

GENETICAL STUDIES ON COMBINING ABILITY FOR YIELD AND ITS COMPONENTS TRAITS IN HYBRID RICE UNDER NORMAL AND SALINE CONDITIONS

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ABSTRACT

In this study, an effort was made to identify good parents and nature of gene action governing yield and its components characters of rice under normal and saline environmental by Line (three cytoplasmic male sterile) x tester (three restorers) analysis. In the present study, the mean square due to genotypes, parents, crosses and parent vs crosses revealed highly significant variations at locations, years and their combined analysis over locations through years. The interactions of genotypes, parents and crosses by years and locations were highly significant for all grain yield and its components traits except 1000-grain weight trait which revealed insignificant interaction over the years. On the other hand the mean squares resulting from the interaction of genotypes, parents and crosses by years x locations were insignificant in all studied traits except number of grains / panicle and the number of filled grains / panicle traits which showed highly significant.

GCA for lines and testers and SCA for Lines x testers were highly significant under all environments and combined analysis for yield and its components traits. Similarly, the genetic variance of interaction of lines and testers by years and locations were highly significant. But the mean squares of interaction of lines and testers by years x locations were often insignificant for all traits except number of grains / panicle and number of filled grains / panicle traits which revealed highly significant. Parents with high x high or low x high general combining ability GCA effects gave the best heterotic combination like the 1R70368A / Giza181R. Meanwhile, the CMS line IR70368A was the best female general combining ability for most of studied traits, while, the restorer lines Giza181R and Giza182R were the best testers capable of to combine their genes with the lines for the most studied traits. Also, the cross combinations IR70368A x Giza 181R and IR58025A x Giza 182R showed high SCA effects for most studied traits and considered as the best combinations. The results showed that all yield and its components traits were largely governed by additive gene action except number of panicles / plant which was governed by non-additive gene action, indicating that the additive variance plays the main role in the inheritance of these traits. Furthermore, the magnitude values of additive by years, locations and years x locations interactions were positive and larger than non-additive interactions for all yield traits. Heritability estimates in the narrow and broad senses were close together in value for most yield and its components traits, indicating that the additive genetic variance plays the master role in the inheritance of these traits.

INTRODUCTION

Rice (*Oryza sativa*, L.) is considered as one of the most important cereal crops not only in Egypt, but also all over the world. In Egypt, the annually cultivated area by rice is almost more than 20% of the total area.

According to the statistics of the Ministry of Agriculture in 2009, the total cultivated area of rice was about 1.2 million feddan all of it under irrigation. During the past 20 years, Egypt's Rice research program has succeeded in raising the national average rice yield more than 70%, from 2.4 million ton national production for the base period (1984-1987) by a steady increase annually to reach its maximum 4.92 million tons of paddy rice in 2009 (Proceeding of 2009, Researcher at RRTC). In spite of the great progress achieved in rice productivity in Egypt, we need to make another breakthrough to increase rice yield per unit area and unit time by raising the national average yield more than 15%. It is hard to achieve through inbred varieties because we have improved commercial varieties with superior genetic background (El-Mowafi *et al.*, 2009).

Salinity effects on plants are complex. The general effects of salinity are the results of both osmotic and ionic stresses (Greenway and Munns, 1980). The initial and primary effect of salinity, especially at moderate salinity concentrations, is due to its osmotic effects (Munns and Termaat, 1986 and Jacoby, 1994). At the whole plant level, ion concentrations in plant tissues increase as a result of salinity stress. Ion toxicity or nutrition deficiency will be caused by the overdominance of a specific ion (Bernstein *et al.*, 1974). The measurable or visible effects of salinity on plants can include reduced growth rate, damage of meristems in growing shoots, reductions in yield components, or typical symptoms of nutritional disorders under osmotic and ionic stress. Grain yield reduction of rice under stress of root-zone salinity can be caused by injuries at both seedling and maturity stages. In most commonly cultivated rice cultivars, young seedlings were very sensitive to root-zone salinity (Pearson and Bernstein, 1959; Kaddah, 1963; Flowers and Yeo, 1981 and Heenan *et al.*, 1988). Yield components related to final grain yield were also severely affected by root-zone salinity. Primary branches per panicle, panicle length, spikelets per panicle, number of filled spikelets and seed weight per panicle were significantly reduced by salinity (Sajjad, 1984; Heenan *et al.*, 1988 and Khatun *et al.*, 1995).

Line x tester analysis provided useful informations about the nature of the genetic parameters. It also helps in identification of parental lines in terms of their combining ability in cross combinations. This may provide a dependable basis in selecting parents in a hybridization program to get desirable segregants. The investigation being reported herein was undertaken with a view to estimate the general and specific combining ability effects under normal and saline conditions and combined for three CMS and three restorer lines useful for hybrid rice breeding program.

MATERIALS AND METHODS

Line x tester mating design was conducted by using three CMS lines namely IR58025A, IR69625A and IR70368A as a female parents and three restorer lines namely Giza178R, Giza181R and Giza182R as a testers parents (Table 1) to obtain 9 F₁ crosses. The trails were conducted in Randomized Complete Block Design with three replications with spacing of 20 cm between rows and 20 cm between plants to comprising 9 hybrids and their

sex parents in the growing seasons of the two years 2006 and 2007 at normal (Sakha) and saline (El-Sirw) conditions. The recommended agricultural practices were followed. Observations were recorded on ten plants taken at random from each test entry replication for No. of panicles / plan, No. of grains / panicle, No. of filled grains / panicle, 1000-grain weight and grain yield / plant. combining ability analysis was carried out as suggested by Kempthorne model (1957).

Table 1: Origin and salient features of the parental genotypes used in this study.

No	Genotypes	Origin (parentage)	Salient features	Reaction to salinity
CMS Lines				
1	IR58025 A	(IRR1) IR 48483 A/8 pus A167-120-3-2//pusA 167-120-3-2	Indica type, late maturing extra long grain, low amylose content and strong aroma.	Moderately
2	IR69625A	(IRR1) -----	Indica type, medium early maturing, medium grain type and medium amylose content.	Tolerant
3	IR70368A	(IRR1) -----	Indica type, mid. early maturing, medium grain type and medium amylose content.	Sensitive
Testers				
4	Giza178R	(Egypt) Giza 175 / Milyang 49	Indica- japonica type, medium early maturing, short statured, tolerance to salinity, short grain, good grain quality, high yielder and good restorer for CMS lines.	Tolerant
5	Giza181R	(Egypt) IR 24 / IR 22	Indica type medium maturing semi- dwarf resistance to blast excellent, long grain and high yielder.	Sensitive
6	Giza182R	(Egypt) Giza 181/IR 39422-163-1-2// Giza 181	Indica type, new released variety, early maturing, semi-dwarf, long grain, resistance to blast, high yielder and good fretter for CMS lines.	Moderately

RESULTS AND DISCUSSION

Analysis of variance:

The analyses of variance for yield and its components traits for all genotypes, for each location in each year and their combined data were calculated and the results are presented in Tables 2 and 3, respectively.

The results show that the genotypes mean squares were found to be larger than their corresponding mean squares of the error. However, the results of the F-test cleared that the mean squares of the genotypes showed highly significant values at the two locations through the two years and their combined data. These findings indicated the presence of large variations among them. Similarly, the mean squares of years were highly significant for the traits of grain yield/plant, No.of panicles/plant, No.of grains/panicle and No.of filled grains/panicle and non significant for 1000-grain weight. Therefore, the mean squares of locations were highly significant for all studied traits. Also, the interactions between years x locations were insignificant

The data is clarify that the mean squares of genotypes, parents , crosses and parents vs. crosses showed high significance values for all yield and its component traits at the two locations in the two years and their combined data. These findings indicated overall wide real differences among these populations.

Table 2: Mean square estimates from ordinary and line x tester analysis for yield and its components traits at the two locations through the two years.

S .o .v	d.f	No. of panicles/plant				No. of grains/panicle			
		Location 1		Location 2		Location 1		Location 2	
		Year1	Year2	Year1	Year2	Year1	Year2	Year1	Year2
Replications	2	0.035ns	0.089 ns	0.072 ns	0.155 ns	5.408**	18.774**	24.668**	14.254**
Genotypes	14	15.441**	31.253**	29.241**	37.029**	2677.441**	2528.535**	2995.239**	3196.277**
Parents	5	11.223**	33.193**	31.181**	45.463**	2481.479**	2060.888**	3386.606**	3656.280**
Crosses	8	13.914**	24.240**	19.459**	24.943**	1617.549**	1754.801**	1843.296**	1850.017**
Par. Vs. C.	1	48.743**	77.656**	97.801**	91.560**	12136.385**	11056.640**	10253.938**	11666.352**
Lines	2	10.452**	17.673**	20.116**	11.923**	1645.684**	1681.753**	1984.067**	2186.703**
Testers	2	13.199**	40.400**	27.358**	39.541**	3365.363**	3929.939**	4249.628**	4218.151**
Lines x testers	4	16.001**	19.443**	15.181**	24.153**	729.574**	703.757**	569.745**	497.606**
Error	28	0.612	1.258	2.049	1.690	84.877	154.159	202.614	236.121

* and ** Significant at 5% and 1% levels of probability, respectively.

Table 2: Continue.

S .o .v	d.f	No. of filled grain/panicle				1000- grain weight			
		Location 1		Location 2		Location 1		Location 2	
		Year1	Year2	Year1	Year2	Year1	Year2	Year1	Year2
Replications	2	3.361*	12.693**	9.521**	7.148**	0.038ns	0.056ns	0.045ns	0.003ns
Genotypes	14	12558.854**	10208.707**	7197.663**	5957.106**	15.359**	17.529**	13.057**	13.602**
Parents	5	10234.772**	7335.990**	5155.414**	3718.291**	17.169**	21.942**	16.285**	18.294**
Crosses	8	2009.167**	1789.815**	1393.863**	1234.813**	13.420**	13.601**	5.951**	6.008**
Par. Vs. C.	1	108576.77**	91923.436**	63839.307**	54929.523**	21.823**	26.892**	53.770**	50.891**
Lines	2	1086.040**	1251.183**	1664.921**	1296.490**	20.596**	12.984**	16.500**	17.006**
Testers	2	5890.204**	4981.963**	1867.214**	1569.323**	21.285**	27.948**	0.442ns	1.173ns
Lines x testers	4	530.211**	463.056**	1021.659**	1036.718**	5.900**	6.735**	3.431*	2.926*
Error	28	109.191	101.757	153.536	126.763	0.326	0.212	0.602	0.422

* and ** Significant at 5% and 1% levels of probability, respectively.

Table 2: Continue.

S .o .v	d.f	Grain yield/plant			
		Location 1		Location 1	
		Year1	Year2	Year1	Year2
Replications	2	2.031ns	2.765ns	0.686ns	0.824ns
Genotypes	14	736.247**	762.098**	483.793**	460.214**
Parents	5	558.611**	534.094**	243.233**	230.590**
Crosses	8	85.018**	147.001**	67.448**	82.503**
Par. Vs. C.	1	6834.261**	6822.896**	5017.357**	4630.011**
Lines	2	8.379**	0.983ns	65.099**	63.776**
Testers	2	277.734**	504.759**	103.287**	128.356**
Lines x testers	4	26.980**	41.130**	50.702**	68.941**
Error	28	16.554	15.449	13.576	16.475

* and ** Significant at 5% and 1% levels of probability, respectively.

The interactions of genotypes, parents and crosses with the two years were highly significant for all grain yield and its component traits with the except of 1000-grain weight which had insignificant mean square. Also, the interaction of parents vs crosses with years was found to be non significant for all yield traits except for No. of filled grains/panicle was highly

significant. As well as, the interactions of genotypes, parents and crosses with the locations were highly significant for all grain yield and its component traits. P.vs C.xloc. which has insignificant values for No. of panicles/plant, significant values for 1000-grain weight and highly significant for the other studied traits. Interactions between genotypes, parents, crosses and parents vs crosses and years x locations were highly significant for No.of grains/panicle and No. of filled grains /panicle traits and non significant for the others studied traits except for the interaction of crosses x years x locations for grain yield/ plant showed significant values.

Table 3: Combined mean square estimates from ordinary and line x tester analysis for yield and its components traits over the two locations through the two years.

Sov	d.f	Grain yield /plant	No. of panicles /plant	No. of grains/ panicle	No. of filled grains/ panicle	1000-grain weight
Years	1	61.098**	61.519**	91.800**	1822.141**	1.342ns
Locations	1	12024.445**	1173.359**	22925.467**	114231.613**	215.124**
Years* Loc.	1	2.509ns	0.001ns	3.931ns	2.069ns	0.015ns
Error	8	1.576	0.088	15.776	8.181	0.035
Genotypes	14	2320.655**	98.235**	11110.718**	34634.83**	49.916**
Parents	5	1357.478**	106.658**	11127.543**	24951.749**	56.291**
Crosses	8	321.912**	66.415**	6855.437**	5834.780**	33.682**
Lines (L.)	2	67.683**	23.123**	7069.256**	4611.721**	65.023**
Testes (T.)	2	906.785**	110.670**	15606.433**	12991.333**	33.643**
L. x T.	4	156.590**	65.935**	2373.030**	2868.034**	18.031**
P. vs C.	1	23126.484**	310.680**	45068.841**	313450.135**	147.913**
G. x Y.	14	4.126**	3.160**	8.594**	120.989**	0.184ns
P. x Y.	5	2.284*	3.660**	6.966**	211.528**	0.231ns
C. x Y.	8	5.538**	3.172**	10.592**	17.323**	0.174ns
L. x Y.	2	6.590**	3.574*	28.260**	7.564**	0.259ns
T. x Y.	2	12.590**	4.468*	5.969**	45.958**	0.377ns
L. x T. x Y.	4	1.487ns	2.323ns	4.071*	7.884**	0.031ns
P. vs C.xY.	1	2.040ns	0.564ns	0.750ns	497.622**	0.029ns
G. x Loc.	14	115.925**	10.886**	263.597**	1158.077**	9.265**
P. x Loc.	5	205.854**	10.330**	424.089**	1268.494**	17.023**
C. x Loc.	8	52.442**	12.174**	195.098**	570.766**	4.910**
L. x Loc.	2	62.285**	33.035**	400.568**	670.722**	1.333ns
T. x Loc.	2	89.160**	4.715**	138.302**	1266.038**	16.805**
L. x T. x Loc.	4	29.162**	5.474**	120.762**	173.152**	0.751ns
P. vs C.xLoc.	1	174.144**	3.362ns	9.129**	5304.480**	5.315*
G. x Y.x Loc.	14	1.645ns	0.683ns	14.582**	8.421**	0.183ns
P. x Y.x Loc.	5	0.913ns	0.412ns	26.655**	12.695**	0.145ns
C. x Y.x Loc.	8	2.078*	0.793ns	4.535**	4.788**	0.213ns
L.xY. x Loc.	2	1.679ns	0.432ns	0.124ns	8.626**	0.471ns
T. x Y. x Loc.	2	5.602**	0.647ns	12.378**	5.375*	0.023ns
L.xT.xY.x Loc.	4	0.514ns	1.047ns	2.820*	2.576*	0.179ns
P.vs C.xY.xLoc.	1	1.841ns	1.158ns	34.593**	16.115**	0.133ns
Error	112	15.513	1.402	119.43	122.812	0.390

* and ** Significant at 5% and 1% levels of probability, respectively.

The results also illustrated that the general combining ability variance (GCA) for both lines and testers and specific combining ability (SCA) of lines x testers showed high significance in both the two years at normal and saline

conditions for all studied traits except for 1000-grain weight trait (GCA) for testers was non significant in saline conditions also grain yield/plant (GCA) for lines was non significant in the second year at normal condition. On the other hand, GCA of lines and testers and SCA for lines x testers were highly significant for all studied traits in combined data. The interactions of years with general combining ability (GCA) of lines and testers were non significant for 1000-grain weight and highly significant and significant for the rest of yield studied traits. But, The interactions of years with (SCA) of lines x testers were highly significant for No. of filled grains/panicle, significant for No. of grains/panicle and non significant for other yield traits. This indicated that the non-additive genetic variance is more stable for most studied traits than additive through years. The interactions of locations with both types of combining ability, (GCA) of lines and testers and SCA of lines x testers were highly significant for all yield studied traits except 1000-grain weight trait which showed non significant mean squares for interactions, GSA of lines and SCA of lines x testers. The interactions of locations and years with GCA of lines were non significant in all yield studied traits except for no. of filled grains /panicle which was highly significant. In the case of GCA of testers, the interaction was highly significant for No. of grains /panicle and grain yield /plant traits, significant for No. of filled grains /panicle trait and non significant for other yield studied traits. Therefore, there is no interaction between years and locations with SCA for lines x testers in all studied traits except for No. of grains /panicle and No. of filled grains / panicle the interactions were significant. These results indicated that both additive and non-additive genetic variances tended to interact with environments for the significant interactions. Therefore, selection for these traits would not be effective in a single environment, but more environments would be required. This finding indicate that the additive type of gene action played a major role in the inheritance of yield and its component traits. These results were in agreement with conclusions made by Lokaprakash *et al.* (1991), El-Refae (2002), El-Mowafi *et al.* (2003), Hammoud (2004), Abd El-Hadi and El-Mowafi (2005), Pradhan *et al.* (2006), Abd Allah (2008), El-Diasty *et al.* (2008), Shereen *et al.* (2009) and Nadali and Jelodar (2010).

Genetic parameters:

The estimates of genetic parameters of the studied yield and its component traits are shown in Table 4. The results cleared that the magnitude of non-additive genetic variance (σ^2D) for all studied traits which were positive at the two locations in the two years. Also, the magnitude of additive genetic variance (σ^2A) were positive for all studied traits in all conditions except for No. of panicles/plant in the first season at the first location. σ^2A was larger than σ^2D under all environments for all studied traits except for No. of panicles/plant at the two locations in the two years and yield /plant in both years of salinity location. This indicate that additive genetic variance is the master player in the inheritance of these traits.

Table 4: Estimation of genetic parameters for yield and its components traits at the two locations in the two years and the combined data over locations through years.

Table 4: Continue.

Genetic parameters	No. of panicles/plant					No. of grains/panicle				
	L1 Y1	L1Y2	L2Y1	L2Y2	Comb.	L1 1	L1Y2	L2Y1	L2Y2	Comb.
σ^2A	0.00	2.13	1.90	0.35	0.053	394.66	467.13	566.02	601.07	498.045
σ^2D	5.13	6.06	4.38	7.49	5.378	214.90	183.20	122.38	87.16	183.632
D.d	0.00	1.69	1.52	4.63	10.073	0.74	0.63	0.46	0.38	0.607
σ^2E	0.61	1.26	2.05	1.69	1.402	84.88	154.16	202.61	236.12	169.443
G	5.13	8.19	6.28	7.84	98.235	609.56	650.33	688.40	688.23	11110.718
σ^2P	5.74	9.45	8.33	9.53	99.637	694.43	804.49	891.01	924.36	11280.161
h^2_b	0.00	0.23	0.23	0.04	0.676	0.57	0.58	0.64	0.65	0.823
h^2_n	0.87	0.87	0.75	0.82	0.007	0.88	0.81	0.77	0.75	0.601
σ^2AY	-	-	-	-	0.189	-	-	-	-	1.449
σ^2AL	-	-	-	-	1.489	-	-	-	-	16.519
σ^2AYL	-	-	-	-	-0.338	-	-	-	-	2.287
σ^2DY	-	-	-	-	0.154	-	-	-	-	-27.562
σ^2DL	-	-	-	-	0.679	-	-	-	-	-8.114
σ^2DYL	-	-	-	-	-0.118	-	-	-	-	-55.541

Table 4: Continue.

Genetic parameters	No. of filled grains/plant					Grain yield / plant					1000-grain weight				
	L1 Y1	L1Y2	L2Y1	L2Y2	Comb.	L1 1	L1Y2	L2Y1	L2Y2	Comb.	L1 1	L1Y2	L2Y1	L2Y2	Comb.
σ^2A	657.31	589.67	165.42	88.04	329.639	7.44	3.05	6.93	1.37	18.369	1.739	1.739	1.739	1.739	1.739
σ^2D	140.34	120.43	289.37	303.32	228.769	2.34	2.17	17.49	0.84	11.750	1.470	1.470	1.470	1.470	1.470
D.d	0.46	0.45	0.31	1.89	0.833	10.28	0.84	1.70	0.92	0.800	0.919	0.919	0.919	0.919	0.919
σ^2E	109.19	101.76	563.54	126.75	5122.812	10.38	0.21	16.40	0.60	4.513	0.390	0.390	0.390	0.390	0.390
G	797.65	710.12	274.80	391.56	14634.830	15.82	5.23	23.52	2.25	20.639	9.916	9.916	9.916	9.916	9.916
σ^2P	906.85	811.86	808.33	518.72	18475.642	35.39	5.44	39.99	2.23	36.160	160.306	160.306	160.306	160.306	160.306
h^2_b	0.73	0.73	0.50	0.27	0.17	0.66	0.785	0.22	0.56	0.15	0.42	0.633	0.790	0.790	0.790
h^2_n	-	-	0.64	-	0.78	0.463	0.59	-	0.59	-	0.428	0.428	0.428	0.428	0.428
σ^2AY	-	-	-	-	2.097	-	-	-	-	0.900	0.032	0.032	0.032	0.032	0.032
σ^2AL	-	-	-	-	88.359	-	-	-	-	0.924	0.924	0.924	0.924	0.924	0.924
σ^2AYL	-	-	-	-	2.950	-	-	-	-	5.173	0.045	0.045	0.045	0.045	0.045
σ^2DY	-	-	-	-	-19.155	-	-	-	-	2.084	-0.060	-0.060	-0.060	-0.060	-0.060
σ^2DL	-	-	-	-	8.390	-	-	-	-	-2.338	0.060	0.060	0.060	0.060	0.060
σ^2DYL	-	-	-	-	-40.079	-	-	-	-	-2.275	-0.070	-0.070	-0.070	-0.070	-0.070
σ^2DYL	-	-	-	-	-	-	-	-	-	-5.000	-	-	-	-	-

Similar results were obtained by El-Mowafi (1988), El-Mowafi (1994), Hammoud (1996), Attia (2001), El-Mowafi (2001), El-Refae (2002) Sarker *et al.* (2002), El-Mowafi *et al.* (2003) Abd Allah (2008), Shereen *et al.* (2009) and Nadali and Jelodar (2010). On the other hand, the estimation of genetic parameters from the combined analysis showed that the additive genetic variance (σ^2A) were positive and larger than those of non-additive genetic variance (σ^2D) for all yield and its components traits. These result accurate the single analysis results and introduce the prove that the additive effects play the major role in the expression of yield traits except for No. of panicles/plant trait which was under control of dominance effects and the over-dominance play the big role in its expression.

Genetic parameters by years, locations and years x locations interactions also revealed that the magnitude of additive by locations ($\sigma^2A \times L$) were positive and larger than the corresponding values of non-additive by locations ($\sigma^2D \times L$) which were positive for all yield studied traits except for

No. of grains/panicle trait. While, the magnitude of additive by years ($\sigma^2A \times Y$) were positive and larger than non-additive by years ($\sigma^2D \times Y$) which recorded negative values for all yield studied traits except for No. of panicles/plant. For the $\sigma^2A \times Y \times L$ effects all traits revealed positive values except for No. of panicles /plant trait which exhibited negative magnitude value while, $\sigma^2D \times Y \times L$ effects revealed negative values for all studied traits. These result suggests that the non-additive effects are more stable over different environments than the additive effects.

The estimated values of heritability at the two locations in the two years and from the combined data over them revealed closed equal h^2_n values to h^2_b in some traits at some environments because of the zero value of dominance effects. The highest estimate of combined narrow sense heritability was observed in the case of No. of grains/panicle (0.601) and that confirms the big role to additive effects while, the lowest recorded in No. of panicles /plant (0.007) and that due to the highly influence of ecological conditions. On the other hand, the estimates of heritability in broad sense ranged from 0.823 for No. of grains/panicle to 0.633 in yield/plant. However, these results are in general agreement with those reported by Kuo and Liu (1987).

Estimation of GCA effects:

The estimated values of general combining ability effects (gi) for parental lines (CMS and restorer lines) for yield and its components in the two years at the two locations and their combined data are presented in Table 5. The restorer line Giza178R exhibited highly significant positive GCA effects for grain yield/plant trait in normal media and from the combined data, proving to be good combiners for this trait. In the same time, the restorer Giza181R exhibited highly significant positive GCA effects at all environments and from the combined data. The former cultivars which proved to be good combiners. For No. of panicles/plant trait, the restorer Giza181R revealed highly significant positive GCA effects at all environmental and from the combined data, this finding indicate that is excellent combiners at normal and saline environments. While, the female line IR69625A and the tester line Giza178R recorded highly significant positive GCA effects under normal environment and from the combined data.

Table 5: Estimation of general combining ability effects (gi) for lines and testers at the two locations in the two years and the combined data over locations in years for yield and its components traits.

Estimation of SCA effects:

Parents	No. of panicles/plant					No. of grains/panicle				
	Location 1		Location 2		Comb.	Location 1		Location 2		Comb.
	Year1	Year2	Year1	Year2		Year1	Year2	Year1	Year2	
CMS Lines										
IR58025A	-0.08	0.72	-1.71**	-1.28**	-0.59**	1.27	-0.72	-6.37	-8.48	-3.58
IR69625A	1.11**	0.90*	0.69	0.96*	0.91**	-14.11**	-13.30**	-10.60*	-9.51	-11.88**
IR70368A	-1.04**	-1.61**	1.03*	0.32	-0.32	12.83**	14.01**	16.97**	17.99**	15.45**
Restorer lines (Testers)										
Giza178R	0.66**	1.60**	0.35	0.74	0.84**	7.76*	7.28	3.46	4.40	5.72*
Giza181R	0.73**	0.81*	1.54**	1.62**	1.18**	14.26**	16.28**	19.79**	19.11**	17.36**
Giza182R	-1.40**	-2.40**	-1.89**	-2.37**	-2.02**	-22.01**	-23.56**	-23.25**	-23.51**	-23.08**
L.S.D 0.05%	0.53	0.77	0.98	0.89	0.39	6.29	8.48	9.72	10.49	4.30
0.01%	0.72	1.03	1.32	1.20	0.52	8.49	11.44	13.11	14.15	5.68

* and ** Significant at 5% and 1% levels of probability, respectively.

Table 5: Continue.

Parents	No. of filled grains/panicle					1000- grain weight				
	Location 1		Location 2		Comb.	Location 1		Location 2		Comb.
	Year1	Year2	Year1	Year2		Year1	Year2	Year1	Year2	
CMS Lines										
IR58025A	-3.60	-3.35	-13.26**	-11.43**	-7.91**	-1.73**	-1.34**	-1.56**	-1.57**	-1.55**
IR69625A	-8.73**	-9.75**	-0.67	-1.07	-5.05**	0.69**	0.34*	0.84**	0.99**	0.72**
IR70368A	12.33**	13.10**	13.92**	12.50**	12.96**	1.04**	0.99**	0.72**	0.58*	0.83**
Restorer lines (Testers)										
Giza178R	7.64*	8.60*	-0.76	1.39	4.22*	-0.85**	-0.86**	-0.12	-0.07	-0.48**
Giza181R	20.89**	18.01**	14.77**	12.46**	16.53**	-0.93**	-1.17**	-0.13	-0.32	-0.64**
Giza182R	-28.53**	-26.62**	-14.01**	-13.84**	-20.75**	1.78**	2.03**	0.26	0.39	1.11**
L.S.D 0.05%	7.13	6.89	8.46	7.69	3.66	0.39	0.31	0.53	0.44	0.21
0.01%	9.62	9.29	11.41	10.37	4.83	0.53	0.42	0.72	0.60	0.27

* and ** Significant at 5% and 1% levels of probability, respectively

Table 5: Continue.

Parents	Grain yield/plant				
	Location 1		Location 1		Comb.
	Year1	Year2	Year1	Year2	
CMS Lines					
IR58025A	0.17	-0.15	-2.99*	-3.05*	-1.51*
IR69625A	-1.04	0.38	0.77	1.23	0.33
IR70368A	0.87	-0.23	2.22	1.83	1.17
Restorer lines (Testers)					
Giza178R	3.23*	3.92**	0.94	1.19	2.32**
Giza181R	3.19*	4.72**	2.82*	3.04*	3.44**
Giza182R	-6.41**	-8.64**	-3.76**	-4.23**	-5.76**
L.S.D 0.05%	2.78	2.68	2.52	2.77	1.30
0.01%	3.75	3.62	3.39	3.74	1.72

* and ** Significant at 5% and 1% levels of probability, respectively.

The results indicate that both of No. of grains/panicle and No. of filled grains/panicle traits tack the same direction, the CMS line IR70368A and the tester line Giza181 showed highly significant positive GCA effects in each year at each location and from the combined data. So these genotypes will be successful in breeding hybrids with high number of total and filled grains at both normal and saline environments.

Concerning 1000-grain weight traits, the results indicated that the two CMS lines, IR69625A and IR70368A showed highly significant and positive

GCA effects at single and combined data. It could be also concluded that these two CMS lines were excellent combiners for 1000-grain weight trait. It could be of practical interest in a hybrid rice breeding program towards developing high yielding genotypes under salinity and normal environments. Also, the restorer line Giza182R exhibited high positive GCA effect at normal and from the combined data.

The estimated values of specific combining ability effects (S_{ij}) for yield and its component traits in years at locations and for the combined data are presented in Table 6. The results revealed that all F_1 hybrids showed insignificant effects for grain yield /plant trait at the two locations in the two years and their combined data except for the hybrids IR58025A x Giza182R and IR70368A x Giza181R, which showed highly significance SCA effects from the combined data. The results also indicated that, four F_1 hybrids out of the nine hybrid combinations showed significant S_{ij} for No. of panicles/plant trait from the combined data. In the same time, the hybrid combination IR58025A x Giza182R consider good combination under all conditions. But the combination IR69625A x G181R was the best under saline media and IR70368A x Giza178R was good at the normal conditions.

Concerning No. of grain/panicle and filled grains/panicle traits, the results indicated that most of F_1 hybrid showed significant positive S_{ij} at the two locations in the two years. However, four and two hybrids recorded highly significant positive S_{ij} from the combined data for No. of grains/panicle and filled grains/panicle, respectively. Furthermore, the hybrid combination IR58025A x Giza178R is considered as best combination for No. of grains/panicle trait. While, the hybrid IR70368A x Giza181R was the best combination for No. of filled grains/panicle.

The results also illustrated that three F_1 hybrids exhibited highly significant desirable S_{ij} from combined data for 1000-grain weight trait, these hybrids were IR58025A x Giza182R, IR69625A x Giza178R and IR70368A x Giza181R. Whereas, the hybrid IR58025A x Giza182R scored high significant effects under all conditions. The hybrids IR69625A x Giza178R and IR70368A x Giza181R were exhibited high SCA effects at normal condition.

It could be mentioned that the significant positive values of S_{ij} which were observed revealed the possibility of using them in hybrid rice breeding program. Generally, the results revealed that the F_1 hybrids IR70368A x Giza181R and IR58025A x Giza182 were the best S_{ij} under all conditions for all studied yield and its component traits.

Table 6: Estimation of specific combining ability effects (S_{ij}) for nine hybrids at the two locations in the two years and their combined data over locations in years for yield and its components traits.

Hybrids	No. of panicles/plant					No. of grains/panicle				
	Location 1		Location 2		Comb.	Location 1		Location 2		Comb.
	Year1	Year2	Year1	Year2		Year1	Year2	Year1	Year2	
IR58025A xGiza178R	-1.56**	-1.62*	-0.50	-0.86	-1.13**	11.09*	11.36	10.65	9.06	10.54**
xGiza181R	-1.14*	-0.76	-2.22*	-2.70**	-1.96**	-19.08**	-19.30*	-17.98*	-16.72	-18.27**
xGiza182R	2.70**	3.38**	2.71**	3.56**	3.09**	7.99	7.94	7.33	7.67	7.73*
IR69625A xGiza178R	-0.35	0.67	0.94	0.78	0.51	0.27	-0.59	-4.06	-3.24	-1.91
xGiza181R	0.64	1.13	0.71	1.63*	1.03**	10.00	8.94	6.17	5.08	7.55*
xGiza182R	-0.29	-1.80*	-1.65	-2.41**	-1.54**	-10.27	-8.35	-2.11	-1.83	-5.64
IR70368A xGiza178R	1.91**	0.95	-0.44	0.08	0.62*	-11.36	-10.77	-6.59	-5.81	-8.63*
xGiza181R	0.50	0.64	1.50	1.07	0.93*	9.08	10.36	11.81	11.64	10.72**
xGiza182R	-2.41**	-1.59*	-1.06	-1.14	-1.55**	2.28	0.41	-5.21	-5.83	-2.09
L.S.D 0.05%	0.93	1.33	1.69	1.54	0.68	10.89	14.68	16.83	18.17	7.44
0.01%	1.25	1.79	2.28	2.07	0.90	14.70	19.81	22.71	24.51	9.83

** Significant at 5% and 1% levels of probability, respectively.

Table 6: Continue.

Hybrids	No. of filled grains/panicle					1000- grain weight				
	Location 1		Location 2		Comb.	Location 1		Location 2		Comb.
	Year1	Year2	Year1	Year2		Year1	Year2	Year1	Year2	
IR58025A xGiza178R	11.40	10.72	10.54	10.76	10.58**	-0.88*	-0.03	-0.87	-0.89*	-0.92**
xGiza181R	-13.38*	-13.36*	-18.68*	-20.21**	-16.41**	-0.88*	-0.83**	-0.47	-0.32	-0.63**
xGiza182R	1.98	2.64	8.13	9.46	5.55	1.75**	1.86**	1.35**	1.21**	1.54**
IR69625A xGiza178R	3.13	1.75	8.46	6.86	5.05	0.98**	0.92**	0.74	0.78*	0.86**
xGiza181R	3.22	5.07	1.10	2.19	2.90	0.01	-0.20	-0.06	0.03	-0.05
xGiza182R	-6.36	-6.83	-9.56	-9.04	-7.95*	-0.99**	-0.72*	-0.69	-0.81*	-0.80**
IR70368A xGiza178R	-14.53*	-12.47*	-19.00*	-17.61*	-15.90**	-0.10	0.11	0.13	0.11	0.06
xGiza181R	10.16	8.29	17.58*	18.02**	13.51**	0.86*	1.03**	0.53	0.30	0.68**
xGiza182R	4.38	4.19	1.42	-0.41	2.39	-0.76*	-1.14**	-0.66	-0.41	-0.74**
L.S.D 0.05%	12.36	11.93	14.65	13.31	6.33	0.68	0.54	0.92	0.77	0.36
0.01%	16.67	16.09	19.77	17.96	8.37	0.91	0.73	1.24	1.04	0.47

* and ** Significant at 5% and 1% levels of probability, respectively.

Table 6: Continue.

Hybrids	Grain yield/plant				
	Location 1		Location 2		Comb.
	Year1	Year2	Year1	Year2	
IR58025A xGiza178R	0.21	-0.26	0.71	0.14	0.09
xGiza181R	-2.80	-3.48	-4.86*	-4.92*	-3.95**
xGiza182R	3.01	3.75	3.88	4.79	3.86**
IR69625A xGiza178R	-1.05	-1.08	1.39	2.34	0.40
xGiza181R	0.70	0.69	0.47	0.29	0.54
xGiza182R	0.35	0.40	-1.87	-2.63	-0.94
IR70368A xGiza178R	1.26	1.35	-2.10	-2.48	-0.49
xGiza181R	2.11	2.80	4.11	4.63	3.41**
xGiza182R	-3.36	-4.14	-2.01	-2.15	-2.92*
L.S.D 0.05%	4.81	4.65	4.36	4.80	2.25
0.01%	6.49	6.27	5.88	6.48	2.98

* and ** Significant at 5% and 1% levels of probability, respectively.

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دراسات وراثية علي القدرة علي التآلف لصفات المحصول ومكوناته تحت كل من الظروف العادية والملحية في بعض هجن الأرز
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أجري هذا البحث بغرض دراسة كل من نوعي القدرة العامة والخاصة على التآلف لصفات المحصول ومكوناته في الأرز الهجين تحت كل من الظروف العادية والملحية باستخدام تحليل السلالة (ثلاثة سلالات عقيمة الذكر سيتوبلازميا CMS) x الكشاف (ثلاثة أصناف معيدة للخصوبة Restorers). أجريت تجربتان حقليتان لتقييم التراكيب الوراثية احدهما تحت الظروف الملحية الطبيعية بمحطة البحوث الزراعية بالسرو والأخرى تحت الظروف العادية بمحطة البحوث الزراعية بسخا- كفر الشيخ وقد تم تكرار هاتان التجربتان في كلا الموقعين عامي 2006-2007. أظهرت النتائج أن متوسط المربعات الراجع إلى كل من التراكيب الوراثية والآباء والهجن كانت عالية المعنوية تحت كل من الظروف العادية والملحية خلال السنتين وكذلك التحليل المشترك بينهم. اظهر التفاعل بين كلا من التراكيب الوراثية والآباء والهجن مع السنين و المواقع تباينات عالية المعنوية لكل صفات المحصول ومكوناته ما عدا صفة وزن الألف حبة التي أظهرت تباينات غير معنوية مع السنين. ومن ناحية أخرى كانت التباينات الناتجة عن تفاعل التراكيب الوراثية والآباء والهجن مع المواقع x السنين غير معنوية لكل الصفات عدا صفتي عدد الحبوب في السنبله وعدد الحبوب الممتلئة للسنبله التي كانت عالية المعنوية.

التباينات الراجعة لكل من نوعي القدرة على التآلف (GCA و SCA) كانت عالية المعنوية تحت كل من الظروف البيئية العادية والملحية والتحليل المشترك بينهم أيضا التباين الوراثي لتفاعل كل من السلالات والكشافات و السلالات x الكشافات مع السنين ومع المواقع كان عالي المعنوية لكل الصفات بينما كان متوسط مربعات التفاعل بين كل من السلالات والكشافات و السلالات x الكشافات مع السنين x المواقع كانت غير معنوية لكل الصفات عدا صفتي عدد الحبوب للسنبله وعدد الحبوب الممتلئة للسنبله. التهجين بين الآباء ذات القدرة العامة على التالف عالي x عالي أو منخفض x عالي أعطى أفضل التراكيب ذات قوة الهجين العالية مثل IR70368A x Giza181R وعلى صعيد متصل كانت السلالة العقيمة الذكر سيتوبلازميا الأفضل بين كل الامهات من حيث قدرتها العامة على التالف مع الكشافات في حين كانت الكشافات Giza181R و Giza182R هما الأقدر على خلط جيناتها مع السلالات لأغلب الصفات المحصولية كذلك فان الهجين IR70368A x Giza181R والهجين IR58025A x Giza182R يعتبران أفضل التوليفات وأظهرا قدرة خاصة على التالف عالية لمعظم الصفات المحصولية. وقد أوضحت النتائج أن التباين المضيف يلعب الدور الأكبر في توريث كل صفات المحصول ومكوناته تحت الدراسة فيما عدا صفة عدد السنابل لكل نبات حيث كان تأثير التباين الغير مضيف هو المتحكم الرئيسي في توريث هذه الصفة. علاوة على ذلك كانت قيم تفاعل التباين المضيف مع المواقع و السنين و المواقع x السنين موجبة و اكبر من قيم تفاعل التباين الغير مضيف لكل صفات المحصول ومكوناته. قياسات المكافئ الوراثي بمعنييه الواسع والضيق كانت متقاربة لبعضها في القيم لأغلب صفات المحصول ومكوناته وذلك يشير أيضا إلى أن التباين المضيف يلعب الدور الأكبر في توارث هذه الصفات.

قام بتحكيم البحث

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