

Research Article**Generation mean analysis for yield and quality traits in F₂ and F₃ generation of rice (*Oryza sativa* L.)****K. Subbulakshmi, N. Shunmugavalli and A. Muthuswamy**Department of Plant Breeding & Genetics, Agricultural College & Research Institute,
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Abstract

The experimental material consisted of five generations (P₁, P₂, F₁, F₂ and F₃) obtained from two crosses using four parents laid out in a randomized block design with three replications to study the generation mean analysis for eleven characters viz., plant height, number of productive tillers per plant, panicle length, days to 50% flowering, number of grains per panicle, 1000 grain weight, hulling percentage, milling percentage, length breadth ratio, amylose content and single plant yield. In (ACK 09009 × ADT 43) the characters like 1000 grain weight, hulling percentage, milling percentage and amylose content were governed by dominance and dominance × dominance gene effects whereas length breadth ratio, amylose content and single plant yield were governed by additive and additive × additive gene effects. In (IR 8 × ASD 16) characters like plant height, number of grains per panicle, 1000 grain weight, hulling percentage, milling percentage and amylose content were predominantly governed by additive and additive × additive gene action. The duplicate dominant epistasis was observed for the traits number of productive tillers per plant, number of grains per panicle, 1000 grain weight, hulling percentage, milling percentage, amylose content and single plant yield. The presence of complementary type of epistasis was noticed for plant height, panicle length, days to fifty per cent flowering, 1000 grain weight, length breadth ratio and amylose content.

Key words

Generation mean analysis, epistasis, additive and dominance

Introduction

Rice is the premier food crop of the world, contributing to 73 per cent of total calorie intake of the population. Self sufficiency and stability in rice production were made possible by development of high yielding varieties. To sustain this self sufficiency and to meet out the demand created by ever increasing population, the production and productivity must be raised yet again. Close observations on the yield performance of high yielding varieties have revealed that the realized yield in such varieties is showing a plateauing trend (Pingali, 1990). This situation warrants the development of innovative technologies to improve rice productivity.

Materials and methods

The present investigation was carried out at Agricultural college and Research institute, Killikulam, Tamil Nadu Agricultural University, Tuticorin District, Tamil Nadu from 2012 to 2014. An LxT mating design involving 14 female and 4 male parents was constituted. Out of 56 two cross combinations viz., ACK 09009 × ADT 43 and IR 8 × ASD 16 alone were selected for the current study based on yield performance and quality parameters.

Result and discussion

Generation mean analysis, a first degree statistics, is a simple but useful technique for characterizing gene effects for a polygenic character (Hayman, 1958) and determines the presence & absence of

non-allelic interactions. The greatest merit of generation mean analysis is that it helps in the estimation of epistatic gene effects namely additive × additive (i), additive × dominance (j) and dominance × dominance (l). The most commonly used design Line × Tester analysis fails to detect the epistasis. The nature of gene action governing the inheritance of yield and its components was therefore studied using generation mean analysis. The generation mean analysis was carried out in selected two crosses obtained from the Line × Tester testing programmes. The variation among the means of different generation in all the eleven characters studied suggesting the usefulness of the estimation of additive, dominance and epistatic interaction. Significant differences among five generation means were noticed for plant height, number of productive tillers per plant, panicle length, days to fifty per cent flowering, number of grains per panicle, 1000 grain weight, hulling percentage, milling percentage, amylose content and single plant yield.

The C, D scaling test for almost all the characters in the two crosses showed that atleast one or both were found significant indicating the presence of non-allelic interaction in the inheritance of the characters under study. However the characters days to fifty per cent flowering, length breadth ratio and single plant yield of cross 2 showed non-significant values for both C and D scales indicating the non-interacting mode of inheritance. Any one or both the scaling tests were found to be

significant in all the traits indicating the presence of epistasis.

The type of epistasis was determined as complementary when dominance (h) and dominance \times dominance (l) gene effects have same sign and duplicate epistasis when the sign was different. Hence, the present study shows that significant additive and epistatic effects exist in this population. Although their presence may vary from cross to cross.

One or both C and D scaling was found significant for all the traits except days to fifty per cent flowering, length breadth ratio and single plant yield in cross 2 (Table 1). Both the crosses exhibiting non-allelic interaction for inheritance of almost all the traits studied. In general, the interaction effect together i.e., additive \times additive (i) and dominance \times dominance (l) found in higher magnitude than the combined main effects of additive (d) and dominance (h) effects for all the traits in both the crosses.

Studies on gene effects in generation mean analysis revealed that additive gene effect (d) was significant in cross 1 for the traits plant height, number of productive tillers per plant, days to fifty per cent flowering, length breadth ratio, amylose content and single plant yield (Table 2). These results indicated that there exist scope for direct selection for grain yield and its contributing traits. Additive effect for number of productive tillers per plant was reported by Robin (1997), Kalita and Upadhaya (2000b) and Kumar *et al.* (2007). In cross 2 significant additive effect was noticed for the traits plant height, days to fifty per cent flowering, number of grains per panicle, 1000 grain weight, hulling percentage, milling percentage, length breadth ratio, amylose content and single plant yield (Table 2). Anbumalarithi (2005) reported additive gene effect for days to first flowering.

The dominance gene effect (h) was significant in cross 1 for the traits 1000 grain weight, hulling percentage, milling percentage and amylose content whereas in the case of cross 2 it was observed significant effect for the traits 1000 grain weight, hulling percentage and milling percentage. The dominant effect was non-significant in both the crosses for the traits plant height, number of productive tillers, panicle length, days to fifty per cent flowering, number of grains per panicle, length breadth ratio and single plant yield (Table 2). Dominance gene effect for number of productive tillers plant was earlier reported by Koodalingam (1994), Kumar *et al.* (2007), Patil *et al.* (2003) and Priya (2003).

The additive \times additive (i) interaction effect was significant in cross1 for the traits 1000 grain

weight, hulling percentage, milling percentage, amylose content and single plant yield but in the case of cross 2 the significant effect was noticed for the traits plant height, panicle length, number of grains per panicle, 1000 grain weight, hulling percentage, milling percentage and amylose content (Table 2). These results were in conformity with Vaithilingam (1995) for the trait number of productive tillers per plant, Robin (1997) for the trait number of grains per panicle, Kumar *et al.* (2007), and Robin (1997), Yogameenakshi (2002).

The dominance \times dominance (l) interaction effect had significant effect in cross 1 for the traits number of productive tillers per plant, number of grains per panicle, 1000 grain weight, hulling percentage, milling percentage, length breadth ratio and amylose content whereas in the case of cross 2 the traits *viz.*, number of productive tillers per plant, panicle length, 1000 grain weight and amylose content were observed significant (l) effect (Table 2). Similar results were earlier reported for number of productive tillers (Koodalingam, 1994 and Vaithilingam, 1995); number of grains per panicle (Robin, 1997), 1000 grain weight (Mahalingam, 2003) and for grain yield (Kumar *et al.*, 2007).

The dominance (h) and dominance \times dominance (l) had opposite sign in cross 1 for the traits number of productive tillers per plant, number of grains per panicle, 1000 grain weight, hulling percentage, milling percentage and single plant yield (Table 2). It indicated the presence of duplicate dominance epistasis. In the cross 2 the predominance of duplicate epistasis was noticed from opposite sign of (h) and (l) for the expression of plant height, number of grains per panicle, hulling percentage, milling percentage and amylose content.

In cross 1 the traits plant height, panicle length, days to fifty per cent flowering, length breadth ratio and amylose content showed the presence of complementary type of epistasis whereas in the case of cross 2 the complementary type of epistasis was recorded for the traits number of productive tillers per plant, panicle length and 1000 grain weight (Table 2). These results are in conformity with the findings of Chauhan (1993).

It could be noted that the presence of additive, dominance, additive \times additive and dominance \times dominance interaction effects were present along with either duplicate dominant epistasis or complementary recessive epistasis for grain yield and most of its contributing traits. Hence, selection in the early segregating generations may not give desirable recombinants. Therefore selection may be delayed to later segregating generations when the dominance and epistasis disappear and resorting to intermating of segregants followed by recurrent selection.

Simple selection procedures or pedigree breeding method is sufficient to harness additive gene action. But the presence of dominance gene action in most of the characters warrants postponement of selection to later generations after effecting crosses. Heterosis breeding procedures are effective in harnessing dominance gene action to the full extent.

Both additive and dominance gene actions play major role in several characters. In such circumstances biparental mating design or reciprocal recurrent selection can be followed for further recombination of alleles to produce desirable segregants. These methods can also be well adopted in order to harness the epistatic interactions by way of breaking the undesirable linkages. Diallel selective mating system proposed by Jensen (1970) could also be followed to break such undesirable linkages between two or more genes and to produce desirable recombinants.

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Table 1. Scaling test of qualitative and quantitative traits of two crosses in rice

Crosses / scales	ACK 09009 × ADT 43	IR 8 × ASD 16
Plant height		
C	24.75 ± 7.85**	15.19 ± 7.64**
D	17.99 ± 7.39**	4.97 ± 5.25
No. of Productive Tillers		
C	-6.04 ± 2.22**	-11.77 ± 2.11**
D	0.89 ± 2.20	-2.69 ± 2.20
Panicle length		
C	3.15 ± 1.43**	-15.29 ± 2.06**
D	1.28 ± 1.32	-7.55 ± 1.58**
Days to 50% flowering		
C	7.72 ± 5.42	-1.22 ± 2.06
D	7.24 ± 3.34**	1.04 ± 1.64
No. of grains /panicle		
C	98.80 ± 17.43**	1.55 ± 18.37
D	4.60 ± 14.98	33.20 ± 15.45**
1000 grain weight		
C	1.69 ± 1.98	12.81 ± 2.37**
D	5.48 ± 1.43**	2.75 ± 0.89**
Hulling percentage		
C	35.93 ± 4.09**	-6.37 ± 2.96**
D	-8.92 ± 3.31**	-12.65 ± 2.71**
Milling percentage		
C	31.90 ± 3.47**	-5.35 ± 2.48**
D	-6.23 ± 2.80**	-10.63 ± 2.27**
Length breadth ratio		
C	-0.74 ± 0.13**	0.06 ± 0.09
D	-0.13 ± 0.12	-0.06 ± 0.07
Amylose content		
C	21.36 ± 0.66**	14.37 ± 0.38**
D	13.67 ± 0.61**	1.89 ± 0.50**
Single plant yield		
C	24.82 ± 10.33**	-3.83 ± 12.39
D	26.16 ± 9.44**	12.61 ± 11.09

**Significant at 1% level



Table 2. Genetic components of generation mean for qualitative and quantitative traits in rice

Genetic effects	ACK 09009 × ADT 43	IR 8 × ASD 16	Genetic effects	ACK 09009 × ADT 43	IR 8 × ASD 16
Plant height			Hulling Percentage		
(m)	113.22 ± 1.90**	99.26 ± 1.87**	(m)	73.79 ± 0.69**	63.93 ± 0.33**
(d)	1.00 ± 0.43 **	-4.60 ± 0.14**	(d)	-0.36 ± 0.98	4.51 ± 0.17**
(h)	-8.34 ± 5.69	6.14 ± 4.46	(h)	5.51 ± 2.19**	8.27 ± 2.05**
(i)	-5.87 ± 5.69	-9.98 ± 4.97**	(i)	11.21 ± 2.92**	16.40 ± 1.80**
(l)	-9.01 ± 17.54	-13.62 ± 15.83	(l)	-59.81 ± 7.04**	-8.37 ± 5.61
No. of productive tillers			Milling percentage		
(m)	16.29 ± 0.46**	15.72 ± 0.50**	(m)	62.72 ± 0.59**	53.70 ± 0.28**
(d)	-0.67 ± 0.23**	0.26 ± 0.41	(d)	-0.30 ± 0.82	3.79 ± 0.15**
(h)	-1.06 ± 1.63	2.22 ± 1.55	(h)	4.68 ± 1.86**	6.94 ± 1.72**
(i)	-2.94 ± 1.58	0.36 ± 1.67	(i)	8.86 ± 2.47**	13.78 ± 1.51**
(l)	9.24 ± 4.77**	12.11 ± 4.69**	(l)	-50.85 ± 5.98**	-7.04 ± 4.71**
Panicle length			Length breadth ratio		
(m)	24.48 ± 0.32**	23.91 ± 0.31**	(m)	2.58 ± 0.02**	2.50 ± 0.01**
(d)	-0.20 ± 0.22	0.26 ± 0.45	(d)	0.64 ± 0.01 **	0.21 ± 0.02**
(h)	-0.79 ± 0.96	1.95 ± 1.08	(h)	0.16 ± 0.09	0.09 ± 0.05
(i)	-0.73 ± 1.01	3.02 ± 1.46**	(i)	0.05 ± 0.09	-
(l)	-2.49 ± 3.00	10.31 ± 3.44**	(l)	0.80 ± 0.27**	-
Days to 50% flowering			Amylose content		
(m)	100.26 ± 1.32**	98.57 ± 0.48**	(m)	34.55 ± 0.03**	31.07 ± 0.06**
(d)	4.13 ± 0.37**	0.56 ± 0.21**	(d)	-4.25 ± 0.29**	2.64 ± 0.09**
(h)	-1.54 ± 2.95	-0.39 ± 1.29	(h)	-2.56 ± 0.13**	0.28 ± 0.33
(i)	4.72 ± 3.43	-	(i)	-14.06 ± 0.32**	6.42 ± 0.34**
(l)	-0.64 ± 10.94	-	(l)	-10.26 ± 0.46**	-16.64 ± 0.85**
No. of grains /panicle			Single plant yield		
(m)	201.43 ± 3.37**	188.02 ± 3.96**	(m)	68.09 ± 2.14**	68.29 ± 2.44**
(d)	3.00 ± 2.39**	-10.26 ± 3.23**	(d)	-3.33 ± 1.36**	-8.20 ± 2.44**
(h)	14.86 ± 11.22	-14.47 ± 11.29	(h)	-9.18 ± 7.02	-6.34 ± 7.79
(i)	19.40 ± 11.39	-42.40 ± 12.31**	(i)	-19.97 ± 7.15**	-
(l)	-125.60 ± 34.39**	42.19 ± 36.38	(l)	1.78 ± 21.26	-
1000 grain weight			**Significant at 1% level		
(m)	21.76 ± 0.21**	24.31 ± 0.20**	(m) = mid parental value, (d) = additive effect, (h) = dominance effect, (i) = additive x additive,		
(d)	-0.69 ± 0.53	-1.58 ± 0.31**	(l) = dominance x dominance		
(h)	-3.19 ± 0.85**	-1.86 ± 0.88**			
(i)	-4.77 ± 1.42**	-2.86 ± 1.09**			
(l)	5.05 ± 2.80**	-13.41 ± 3.35**			