GENETIC AND COMBINING ABILITY ANALYSIS OF GRAIN QUALITY CHARACTERS IN HYBRID RICE

El-Mowafi H. F.
Rice Research and Training Center (RRTC), Sakha, Kafr El-Sheikh Egypt, 33717, Field Crops Research Inst.(FCRI), Agric. Research Center

ABSTRACT

The present investigation was conducted to realize the feasibility of heterosis breeding method using three lines system in rice (CMS, maintainer and restorer lines). The experiments were carried out during 2002, 2003 and 2004 growing seasons at RRTC Farm, Sakha, Kafr El-Sheikh, Egypt. Twelve hybrids obtained from crossing four diverse CMS lines as females with three Egyptian restorer lines were evaluated along with the parents for genotypic variation. The mean squares of the genotypes showed significant values for all studied grainn quality characters at the two years and their combined data, indicating the presence of large variations among them. The interactions of genotypes and parents with years were insignificant for all grain quality characters with the exception of total milled rice % (TMR %) and Head rice %(HR %) which should highly significance mean squares. The interaction of crosses with the years was found to be insignificant for all characters except HR%. In the mean time, the interaction of parents vs. crosses with the years was significant for TMR%, HR%, grain shape and Chalkiness of endosperm (CLK) and insignificant for BR%, Brown rice length (BRL), gelatinization temperature(GT) and amylose content % characters.

The analysis of variances for combining ability revealed significant differences among CMS lines for BR%, BRL%, grain shape, CLK, GT and amylose content %. Therefore, the testers exhibited significant differences for BRL, grain shape and GT. The line x tester (SCA) variance exhibited significant differences at the two years and their combined data for HR% and amylose content % and varied for the rest of grain quality studied characters. The result ,alsoindecated that the parents , IR58025A, IR68885A, Giza 178 R and Giza 182 R were found to have favorable genes for one or more characters along with grain quality. Out of 12 hybrids one hybrid for BR%, two for HR%, one for grain shape and three for low amylose content exhibited significant desirable SCA effects in the two years and their combined data. The superior hybrids for most grain quality characters were SK 2003 H (G. 46A/Giza 178 R), SK2010 H (G. 46A/Giza 182 R) and SK 2011 H (large stigma A/Giza 182 R). The estimates of genetic parameters revealed that additive variance values and relative importance of GCA% were higher than these dominant variance and relative important of SCA% for all grain quality studied characters except in case of BR%.

INTRODUCTION

Hybrid rice has given yield advantage of about 20% over popular conventional varieties and is accepted by the farmers. However, grain quality of rice is of primary importance everywhere, more 80 because rice is consumed hole after cooking (Kumar *et al.*, 1994; Virmani and Zaman, 1998 and Zaman *et al.*, 2003). The main attributes deciding quality are 1) high milling and head rice recovery, 2) grain size, shape and endosperm appearance, and 3) cooking and eating characteristics of grains harvested from F_1 plants are of great concern.

The economic product of rice hybrids is the seed borne on F_1 plants. These are F_2 seeds, and they show genetic segregation for endosperm traits in the grain due to genetic differences among parents. The product that reaches the consumer is therefore basically a bulk of grains segregating for endosperm traits (Kumar *et al.,* 1994). Besides having higher yield potential for general consumer acceptance, it is essential that the hybrids developed should possess good quality characteristics, Some hybrids yielded 15-20% more than prevalent high-yielding inbred varieties but their grain quality did not fined acceptability by consumers. This has prompted the use of the best parental lines for grain quality to overcome quality problems. If parental lines are chosen carefully, grain quality as good as that of any good-quality conventional rice variety can be achieved (Khush *et al.,* 1988).

In most countries long-grain Indica rice, which is soft and non sticky on cooking, is preferred; in others, low amylose short grain japonica rice, which is soft and sticky on cooking, is liked.

The choice of parents, especially for heterosis breeding, should be based on the combining ability test and their mean performances (Yaddav and Murty, 1966). The present investigation was aimed to study the mature of combining ability of four diverse CMS lines, three Egyptian restorer lines and their hybrid combinations for grain quality characteristics in hybrid rice.

MATERIALS AND METHODS

The genetic materials used in this study involved four rice cytoplasmic male sterile (CMS) and their maintainer (B) lines from four diverse cytostrility sources viz., IR58025 A/B (WA), IR68885A/B (Mutant IR62829A), G46A/B (Gambiaca) and large Stigma A/B (Kalinga). In addition, three Egyptian restorer lines viz. Giza 178R, Giza 181R and Giza 182R were also used the obtained 12 F1 hybrids produced through crossing four CMS and three restorer lines are presented in Table 1 these genotypes were evaluated in a randomized blocks design with four replications during the two successive growing seasons of 2003 and 2004. the experiments were conducted at Rice Research and Training Center (RRTC) Farm, Sakha, Kafr El-Sheikh, Egypt. 30-days-old seedlings were transplanted in rows 5.0 m. long, 20cm apart, 20cm spaced and one seedling /hill. One genotype was planted in 7 rows.

All the materials were milled raw and analyzed for grain quality traits. Milling out turn was determined by dehulling 200 g rough rice in a Stake Rice Mill. followed by 45 second polishing in a stake.

Grain Testing Mill. 05. Head rice out turn was determined by separating broken rice. Milled and head rice out turn was expressed as percent. Seeds hulled was used to measure kernel length in mm with Mitutoyo micrometer. Length and shape of brown rice were measured according to IRRI Standard Evaluation (1996) as follow:

Scale (length)
1   Extra long (more than 7.5 mm).
3   Long (6.6 to 7.5).
5   Medium (5.5 to 6.6).

7   Short (5.5 mm or less).
Brown rice shape (BRL)

Scale	Shape	Ratio
1	Slender	Over 3.0
3	Medium	2.1 to 3.0
5	Bold	1.1 to 2.0
9	Round	Less than 1.1

Chalkiness of endosperm (CIK)
Scale (% of kernel area)
0   None
1   Small (less than 10%)
5   Medium (11% to 20%)
9   Large (more than 120)

Table (1): Hybrid rice combinations generated through crossing CMS lines x restorer lines used for the study.

Hybrid name	Parentage
SK2025H	IR58025A/Giza 178R
SK2037H	IR58025A/Giza 181R
SK2049H	IR58025A/Giza 182R
SK2027H	IR68885A/Giza 178R
SK2039H	IR68885A/Giza 181R
SK2051H	IR68885A/Giza 182R
SK2003H	G 46A/Giza 178R
SK2005H	G 46A/Giza 181R
SK2010H	G 46A/Giza 182R
SK2004H	Large Stigma A/Giza 178 R
SK2006H	Large Stigma A/Giza 181R
SK2011 H	Large Stigma A/Giza 182R

Alkali spreading value was classified into three ranges i.e. 1.0-3.00 corresponds to high, 3.0-5.0 corresponds to intermediate and 6.0-7.0 corresponds to low gelatinization temperature (GT). Amylose content was determined by the procedure of Juliano (1971).

The combining ability analysis was carried out as suggested by Kempthorne (1957).

RESULTS AND DISCUSSION

Genotypic variations, analysis of variance and combining ability:

In the two growing seasons of 2003 and 2004, all genotypes were evaluated to study the magnitude of genotypic variations which are presented among them. These genotypes included 19 entries (four cytoplasmic male sterile lines as female, three Egyptian restorer lines as male testers and their 12 F_1 hybrid combinations.

The analysis of variances and combining ability were made for each year and over all two years all studied characters and the results are shown in Table (2).

Table (2): The e stimates of mean squares of ordinarY analysis for grain quality traits in the two years and their combined data.

S.V.	d.F.		BR %			TMR %			HR %			BRL		
	Single	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
Years (Y)		1	-	-	$0.063^{n.s}$	-	-	$2.155^{n.s}$	-	-	21.75*	-	-	$0.007^{n.s}$
Reps/(Y)	3	6	-	-	0.697	-	-	1.145	-	-	1.049	-	-	0.279
Genotypes (G)	18	18	3.306*	4.5911**	6.587**	10.117**	5.398**	12.09**	138.36**	81.175**	211.68**	10.440**	10.557**	20.949**
Parent (P)	6	6	5.643**	6.738**	11.851**	23.667**	12.286**	28.43**	328.12**	179.47**	494.73**	19.560**	20.57**	40.113**
Crosses (C)	11	11	$2.311^{n.s}$	3.794**	4.253**	$1.902^{n.s}$	1.384**	1.889*	22.96**	26.73**	46.03**	6.339**	5.915**	12.189**
P.Vs. (C)	1	1	0.226	$0.474^{n.s}$	$0.677^{n.s}$	19.189**	8.214**	26.256**	269.22**	90.24**	335.59**	$0.835^{n.s}$	1.535**	2.317**
G x Y		18	-	-	$1.310^{n.s}$	-	-	3.425**	-	-	7.855**	-	-	$0.048^{n.s}$
P x Y		6	-	-	$0.530^{n.s}$	-	-	7.523**	-	-	12.86**	-	-	$0.017^{n.s}$
C x Y		11	-	-	$1.852^{n.s}$	-	-	$1.397^{n.s}$	-	-	3.66*	-	-	$0.065^{n.s}$
P.Vs. C x Y		1	-	-	$0.023^{n.s}$	-	-	1.147*	-	-	23.87**	-	-	$0.053^{n.s}$
Lines (GCA)	3	3	$4.250^{n.s}$	4.688*	$7.760^{n.s}$	5.472*	$1.410^{n.s}$	$3.844^{n.s}$	$53.74^{n.s}$	69.35*	117.014*	10.854**	9.299**	20.083**
Testers (SCA)	2	2	$0.771^{n.s}$	$1.271^{n.s}$	0.031*	$0.333^{n.s}$	$0.771^{n.s}$	$0.969^{n.s}$	$5.813^{n.s}$	$14.31^{n.s}$	$17.28^{n.s}$	18.146**	17.063**	35.167**
L x T (SCA)	6	6	$1.854^{n.s}$	4.188**	3.906**	$0.639^{n.s}$	1.576**	$1.219^{n.s}$	13.28**	9.563**	20.13**	$0.146^{n.s}$	$0.507^{n.s}$	$0.583^{n.s}$
L x Y		3	-	-	$1.178^{n.s}$	-	-	$3.038^{n.s}$	-	-	$6.075^{n.s}$	-	-	$0.07^{n.s}$
T x Y		2	-	-	$2.011^{n.s}$	-	-	$0.135^{n.s}$	-	-	$2.843^{n.s}$	-	-	$0.042^{n.s}$
L x T x Y		6	-	-	$2.136^{n.s}$	-	-	$0.996^{n.s}$	-	-	$2.713^{n.s}$	-	-	$0.070^{n.s}$
Error	54	108	1.512	0.487	0.932	1.148	0.351	0.791	4.15	1.135	2.584	0.483	0.323	0.422
GCA/SCA														
C.V %			1.58	0.90	1.24	1.60	0.890	1.33	3.88	2.00	3.04	16.10	13.13	15.04

* and ** significant at 0.05 and 0.01 probability levels, respectively.

J. Agric. Sci. Mansoura Univ., 31 (8), August, 2006

4933

Cont. Table (2):Estimates of the mean squares of ordinaries analysis for grain quality traits in the two years and their combined data.

S.V.	d.F.		Shape			CLK			Gel. Temp.			Amylose content %		
	Single	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
Years (Y)		1	-	-	1.837**	-	-	1.663$^{n.s}$	-	-	0.658$^{n.s}$	-	-	1.240**
Reps/(Y)		6	-	-	0.220	-	-	3.197	-	-	0.798	-	-	0.116
Genotypes(G)	18	18	19.291**	25.08**	43.132**	16.064**	17.649**	32.83**	3.349**	4.501**	7.096**	13.425**	14.523**	27.737**
Parent (P)		6	34.405**	38.226**	72.43**	28.571**	25.65**	53.708**	6.326**	8.000**	14.113**	23.833**	26.726**	50.405**
Crosses (C)		11	41.375**	19.455**	28.96**	10.455**	14.58**	24.428**	2.021**	2.977**	3.829**	8.460**	8.583**	16.785**
P.Vs. (C)		1	15.642**	8.143**	23.18**	2.729$^{n.s}$	3.339$^{n.s}$	0.015$^{n.s}$	0.703$^{n.s}$	0.276$^{n.s}$	0.931$^{n.s}$	5.595**	6.647**	12.220**
G x Y		18	-	-	1.239$^{n.s}$	-	-	0.883$^{n.s}$	-	-	0.754$^{n.s}$	-	-	0.211
P x Y		6	-	-	0.201$^{n.s}$	-	-	0.513$^{n.s}$	-	-	0.213$^{n.s}$	-	-	0.154$^{n.s}$
C x Y		11	-	-	1.870$^{n.s}$	-	-	0.607$^{n.s}$	-	-	1.169$^{n.s}$	-	-	0.258$^{n.s}$
P.Vs. C x Y		1	-	-	0.605*	-	-	6.053*	-	-	0.048$^{n.s}$	-	-	0.022$^{n.s}$
Lines (GCA)		3	17.111*	38.000**	50.22**	36.111**	47.806**	82.847**	4.076*	8.250*	11.149**	27.799**	26.139**	53.372**
Testers(SCA)		2	30.646**	48.250**	77.82**	1.750$^{n.s}$	4.083$^{n.s}$	5.542$^{n.s}$	3.521*	1.000$^{n.s}$	3.260*	1.188$^{n.s}$	3.521$^{n.s}$	4.385$^{n.s}$
L x T (SCA)		6	2.090*	0.583$^{n.s}$	2.045*	0.528$^{n.s}$	1.472$^{n.s}$	1.514$^{n.s}$	0.493$^{n.s}$	1.000$^{n.s}$	0.358$^{n.s}$	1.215**	1.493**	2.622**
L x Y		3	-	-	4.890$^{n.s}$	-	-	1.070$^{n.s}$	-	-	1.177$^{n.s}$	-	-	0.566$^{n.s}$
T x Y		2	-	-	1.076$^{n.s}$	-	-	0.291$^{n.s}$	-	-	1.261$^{n.s}$	-	-	0.324$^{n.s}$
L x T x Y		6	-	-	0.628$^{n.s}$	-	-	0.486$^{n.s}$	-	-	1.135$^{n.s}$	-	-	0.086$^{n.s}$
Error	54	108	0.909	0.873	0.906	1.805	1.963	1.875	0.449	0.574	0.511	0.192	0.176	0.157
GCA/SCA														
C.V %			23.76	21.98	23.17	46.41	44.74	45.83	13.26	15.39	14.34	2.12	2.02	1.91

* and ** significant at 0.05 and 0.01 probability levels, respectively.

This table presented the partitioning of the total variance among genotypes into general combining (GCA) of cytoplasmic male sterile lines (CMS) and restorer lines (R) and specific combining.

The results indicated that the mean squares of genotypes were larger than their corresponding mean squares of the error. Therefore, the results of the F-test indicated that the mean squares of the genotypes showed significant and highly significant values for all studied grain quality characters at the two years and their combined data, indicating the presence of large variations among genotypes. Similarly, the mean squares of years were significant for head rice %, grain shape and amylose content % characters and insignificant for BR%, TMR%, BRL, CLK and GT characters.

The results cleared that the parental lines and the hybrids showed significant and highly significant differences for studied characters at the two years and their combined data except for BR% and TMR% at the first year only that were insignificant. Parents vs. crosses mean squares indicated that the average heterosis aws significant in all hybrids at the two years and their combined data for TMR%, HR%, grain shape, and amylose content %, while was significant at the second year and the combined data for BRL character. On the other hand, the mean squares of parents vs. crosses were found to be insignificant for BR%, CLK and GT characters.

The interactions of genotypes and parents with the two years were insignificant for all grain quality characters with the exception of TMR% and HR% which had highly significant mean squares. The interaction of crosses with the years was found to be insignificant for all studied grain quality characters except for HR% which was significant. In the same time, the interaction of parents vs. crosses with the years was found to be significant for TMR%, HR%, grain shape and CLK and insignificant for BR%, BRL, GT and amylose content % characters. It could be also concluded that the evaluation of potentiality of parents for the expression of heterosis should could be necessarily be conducted over a number of environmental conditions and that genetic diversity alone would not guarantee the expression of heterosis but the suitability of the environmental conditions is required. Similar results were obtained by El-Hissewy (1985), El-Abd (1999) and Moustafa (2000).

The analysis of variances for combining ability given in the Table 2 revealed significant differences among CMS lines for BRL, grain shape, CLK, GT and amylose content % at the two years and their combined data. The results also revealed that the presence significant differences for HR% at the second year and the combined data, significant differences for BR% at the second year and significant differences for TMR% at the first year. In the same time, the testers exhibited significant differences for BRL and grain shape at the two years and their combined data and significant differences for GT at the first year and the combined data. However , some genotypes showed insignificant values were regarded for BR%, TMR%, HR%, CLK and amylose content %. The lines x testers (SCA) obtained highly significant mean squares of lines x testers (SCA) for HR% and amylose content % characters at the two years and their combined data, while showed highly

significant for BR% at the second year and the combined data, highly significant only at the second year for TMR%, significant at the first year and the combined data for grain shape characters and insignificant for all the other studied grain quality characters. These findings of significant values indicated and pronounced markedly different combining ability effects. This might be due to the wide genetic diversity of CMS and restorer lines.

The interactions of years with both types of combining ability, general combining ability (GCA) of lines and testers and specific combining ability (SCA) of lines x testers were found to be insignificant for all studied characters.

For general consumer acceptance, it is essential that the hybrids developed could possess good quality characteristics besides having higher yield potential. Therefore, the hybrids included in this investigation and parental lines, CMS, maintainers and restorer lines have been critically screened for various quality characteristics.

Milling quality is the measure of rough rice performance during milling process. It is the total quality of head and broken grain recovered from unit quality of rough rice mean (Biswas *et al.*, 1992).

The mean performances of the parental lines (CMS, maintainer and restorer lines) and their hybrid combinations for all grain quality characters are presented in Table (3). The results revealed that the CMS lines and their maintainer lines, IR68885A, IR68885B, IR58025A and IR58025B showed the highest mean values for milling quality characters, BR%, TMR% and HR% at the two years and their combined data. However, the restorer lines Giza 182R and Giza 181R showed the highest mean values for these characters. The most desirable mean values were detected by the hybrid. Combinations, IR6885A/Giza 178 (SK2027H), IR58025A/Giza 178R (SK2025 H), IR68885A/Giza 182R (SK 2051 H). However, with higher advantage of grain yield the hybrid combination G46A/Giza 178R (SK2003H) was accepted by the farmers for cooking and eating quality characters and short grain with medium amylose content. Any hybrid with good quality, have head rice recovery of more than 55 percent, intermediate alkali value (4-5) and translucent grain without chalkiness. Head rice recovery for the hybrid combinations ranged from 56.66% for the hybrid combination IR68885A x Giza 178R (SK 2027 H) to 50.64% for the hybrid combination large Stigma A/ Giza 181R (SK 2006H). Almost half of the experimental hybrids have long slender to medium long with few expections which are having bold to medium bold grains. One hybrid combination namely G46A/Giza 178R (SK2003H) have short to medium short grain.

Some promising hybrid combinations such as SK2003H, SK2010 H and SK2011 H had intermediate amylose content and intermediate alkali value (GT) indicating their acceptability in terms of quality parameters. Giza 178 (Check variety) which is a popular variety in Egypt is characterized by low to intermediate amylose content and alkali value. Unless rice hybrids have milling quality equal to or higher than either parent, the full advantage of their high yielding ability can not be realized (Khush *et al.*, 1988). If a hybrid has a higher broken percentage, its marketability will be reduced.

Table (3): The mean performance of all genotypes for grain quality characters for the two years and their combined.

Genotypes	BR %			TMR %			HR %			BRL		
	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
CMS Lines (A):												
IR 58025 A	76.30	76.18	76.24	67.30	67.25	67.27	45.10	45.98	45.54	1.33	1.00	1.17
IR 68885 A	77.15	75.62	76.39	66.22	66.13	66.18	54.55	54.80	54.68	2.98	3.00	2.99
G 46 A	75.58	75.88	75.73	64.50	64.98	64.74	48.58	48.10	48.34	7.00	7.00	7.00
Large Stigma A	76.90	75.58	76.24	66.15	65.78	65.97	45.60	44.83	45.21	5.00	5.50	5.25
Lines (B):												
IR 58025 B	76.65	76.98	76.81	65.78	66.30	66.04	48.08	48.65	48.36	1.25	1.00	1.13
IR 68885 B	78.08	78.08	78.08	66.88	66.98	66.93	55.48	54.95	55.21	3.00	3.00	3.00
G 46 B	75.93	75.35	75.64	64.13	64.60	64.36	42.58	46.10	44.37	7.00	7.00	7.00
Large Stigma B	77.65	77.75	77.70	66.93	66.43	66.68	34.15	40.78	37.46	5.00	5.00	5.00
Restorer lines (R):												
Giza 178 R	79.85	79.60	79.73	70.05	65.63	67.84	57.60	58.33	57.96	7.00	7.00	7.00
Giza 181 R	77.73	78.10	77.91	68.85	69.33	69.09	56.73	57.13	56.93	3.00	3.00	3.00
Giza 182 R	78.30	77.53	77.91	70.30	69.35	69.83	56.68	57.23	56.95	3.00	3.00	3.00
Hybrid combinations:												
SK2025H	77.80	78.40	78.10	66.90	66.08	66.49	56.23	56.83	56.53	5.00	5.25	5.13
SK2037H	77.35	77.45	77.40	67.20	66.78	66.99	54.90	55.68	55.29	3.00	3.00	3.00
SK2049H	77.80	77.75	77.78	66.58	66.93	66.75	54.68	54.28	54.48	3.00	3.25	3.13
SK2029H	78.40	77.25	77.83	66.75	65.78	66.26	56.43	56.90	56.66	5.00	5.00	5.00
SK2039 H	77.18	78.58	77.88	66.75	66.25	66.50	55.98	56.38	56.18	3.00	3.00	3.00
SK2051H	76.38	77.93	77.15	67.75	66.88	67.31	55.85	56.85	56.35	3.00	3.00	3.00
SK2003H	78.68	78.68	78.68	65.98	66.58	66.28	56.00	53.83	54.91	7.00	7.00	7.00
SK2005H	79.03	78.78	78.90	65.93	65.53	65.58	52.20	49.83	51.01	5.00	4.75	4.88
SK2010H	78.30	77.78	78.04	66.08	65.53	65.80	50.55	51.75	51.15	5.00	5.00	5.00
SK2004H	76.88	75.83	76.35	65.55	66.95	66.25	50.00	51.93	50.96	5.50	5.25	5.38
SK2006H	77.50	76.35	76.93	65.90	66.15	66.03	50.75	50.53	50.64	4.00	4.25	4.13
SK2011H	77.98	78.53	78.25	65.50	66.92	66.21	53.55	54.85	54.20	4.25	4.50	4.38
L.S.D. 5%	1.75	0.99	0.96	1.15	0.84	0.88	2.90	1.51	1.59	0.99	0.81	0.64
1%	2.33	1.32	1.26	1.54	1.12	1.64	3.86	2.02	2.10	1.31	1.08	0.85

Cont. Table (3):The mean performances of all genotypes for grain quality characters for the two years and their combined.

Genotypes	Shape			CLK			Gel. Temp.			Amlyose content %		
	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
CMS Lines (A):												
IR 58025 A	1.00	1.00	1.00	1.98	1.00	1.49	6.75	6.75	6.75	15.60	16.23	15.91
IR 68885 A	3.00	3.00	3.00	1.00	1.00	1.00	3.25	3.00	3.13	20.30	20.30	20.30
G 46 A	8.38	8.50	8.44	8.00	7.00	7.50	5.00	4.75	4.88	21.65	21.63	21.64
Large Stigma A	5.00	5.00	5.00	8.00	8.00	8.00	4.00	4.00	4.00	22.35	22.45	22.40
Lines (B):												
IR 58025 B	1.00	1.00	1.00	2.00	1.00	1.50	6.75	7.00	6.88	16.85	16.93	16.89
IR 68885 B	3.00	3.00	3.00	2.00	1.75	1.88	3.25	3.00	3.13	20.90	21.05	20.98
G 46 B	8.75	8.75	8.75	7.00	6.00	6.50	5.25	5.00	5.13	23.17	23.23	23.20
Large Stigma B	5.00	5.00	5.00	7.00	7.00	7.00	4.50	4.00	4.25	23.73	24.33	24.03
Restorer lines (R):												
Giza 178 R	8.23	8.80	8.51	2.00	2.00	2.00	4.25	4.00	4.13	18.75	19.13	18.94
Giza 181 R	3.00	3.00	3.00	1.00	1.00	1.00	6.00	6.00	6.00	19.18	19.20	19.19
Giza 182 R	3.03	3.00	3.01	1.00	1.00	1.00	6.25	6.00	6.13	19.30	19.30	19.30
Hybrid												
combinations:	4.00	4.00	4.00	1.25	2.00	1.63	5.00	5.50	5.25	18.29	18.70	18.50
SK2025H	2.00	1.50	1.75	1.20	1.00	1.10	6.00	6.25	6.13	18.63	18.86	18.75
SK2037H	2.50	2.00	2.25	0.95	1.00	0.98	6.00	6.00	6.00	19.15	18.96	19.06
SK2049H	5.00	4.63	4.81	1.75	3.00	2.38	3.75	4.50	4.13	21.04	21.73	21.38
SK2029H	1.00	1.00	1.00	1.25	1.00	1.13	4.75	3.75	4.25	21.03	21.66	21.34
SK2039 H	1.50	1.50	1.50	0.88	1.00	0.94	5.25	3.50	4.38	20.63	20.61	20.62
SK2051H	5.00	8.00	6.50	4.00	5.00	4.50	5.00	4.50	4.75	22.18	22.03	22.10
SK2003H	4.00	5.00	4.50	4.50	6.00	5.25	5.25	5.50	5.38	22.22	22.58	22.40
SK2005H	4.00	5.00	4.50	4.00	5.00	4.50	5.50	5.00	5.25	20.91	20.48	20.70
SK2010H	7.00	7.00	7.00	5.00	5.00	5.00	4.25	4.00	4.13	22.66	23.05	22.86
SK2004H	3.75	4.00	3.88	4.50	5.00	4.75	4.00	5.00	4.50	21.84	21.93	21.88
SK2006H	4.25	4.00	4.13	3.50	4.00	3.75	5.00	5.00	5.00	21.78	2.93	21.85
SK2011H												
L.S.D. 5%	1.36	1.33	0.94	1.91	1.99	1.36	0.95	1.08	0.71	0.62	0.60	0.39
1%	1.81	1.77	1.25	2.55	2.66	1.79	1.27	1.44	0.94	0.83	0.80	0.52

All the hybrids tested were subjected to quality analysis over the years. The hybrids possess HR% 55%, intermediate amylose content of (20-25%) intermediate alkali value of (4-5) and long slender to medium slender for long grain type or short to medium short for short grain type without chalkiness are listed in Table (1). Among the parental lines, the commonly utilized CMS line IR58025A is characterized by lower amylose content and higher alkali where as IR68885A, G46A and large stigma A possess intermediate amylose and alkali value. Hybrids viz., IR58025A/Giza 178R (SK2025 H), IR68885A/Giza 178R (SK2027H), G46A/Giza 178R (SK2003), G46A/Giza 182R (SK2010H) and large Stigma A/Giza 182R (SK2011 H) possess desirable range of amylose content and alkali value even though the female parents has lower or high amylose and higher or intermediate alkali value. This finding indicate that desirable quality in these hybrids have been contributed by the respective male parents (Virmani, 1994).

Amylose content was highly related to cooking and eating quality. Hybrid rice grains have different cooking and eating qualities from the parents because of the segregation in amylose content. Generally, cooking and eating qualities are intermediate. However, in some cases, the influence of the high amylose parent remains strong. Gelatinization temperature may also be related to cooking quality but does not effect it severely and therefore, may not influence the acceptability of hybrid rice (Khush *et al.* (1988) and Virmani, 1994).

General and specific combining ability effects:

Among the eight quality characters of cytoplasmic genctic male sterile lines CMS), the GCA effects of TMR%, HR% BRL and grain shape (for long grain type), and CLK in IR58025A and IR68885A were higher than the other female lines (Table 4). The G46A line had the highest GCA effect for BR% and BRL (for short grain type).

Among male lines, Giza 178R was the best general combiner as it showed consistently significant GCA effects for HR%, BRL, grain shape, slow GT and medium amylose content. Giza 182R was the best general combiner for BR% TMR%, CLK and low amylose content while, both restorer lines Giza 1812R and Giza 182R were the best general combiners for BRL and grain shape (for long grain type).

The results illustrated that to the grain length and grain shape revealed that two female CMS lines G46A and large Stigma A and one male restorer line, Giza 178R to show significant and positive GCA effects suggesting their usefulness in Egyptian hybrid rice improvement programme where short grains are preferred. The CMS female lines, IR58025A and IR68885A and the restorer lines Giza 181 R and Giza 182 R revealed significant and negative estimates. These parental lines could be considered as good combiners for long grain in rice hybrids. This findings were in agreement with El-Mowafi (1994) and El-Refae (2002).

Estimates of SCA effects of the hybrid combinations, at the two years and heir combined data for grain quality characters are given in Table (4).

Table (4): The estimates of GCA effects of CMS and restorer lines for grain quality traits at the two years and their combined data.

Lines	BR %			TMR %			HR %			BRL		
	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
CMS lines (A):												
IR 58025	$-0.1250^{n.s}$	$0.0625^{n.s}$	$-0.0313^{n.s}$	$0.5417^{n.s}$	$0.2292^{n.s}$	$0.3854^{n.s}$	1.3958^{*}	1.3958^{**}	1.3958^{**}	-0.7292^{**}	-0.6042^{**}	-0.6667^{**}
IR 68885	$-0.3750^{n.s}$	$0.1458^{n.s}$	$-0.1146^{n.s}$	0.6250^{*}	$-0.1042^{n.s}$	$0.2604^{n.s}$	2.0625^{**}	2.6458^{**}	2.3542^{**}	-0.7292^{**}	-0.7708^{**}	-0.7500^{**}
G 46	0.8750^{*}	0.6458^{**}	0.7604^{**}	$-0.5417^{n.s}$	-0.4375^{*}	-0.4896^{*}	$-0.9375^{n.s}$	-2.3542^{**}	-1.6458^{**}	1.2708^{**}	1.1458^{**}	1.2083^{**}
Large StIGMA	$-0.3750^{n.s}$	-0.8542^{**}	-0.6146^{**}	-0.6250^{*}	$0.3125^{n.s}$	$-0.1563^{n.s}$	-2.5208^{**}	-1.6875^{**}	-2.1042^{**}	$0.1875^{n.s}$	$0.2292^{n.s}$	$0.2083^{n.s}$
Restorer lines (testers)												
G. 178 R	$0.2083^{n.s}$	$-0.2708^{n.s}$	$-0.0313^{n.s}$	$-0.833^{n.s}$	$0.208^{n.s}$	$-0.0313^{n.s}$	$0.6875^{n.s}$	0.7500^{**}	0.7188^{*}	1.2292^{**}	1.1875^{**}	1.2083^{**}
G. 181 R	$0.0208^{n.s}$	$-0.0208^{n.s}$	$0.0000^{n.s}$	$-0.0833^{n.s}$	$0.2292^{n.s}$	$-0.1563^{n.s}$	$-0.4375^{n.s}$	-1.0625^{**}	-0.7500^{*}	-0.6458^{**}	-0.6875^{**}	-0.6667^{**}
G. 182 R.	$-0.2292^{n.s}$	$0.2917^{n.s}$	$0.0313^{n.s}$	$0.1667^{n.s}$	$0.2083^{n.s}$	$0.1875^{n.s}$	$0.2500^{n.s}$	$0.3125^{n.s}$	$0.0313^{n.s}$	-0.5833^{**}	-0.5000^{**}	-0.5417^{**}
L.S.D. for CMS lines 5%	0.710	0.285	0.413	0.619	0.342	0.430	1.176	0.615	0.744	0.4012	0.3282	0.2400
1%	0.944	0.758	0.546	0.823	0.455	0.568	1.564	0.818	0.983	0.5336	0.4365	0.3172
L.S.D. for restorer lines 5%	0.615	0.349	0.358	0.536	0.296	0.372	1.019	0.533	0.644	0.3474	0.2842	0.2077
1%	0.818	0.464	0.473	0.713	0.394	0.492	1.355	0.708	0.851	0.4620	0.3780	0.2745

Cont. Table (4): The estimates of GCA effects of CMS and restorer lines for grain quality traits at the two years and their combined data.

Lines	Shape			CLK			Gel. Temperature			Amylose content %		
	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
CMS lines (A):												
IR 58025	-0.8333^{**}	-1.5000^{**}	-1.1667^{**}	-1.5833^{**}	-1.8750^{**}	-1.7292^{**}	0.6875^{**}	1.0417^{**}	0.8646^{**}	-2.1458^{**}	-2.1250^{**}	-2.1354^{**}
IR 68885	-1.1667^{**}	-1.50000^{**}	-1.333^{**}	-1.4167^{**}	-1.5417^{**}	-1.4792^{**}	-0.3958^{*}	-0.9583^{**}	-0.6771^{**}	$0.0208^{n.s}$	0.3750^{**}	0.1979^{*}
G 46	0.6667^{*}	2.000^{**}	1.3333^{**}	1.4167^{**}	2.0417^{**}	1.7292^{**}	$0.2708^{n.s}$	$0.1250^{n.s}$	$0.1979^{n.s}$	0.8542^{**}	0.4583^{**}	0.6563^{**}
Large St.	1.3333^{**}	1.000^{**}	1.1667^{**}	1.5833^{**}	1.3750^{**}	1.4792^{**}	-0.5625^{**}	$-0.2083^{n.s}$	-0.3854^{*}	1.2708^{**}	1.2917^{**}	1.2813^{**}
Restorer lines (testers)												
G. 178 R	1.5833^{**}	$2.000^{n.s}$	1.7917^{**}	$0.2500^{n.s}$	$0.4583^{n.s}$	$0.3542^{n.s}$	-0.4792^{**}	$-0.2500^{n.s}$	-0.3646^{**}	$0.1875^{n.s}$	0.2708^{*}	0.2292^{**}
G. 181 R	-0.9792^{**}	-1.1250^{**}	-10521^{**}	$0.1250^{n.s}$	$0.0833^{n.s}$	$0.1042^{n.s}$	$0.0208^{n.s}$	$0.2500^{n.s}$	$0.1354^{n.s}$	$0.1250^{n.s}$	0.2708^{*}	0.1979^{*}
G. 182 R.	-0.6042^{*}	-0.8750^{**}	-0.7396^{**}	$-0.3750^{n.s}$	$-0.5417^{n.s}$	$-0.4583^{n.s}$	0.4583^{**}	$0.0000^{n.s}$	$0.2292^{n.s}$	-0.3125^{**}	-0.5417^{**}	-0.4271^{**}
L.S.D. for CMS lines 5%	0.5504	0.5394	0.3920	0.7756	0.809	0.5332	0.3868	0.4372	0.2986	0.2526	0.2424	0.1752
1%	0.7320	0.7177	0.5182	1.0315	1.076	0.7047	0.5144	0.5815	0.3946	0.3359	0.3224	0.2316
L.S.D. for restorer lines 5%	0.4766	0.4672	0.3396	0.6718	0.7006	0.4617	0.335	0.3786	0.2586	0.2188	0.210	0.1517
1%	0.6339	0.6214	0.4488	0.8935	0.9312	0.6103	0.4455	0.5035	0.3418	0.2910	0.2793	0.2005

4939

J. Agric. Sci. Mansoura Univ., 31 (8), August, 2006

High positive values would be of interest in BR%, TMR% and HR%. High negative values would be useful from the breeder's point of view for CLK, gelatinization temperature (GT) and Amylose content %.

Out of 12 hybrid combinations, one for BR%, two for HR%, one for grain shape and three for low amylose content exhibited significant desirable SCA effects in the two years and their combined data. From the foregoing discussion, it could be indicated that the superior hybrid combinations for most grain quality characters were G46A/Giza 178R (SK2003H), G46A/Giza 182 (SK2010 H) and large Stigma A/Giza 182R (SK 204H).

Genetic parameters:

Genetic parameters as well as heritability values were estimated for all studied quality characters and the results are presented in Table (6). The results indicated that the estimates of the additive genetic variance (σ^2A) and the relative importance of GCA% of TMR%, HR%, BRL, grain shape, CLK, GT and AC% were higher than those of non-additive genetic variance including dominance (σ^2D) and relative importance of SCA %. These results indicated that these characters, were mainly governed by additive gene effect. Similar results were obtained by Hong *et al.* (1985a), Kuo and Liu (1986), El-Mowafi (1994), Panamasivam *et al.* (1995), Hammoud (1996) and El-Refae (2002) for grain dimensions characters, Srivastava *et al.* (1978), Gravois (1994), Paramasivam *et al.* (1995) and Moustafa (2000) for milling recovery characters and Hussein (1982), Puri *et al.* (1983), Kuo *et al.* (1985), Hammoud (1996), El-Abd (1999) and Moustafa (2000) for cooking and eating quality characters. On the other hand, the dominance variance value (σ^2D) and relative importance of SCA% for BR% character were higher than those of the additive variance (σ^2A) and relative importance of GCA%. This finding indicated that BR% character was mainly governed by non-additive gene action. Similar results was obtained by Salem (1997).

Concerning heritability, the results cleared that the estimated values of heritability in broad sense (h^2_b%) were high for HR%, BRL, grain shape, CLK and amylose content %, moderate for GT and low for BR% and TMR%. On the other hand, heritability values in narrow sense were relatively high for BRL, grain shape, CLK and amylose content %, moderate for GT and low for BR%, TMR% and HR%.

The results also indicated that a major part of the total phenotypic variance (σ^2P) was due to additive genetic variance (σ^2A) for HR%, BRL, grain shape CLK, GT and amylose content % characters. Accordingly, it was expected that an effective phenotypic selection to improve parental cytoplasmic male sterile, lines (CMS), maintainer and restorer lines for grain dimensions, milling recovery and cooking and eating quality characters for hybrid rice breeding programmes could be achieved with a satisfactory degree of accuracy.

Table (5):The estimates of SCA effects for the 12 F_1 hybrid combinations at the two years and their combined data for grain quality traits.

Hybrid combinations	BR %			TMR %			HR %			BRL		
	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
SK 2025 H	0.1250 n.s	0.6875 n.s	0.4062 n.s	0.0833 n.s	-0.6042 n.s	-0.2604 n.s	0.2292 n.s	0.6667 n.s	0.4479 n.s	0.1042 n.s	0.2292 n.s	0.1667 n.s
SK 2037 H	-0.4375 n.s	-0.3125 n.s	-0.3750 n.s	0.3333 n.s	0.3958 n.s	0.3646 n.s	0.1042 n.s	0.9792 n.s	0.5417 n.s	-0.0208 n.s	-0.1458 n.s	-0.0833 n.s
SK 2049 H	0.3125 n.s	-0.3750 n.s	-0.0312 n.s	-0.4167 n.s	0.2083 n.s	-0.1042 n.s	-0.3333 n.s	-1.6458 n.s	-0.9896**	-0.0833 n.s	-0.0833 n.s	-0.0833 n.s
SK 2027 H	0.8750 n.s	-0.3958 n.s	0.2396 n.s	-0.2500 n.s	-0.5208 n.s	-0.3854 n.s	-0.4375 n.s	-0.5833 n.s	-0.5104 n.s	0.1042 n.s	0.1458 n.s	0.1250 n.s
SK 2039 H	-0.1875 n.s	0.6042 n.s	0.2083 n.s	-0.2500 n.s	0.2292 n.s	-0.01042 n.s	0.4375 n.s	0.7292 n.s	0.5833 n.s	-0.0208 n.s	0.0208 n.s	0.0000 n.s
SK 2051 H	-0.6875 n.s	-0.2083 n.s	-0.4479 n.s	0.5000 n.s	0.2917 n.s	0.3958 n.s	0.0000 n.s	-0.1458 n.s	-0.0729 n.s	-0.0833 n.s	-0.1667 n.s	-0.1250 n.s
SK 2003 H	-0.3750 n.s	0.6042 n.s	0.1146 n.s	0.1667 n.s	0.8125 n.s	0.4896 n.s	2.3125*	1.1667*	1.7396**	0.1042 n.s	0.2292 n.s	0.1667 n.s
SK 2005 H	0.5625 n.s	-0.3542 n.s	0.4583 n.s	-0.333 n.s	-0.1875 n.s	-0.2604 n.s	-0.3125 n.s	-0.7708 n.s	-0.5417 n.s	-0.0208 n.s	-0.1458 n.s	-0.0833 n.s
SK 2010 H	-0.1875 n.s	-0.9583**	-0.5729 n.s	0.1667 n.s	-0.6250 n.s	-0.2292 n.s	-2.0000 n.s	-0.3958 n.s	-1.1979**	-0.0833 n.s	-0.0833 n.s	-0.0833 n.s
SK 2004 H	-0.6250 n.s	-0.8958*	-0.7604*	0.000 n.s	0.3125 n.s	0.1562 n.s	-2.1042*	-1.2500*	-1.6771*	-0.3125 n.s	-0.6042*	-0.4583*
SK 2006 H	0.0625 n.s	-0.6458 n.s	-0.2917 n.s	0.2500 n.s	-0.4375 n.s	-0.0937 n.s	-0.2292 n.s	-0.9375 n.s	-0.5833 n.s	0.0625 n.s	0.2708 n.s	0.1667 n.s
SK 2011 H	0.5625 n.s	1.5417**	1.521**	-0.2500 n.s	0.1250 n.s	-0.0625 n.s	2.3333*	2.1875*	2.2604**	0.2500 n.s	0.3333 n.s	0.2917 n.s
L.S.D.5%	1.23	0.698	0.715	1.072	0.592	0.745	2.037	1.065	1.288	0.6950	0.5684	0.4156
1%	1.64	0.928	0.945	1.430	0.394	0.984	2.709	1.417	1.703	0.9243	0.7560	0.5493

*, ** significant at 0.05 and 0.01 probability levels, respectively.

Cont. Table (5):The estimates of SCA effects for the 12 F_1 hybrid combinations at the two years and their combined data for grain quality traits.

Hybrid combinations	Shape			CLK			Gel. Temperature			Amylose content %		
	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
SK 2025 H	-0.4167 n.s	-0.5000 n.s	-0.4583 n.s	-0.1667 n.s	0.1250 n.s	-0.0208 n.s	-0.1875 n.s	-0.1667 n.s	-0.1771 n.s	-0.6042**	-0.4375*	-0.5208**
SK 2037 H	0.1458 n.s	0.1250 n.s	0.1354 n.s	-0.0417 n.s	-0.2500 n.s	-0.1458 n.s	0.3125 n.s	0.0833 n.s	0.1979 n.s	-0.0417 n.s	-0.1875 n.s	-0.1146 n.s
SK 2049 H	0.2708 n.s	0.3750 n.s	0.3229 n.s	0.2083 n.s	0.1250 n.s	0.1667 n.s	-0.1250 n.s	0.0833 n.s	-0.0208 n.s	0.6458**	0.6250**	0.6354**
SK 2027 H	0.9167 n.s	0.5000 n.s	0.7033*	0.1667 n.s	0.7917 n.s	0.4792 n.s	-0.3542 n.s	0.8333*	0.2396 n.s	-0.20208 n.s	0.0625 n.s	0.208 n.s
SK 2039 H	-0.5208 n.s	-0.3750 n.s	-0.4479 n.s	-0.2083 n.s	-0.5833 n.s	-0.3958 n.s	0.1458 n.s	-0.4167 n.s	-0.1354 n.s	0.0417 n.s	0.0625 n.s	0.0521 n.s
SK 2051 H	-0.3958 n.s	-0.1250 n.s	-0.2604 n.s	0.0417 n.s	-0.2083 n.s	-0.0833 n.s	0.2083 n.s	-0.4167 n.s	-0.1042 n.s	-0.0208 n.s	-0.1250 n.s	-0.0729 n.s
SK 2003 H	-0.9167 n.s	0.0000 n.s	-0.4583 n.s	-0.4167 n.s	-0.7917 n.s	-0.6042 n.s	0.2292 n.s	-0.2500 n.s	-0.0104 n.s	0.1458 n.s	-0.0208 n.s	0.0625 n.s
SK 2005 H	0.6458 n.s	0.1250	0.3854 n.s	0.2083 n.s	0.5833 n.s	0.3958 n.s	-0.0208 n.s	0.2500 n.s	0.1146 n.s	0.4583*	0.7292**	0.5937**
SK 2010 H	0.2708 n.s	-0.1250 n.s	0.0729 n.s	0.2083 n.s	0.2083 n.s	0.2083 n.s	-0.2083 n.s	0.000 n.s	-0.1042 n.s	-0.6042**	-0.7083**	-0.6562**
SK 2004 H	0.4167 n.s	0.0000 n.s	0.2083 n.s	0.4167 n.s	-0.1250 n.s	0.1458 n.s	0.3125 n.s	-0.4167 n.s	-0.0521 n.s	0.4792*	0.3958**	0.4375**
SK 2006 H	-0.2708 n.s	0.1250 n.s	-0.0729 n.s	0.0417 n.s	0.2500 n.s	0.1458 n.s	-0.4375 n.s	0.0833 n.s	-0.1771 n.s	-0.4583*	-0.6042**	-0.5312**
SK 2011 H	-0.1458 n.s	-0.1250 n.s	-0.1354 n.s	-0.4583 n.s	-0.1250 n.s	-0.2917	0.1250 n.s	0.3333 n.s	0.2292 n.s	-0.0208 n.s	0.2083 n.s	0.0937 n.s
L.S.D.5%	0.9534	0.9342	0.6791	1.344	1.401	0.9237	0.6700	0.7574	0.5174	0.4376	0.4200	0.3035
1%	1.268	1.2425	0.8976	1.787	1.863	1.221	0.87911	1.007	0.6838	0.5820	0.5586	0.4012

*, ** significant at 0.05 and 0.01 probability levels, respectively.

Table (6):Estimates of genetic parameters and heritability in broad and narrow senses for grain quality characters for the two years and their combined data.

Parameters	BR %			TMR %			HR %			BRL		
	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
$(\sigma^2 A)$	0.132	-0.1407	0.039	0.3836	-0.0641	0.203	2.904	5.279	3.948	0.5173	0.388	0.4525
$(\sigma^2 D)$	0.0855	0.925	0.372	-0.1272	0.3062	0.107	2.283	2.107	4.386	-0.0742	0.046	0.201
$(\sigma^2 E)$	0.512	0.487	0.932	1.148	0.3510	0.791	4.151	1.135	2.584	0.483	0.323	0.422
$(\sigma^2 G)$	0.2175	0.7843	0.411	0.2564	0.2421	0.310	5.187	7.386	8.334	0.4331	0.434	0.4726
$(\sigma^2 P)$	1.729	1.2713	1.343	1.404	0.5931	1.101	9.338	8.521	10.92	0.9161	0.757	0.8946
$(h^2. b)$ %	12.57	61.69	30.60	18.26	40.82	28.16	55.55	86.68	76.32	47.28	57.33	52.83
$(h^2. n)$ %	7.63	-11.06	2.90	27.32	-10.81	18.44	31.10	61.95	36.15	56.47	51.25	50.58
Relative importance of gca %	60.69	-17.94	9.49	149.61	-26.48	65.48	55.99	71.47	47.37	119.44	89.40	95.75
Relative importance of sca %	39.31	117.94	90.51	-49.61	126.48	34.52	44.01	28.53	52.63	-19.44	10.60	4.25

Cont. Table (6):The estimates of genetic parameters and heritability in broad and narrow senses for grain quality characters for the two years and their combined data.

Parameters	Shape			CLK			Gel. Temp.			Amylose content %		
	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
$(\sigma^2 A)$	3.037	6.097	1.218	3.0414	4.024	3.5149	0.4878	0.6667	0.5403	2.213	2.181	0.266
$(\sigma^2 D)$	0.2952	-0.0725	0.1424	-0.3192	-0.123	-0.0451	0.011	0.1065	-0.019	0.2557	0.329	0.308
$(\sigma^2 E)$	0.909	0.873	0.906	1.805	1.963	1.875	0.449	0.574	0.511	0.192	0.176	0.157
$(\sigma^2 G)$	3.332	6.024	1.360	2.7222	3.901	3.4698	0.4988	0.7732	0.5213	2.469	2.510	0.574
$(\sigma^2 P)$	4.241	6.897	2.266	4.5227	5.864	5.3448	0.9478	1.347	1.032	2.661	2.686	0.731
$(h^2. b)$ %	78.57	87.34	60.02	60.19	66.52	64.92	52.63	57.40	50.51	92.78	93.45	78.52
$(h^2. n)$ %	71.61	88.40	53.75	67.25	68.62	65.76	51.47	49.49	52.35	83.16	81.20	36.39
Relative importance of gca %	91.14	101.21	89.56	111.72	103.15	101.30	97.80	86.23	103.64	89.63	86.89	46.34
Relative importance of sca %	8.86	-1.20	10.47	-11.72	-3.15	-1.30	2.20	13.77	-3.64	10.36	13.11	53.66

Similar results were obtained by Sood and Siddiq (1980), Hussein (1982), El-Hissewy (1985), Kuo *et al.* (1985), Kuo and Liu (1986), El-Mowafi (1994), Honarnejad (1994, Moustafa (2000) and El-Refae (2002) for grain dimensions characters, Hussein (1982), El-Abd (1999) and Moustafa (2000) for milling recovery characters and Hussein (1982), Kuo *et al.* (1985), El-Abd (1999) and Moustafa (2000) for cooking and eating quality characters. The cases of BR%, TMR% and HR% characters, which showed low estimates of heritability in narrow sense (h^2_n), suggested that a major part of the total phenotypic variance was due dominance genetic variance and environmental effects. These findings indicated that the selection for these characters should be done in the late generations. In case of GT character, the estimate of heritability in narrow sense was moderate indicating that a major part of total phenotypic variance was due to both additive and dominance genetic variance. Accordingly, it was expected that the effective phenotypic selection for this character could be achieved with satisfactory degree of accuracy.

REFERENCES

Biswas, S.K.; K.A. Kabir; F. Pegum and N.H. Choudhury (1992). Physiochemical properties of modern and local rice varieties of Bangladesh. Bangladesh Rice. J., 3: 128-131.

El-Abd, A.B.A. (1999). A study on the inheritance of rice grain quality and its relation with yield and some yield related characters. Ph.D., Thesis, Faculty of Agric., Al-Azhar Univ., Egypt.

El-Hissewy, A.A. (1985). Studies on genetic variation and combining ability in diallel of some rice (*Oryza sativa* L.) strains and cultivars. Ph.D. Thesis, Fac. of Agric., Univ. of Alexandria, Egypt.

El-Mowafi, H.F. (1994). Studies on rice breeding. Ph.D. Thesis, Faculty of Agric., Kafr El-Sheikh Tanta Univ., Egypt.

El-Refae; Y.Z.E. (2002). Genetical and biochemical studies on heterosis and combining ability in rice. M.Sc. Thesis, Fac. Agric., Tanta Univ., Kafr El-Sheikh, Egypt.

Gravois, K.A. (1994). Diallel analysis of head rice percentage, total milled rice percentage and rough rice yield. Crop Sci., 34: 42-45.

Hammoud, S.A. (1996). Breeding studies on some characters of rice (*Oryza sativa* L.).. M.Sc. Thesis, Faculty of Agriculture, Menofiya Univ., Menofiya, Egypt.

Honarnejad, R. (1994). Genetical characteristics and combining ability of six Iranian rice cultivars (*Oryza sativa* L.). Iran. J. Agric. Sciences, 25(4): 31-50.

Hong, M.C.; S.S. Huang; J.L. Lin; S.T. Wu and F.S. Thseng (1985a). Systematic approach to the physiological genetics of assimilate production and partitioning processes during grain filling period in paddy rice. IV. Diallel analysis of grain characters. J. Agric. and Forestry, 34(1): 13-21.

Hussein, M.M. (1982). Genetic studies for some physical and technological characteristics in rice grain. Ph.D. Thesis, Faculty of Agriculture, Al-Azhar Univ., Cairo, Egypt.

International Rice Research Institute (1996). Standard Evaluation System in Rice. IRRI, Manila, Philippines.

Juliano, B.O. (1971). A simplified assay for milled rice amylose. Cereal Sci. Today. 16: 334-338, 340-360.

Kempthorne, O. (1957). An introduction to genetic statistics. John Wiley and Sons Inc., New York, 458-471.

Khush, G.S.; I. Kumar and S.S. Virmani (1988). Grain quality of hybrid rice. In: Hybrid rice. Manila (Philippines): International rice Research Institute. p. 201-215.

Kumar, I.; K. Maruyama and H.P. Hoon (1994). Grain quality consideration in hybrid rice. In. Hybrid Rice Technology new developments and future prospects, selected papers from the International Rice Research Conference, Edited by S.S. Virmani, IRRI.

Kuo, Y.C. and C. Liu (1986). Genetic studies on large kernel size of rice. II. Inheritance of grain dimensions of brown rice. Journal of Agricultural Research of China, 35(4): 401-412.

Kuo, Y.C.; C. Liu; T.M. Chang and S.C. Hsieh (1985). Inheritance of quality and grain characteristics in Indica rice. Journal of Agricultural Research of China, 34(3): 243-257.

Moustafa, A.A. (2000). Breeding studies on rice (*Oryza sativa* L.). Ph.D. Thesis, Fac. Agric. Menoufiya Univ., Egypt.

Paramasivam, K.; S. Giridharan; A.P.M.K. Soundararaj; P. Vivekanandan and P. Parthasarathy (1995). Combining ability of some varieties for grain quality traits mating system. IRRN, IRRI, 20(1): 4.

Puri, R.P.; E.A. Siddiq and R.B. Mehra (1983). Studies on cooking and nutritive qualities of cultivated rice, *Oryza sativa* L. II-Qualitative genetic characterisation of amylose content. Genetica Agraria, 34: 15-34.

Sood, B.C. and E.A. Siddiq (1980). Studies on component quality attributes of Basmati rice, *Oryza sativa* L. Zeitschrift fur Pflanzenzuchtung, 84(4): 294-301.

Srivastava, R.B.; H.G. Singh and Y.S. Chauhan (1978). Genetic architecture of some quality traits in the F_2 populations of rice. Indi. J. Agric. Sciences, 48(10): 568-572.

Virmani, S.S. (1994). Heterosis and hybrid rice breeding. V. Grain quality considerations in hybrid rice. Monographs on theoretical and applied genetics 22, Springer Verlag. IRRI, pp. 187.

Virmani, S.S. and F.U. Zaman (1998). Improving grain quality of hybrid rice: Challenges, strategies, and achievements. In: Virmani S.S., E.A. Siddiq and K. Muralidharan, Editors. Advances in hybrid rice technology. Proceedings of the 3rd Int. Symp. Inter., 14-16 Nov. 1996. Hyderabad, India, Manila (Philippines). IRRI. p. 177-186.

Yadav, S.P. and B.R. Murty (1966). Heterosis and combining ability of different height categories in bread wheat. Indian J.Genet. 36, 184-196.

Zaman, F.U.; B.C. Viraktamath and S.S. Virmani (2003). Improving grain quality in hybrid rice. Hybrid rice for food security, poverty alleviation and environmental protection, edited by S.S. Virmani, C.X. Mao, and B. Hardy, IRRI, p. 69-84.

التحليل الوراثى والقدرة على الإئتلاف فى صفات جودة حبوب الآرز الهجين

حمدى فتوح الموافى

مركز البحوث والتدريب فى الارز ـ سخا ـ كفرالشيخ ـ مصر ٣٣٧١٧ ـ معهد بحوث المحاصيل الحقلية ـ مركز البحوث الزراعية

أجرى هذا البحث لدراسة إمكانية الاستفادة من ظاهرة قوة الهجين بإستخدام نظام الــثلاث فـى الارز سلالة العقم الذكرى السيتوبلازمى الوراثى CMS والسلالة المحافظة على خصوبتها B والســلالة المعيدة للخصصوبة والمعنتة للارز الهجين R) وذلك لائتداد الارز الهجين عالى الجــودة علــى النطــاق التجارى.

أجريت التجارب خلال مواسم زراعة الارز سنة ٢٠٠٢ ، ٢٠٠٣ ، ٢٠٠٤ بمزرعة ومعامــل مركز البحوث والتدريب فى الارز بمحطة البحوث الزراعية بسخا ـ كفرالشيخ وذلك باستخدام نظام تحليل السلالة × الكشاف لاربع سلالات عقيمة ذكريا وراثيا من مصادر متنوعة هى Large Stigma A, G 46A, IR68885A, IR58025A هجنت فى القطع المنعزلة مع الملحقات المصرية المعيدة للخصوبة جيزة ١٧٨ أر ، جيزة ١٨١ أر وجيزة ١٨٢ أر لائتاج هجن تقاوى الدراسة.

وكان الغرض دراسة التباين الوراثى والقدرة على الائتلاف والتفاعلات المختلفة مع الســنوات وفعل الجين لصفات جودة الحبوب فى الارز الهجين

ويمكن تلخيص نتائج هذه الدراسة فى النقاط التالية.

1- أظهر تحليل التباين وجودة تباينات معنوية للتراكيب الوراثية لكل صــفات جــودة الحبــوب وكانــت تفاعلات كل من التراكيب الوراثية والآباء غير معنوية لكل صفات جودة الحبوب عدا صــفتى نسبة تصافى التبييض ونسبة الحبوب الكاملة وفى نفس الوقت كانت تفاعلات متوسط الهجين المعبرة عــن قوة الهجين مع السنوات معنوية لصفات نسبة تصافى التبييض ، نسبةالحبوب السليمة (الحبوب السليمة %) ، شكل الحبة ونسبة الحبوب الطباشيرية(الشفافية) وغير معنوية لصفات نسبة تصــافى التقشــير وطول الحبة المقشورة ودرجة حرارة الجلتنة ونسبة الاميلوز .

2- كانت قيم التباين الوراثى الراجع للقدرة العامة على الائتلاف للسلالات العقيمة معنوية لصفات النسبة المئوية لتصافى التقشير ، طول الحبة المقشورة ، شكل الحبة ، نسبة الحبوب الطباشيرية(الشــفافية) ، درجة حرارة الجلتنة ونسبة الاميلوز. كما كان معنويا لسلالات الخصوبة الكشافة لصفات طول الحبة ، شكل الحبة ودرجة حرارة الجلتنة.

3- أظهرت تباينات القدرة الخاصة على الائتلاف الناتجة عن تفاعل السلالة × الكشاف معنونية لصــفات النسبة المئوية للتقشير ونسبة الاميلوز % فى السنتين والتحليل المشترك بينهما وتفاوتت فى بقية صفات جودة الحبوب تحت الدراسة.

4- أظهرت دراسة تأثير القدرة العامة على الائتلاف لكل سنة تفوق كل مــن ســلالات العقــم الــذكرى السيتوبلازمى الوراثى IR68885A, IR58025A ,سلالات إعادة الخصوبة جيزة ١٧٨ أر وجيــزة ١٨٢ أر فى واحدة او اكثر من صفات جودة الحبوب المرغوبة.

5- أوضحت تأثيرات القدرة الخاصة على الائتلاف لكل سنة والتحليل المشترك تفوق عــدد مــن الهجــن المبشرة فى صفة أو اكثر من الصفات المرغوبة لجودة الحبوب وكان من أهم الهجن المبشــرة فــى المحصول مع صفات جــودة الحبــوب الهجينــين SK2010 H, SK2003H وكــذلك الهجيــن SK2011H.

6- اتضح الدور الاهم للفعل المضيف للجين فى وراثة كل صفات جودة الحبوب فى الارز الهجــين مــن خلال أهمية القدرة العامة على الائتلاف عدا فى صفة النسبة المئوية للتقشير . وأهمية الاستفادة منها فى تحسين السلالات الأبوية للأرز الهجين.