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Research Article

Genetic analysis of yield and its components traits in rice (*Oryza sativa* L.)

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Abstract
The nature of gene interaction in the inheritance of 12 yield and its components traits was studied deploying generation mean analysis following 5 parameter model for parents, F_1, F_2, and F_3generations of four crosses of rice. The results indicated that gene action differs over crosses. In general, most of the traits are governed by non- additive gene action.

Keywords :
Rice, epistasis, gene effects, generation mean analysis.

Introduction

Rice, the world's most important cereal crop, is theprimary source of food and calories for about half of themankind (Khush, 2005). Unlike wheat and corn, rice is almost entirely consumed by humans. It provides 20 *per cent* of the calories and 15 *per cent* of protein consumed by world's population. Besides being the chief source of carbohydrate and protein, it also provides minerals and dietary fibre (Verma*et al*., 2006). It is also a good source of thiamine, riboflavin, and niacin. Every year, rice consumption is increasing at a rate of 1.8%. To meet the growing need of rice consumption, it is estimated that at least 50% rise in the production of rice should be brought about by 2025 (Saharan *et al*., 2004).

Yield is an important economic character and is an outcome of multiplicative interaction of component characters. For breeding high yielding varieties of crop plants, breeders usually face problem of selection of desirable parents. In general, parents are selected on the basis of their *per se* performance, but many times high yielding genotype may/may not transmit its superiority to progeny. Hence, critical choice of parents is most importance, particularly for improvement of complex quantitative characters such as yield and its components. Different mating designs have been used by different workers as an aid in the choice of parents, and to understand their genetic nature. The most commonly used mating designs Diallel and Line x Tester provide estimates of additive and dominance/non-additive components of gene effect in relation to whole population studied. However, partitioning of genetic variance into its all the probable components *i.e*, additive, dominance and all types of epistasis with regard to individual cross is of immense value in formulating an effective and sound breeding programme. Among the common approaches followed to understand the nature of gene effect, generation mean analysis using first degree statistics is an accurate one, and gives detail account of gene effects and quality of the genes carried by the parents.Thus, the present study was carried out to estimate different kinds of gene effects in the inheritance of yield and its related traits through generation mean analysis.

Material and methods

The experimental materials consisted of six parents *viz.*,Gurjari, NWGR-7028, IR-64, IET-20575, GR-7 and NWGR-7064 among which four crosses namely Gurjari × NWGR – 7028, Gurjari × IR – 64, Gurjari × IET – 20575 and GR - 7 × NWGR – 7064 were carried out. The experimental material consisting of four families, each having five generations (P_1, P_2, F_1, F_2, and F_3) was grown in nursery during 15 June, 2012 at Main Rice Research Station, Nawagam in Gujarat. The final experimental material was planted during 15 July, 2012 in compact family block design with three replications, whereas, different generations *viz.*, P_1, P_2, F_1, F_2, and F_3 of each family represented individual experimental unit within family. The individual replication was represented by four family blocks, one row each of P_1, P_2 and F_1, four rows each of F_2 and F_3 generation. Total 12 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 data were recorded on 10 plants per replication in parents and F_1's and 40 plants per replication in F_2's and F_3's for the character days to flowering initiation, plant height (cm), panicle length (cm), number of productive tillers per plant, number of total grains per panicle, test weight of 1000 - grains (g), grain length (mm), grain breadth (mm), L: B ratio, grain yield per plant (g), straw yield per plant (g) and harvest index (%).An individual observation of each generation of each family was considered for statistical analysis.

The recorded observations for each character were subjected to statistical analysis to test the significance of differences among various families and generations of each family. The family differences were tested through complete family block design as reviewed by Panse and Sukhatme (1967); whereas, differences among generations were tested through randomized complete block design as suggested by G. W. Snedecor (1938) and reviewed by Panse and Sukhatme (1967). Means of the different generations were utilized for obtaining the various gene effects. The crosses which showed significant differences among various generations for each of the character under study were subjected to generation mean analysis. For estimation of components of gene effect simple scaling tests (Hayman and Mather, 1955) were applied. The non-significance test of all the simple scaling tests suggests adequacy of additive dominance model; hence, principle gene effects additive and dominance were estimated as per Jinks and Jones (1958) three parameters model (m, $\hat{d}$ and $\hat{h}$). For the families and characters, where in any of the simple scaling test was significant, five parameters (m, $\hat{d}$, $\hat{h}$, $\hat{i}$, and $\hat{l}$) model as suggested by Hayman (1958) was applied to partition gene effect into epistatic components including principle gene effects. However, for confirmation of adequacy of additive dominance model, and to realize presence of higher order interallelic interactions, joint scaling test as suggested by Cavalli (1952) was also applied.

Results and Discussion

Analysis of variance between family comparisons depicted significant differences for all growth attributes except number of productive tillers per plant. Whereas, analysis of variance between progenies within family comparisons depicted significant differences for most of characters except panicle length (cross II) and harvest index (cross III).

The individual scaling test/s and/or ’x^2’ value of joint scaling tests were significant with all the families for all the characters except plant height (cross II), test weight of 1000 - grains (cross IV), grain length (cross II), grain breadth (crosses I, III and IV), Grain length : grain breadth ratio(cross III), straw yield per plant (cross I) and harvest index (cross IV) indicating inadequacy of additive dominance model and possibility for the presence of inter-allelic gene interactions in the inheritance of these traits (Table. 1).

A perusal of five parameter model suggested by Hayman (1958) indicated that additive effect ($\hat{d}$) was significant for all the character except for harvest index in cross I, for plant height and panicle length in cross II, for harvest index in cross III and none of the character in cross IV. The results of present study are in akin with findings of Lokaprakash*et al.*(1991), Chakraborty*et al*. (1994), Robin (1997), Dhanakodi and Subramanian (1998), Singh (2002), Vanaja*et al.* (2003), Senthilkumar(2011) and Roy and Senapati (2011) as they reported importance of additive gene effects.While dominance effect ($\hat{h}$) was significant for all the characters except for plant height, panicle length, test weight of 1000 grains, grain length and grain breadth in cross I, for days to flowering initiation in cross II, for days to flowering initiation, number of productive tillers per plant, grain length, grain breadth, Grain length : grain breadth ratioand grain yield per plant in cross III and for days to flowering initiation, number of productive tillers per plant, number of total grains per panicle, grain length, grain breadth, L:B ratio, grain yield per plant and straw yield per plant in cross IV. However all the genetic components were significant for the traits number of productive tillers per plant, number of total grains per panicle, Grain length : grain breadth ratioand grain yield per plant in the cross I, for number of total grains per panicle, Grain length : grain breadth ratioand grain yield per plant in the cross II, for number of total grains per panicle in the cross III and none of character in the cross IV (Table. 1).

Among the components of epitasis, additive × additive ($\hat{i}$) interaction was significant and important in all the crosses for number of total grains per panicle and grain yield per plant. Dhanakodi and Subramanian (1998) and Roy and Senapati (2011) for grain yield, reported similar results. Whereas, dominance × dominance ($\hat{l}$) was significant in all the crosses for number of total grains per panicle. These results are in close agreement with earlier findings of Khaleque*et al.* (1978) and Manna *et al*. (2002). The higher magnitude of estimates of dominance × dominance interaction as compared to additive × additive interaction for grain yield and their components which corroborated with the observation of Chauhan *et al.* (1993), Kumar *et al* (2007), who reported the importance of all the two types interactions in the inheritance of different traits.

Considering the sign of dominance ($\hat{h}$) and dominance × dominance ($\hat{l}$), the nature of epistasis was identified as duplicate in majority of the crosses for most of the yield and its component traits except for plant height, grain breadth, Grain length : grain breadth ratioand straw yield per plant in cross I, for plant height, number of productive tillers per plant, grain length, grain breadth, L:B ratio, grain yield per plant, straw yield per plant and harvest index in cross II, for days to flowering, plant height, number of productive tillers per plant, grain length, grain breadth, Grain length : grain breadth ratioand grain yield per plant in cross III and for test weight of 1000 grains, grain breadth, grain yield per plant and harvest index in cross IV. Duplicate epistasis as observed in most of the crosses for majority of the characters may result in decreased variation in F_2 and subsequent generations and may decrease heterosis and also hinder the pace of progress through selection (Singh *et al.*, 2006).

The present study demonstrates the importance of additive, dominance and epistatic gene effects in the inheritance of grain yield and their attributing traits. Hence, selection in the early segregating generations may not give desirable recombinants. This may possibly be overcome by delaying the selection to later segregating generations when the dominance and epistasis disappear and resorting to intermatingof segregants followed by recurrent selection. Delogu*et al*. (1998) suggest recurrent selection as a basic breeding approach in autogamous crops. Diallel selective mating design suggested by Jenson (1970) can also be adopted, which will promote more recombination.

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Table 1. Estimates of Simple Scaling Test and gene effects for various traits in four crosses of rice.

Cross	Scaling Test		Gene effect Five parameters model					Three parameters model			'x^2'at 2 d.f.	Types of epistasis
	C	D	m	$\hat{d}$	$\hat{h}$	$\hat{i}$	$\hat{l}$	m	$\hat{d}$	$\hat{h}$		
Days to flowering initiation												
I	3.70	11.08**	91.51**	1.97**	-6.80**	-2.84*	9.84	-	-	-	36.33**	D
II	4.93	6.50*	100.42**	-4.73**	-3.14	-12.98**	2.09	-	-	-	14.38**	D
III	-10.06**	-9.97**	91.15**	-1.90**	1.70	1.17	0.13	-	-	-	48.89**	-
IV	12.60**	8.85**	96.11**	0.68*	3.02	-2.43*	-5.00	-	-	-	51.76**	D
Plant height (cm)												
I	16.55**	13.07**	112.36**	5.46**	-0.06	4.96*	-4.64	-	-	-	28.86**	-
II	2.30	5.10	-	-	-	-	-	166.71**	0.57	6.17**	1.44	-
III	-10.03**	-2.42	108.76**	4.97**	7.87*	9.87**	10.15	-	-	-	3.68	-
IV	1.23	6.50*	114.15**	-4.48**	-4.68*	-13.09**	7.02	-	-	-	40.41**	D
Panicle length (cm)												
I	1.23*	2.59**	20.68**	-0.68**	-0.49	-2.89**	1.80	-	-	-	26.27**	D
II	0.91	5.78**	20.99**	0.12	-3.92**	-3.45**	6.49**	-	-	-	35.75**	D
III	3.19**	4.06**	21.84**	-1.81**	-2.23**	5.81**	1.15	-	-	-	26.76**	D
IV	0.26	-3.89**	25.18**	-0.87*	4.85**	0.89	-5.54*	-	-	-	8.23*	D
No. of productive tillers per plant												
I	-4.10*	5.57**	8.47**	-1.66**	-2.31*	-4.43**	12.89**	-	-	-	25.61**	D
II	-4.60*	-0.72	9.00**	0.98*	2.79**	1.68*	5.18	-	-	-	9.17*	-
III	-1.90	2.85*	9.04**	0.70**	0.55	-0.81**	6.33	-	-	-	6.13*	-
IV	-5.20**	-3.77**	8.13**	-1.63**	-0.29	-1.62	1.91	-	-	-	33.05**	D

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

.I. Gurjari × NWGR - 7028 II. Gurjari × IR - 64 III. Gurjari × IET - 20575 IV. GR - 7 × NWGR - 7064

Table 1. Contd...

Cross	Scaling Test		Gene effect Five parameters model					Three parameters model			‘x^2’at 2 d.f.	Types of epistasis
	C	D	m	$\hat{d}$	$\hat{h}$	$\hat{i}$	$\hat{l}$	m	$\hat{d}$	$\hat{h}$		
					No. of total grains per panicle							
I	47.60**	23.17**	134.50**	10.67**	21.55**	13.82**	-32.58**	-	-	-	53.24**	D
II	78.73**	81.63**	137.88**	7.87**	-9.97*	-25.57*	3.87*	-	-	-	83.64**	D
III	84.43**	95.10**	136.43**	9.71**	-19.38**	-29.89**	14.22**	-	-	-	337.11**	D
IV	81.63**	55.02**	137.34**	-10.33**	7.79	-43.74**	-35.49	-	-	-	19.88**	D
					Test weight of 1000 – grains (g)							
I	2.67	10.02**	25.19**	1.65**	-2.35	-2.93*	9.80	-	-	-	21.93**	D
II	7.49**	6.21**	24.58**	2.26**	2.57**	1.62	-1.69**	-	-	-	11.51**	D
III	-2.14	-4.72*	24.64**	3.19**	4.01*	9.18**	-3.44	-	-	-	3.97	D
IV	-1.64	-1.60	-	-	-	-	-	19.35**	2.62**	1.69*	1.64	-
					Grain length (mm)							
I	1.31**	1.34**	9.51**	0.70**	-0.07	0.73**	0.03		-	-	32.95**	D
II	0.53	0.30	-	-	-	-	-	9.90**	-0.51**	-0.58*	2.18	-
III	1.09*	0.86*	9.61**	-0.36**	-0.29	-1.11**	-0.32	-	-	-	11.50**	-
IV	0.69	1.03*	9.25**	0.47**	-0.39	0.38	0.45	-	-	-	10.07**	D
					Grain breadth (mm)							
I	-0.42	-0.12	-	-	-	-	-	2.64**	0.14**	0.05	4.12	-
II	-0.76**	-0.64**	2.37**	0.38**	0.36**	1.06*	0.16	-	-	-	30.93**	-
III	0.31	0.39	-	-	-	-	-	2.53**	0.40**	-0.05	5.46	-
IV	-0.07	-0.15	-	-	-	-	-	2.23**	0.26**	0.01	1.17	-

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

.I. Gurjari × NWGR - 7028 II. Gurjari × IR - 64 III. Gurjari × IET - 20575 IV. GR - 7 × NWGR - 7064

Table 1. Contd...

Cross	Scaling Test		Gene effect Five parameters model					Three parameters model			'x^2'at 2 d.f.	Types of epistasis
	C	D	m	$\hat{d}$	$\hat{h}$	$\hat{i}$	$\hat{l}$	m	$\hat{d}$	$\hat{h}$		
L:B ratio												
I	1.28**	0.91*	3.80**	0.07*	-0.13**	-0.25**	-0.49**	-	-	-	24.32**	-
II	1.38**	1.15**	4.18**	-0.77**	-0.95**	-2.08**	-0.31**	-	-	-	28.51**	-
III	-0.14	-0.07	-	-	-	-	-	3.87**	-0.74**	0.11	0.12	-
IV	0.41	0.77*	4.21**	-0.27**	-0.33	-0.99**	0.48	-	-	-	8.21*	D
Grain yield per plant												
I	14.92**	13.25**	26.10**	2.03**	0.30*	-2.27*	-2.23*	-	-	-	15.67**	D
II	32.97**	20.38**	29.46**	1.89*	-0.68*	-4.31*	-16.79*	-	-	-	74.45**	-
III	26.03**	17.76**	28.94**	1.14*	-3.14	-5.23*	-11.02	-	-	-	55.32**	-
IV	23.48**	16.81**	26.93**	-2.60**	-2.07	-12.51**	-8.89	-	-	-	60.21**	-
Straw yield per plant												
I	5.32	4.16	-	-	-	-	-	24.58**	14.81*	4.24**	4.89	-
II	1.61	7.12*	28.06**	2.19*	4.53*	-0.09**	7.34	-	-	-	6.49*	-
III	8.43**	6.96**	25.85**	2.60**	5.13**	1.97	-1.96**	-	-	-	14.05**	D
IV	16.56**	18.41**	31.04**	-2.28**	-1.83	-14.08**	2.46		-	-	67.60**	D
Harvest Index												
I	3.01	11.90**	48.75**	0.25	-1.54**	-6.93**	11.85*	-	-	-	10.22**	D
II	18.57**	27.50**	57.52**	4.08**	9.19**	-7.07	11.9*	-	-	-	62.01**	-
III	10.68**	10.73**	52.75**	-2.05	-6.94**	-9.47**	0.07	-	-	-	9.66**	D
IV	4.44	4.52	-	-	-	-	-	44.46**	2.82**	3.86**	3.59	-

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

.I. Gurjari × NWGR - 7028 II. Gurjari × IR - 64 III. Gurjari × IET - 20575 IV. GR - 7 × NWGR - 7064