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Genetic architecture of grain quality characters in rice (*Oryza sativa* L.)

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ABSTRACT

Analysis of generation mean was carried out in six crosses of rice viz., ADT 41 / ADT 46, ADT 41 / CO 47, ADT 41 /TKM 9, ADT 41/ Jeeragasamba, ADT 41/ACM 98003 and ADT 41/AS 90033 for hulling percentage, milling percentage, head rice recovery, kernel length, kernel breadth, kernel L/B ratio, kernel length after cooking, linear elongation ratio and alkali spreading value. The scaling test showed the presence of epistatic interactions for all the nine grain quality traits studied. Milling percentage and linear elongation ratio were governed by additive, dominance and epistatic interactions of additive x additive, dominance x dominance and duplicate epistasis. Hulling percentage was governed by additive, dominance and duplicate type. Head rice recovery was under the control of additive, dominance, dominance x dominance and duplicate epistasis. Kernel length and kernel breadth were predominantly under the control of additive, dominance, additive x dominance and duplicate gene interactions. Kernel L/B ratio and kernel length after cooking were influenced by additive, additive x dominance and duplicate type. Dominance, additive x additive and duplicate type of gene actions influenced alkali spreading value. The other four grain quality traits viz., water uptake, volume expansion ratio, amylose content and gel consistency were under the control of non-additive gene action. To explore both additive and non-additive type of gene action it was suggested to postpone the selection to later generation in pedigree breeding programme.

Key words: Generation mean, quality, crosses, additive, dominance.

INTRODUCTION

Rice is a premium food grain crop and is often the main source of calories and principal food of millions of people. With a rising living standard, the demand for high quality rice is increasing. Super fine varieties of rice with aromatic grains, superior cooking and eating characteristics get a premium price in the market. Basmati fetches comparatively a higher price, which is not affordable by rural consumers and those with low income. Therefore breeding for quality has to be emphasized to bring out fine grained rice fetching optimum price, which will be easily within the reach to the rural consumers. Hence the rice grain quality has become a necessity for the acceptance of varieties to be released.

Among the quality characters, cooking quality inclusive of milling quality parameters like hulling, milling, head rice recovery etc. are of particular interest, as a very large proportion of the world's rice is consumed as cooked rice [1]. Incorporation of these characters into high yielding semi dwarf varieties is essential in this era of quality breeding.

For the improvement of yield and quality characters, a sound breeding methodology has to be formulated which in turn rests on the correct understanding of the gene action involved. Many reports are available on the nature of gene action governing the yield and its component traits while studies on the genetics of milling and cooking qualities are limited. Therefore, an attempt was made in the present study to unravel the genetic architecture of some of the grain quality traits of rice.

MATERIALS AND METHODS

The present investigation was carried out using five cultivars of rice *viz.*, ADT 41- extra long slender grain type, ADT 46 – long slender, CO 47– medium slender, Jeeragasamba- short slender and TKM 9 – short bold and two advanced cultures *viz.*, ACM 98003 – medium bold and AS 90033 – long bold which were selected based on grain type. Crossing block was raised with seven parents at the research farm of Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai. Seven parents were crossed in a half diallel fashion (excluding reciprocals) and 21 cross combinations were effected. The parent ADT 41 was superior to rest of the parents with respect to grain quality characters besides being considerably a good yielder. Hence, out of 21 crosses, six crosses involving ADT 41 as the female parent *viz.*, ADT 41 / ADT 46, ADT 41 /CO 47, ADT 41/TKM 9, ADT 41/ Jeeragasamba, ADT 41/ ACM 98003 and ADT 41/ AS 90033 were chosen for generation mean analysis. Six generations *viz.*, P₁, P₂, F₁, F₂, B₁ and B₂ for each of the six cross combinations were constituted.

All the six generations in each of the six crosses were raised in a randomized block design with three replications. Single seedling was planted per hill adopting a spacing of 20 x 15 cm and recommended crop management practice was done. Thirty seedlings in all generations were planted except F₂ with 200 seedlings per replication in each cross. Ten plants from each of the parents and F₁ and thirty plants from B₁ and B₂ and 75 plants from F₂ per replication were randomly sampled to record the observations. The seed samples from the selected plants were hulled and milled using Satake type THU 35A dehusker and Satake type TM O5 miller, respectively. Percentage of hulling, milling and head rice recovery were calculated as per the method suggested [2]. Kernel length, kernel breadth, kernel L/B ratio and kernel length after cooking were estimated by standard procedures. Linear elongation ratio was calculated [3] and the alkali spreading value was estimated [4]. The mean values and the variance of mean were computed for all six generations *viz.*, P₁, P₂, F₁, F₂, B₁ and B₂ for each cross. The adequacy of the data for a simple additive - dominance model was tested utilizing the A, B and C scaling tests [5] and [6]. Genetic components of generation mean *viz.*, m, (d), (h), (i), (j) and (l) were estimated following the six parameter model [7].

RESULTS AND DISCUSSION

The means of each generation were calculated from the replicated trial and the scaling test was applied to study the adequacy of additive dominance model. The estimates of scaling tests and genetic components of generation mean for quality characters are presented in Table 1 and 2, respectively. The scaling test was significant for one scale in all the crosses for all the quality traits studied, indicating inadequacy of simple additive dominance model.

In the case of hulling percentage, the mid parental value (m) was significant for all the crosses and the additive effect (d) was significant in four crosses *viz.*, ADT 41 /ADT 46, ADT 41 / TKM 9, ADT 41 / Jeeragasamba and ADT 41/AS 90033. The crosses ADT 41 / TKM 9 and ADT 41/ Jeeragasamba showed significant dominance (h) and additive x additive (i) effects. Significant dominance x dominance (l) interaction effect was observed in ADT 41 / CO 47, ADT 41 / TKM 9 and ADT 41 / ADT 41/ Jeeragasamba. The unlike signs of (h) and (l) revealed the duplicate epistasis. Since both additive, dominance x dominance and duplicate gene interactions were important for this trait, improvement may be possible by delaying selection to later generations.

For milling percentage and head rice recovery, the parameter (m) was significant in all the crosses. However, the additive effect (d) was significant in four crosses *viz.*, ADT 41 / ADT 46, ADT 41 / TKM 9, ADT 41 / ACM 98003 and ADT 41 / AS 90033. Significant dominance effect (h) was observed in four crosses. Both the (i) and (l) interactions were significant only in fourth and fifth crosses. Duplicate epistasis was evident from the opposite signs of (h) and (l) in all the crosses. Additive effect of head rice recovery was significant in all crosses except ADT 41/AS 90033. Additive x additive and dominance x dominance interaction effects were significant in third and fourth crosses, respectively. The (h) and (l) effects were significant in four crosses and showed opposite signs in all

crosses which exhibited the presence of duplicate gene interaction. Thus the results suggest that improvement for milling percentage and head rice recovery can be achieved through reciprocal recurrent selection.

Table 1. Scaling test of quality characters of six crosses in rice

Crosses	ADT 41/ ADT 46	ADT 41/ CO 47	ADT41 / TKM 9	ADT 41/ Jeeraga samba	ADT 41/ ACM 98003	ADT 41 / AS 90033
Scales	1	2	3	4	5	6
Hulling percentage						
A	2.04	-17.97*	-7.60*	0.28	4.99*	5.05*
B	-6.17*	-15.77*	-2.72	-8.67*	1.75	4.11
C	-4.59	-21.37*	-1.72	2.27	6.88*	6.21*
Milling Percentage						
A	-1.29	-14.25	-7.52*	-1.24	0.79	5.34
B	-12.04*	-12.43*	-0.39	-8.47*	-3.50	7.59*
C	-8.31*	-1.76	2.92	2.87	-7.56*	-2.04
Head rice recovery						
A	0.28	-3.45*	-5.46*	-2.52	-9.65*	-5.08*
B	-2.09	0.60	-8.90*	-5.76*	-9.21*	-1.73
C	9.70	-4.92	-7.43	14.73*	-8.96*	4.23
Kernel length						
A	-0.57	-0.79	-1.95*	-1.43*	-1.49*	-1.85*
B	0.09	-0.03	-0.01	1.33*	0.28	-0.07
C	-2.46*	-1.31*	-1.66*	-0.16	0.37	-2.40*
Kernel breadth						
A	-0.02	0.37*	0.36*	0.09	0.47*	0.34*
B	-0.14*	0.13	-0.12	0.29*	0.07	-0.16
C	-0.09	0.27*	0.11	0.21	0.23*	1.36
Kernel L/B ratio						
A	-0.31	-1.00*	-1.53*	-0.95*	-1.48*	-1.47*
B	0.24	-0.20	0.04	0.33	-0.02	0.10
C	-1.03*	-1.04*	-1.21*	-0.43	-0.37	-1.94*
Kernel length after cooking						
A	-0.51*	-2.41*	-2.82*	-2.95*	-1.24*	-1.31*
B	-0.77*	-1.59*	-1.02*	1.01*	0.68*	-0.43
C	-2.89*	-3.43*	-4.64*	-2.29*	0.47	-4.03*
Linear elongation ratio						
A	0.04	-0.18*	-0.01	-0.14*	0.14*	0.22*
B	-0.13*	-0.25*	-0.17*	-0.20*	0.04	-0.05
C	0.16*	-0.19*	-0.38*	-0.33*	-0.03	-0.05
Alkali spreading value						
A	-0.66*	-0.11	-0.96*	-0.58*	-0.12	0.41*
B	-0.53*	0.60*	-0.28*	0.34*	0.17	0.69*
C	-0.98*	0.13	-2.52*	-1.48*	-0.92*	-2.21

* - Significant at 5 % level

In the case of kernel length, kernel breadth and kernel L/B ratio, the values of (m) and (d) were significant in all the crosses. For kernel length, (h) was significant in four crosses viz., ADT 41/ADT 46, ADT 41/TKM 9, ADT41/ACM 98003 and ADT 41/ AS 90033. Significant (j) effect was observed in four crosses and the crosses ADT 41/TKM 9, ADT 41/ACM 98003 and ADT 41/AS 90033 showed significant (l) interaction. The duplicate epistasis was also found in all the crosses. The additive, additive x additive, dominance x dominance and duplicate interactions for this trait was observed [8]. Dominance effect (h) and interaction effect (l) of kernel breadth were significant in three crosses viz., ADT 41/CO 47, ADT 41/ Jeeragasamba and ADT 41/ACM 98003. The additive x dominance interaction was significant in four crosses in addition to duplicate epistasis. It was inferred that kernel breadth was under the control of additive, additive x dominance and epistatic interactions. In the case of kernel L/B ratio, all crosses except ADT 41 / ADT 46 and ADT 41/CO 47 exhibited significant (j) interaction effect. Two crosses viz., ADT 41/TKM 9, ADT 41/ACM 98003 showed significant (h), (j) and (l) effects. It was clear that kernel breadth and kernel L/B ratio was controlled by additive, additive x dominance and duplicate gene interactions and improvement for these characters may be possible by postponement of selection to later generations in pedigree breeding programme.

The estimates of (m), (d) and (j) effects for kernel length after cooking were significant in all the crosses except (j) effect in ADT 41/ADT 46 and ADT 41/CO 47. In addition to this, the cross ADT 41/AS 90033 also showed

significant (h) and (i) effects. Duplicate epistasis is also important for this character. Additive, dominance and epistatic interaction of all three kinds was reported for this trait [9].

For linear elongation ratio, (m), (d) and (i) effects were significant in all the six crosses studied except (i) effect in ADT 41/ Jeeragasamba. The crosses ADT 41/CO 47, ADT 41/TKM 9, ADT 41/ACM 98003 and ADT41/AS 90033 exhibited significant (h) effects. The additive x dominance (j) interaction was significant in three crosses whereas significant (l) effect was noticed in five crosses. This revealed that, improvement for this character through direct selection is not easy. Recurrent selection utilizing suitable male sterility system may be more suitable for improvement of this trait.

For alkali spreading value, (m) was significant in all the crosses and (d) effect was significant in three crosses, ADT 41/CO 47, ADT 41/ Jeeragasamba and ADT 41/ ACM 98003. The dominance effect (h) and (i) interaction effects were significant in four crosses. The (h) and (l) effects had dissimilar signs in all the crosses which conferred the duplicate epistasis. Thus, this character was under the influence of dominance, additive x additive and duplicate interaction. An additive and additive x additive interaction effect for this trait was reported [10].

Table 2. Genetic components of generation mean for quality characters in rice

Crosses / Genetic effects	ADT 41/ ADT 46	ADT 41/ CO 47	ADT41/ TKM 9	ADT 41/ Jeeraga samba	ADT 41/ ACM 98003	ADT 41/ AS 90033
	1	2	3	4	5	6
Hulling percentage						
m	76.11*	84.73*	84.81*	85.09*	75.95*	73.45*
(d)	-2.35*	1.05	-2.23*	-2.53*	-1.06	-1.30*
(h)	-4.92	-53.62	-24.29*	-27.64*	7.15	12.74
(i)	0.46	-12.36	-8.60*	-10.66*	-0.15	2.94
(j)	4.11*	-1.10	-2.44	4.48*	1.62	0.47
(l)	3.67	46.10*	18.92*	19.05*	-6.59	-12.10
Milling percentage						
m	76.80*	91.39*	78.57*	80.71*	65.87*	55.72*
(d)	-2.74*	0.14	-1.89*	-1.14	-2.03*	-1.97*
(h)	-26.32*	-70.67*	-24.14	-31.04*	7.24	40.87*
(i)	-5.03	-24.93*	-10.83*	-12.59*	4.85	14.98*
(j)	5.37*	-0.91	-3.57	3.61	2.15	-1.12
(l)	18.36*	51.61*	18.74*	22.30*	-2.14	-27.91*
Head rice recovery						
m	65.64*	53.37*	61.31*	78.14*	58.99*	63.49*
(d)	-2.14*	-3.43*	-2.35*	-3.34*	2.60*	-0.78
(h)	-25.44	-0.71	-31.79*	-56.40*	-27.65*	-22.63*
(i)	-11.51	2.07	-6.93	-23.01*	-9.90*	-11.04*
(j)	1.18	-2.03*	1.72	1.62*	-0.22	-1.68
Kernel length						
m	5.42*	6.39*	6.97*	6.02*	8.71*	6.61*
(d)	0.54*	1.12*	1.29*	1.84*	0.86*	0.89*
(h)	2.70*	-0.15	-3.24*	-0.21	-4.57*	-1.67*
(i)	1.98*	0.49	-0.30	0.06	-1.58*	0.48
(j)	-0.33	-0.38	-0.97*	-1.38*	-0.89*	-0.89*
(l)	-1.50	0.33	2.26*	0.04	2.79*	1.44*
Kernel breadth						
m	2.15*	1.83*	2.12*	1.62*	1.95*	3.40*
(d)	-0.20*	-0.16*	-0.35*	0.09*	-0.36*	-0.30*
(h)	-0.18	0.95*	0.31	1.05*	1.07*	-2.37
(i)	-0.07	0.23	0.13	0.17	0.31*	-1.18
(j)	0.06	0.12*	0.24*	-0.10	0.20*	0.25*
(l)	0.23	-0.73*	-0.37	-0.55*	-0.85*	1.00
Kernel L/B ratio						
m	2.65*	3.57*	3.41*	3.54*	4.43*	2.76*
(d)	0.61*	0.81*	1.06*	0.86*	0.91*	0.85*
(h)	1.25	-1.72	-2.26*	-1.55	-3.84*	-0.45
(i)	0.97*	-0.16	-0.28	-0.18	-1.12*	0.56*
(j)	-0.27	-0.40	-0.78*	-0.64*	-0.73*	-0.79*
(l)	-0.90	1.36	1.77*	0.79	2.62*	0.82*

Crosses / Genetic effects	ADT 41/ ADT 46	ADT 41/ CO 47	ADT41/ TKM 9	ADT 41/ Jeeraga samba	ADT 41/ ACM 98003	ADT 41/ AS 90033
	1	2	3	4	5	6
Kernel length after cooking						
m	9.50*	10.91*	9.37*	8.82*	11.72*	8.56*
(d)	0.39*	1.18*	1.23*	2.25*	0.77*	0.53*
(h)	2.03	-5.04*	-2.25	-0.85	-2.59	2.90*
(i)	1.61*	-0.57	0.80	0.35	-1.03	2.29*
(j)	0.13	-0.41	-0.90*	-1.98*	-0.96*	-0.44*
(l)	-0.33	4.57*	3.04*	1.59	1.59	-0.55
Linear elongation ratio						
m	1.76*	1.75*	1.35*	1.56*	1.29*	1.33*
(d)	-0.06*	-0.08*	-0.11*	-0.10*	-0.07*	-0.12*
(h)	-0.41	-0.83*	0.37*	-0.29	0.66*	0.78*
(i)	-0.25*	-0.24*	0.20*	-0.02	0.22*	0.22*
(j)	0.09*	0.04	0.08*	0.03	0.05	0.13*
(l)	0.34*	0.66*	-0.02	0.37*	-0.40*	-0.40*
Alkali spreading value						
m	2.86*	1.83*	1.36*	1.09*	1.38*	1.32*
(d)	0.02	0.46*	0.02	0.33*	0.30*	0.02
(h)	-1.64*	0.47	1.31*	2.09*	1.24	2.59*
(i)	-0.21	0.36	1.27*	1.24*	0.97*	1.31*
(j)	-0.07	-0.36*	-0.34*	-0.46*	-0.14	-0.14
(l)	1.40*	-0.85	-0.02	-1.00*	-1.01	-2.41*

m = mid parental value, *(d)* = additive effect, *(h)* = dominance effect, *(i)* = additive x additive, *(j)* = additive x dominance, *(l)* = dominance x dominance

* - Significant at 5 % level

CONCLUSION

From the foregoing discussion on gene action for quality traits, it was clear that additive, dominance and epistatic genetic components are important for the expression of characters studied. In such situations simple pedigree method of selection alone is ineffective. Probably this could be one of the reasons for the inability of rice breeders to effectively combine desired quality characteristics. To overcome this problem, biparental mating followed by selection of desired recombinants from the segregating population is desirable. Since considerable amount of dominance effect was also present for most of the traits, selection of superior segregants has to be postponed to later generations until homozygosity is achieved.

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