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Gene effects for certain Physical quality traits and Grain yield in Rice

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Abstract : Genetic analysis of certain physical quality traits of grain in four selected rice crosses indicated that milling recovery in Chandan/Sambamahsuri, head rice recovery in IR-64/Rasi and length/breadth ratio in all the crosses studied were under the control of additive gene action indicating the possibility of true breeding progenies for these parameters. However, the inheritance of traits like kernel length and breadth was influenced by both additive and non -additive type gene actions. Importance of all types of epistatic interactions were found to be governing the inheritance of grain yield. Postponement of selection of desirable segregants, to advanced generations could be suggested to exploit such complex genetic makeup.

Key words: Milling recovery, Head rice recovery, Length/breadth ratio, epistatic gene effects.

Introduction

A paradigm shift in the rice breeding strategies from quantity centered approach to quality-oriented efforts was inevitable, since India has not only become self sufficient in food grain production but also is the second largest exporter of quality rice in the world. Evolving cultures which suit consumer demands of international and national markets has become imperative. Recent studies on genetics of quality characters interpret polygenic control and non-allelic interactions while, earlier studies explained these traits on the basis of simple Mendelian inheritance (Pandey *et al.* 1985). The present investigation on generation mean analysis by six parameter model (Jinks and Jones, 1958) in four crosses revealed significance of A,B,C scaling tests suggesting that all physical quality characters and grain yield were influenced by epistatic gene effects.

Material and Methods

The material comprised of parents (P_1 and P_2), F_1, F_2, Bc_1, and Bc_2 generations of four crosses viz; Chandan/Sambamahsuri, Sambamahsuri/ Tellahamsa, Erramallelu/Rasi and IR-64/Rasi. Parents Chandan, Erramallelu, IR-64 and Tellahamsa possessed long slender grain, while Sambamahsuri had medium slender grain and Rasi was medium bold type. Sets of these six family progenies were raised in randomized block design with three replications. All the F_1s, parents and backcrosses were planted in three rows of 1.5 metre length and the F_2s were planted in ten rows. A spacing of 20 x 15 cm was adopted. Observations were recorded on five random plants from each of the parents and F_1S while, 20 plants from Bc_1, Bc_2 and 30 F_2 plants in each replication. Recommended agronomic, cultural and plant protection measures were adopted in conducting the experiment.

Estimation of traits like milling recovery and headrice recovery was done using a paddy sample of 10 g. Satake huller and Kett type T_2 polisher were used for hulling and milling of rice samples. Dial micrometer was employed to generate data on grain dimensions. For grain yield per plant; matured panicles of five plants were individually harvested, threshed, cleaned and dried to 12-14 per cent moisture level. The grain yield was recorded in grams.

Table 1. Estimates of generation means and gene effects for physical quality characters and grain yield

Generation	Milling recovery				Head rice recovery			
	Chandan/ Sambamahsuri	Sambamahsuri/ Tellahamsa	Erramallelu/ Rasi	IR-64/ Rasi	Chandan/ Sambamahsuri	Sambamahsuri/ Tellahamsa	Erramallelu/ Rasi	IR-64/ Rasi
P_1	72.04+0.093	67.22+0.056	70.37+0.168	67.64+0.117	50.29+0.098	64.37+0.156	42.29+0.099	54.12+0.129
P_2	69.32+0.095	72.86+0.072	72.38+0.089	72.23+0.235	65.71+0.104	58.70+0.123	51.71+0.101	51.81+0.107
F_1	65.60+0.116	72.86+0.052	73.12+0.208	73.50+0.218	48.26+0.162	58.41+0.115	58.84+0.061	62.41+0.119
F_2	62.79+0.051	69.96+0.084	70.38+0.039	67.78+0.032	45.17+0.049	51.30+0.063	46.03+0.023	58.63+0.109
BC_1	61.71+0.050	64.59+0.059	68.58+0.092	66.49+0.083	47.24+0.139	60.34+0.116	41.73+0.115	53.24+0.190
BC_2	60.37+0.112	69.41+0.079	69.99+0.029	69.74+0.068	51.76+0.053	55.47+0.092	44.07+0.061	50.54+0.109
Parameter								
A	0.032**+0.179	0.020**+0.142	0.105**+0.324	0.089**+0.298	0.113**+0.337	0.091**+0.302	0.066**+0.257	0.176**+0.419
B	0.073**+0.269	0.033**+0.182	0.054**+0.233	0.121**+0.348	0.048**+0.219	0.062**+0.248	0.029**+0.169	0.073**+0.270
C	0.114**+0.337	0.133**+0.365	0.233**+0.483	0.275**+0.525	0.163**+0.404	0.156**+0.395	0.043**+0.208	0.274**+0.523
m	62.797**+0.051	69.960**+0.084	70.380**+0.039	67.777**+0.032	45.167**+0.049	51.300**+0.063	46.033**+0.023	58.630**+0.109
d	1.343**+0.123	-4.813**+0.099	-1.410**+0.096	-3.243**+0.108	-4.513**+0.149	4.867**+0.148	-2.340**+0.129	2.707**+0.219
h	-12.095**+0.347	-9.003**+0.398	-2.650**+0.337	4.930**+0.357	7.593**+0.398	23.287**+0.417	-0.698**+0.291	-17.512**+0.634
i	-7.020**+0.320	-11.827**+0.392	4.393**+0.248	1.367**+0.251	17.333**+0.357	26.413**+0.388	-12.533**+0.275	-26.160**+0.617
j	-0.015+0.139	-1.990**+0.109	-0.407*+0.135	-0.947**+0.169	3.193**+0.165	2.033**+0.178	2.368**+0.148	1.552**+0.235
l	35.417**+0.595	29.619**+0.539	16.260**+0.618	13.033**+0.679	-2.813+0.719	-18.147**+0.710	52.623**+0.559	50.143**+1.021

Results and Discussion

In the present investigation, the generation mean analysis using six parameter model (Jinks and Jones, 1958) in four crosses revealed significance of A,B,C scaling tests (table 1) suggesting that all the traits (physical quality) and grain yield were influenced by epistatic gene effects. The significant Chi-square for all the traits indicated the inadequacy of six parameter model and pointed to the involvement of higher order interactions in controlling these traits.

For milling recovery it was observed that additive effects were important for Chandan / Sambamahsuri suggesting about the possibility of existence of progenies with higher milling recovery. However dominance component and additive/additive interaction effect was significant in IR-64/Rasi and dominance/ dominance effects were significant for all those crosses studied. The presence of non-additive gene action is expected to restrict the prospects of selection in evolving a pureline with desirable milling recovery. Such situations warrant retention of high degree of heterozygosity in segregating generations through intermating of selected genotypes or by following some form of recurrent selection. Similar signs for (h) and (1) estimates in IR-64/Rasi indicated presence of complimentary gene action and considerable amount of heterosis in this combination for milling recovery. Tomar (1987) indicated the importance of additivity for

Table-1. Contd.

Generation	Kernel length				Kernel breadth			
	Chandan/ Sambamahsuri	Sambamahsuri/ Tellahamsa	Erramallelu/ Rasi	IR-64/ Rasi	Chandan/ Sambamahsuri	Sambamahsuri/ Tellahamsa	Erramallelu/ Rasi	IR-64/ Rasi
P_1	7.51+0.006	5.19+0.003	6.86+0.012	6.97+0.009	1.88+0.005	1.59+0.002	1.56+0.007	1.76+0.005
P_2	5.13+0.006	6.39+0.007	5.94+0.005	5.92+0.004	1.62+0.004	1.86+0.007	2.05+0.008	1.90+0.003
F_1	6.65+0.016	6.08+0.018	6.12+0.023	6.13+0.008	1.91+0.003	2.06+0.011	2.13+0.008	2.17+0.006
F_2	6.64+0.004	5.67+0.004	6.39+0.003	6.39+0.003	1.84+0.001	2.02+0.003	1.96+0.003	2.32+0.003
BC_1	7.00+0.003	5.09+0.005	6.28+0.003	6.39+0.006	1.78+0.003	1.55+0.005	1.57+0.009	1.64+0.009
BC_2	5.09+0.009	5.62+0.004	5.76+0.005	6.05+0.008	1.61+0.006	1.80+0.006	1.94+0.006	1.98+0.002
Parameter								
A	0.0003**+0.018	0.0004**+0.020	0.001**+0.027	0.0003**+0.016	0.0001**+0.008	0.0002**+0.016	0.0004**+0.021	0.0004**+0.019
B	0.0006**+0.024	0.0004**+0.020	0.001**+0.026	0.0003**+0.018	0.0001**+0.007	0.0003**+0.018	0.0003**+0.017	0.0001**+0.008
C	0.001**+0.036	0.002**+0.039	0.003**+0.049	0.001**+0.024	0.0001**+0.010	0.001**+0.026	0.001+0.022	0.0003**+0.017
m	6.440**+0.004	5.670**+0.004	6.390**+0.003	6.397**+0.003	1.843**+0.001	2.017**+0.003	1.957**+0.003	2.320**+0.003
d	1.913**+0.009	-0.527**+0.006	0.513**+0.006	0.337**+0.009	0.167**+0.004	-0.247**+0.008	-0.378**+0.011	-0.347**+0.009
h	-1.262**+0.029	-0.953**+0.027	-1.763**+0.029	-1.017**+0.025	-0.432**+0.010	-1.027**+0.023	-0.477**+0.027	-1.697**+0.023
i	-1.587**+0.024	-1.240**+0.019	-1.480**+0.018	-0.700**+0.023	-0.587**+0.009	-1.360**+0.019	-0.807**+0.025	-2.040**+0.022
j	0.722**+0.010	0.070**+0.007	0.053**+0.009	-0.187**+0.011	0.035**+0.005	-0.113**+0.009	-0.133**+0.021	-0.273**+0.010
l	3.350**+0.052	3.547**+0.046	2.447**+0.055	0.953**+0.045	1.117**+0.019	2.213**+0.041	1.660**+0.049	2.807**+0.042

this trait. Another important milling attribute, head rice recovery was found to be positively influenced by additive effect in IR-64/Rasi and additive/additive interaction was showing enhancing effect in Chandan/Sambamahsuri and Sambamahsuri/Tellahamsa. However, dominance/dominance interaction effects were predominant for crosses Erramallelu/Rasi and IR-64/Rasi. The opposite signs of (h) and (l) indicated duplicate gene action for all crosses indicating hindrance in improvement through selection. In these circumstances procedures capable of exploiting both additive and non -additive gene action would be helpful. Epistatic control for head rice recovery was earlier reported by Tomar (1987).

Importance of both additive and dominance effects for kernel length was reported by Roy and Panwar (1993) and Vivekanandan and Giridharan (1995). They have also indicated the importance of all interaction effects. In the present investigation also additive effects were found to govern the inheritance in all crosses except in Sambamahsuri/Tellahamsa. Among the epistatic types dominance/dominance had higher magnitude in positive direction for all the crosses. As considerable amount of additivity was observed pedigree method of breeding will be rewarding to improve kernel length. Presence of dominance effects in negative direction also necessitates the selection to be postponed to later generations till homozygosity is attained. One or two cycles of

Table-1. Contd.

Generation	Length/breadth ratio				Grain yield/plant			
	Chandan/ Sambamahsuri	Sambamahsuri/ Tellahamsa	Erramallelu/ Rasi	IR-64/ Rasi	Chandan/ Sambamahsuri	Sambamahsuri/ Tellahamsa	Erramallelu/ Rasi	IR-64/ Rasi
P_1	3.99+0.012	3.27+0.004	4.40+0.024	3.97+0.015	18.17+0.162	17.18+0.242	17.85+0.129	17.14+0.055
P_2	3.17+0.009	3.44+0.014	2.91+0.011	3.11+0.008	19.04+0.034	17.20+0.071	15.13+0.099	16.88+0.143
F_1	3.48+0.009	2.96+0.013	2.87+0.008	2.82+0.004	24.34+0.185	29.46+0.171	23.49+0.191	25.12+0.169
F_2	3.50+0.001	2.84+0.002	3.29+0.003	2.78+0.002	16.61+0.039	17.30+0.297	15.16+0.042	24.32+0.021
BC_1	3.93+0.006	3.28+0.014	4.01+0.026	3.91+0.024	15.59+0.055	15.35+0.163	13.52+0.105	16.71+0.054
BC_2	3.15+0.005	3.12+0.012	2.97+0.010	3.05+0.007	5.23+0.071	15.13+0.102	12.17+0.101	16.43+0.112
Parameter								
A	0.0004**+0.019	0.001**+0.031	0.003**+0.057	0.003**+0.051	0.072**+0.269	0.194**+0.441	0.098**+0.3 12	0.043**+0.208
B	0.0003**+0.016	0.001**+0.030	0.001**+0.024	0.0003**+0.016	0.055**+0.235	0.076**+0.276	0.087**+0.295	0.099**+0.3 15
C	0.001**+0.024	0.001**+0.030	0.001**+0.033	0.0004**+0.019	0.188**+0.434	1.595**+1.263	0.201**+0.448	0.145**+0.381
m	3.500**+0.001	2.843**+0.002	3.297**+0.003	2.777**+0.002	16.607**+0.039	17.303**+0.297	15. 160**+0.042	24.320**+0.021
d	0.780**+0.008	0.157**+0.018	1.043**+0.028	0.860**+0.025	0.357**+0.089	0.220+0.193	1.353**+0.146	0.280*+0.124
h	0.078**+0.020	1.033**+0.039	-0.017+0.059	2.095**+0.051	0.952**+0.3 12	4.030**+1.268	-2.252**+0.395	-22.893**+0.322
i	0.173**+0.016	1.433**+0.037	0.767**+0.057	2.813**+0.051	-4.780**+0.237	-8.240**+1.249	-9.253**+0.336	-3 1.000**+0.263
j	0.372**+0.011	0.243**+0.019	0.297**+0.031	0.432**+0.026	0.792**+0.122	0.230+0.230	-0.008+0.167	0.147+0.146
l	-0.223**+0.039	-1.613**+0.078	-1.673**+0.1 16	-4.017**+0.102	29.017**+0.562	40.567**+1.479	37.823**+0.736	48.973**+0.626

intermating among the superior selects would be useful considering higher magnitude of "1". The opposite sign of (h) and (1) for all crosses indicated prevalence of duplicate gene action.

For kernel breadth significant additive and dominance effects and additive/additive interaction effects in negative direction were noticed. This indicates the diminishing effect on expression of kernel breadth which is highly desirable. Preponderance of additivity suggests merit of simple selection procedures for this trait. These results are in accordance with Roy and Panwar (1993), Vivekanandan and Giridharan (1995). The results indicated predominance of duplicate gene action in all the crosses examined. For length/breadth ratio predominance of additive and non-additive epistasis was found in positive direction indicating the enhancing effect. The dominance/dominance type had diminishing effect in all - crosses studied. The additivity suggested that the progenies isolated from these crosses will have high length/breadth ratio. Somrit *et al.*, (1979) reported additive and non-additive gene action for this trait. Presence of duplicate gene action in all crosses except in Erramallelu/Rasi was noticed.

With regard to grain yield per plant additive effects were important for all crosses, dominance effects positively governed the inheritance of yield in Chandan / Sambamahsuri and Sambamahsuri/Tellahamsa. All three types of epistatic interactions were found to be important for all crosses with higher magnitude of dominance/ dominance component. Duplicate epistasis was found in Erramallelu/Rasi and IR-64/Rasi. Similar results were reported by Somrit (1974) and Chauhan *et al.*, (1993). Presence of significant dominance effects combined with duplicate epistasis restricted the scope of simple selection for yield.

In the present investigation digenic interactions were significant for most of the traits in all the four crosses analysed. Epistatic components are supposed to constitute a sizeable part of trait variation in characters influenced by higher estimates of dominance effects. Preponderance of 'h' was noticed for head rice recovery (Chandan/Sambamahsuri, Sambamahsuri/ Tellahamsa) and kernel breadth. For physical quality traits and yield importance of additive, non-additive and epistatic effects were noticed. To exploit such complex genetic makeup selection of desirable segregants may be postponed to advanced generations so that epistatic gene action gets fixed in the segregants.

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