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Genetics of yield and quality characters in rice (*Oryza sativa* L.)

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Abstract

The material comprised of five generation of two crosses namely AURC 8 × ADT 36 and AURC 10 × ADT 43. Among the parents, ADT 43 was found to be good performer for grain length, grain L/B ratio, kernel L/B ratio and grain yield per plant. The cross AURC 8 × ADT 36 exhibited high *per se* performance for grain length, grain breadth, kernel length, kernel breadth and grain yield per plant. From generation mean analysis, the grain length, grain L/B ratio, kernel length, kernel breadth and grain yield per plant were predominantly, controlled by additive gene effects followed by additive × additive interaction effects. Hence simple pedigree breeding procedure is suggested for improvement of these characters.

Keywords: Generation mean analysis, Gene action

Introduction

Rice is the staple food for the largest number of people on Earth. The global rice production has to be enhanced by 70 per cent by 2050 to meet the demand of growing population (FAO, 2009; NRRI, 2013). The current rice production of India is 105 million tons per annum that needs to be enhanced to 150 million tons by coming 30 years (NRRI, 2013). To achieve the target yield level, rice varieties with a yield advantage of about 20 per cent over widely grown varieties must be developed with higher yield potential. Information on genetic parameters of yield and its component characters can help in deciding an appropriate breeding methods. Therefore, gene effects governing yield and quality related traits in two crosses of rice (*Oryza sativa* L.) were estimated following Mather (1949), Hayman (1958) and Cavalli (1952).

Materials and Methods

The five generations namely P₁, P₂, F₁, F₂ and F₃ of two crosses namely, AURC 8 × ADT 36 and AURC 10 × ADT 43 were raised in RBD, replicated thrice during December 2013 at Plant Breeding Farm, Faculty of Agriculture, Annamalai University. A spacing of 20 cm between rows and 15 cm between plants was followed. Data from 60 plants in P₁, P₂ and F₁ generations, 600 plants in F₂ generations, 300 plants in F₃ generations were recorded for both the crosses for seven characters namely, grain length, grain breadth, grain L/B ratio, kernel length, kernel breadth, kernel L/B ratio and grain yield per plant. The biometrical techniques to detect and estimate the additive (d), dominance (h) and genetic interactions *viz.*, additive × additive (i), dominance × dominance (l) from five generations have been analysed according to Mather (1949), Hayman (1958) and Jinks and Jones (1958) using Windostat.

Results and Discussion

The prime objective of hybridization between any two parents is to combine the desirable characters dispersed among them to compensate deficiencies found in one parent by the other. The progenies of these crosses will throw all possible combinations to promote yield. Therefore, the parents selected should inherit the characters to their progenies. The choice of parent was based on the general principle that the parents under selection should have a high *per se* performance for the desirable traits. For a systematic breeding programme, it is necessary to identify the parents which can be the exploited for genetic improvement through hybrid progenies. For which, the breeders are in absolute need of high mean value which is considered as a main criterion for effective selection for ever.

Among the parents studied in the present investigation, ADT 43 showed promise for grain.

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yield per plant, grain length, grain L/B ratio and kernel L/B ratio. AURC 8 recorded high kernel length and kernel breadth. ADT 36 recorded high grain breadth. Another thing, forwarding the F_1 by mean basis is necessary. F_1 of AURC 8 \times ADT 36 showed high grain yield per plant, grain length, grain breadth, kernel length and kernel breadth. The present investigation revealed that the parent AURC 8 and ADT 36 contributed their expression of characters to their progenies (Table 1).

The scaling test indicated either C or D significantly deviated from zero for all the characters in both crosses. In cross AURC 10 \times ADT 43 both C and D significantly for grain length, grain L/B ratio, kernel breadth, kernel L/B ratio and grain yield per plant indicating the presence of epistatic interactions. Five parameter model fitted for separating epistasis.

The estimate of gene effects revealed additive gene effects (d) for grain length, grain L/B ratio, kernel length, kernel breadth and grain yield per plant in the cross

AURC 10 \times ADT 43. Similar results were obtained by earlier workers (Singh *et al.*, 2007, Muhammad Yussouf Saleem *et al.*, 2009, Gnanamalar and Vivekanandan, 2013). Dominance gene effects (h) were significant and positive for grain L/B ratio in the cross AURC 8 \times ADT 36 (Table 2).

Among the epistatic effects, additive \times additive were found positive and significant for all the characters except grain breadth in the cross AURC 10 \times ADT 43. Similar results were obtained by Sabesan (2005), Thirugnanakumar *et al.* (2007), Mahalingam and Nadarajan (2010) and Chamundeswari *et al.* (2013) as well as dominance \times dominance gene effects were

observed positive and significant for kernel breadth and kernel L/B ratio.

The cross AURC 8 \times ADT 36 showed negative and significant additive \times additive effect for grain length, grain breadth, kernel breadth, kernel L/B ratio and grain yield per plant. While the same cross observed positive and significant dominance \times dominance effect for kernel L/B ratio.

Among seven characters studied, grain length, kernel breadth, kernel L/B ratio and grain yield per plant showed opposite signs of (h) and (l) indicating duplicate type of epistasis in both crosses. The trait grain breadth, grain L/B ratio and kernel length observed complementary type of gene interaction as same signs of (h) and (l) in the cross AURC 10 \times ADT 43. The cross AURC 8 \times ADT 36 showed duplicate gene action for grain breadth, grain L/B ratio and kernel length. This is in concurrence with the earlier reports by Nayak *et al.* (2007), Gnanamalar and Vivekanandan (2013) and Yadav *et al.* (2013) indicating the presence of duplicate gene action for grain length, kernel breadth, kernel L/B ratio and grain yield per plant. From the foregoing discussion, it is concluded that the most important yield contributing traits as well as yield *per se* were governed by predominantly additive gene action followed by additive \times additive type of interaction effect. For grain yield per plant along with quality characters *viz.*, grain length, grain L/B ratio, kernel length and kernel breadth were controlled by additive effect and additive \times additive interaction effects in the cross AURC 10 \times ADT 43. Simple pedigree breeding procedure can be used for improvement of these traits.

Table 1: Mean \pm SE performance of five generations for yield and yield components characters

Characters	Crosses	P ₁	P ₂	F ₁	F ₂	F ₃
Grain length (mm)	1	8.00 \pm 0.09	8.05 \pm 0.04	8.19 \pm 0.07	8.24 \pm 0.04	8.29 \pm 0.04
	2	7.98 \pm 0.15	8.14 \pm 0.14	8.03 \pm 0.08	7.88 \pm 0.04	7.81 \pm 0.04
Grain breadth (mm)	1	3.00 \pm 0.14	3.07 \pm 0.07	3.04 \pm 0.10	3.06 \pm 0.01	3.09 \pm 0.01
	2	2.00 \pm 0.05	2.03 \pm 0.02	2.00 \pm 0.01	2.08 \pm 0.06	2.11 \pm 0.02
Grain L/B ratio	1	2.64 \pm 0.12	2.62 \pm 0.05	2.70 \pm 0.11	2.63 \pm 0.01	2.56 \pm 0.01
	2	3.98 \pm 0.12	4.04 \pm 0.10	4.02 \pm 0.06	3.86 \pm 0.02	3.75 \pm 0.03
Kernel length (mm)	1	5.98 \pm 0.12	5.03 \pm 0.18	6.03 \pm 0.07	6.12 \pm 0.03	6.18 \pm 0.03
	2	5.46 \pm 0.13	5.75 \pm 0.09	6.02 \pm 0.16	6.16 \pm 0.03	6.21 \pm 0.03
Kernel breadth (mm)	1	2.38 \pm 0.13	2.05 \pm 0.05	2.02 \pm 0.04	2.12 \pm 0.03	2.20 \pm 0.05
	2	1.42 \pm 0.03	1.44 \pm 0.02	1.98 \pm 0.03	2.02 \pm 0.01	2.06 \pm 0.01
Kernel L/B ratio	1	2.48 \pm 0.24	2.46 \pm 0.06	2.99 \pm 0.07	3.06 \pm 0.01	3.11 \pm 0.02
	2	3.82 \pm 0.07	3.94 \pm 0.09	3.03 \pm 0.09	3.10 \pm 0.01	3.14 \pm 0.01
Grain yield per plant (g)	1	27.14 \pm 0.51	28.23 \pm 0.17	32.49 \pm 0.18	33.14 \pm 0.14	33.89 \pm 0.13
	2	23.43 \pm 0.35	33.60 \pm 0.08	32.10 \pm 0.21	31.17 \pm 0.19	31.83 \pm 0.17

Cross 1 : AURC 8/ADT 36

Cross 2 : AURC 10/ADT 43

Table 2: Scaling test and gene effects for yield and yield components characters in rice

Genetic parameters	Grain length		Grain breadth		Grain L/B ratio	
	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2
C	0.53 \pm 0.25*	-0.66 \pm 0.31*	0.09 \pm 2.07*	0.29 \pm 0.07*	-0.14 \pm 0.27	-0.62 \pm 0.23*
D	0.63 \pm 0.22*	-0.64 \pm 0.29*	0.17 \pm 0.17*	0.25 \pm 0.05	-0.28 \pm 0.15*	-0.74 \pm 0.20*
Gene effects						
(m)	8.24 \pm 0.04*	7.88 \pm 0.04*	3.06 \pm 0.01*	2.08 \pm 0.06*	2.63 \pm 0.01*	3.86 \pm 0.02*
(d)	-0.02 \pm 0.05	0.28 \pm 0.15*	-0.03 \pm 0.08	-0.01 \pm 0.02	0.01 \pm 0.06	0.40 \pm 0.10*
(h)	-0.16 \pm 0.15*	-0.08 \pm 0.10	-0.09 \pm 0.08*	-0.13 \pm 0.01	0.23 \pm 0.09*	-0.03 \pm 0.08
(i)	-0.38 \pm 0.18*	0.15 \pm 0.23*	-0.16 \pm 0.18*	-0.14 \pm 0.06	0.18 \pm 0.17	0.33 \pm 0.18*
(l)	0.13 \pm 0.45	0.02 \pm 0.46	0.10 \pm 0.31	-0.05 \pm 0.07	-0.18 \pm 0.33	-0.16 \pm 0.30*
	D	D	D	C	D	C

* - Significant at 5 per cent level

** - Significant at 1 per cent level

D - Duplicate C - Complementary

Cross 1 : AURC 8/ADT 36

Cross 2 : AURC 10/ADT 43

Table 2: Scaling test and gene effects for yield and yield components characters in rice

Genetic parameters	Kernel length		Kernel breadth		Kernel L/B ratio		Grain yield per plant	
	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2
C	1.41 ± 0.29*	1.39 ± 0.37	0.01 ± 0.17*	1.26 ± 0.08*	1.32 ± 0.30	-1.42 ± 0.22*	12.21 ± 0.87	3.45 ± 0.95*
D	1.47 ± 0.25	1.31 ± 0.20*	0.13 ± 0.14	1.34 ± 0.06*	1.38 ± 0.26*	-1.40 ± 0.13*	13.91 ± 0.82*	7.95 ± 0.88*
Gene effects								
(m)	6.12 ± 0.03*	6.16 ± 0.03*	2.12 ± 0.03*	2.02 ± 0.01*	3.06 ± 0.01*	3.10 ± 0.01*	33.14 ± 0.14*	31.17 ± 0.19*
(d)	-0.14 ± 0.07*	0.47 ± 0.11*	-0.01 ± 0.02	0.16 ± 0.07*	0.01 ± 0.12	-0.06 ± 0.06	-0.54 ± 0.27*	5.08 ± 0.18*
(h)	-0.22 ± 0.11	-0.22 ± 0.14*	-0.28 ± 0.03*	-0.13 ± 0.04*	-0.18 ± 0.05*	-0.15 ± 0.07*	-2.43 ± 0.48*	-1.14 ± 0.62*
(i)	-0.93 ± 0.21	0.20 ± 0.19*	-0.70 ± 0.05*	0.24 ± 0.16*	-0.68 ± 0.28*	0.57 ± 0.12*	-8.32 ± 0.74*	5.44 ± 0.62*
(l)	0.08 ± 0.36	-0.10 ± 0.51	0.16 ± 0.12	0.10 ± 0.13*	0.08 ± 0.21*	0.02 ± 0.26*	2.26 ± 1.45	6.00 ± 1.90
	D	C	D	D	D	D	D	D

* - Significant at 5 per cent level
 ** - Significant at 1 per cent level
 D - Duplicate
 C - Complementary

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