

Inferences on Magnitude and Nature of Gene Effects for Morpho-Physiological Traits in Rice [*Oryza Sativa* L.]

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ABSTRACT

The gene effects for grain yield and its components including grain yield and its contributing characters were studied using parental, F₁, F₂, BC₁ and BC₂ generations in four crosses of rice. The estimates of gene effects in cross I (GURJARI x IR-28) showed that additive, dominance and all interactions (additive x additive, additive x dominance and dominance x dominance) were important for inheritance of grain breadth; additive and additive x dominance for plant height, additive, dominance, and additive x additive for 100 seed weight, grain yield per plant and chlorophyll content at flowering stage; gene effects dominance and epistatic (additive x additive and dominance x dominance) for harvest index and chlorophyll content at panicle initiation stage; and additive, dominance, additive x additive and additive x dominance for photosynthetic rate at panicle initiation stage were found significant and important for inheritance. Additive-dominance model was found inadequate in cross II (NAUR-1 x DANTESHWARI) for all the characters. Inadequate estimates of additive-dominance model were recorded in cross IV (GAR-13 x PUSA SUGANDHA-5) for all the characters. In general, both additive and non-additive gene action were important for the expression of almost all characters studied. Biparental mating, recurrent selection and diallel selective mating system could be used to obtain desirable recombination like early plants with higher yield.

Key words: Gene action, Gene effects, Morpho-Physiological traits, rice.

INTRODUCTION

Rice (*Oryza sativa* L., 2n=24) belongs to family Poaceae and subfamily Oryzoidae. India is the largest rice growing country, while China is the largest producer of rice. In India, rice grown in 42.75 million hectares during

2013 with production of 105.24 million tonnes and productivity of 2462 kg per hectare¹. In Gujarat, rice is cultivated 7.01 lakh hectares with production of 15.41 lakh tonnes and productivity of 2198 kg per hectare¹.

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The rice has good export value in the international market but they are poor yielders. Hence, it is very much essential to improve the rice with higher yield. The grain yield is a highly complex character, generally governed by genes and the interaction between them. To know the pattern of inheritance among different traits in rice, diallel mating is frequently used but a few reports are available on generation mean analysis. So the present experiment was undertaken to know the nature and magnitude of gene effects by generation mean analysis which is a simple and successful method in self pollinated crop like rice.

MATERIAL AND METHODS

Six basic generations *viz.*, P1 (Parent 1), P2 (Parent 2), F1 (P1 x P2), F2 (selfing of F1), BC1(P1 x F1) and BC2 (P2 x F1) of four crosses *viz.*, Gurjari x IR-28, NAUR-1 x Danteshwari, GAR-13 x RP-Bio-226 and GAR-13 x Pusa sugandha-5 were raised in compact family block design replicated thrice at Main Rice Research Center, Navsari Agricultural University, Navsari, during kharif-2014. The individual replication was represented by four family blocks, one row each of P1, P2 and F1, four rows of F2 and two rows each of BC1 and BC2. Total 10 plants were accommodated in each row. The inter and intra row spacing was 20 cm and 15 cm, respectively. All the recommended agronomical practices and plant protection measures were followed as and when required for raising good crop.

The individual scaling tests^{7,12} and joint scaling test² were applied to test the adequacy of additive-dominance model. When the model was adequate the genetic parameters 'm', 'd' and 'h' were estimated following Cavalli². Otherwise six- parameters model following weighted least square technique was used to estimate the components of different parameters *viz.*, 'm', 'd', 'h', 'i', 'j' and 'l'.

RESULTS AND DISCUSSION

The estimates of genetic parameters like mean (m), additive (d), dominance (h), additive

x additive (i), additive x dominance (j), dominance x dominance (l) for different characters in four crosses are presented in table 1. Significant deviation of observed generation mean from the expected mean for most of the characters suggested that the non-allelic interactions were present in these crosses. The data on Days to Flowering revealed that the dominant effect had major role in controlling this character. In crosses GURJARI x IR-28 and NAUR-1 x DANTESHWARI, additive (d), additive x dominance (j), dominance x dominance (l) type of interactions were important. In crosses GAR-13 x RP BIO- 226 and GAR-13 x PUSA SUGANDHA-5 dominance (h), additive x additive (i) and dominance x dominance (l) type of interactions were important.

Duplicate type of epistasis was found in all the crosses except NAUR-1 x DANTESHWARI supported by the findings of Roy and Panwar¹³, Hasib *et al.*⁶ and Roy and Senapati¹⁴. Inheritance of this trait in crosses *viz.*, NAUR-1 x DANTESHWARI and GAR-13 x RP BIO- 226 was under the control of duplicate type of epistasis. The importance of both additive and non additive types of gene effects were also observed by Roy and Panwar¹³ and Roy and Senapati¹⁴. Additive type of gene action mainly controls panicle length in all the crosses.

The additive effect predominated over dominant effect have been reported by Roy and Panwar¹³, Roy and Senapati¹⁴ and Kiani *et al.*⁹. Duplicate type of epistasis was present in GAR-13 x RP BIO- 226. The duplicate type gene interaction played a prominent role in crosses *viz.*, GURJARI x IR-28, NAUR-1 x DANTESHWARI and GAR-13 x RP BIO-226 while, in cross GAR-13 x PUSA SUGANDHA-5. The similar results were reported by Chauhan *et al.*⁴, Roy and Panwar¹³, Hasib *et al.*⁶ and Kiani *et al.*⁹.

Complementary type of epistasis was present in two crosses *viz.*, NAUR-1 x DANTESHWARI and GAR-13 x RP BIO-226, while duplicate gene interaction was found in crosses *viz.*, GURJARI x IR-28 and GAR-13 x PUSA SUGANDHA-5. The same

results also reported by Chauhan *et al.*⁴, Hasib *et al.*⁶, Kumar *et al.*¹¹, Kumar *et al.*¹⁰, Roy and Senapati¹⁴, Chamundeswari *et al.*³ and Kiani *et al.*⁹.

For grain length additive gene action was significant and positive in crosses GURJARI x IR-28 and NAUR-1 x DANTESHWARI suggested the potential for obtaining further improvement in this trait through selection. Similar results were quoted by Hasib *et al.*⁶, Kumar *et al.*¹⁰ and Gnanamalar and Vivekanandan⁵. The influence of dominance gene effects was more than additive for grain breadth. The duplicate type gene interaction played a prominent role in all the crosses. Similar results were quoted by Hasib *et al.*⁶, Kumar *et al.*¹⁰ and Gnanamalar and Vivekanandan⁵.

For grain L: B ratio additive gene action was significant and negative in all the crosses except GAR-13 x RP BIO- 226. Additive x additive and dominance x dominance gene interaction were significant in all the crosses while additive x dominance gene interaction was significant in NAUR-1 x DANTESHWARI and GAR-13 x PUSA SUGANDHA-5. Duplicate epistasis was present in all the crosses. Similar results were quoted by Hasib *et al.*⁶, Kumar *et al.*¹⁰ and Gnanamalar and Vivekanandan⁵.

In cross GURJARI x IR-28 and GAR-13 x RP BIO- 226 dominance effect contributed more to grain yield per plant than

additive, while in other crosses additive contributed more. However, impact of interallelic interactions along with additive and dominance was found in all the crosses. The similar findings were reported by Chauhan *et al.*⁴, Roy and Panwar¹³, Hasib *et al.*⁶, Roy and Senapati¹⁴, Chamundeswari *et al.*³ and Kiani *et al.*⁹.

For straw yield per plant additive gene effect was significant and positive in cross GURJARI x IR-28 and GAR-13 x RP BIO-226 while dominance gene effect was significant in cross NAUR-1 x DANTESHWARI and GAR-13 x PUSA SUGANDHA-5. All the three types of gene interaction found highly significant in cross NAUR-1 x DANTESHWARI and GAR-13 x PUSA SUGANDHA-5. Similar kind of results was reported by Kumar *et al.*¹¹ and Kumar *et al.*¹⁰.

Thus, both additive and non-additive gene effects were important for the inheritance of almost all the characters studied. The use of population improvement concept may become an amenable solution. Biparental mating, recurrent selection and diallel selective mating system might be profitable in exploiting both additive and nonadditive gene action to obtain desirable recombinants having the characteristics of reduced height with high yielding rice plants developed.

Table 1: Estimates of Simple Scaling Test and gene effects for days to flowering, plant height, panicle length, productive tillers per plant, grains per panicle and 100 seed weight in four crosses of rice.

Cross	Gene effect									
	Scaling Test				Six parameters model					
	A	B	C	D	m	d	h	i	j	l
Days to flowering										
I	-20.60**	-5.60**	-23.40**	-13.48**	77.90**	-2.00**	-4.59	-2.81	-7.50**	29.02**
II	-12.60**	-8.26**	-26.33**	-15.70**	82.28**	7.10**	2.93	5.46	-2.16**	15.40**
III	2.46	2.40	22.13**	5.53**	106.36**	-2.10*	-22.8**	-17.26**	0.03	12.40**
IV	4.86*	10.58	-12.31**	-10.68**	94.98**	0.15	23.24**	27.76**	-2.86	-43.22**
Plant height (cm)										
I	9.13**	-2.20	5.39	2.23	102.7**	10.00**	1.06	1.53	5.66**	-8.46
II	-4.85	-1.58	-40.89**	-16.44*	89.29**	9.23**	38.45**	34.45**	-1.63	-28.01*
III	-4.00	-8.26*	2.93	6.13	100.46**	3.20*	-10.53	-15.20	2.13	27.46*
IV	3.00	7.40**	6.80*	-4.63	101.65**	-6.63**	-4.43	3.60	-2.20	-14.00**
Panicle length (cm)										
I	-1.20	1.63**	0.20	1.05	23.32**	-0.67*	1.17	0.22	-1.42**	-0.66

II	-1.91	-3.36**	-4.85*	-0.68	25.07**	5.35**	1.32	-0.42	0.72	5.69*
III	-2.71**	1.29**	-4.90*	-0.45	22.71**	1.37**	5.47**	3.47	-2.06**	-2.04
IV	-2.32	-5.96**	-8.69**	-1.79	26.14**	2.19**	2.96	0.40	1.82*	7.87
Productive tillers per plant										
I	-1.28**	0.04	-2.90**	-1.62	6.30**	-1.09**	1.50	1.66	-0.66**	-0.42
II	-0.41	0.11	-1.56*	-1.32*	7.22**	0.74**	0.73	1.26**	-0.26*	-0.96
III	-0.84	1.66**	7.55**	3.31**	11.35**	-2.41**	-7.19**	-6.73**	-1.25**	5.91**
IV	-1.91**	-0.73*	-4.29**	-2.18*	7.36**	0.19	1.61*	1.64*	-0.59*	1.00
Grains per panicle										
I	-29.90*	-44.44**	4.03	72.85**	152.76**	36.76**	-7.53	-78.37**	7.26	152.71**
II	15.47	-15.12	-56.25*	-15.52	148.76**	33.23**	69.20**	56.60**	15.30	-56.94
III	55.81**	-28.12	-60.35	-30.37	187.46**	75.16**	87.83**	88.04**	41.96**	-115.73**
IV	-30.41**	-80.31**	-144.73**	-3.35	215.45**	46.63**	103.03**	34.01	24.94**	76.71*
100 seed weight (g)										
I	-0.05	-0.20	-0.78**	-0.17	2.60**	0.36**	1.08**	0.52*	0.07	-0.27
II	-0.59**	-0.23*	-0.97**	-0.36	2.29**	-0.12**	0.27**	0.14	-0.17	0.68*
III	0.02	-0.20*	0.08	0.35*	1.70**	0.22**	0.03	-0.27	0.11**	0.46*
IV	0.10	0.58**	-0.62**	-0.35**	1.92**	-0.69**	1.28**	1.32**	-0.24**	-2.01**

N.B. :*,**significant at 5% and 1% level of significance, respectively.

I. Gurjari x IR – 28, II. NAUR-1 x Danteshwari III. GAR-13 x RP-Bio-226, IV. GAR - 13 x Pusa sugandha-5

Table 2: Estimates of Simple Scaling Test and gene effects Grain length, Grain breadth, L:B ratio, Grain yield per plant, Straw yield per plant and Harvest Index for in four crosses of rice

Cross	Gene effect									
	Scaling Test				Six parameters model					
	A	B	C	D	m	D	h	i	j	L
Grain length (mm)										
I	-0.12*	-0.29**	-0.33	-0.03	9.42**	0.16**	0.11*	-0.08	0.08	0.49
II	-0.13	-0.60**	-0.02	0.49*	9.55**	0.16**	-0.20	-0.70**	0.23**	1.43**
III	-0.58**	-0.02	0.04	0.10	7.75**	-0.30**	-0.57	-0.65*	-0.28*	1.26*
IV	-1.62**	-0.03	-3.08**	-0.84	8.39**	-2.04**	2.11*	1.42	-0.79**	0.24
Grain breadth (mm)										
I	0.04	-0.24**	-0.89**	-0.11	2.65**	0.46**	1.03**	0.69**	0.14**	-0.49*
II	0.15	0.19**	0.01	0.29**	2.46**	0.30**	0.61**	0.33**	-0.02	-0.67**
III	-0.003	0.17**	-0.23**	-0.09	2.25**	0.01	0.61**	0.40**	-0.08*	-0.57**
IV	0.02	-0.50**	0.28**	0.32**	2.34**	0.39**	-0.59**	-0.76**	0.26**	1.24**
L:B ratio										
I	-0.10	0.12	0.76**	0.02	3.53**	-0.49**	-1.09**	-0.74**	-0.111	0.72*
II	-0.25*	-0.72**	-0.23	-0.45**	3.87**	-0.38**	-1.07**	-0.74**	0.23**	1.71**
III	-0.24*	-0.28*	0.30**	-0.12	3.43**	-0.14	-1.11**	-0.84**	0.02	1.37**
IV	-0.29**	1.49**	-1.07*	-1.01*	3.59**	-1.71**	1.79**	2.27**	-0.89**	-3.47**
Grain yield per plant (g)										
I	-6.02**	-4.57	-17.58**	-3.39	22.62**	2.23**	12.33**	6.98*	-0.72	3.61
II	0.32	0.05	19.73**	14.57**	26.67**	2.58**	-14.65**	-19.36**	0.13	18.99**
III	-0.027	-0.16	-6.87**	-3.34**	15.88*	3.33**	19.40**	6.68**	0.06	-6.49**
IV	-4.40*	4.54	9.36*	5.59**	27.04**	-2.81**	-8.30**	-9.22**	-4.47*	9.08*
Straw yield per plant (g)										
I	-1.90	-3.36*	-4.85*	-0.68	25.07*	5.35*	1.32	-0.41	0.73	5.68
II	-9.41*	3.65	10.35**	7.02**	33.84**	-2.06	-13.97**	-15.81**	-6.68**	21.27**
III	-1.57	-5.44**	-12.70**	-5.56	28.12**	4.11**	6.47	5.68*	1.93	1.33
IV	0.05	-5.96**	3.52*	-3.35*	31.94**	2.36**	-14.58**	-9.42**	3.00**	15.33**
Harvest Index (%)										
I	1.31	2.57*	-6.88	0.20	43.50**	0.64	14.41**	10.77*	-0.63	-14.66**
II	7.82**	-2.90	12.55**	10.03**	44.02**	4.68**	-3.87	-7.63**	5.36**	2.71
III	1.07	5.26**	4.36**	-0.98**	40.06**	1.91**	15.89**	1.96**	-2.09**	-8.29**
IV	-4.53*	9.36**	6.13	7.93**	45.85**	-4.78**	3.56	-1.30	-6.95**	-3.53

N.B. :*,**significant at 5% and 1% level of significance, respectively.

I. Gurjari x IR – 28, II. NAUR-1 x Danteshwari III. GAR-13 x RP-Bio-226, IV. GAR - 13 x Pusa sugandha-5

Table 3: Estimates of Simple Scaling Test and gene effect for Chlorophyll content and Photosynthetic rate in four crosses of rice

Cross	Gene effect									
	Scaling Test				Six parameters model					
	A	B	C	D	m	d	h	i	j	L
Chlorophyll content at panicle initiation stage										
I	1.25	-1.34	-22.5**	-9.86	36.63**	2.67	23.82**	22.42*	1.29	-22.33**
II	0.86	-2.96*	-13.80**	-6.74**	4.15**	0.62	11.85**	11.70**	1.91*	-9.59*
III	-0.18	2.11	-7.23*	-1.82	35.54**	-0.32	10.95**	9.16*	-1.15	-11.08**
IV	-3.86**	-4.39*	-1.80	0.34	38.69**	-1.47	-5.22*	-6.46**	0.26	14.72**
Chlorophyll content at flowering stage										
I	-7.01*	-6.36**	-23.31**	-4.69**	28.68**	6.62**	16.90**	9.94**	-0.32	3.43
II	-0.59	1.60*	-5.35**	-0.87	24.06**	3.25**	8.17**	6.36**	-1.10*	-7.38**
III	6.95**	3.37**	-14.80**	-8.96**	25.34**	1.46*	23.50**	25.12**	1.79*	-35.44**
IV	-2.12*	-1.86	-19.70**	-7.14**	28.75**	-1.49	18.41**	15.70**	-0.13	-11.71**
Photosynthetic rate at panicle initiation stage ($\mu\text{mol}/\text{m}^2/\text{s}$)										
I	-0.44	-1.67**	-3.16**	0.17	5.87**	1.89**	2.70**	0.98*	0.61**	1.14
II	6.15**	3.54**	4.53**	2.27**	9.52**	0.67**	5.17**	5.16**	1.30**	-14.86**
III	-0.93*	1.21**	-3.42**	1.25*	8.86**	-1.64**	6.67**	3.70**	-1.07**	-3.99**
IV	1.17**	-0.35	-0.63	0.39	8.57**	-0.06	2.16**	1.45**	0.76**	-2.27**
Photosynthetic rate at flowering stage ($\mu\text{mol}/\text{m}^2/\text{s}$)										
I	0.08	-0.89**	1.97*	5.18**	9.96**	2.31**	1.40	-2.79*	0.48	3.61*
II	-2.38**	-4.75**	-1.63*	0.21	11.06**	-1.02**	-4.48**	-5.51**	1.18**	12.65**
III	0.39	-0.63*	-1.43*	-1.62**	10.25**	0.33*	0.28	1.19*	0.51*	-0.95
IV	0.15	-3.02**	-1.26	-0.25	10.95**	0.91**	-1.22	-1.60*	1.58**	4.46**

N.B. :*,**significant at 5% and 1% level of significance, respectively.

I. Gurjari x IR – 28, II. NAUR-1 x Danteshwari III. GAR-13 x RP-Bio-226, IV. GAR - 13 x Pusa sugandha-5

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