**	0.08	-0.42**	0.08
(l)	2.16**	0.53	0.47	0.31	-0.34	0.44	-0.57	0.37	-1.07**	0.36

Table 10: Estimation of gene effects for amylose content in five crosses of rice

Gene effects	Cross I		Cross II		Cross III		Cross IV		Cross V	
	Value	SE (±)	Value	SE (±)	Value	SE (±)	Value	SE (±)	Value	SE (±)
(m)	24.64**	0.31	--	--	24.26**	0.23	--	--	23.33**	0.28
(d)	-0.64	0.55	--	--	0.21	0.39	--	--	0.44	0.49
(h)	1.89	1.68	--	--	-1.14	1.22	--	--	0.90	1.53
(i)	0.39	1.67	--	--	-0.73	1.19	--	--	1.16	1.49
(j)	0.10	0.57	--	--	-0.53	0.44	--	--	-0.02	0.54
(l)	2.93	2.58	--	--	2.70	1.88	--	--	1.08	2.34

Table 11: Estimation of gene effects for alkali spreading value in five crosses of rice

Gene effects	Cross I		Cross II		Cross III		Cross IV		Cross V	
	Value	**SE (±)**	**Value**	**SE (±)**	**Value**	**SE (±)**	**Value**	**SE (±)**	**Value**	**SE (±)**
(m)	4.78**	0.09	4.73**	0.09	3.53**	0.09	4.92**	0.11	4.43**	0.09
(d)	0.63**	0.14	-0.13	0.15	-0.30*	0.15	0.03	0.18	0.07	0.15
(h)	0.40	0.51	0.23	0.54	1.20*	0.53	-3.27**	0.62	0.87	0.54
(i)	-0.13	0.46	-0.67	0.47	0.07	0.48	-4.40**	0.58	0.00	0.48
(j)	0.57**	0.20	-0.30	0.24	0.17	0.23	0.90**	0.25	-0.07	0.24
(l)	2.20**	0.78	3.00**	0.87	4.80**	0.83	9.27**	0.96	1.87*	0.87

Across all eight traits, the predominance of both additive and non-additive gene effects in the majority of crosses indicates the complex genetic control of these characters. The concurrent involvement of fixable (additive) and non-fixable (dominance and epistatic) components suggests that reciprocal recurrent selection would be an effective breeding strategy for accumulating favorable alleles governing these quantitative traits. This approach facilitates the development of superior homozygous recombinants while maintaining genetic variability within the population. Nevertheless, additional cycles of selection and subsequent inbreeding are necessary to stabilize desirable gene combinations and to ultimately release an improved cultivar from the recurrent selection population (Panchal *et al.*, 2023). But, main challenge in reciprocal recurrent selection is difficulty in intermating and more number of crosses to be performed.

A selection of desirable phenotypes in early stage or generation would be beneficial in case where additive gene effect are more than dominant or non-additive gene effect; whereas, improvement of any traits requires intense form of selection through later stage where non-additive gene effects are more (Jagtap, 1986).

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