

STUDIES ON COMBINING ABILITY FOR YIELD AND ITS COMPONENTS IN RICE USING LINE X TESTER MATING DESIGN UNDER SALINE SOIL CONDITIONS

Sultan, M. S.¹; M. A. Abdel-Moneam¹; H. M. Hassan² and E. M. Daher²

¹Agronomy Department, Fac. of Agric. Mansoura University, Egypt.

²Rice Research Section, Field Crops Res. Inst., ARC, Giza, Egypt.

ABSTRACT

A Study on combining ability and genetic parameters were conducted on 39 F1 hybrids along with sixteen rice genotypes (thirteen lines and three testers) to understand the pattern of inheritance of yield and its components for selecting superior genotypes. The experiment was carried out using line x tester mating design, during 2011 and 2012 rice growing seasons at the Lysimeter and the Experimental Farm of Rice Research and Training Center, Sakha, Kafr El-Sheikh, Egypt. Both GCA and SCA variances were found to be significant or highly significant for all studied traits. Sakha 102 and Giza 177 rice genotypes were the best general combiners due to highly significant GCA effects for number of days to 50% heading under normal conditions. Moreover, Sakha 106 was the best general combiner for number of days to 50% heading at two levels 4000 ppm (S1) and 6000 ppm (S2) of salinity. The genotype, Gaori was the best general combiner for plant height under all conditions and for number of filled grains/panicle and sterility% under normal conditions. IEET1444 was the best general combiner for number of panicles/plant, salinity index and grain yield/plant under two levels (S1 and S2) of salinity. While, Wab 880SG-33 was the best general combiners for 1000-grain weight under all conditions, and for number of filled grains/panicle under two levels(S1 and S2) of salinity. Suweon 345 was the best general combiner for number of panicles/plant under normal conditions and for sterility% under two levels (S1 and S2) of salinity. On the other hand, the crosses, IET 1444 x Sakha 104, Wab 880SG-33 x Sakha104, BG 34-8 x Giza 178 and Gz 1368-S-5-4 x Giza 178 were found to be the best cross combinations for most of the studied traits, these crosses had high and significant SCA in desirable direction under normal and two levels of salinity condition. The highest estimated values of phenotypic (V_{ph}) and genotypic (V_g) variances were observed for number of filled grains/panicle and sterility % indicating better scope for the genetic improvement in these two mentioned traits. High broad-sense heritability, coupled with high genetic advance, were observed for number of filled grains/panicle, sterility% and plant height under normal and two levels of salinity condition, indicating the role of additive genetic variance in the expression of these traits and direct selection might be highly effective in early generations to improve these traits under normal and two levels of salinity. Highly significant positive correlation coefficients were recorded between grain yield per plant and each of number of panicles/plant, number of filled grains/panicle and 1000- grain weight under normal and two levels of salinity conditions.

Keywords: Rice, combining ability, salinity, genetic advance, yield and line x tester design

INTRODUCTION

Rice is one of the most important cereal crops, which is a very popular staple food in many developing countries such as Egypt. Grain yield is one of the most breeding objectives. Considerable efforts have been made by breeders to study the genetic expression for numerous characters contributing to yield potential including days to 50% heading, plant height, number of panicles/ plant, 1000-grain weight, number of filled grains/ panicle, salinity index, sterility % and grain yield traits.

Rice is considered a salt-sensitive crop species it has a salinity threshold of 3 dS/m, with a 12% reduction in yield per dSm^{-1} , beyond this threshold. Therefore, rice yields can be reduced by up to 50% when grown under moderate (6 dSm^{-1}) salinity conditions (Zeng *et al.*, 2002). In general, rice plants are very sensitive to salinity stress at young seedling stages, relatively tolerant at the later vegetative stages, and sensitive again during reproduction (Flowers and Yeo., 1981 and Lutts *et al.*, 1995).

The decreasing of rice productivity in salt-affected areas can be addressed through an integrated approach involving both reclamation and management strategies, as well as enhanced genetic tolerance. However, management practices are not always feasible in the long run, as in coastal areas where salt stress is seasonal or in inlands when reclamation costs are prohibitive. In both cases, developing salt-tolerant varieties seems more feasible to enhance the productivity of these marginal lands. Rice is recommended as a crop best suited for salt affected soils because it can grow well under flooded conditions that can help in leaching harmful salts (Ismail *et al.*, 2008)

The success of a plant breeding program greatly depends on right choice of parents for hybridization and the gene action of different economic traits. Combining ability analysis provides such information so as to frame the breeding program effectively. The line x tester analysis gives reliable information about the nature and magnitude of gene action and combining ability effects present in the genetic materials. Dhillon. (1975) pointed out that the combining ability gives useful information on the choice of parents in terms of expected performance of the hybrids and their progenies. The line x tester analysis method is used to breed both self and cross-pollinated plants and to estimate favorable parents and crosses, and their general and specific combining abilities (Kempthorne, 1957).

The performance of parent may not necessarily reveal it to be a good or poor combiner. Therefore, gathering information on nature of gene effects and their expression in terms of combining ability is necessary. At the same time, it also elucidates the nature of gene action involved in the inheritance of characters. General combining ability (GCA) is attributed to additive gene effects and additive x additive epistasis and is theoretically fixable. On the other hand, specific combining ability attributable to non-additive gene action may be due to dominance or epistasis or both and is non-fixable. The presence of non-additive genetic variance is the primary justification for initiating the hybrid program (Pradhan *et al.*, 2006). The main objectives of

the present investigation are to: 1- Study the general and specific combining abilities and genetic parameters for yield and its components traits under normal and saline conditions. 2- Study the phenotypic correlation coefficients among all possible pairs of the studied characters under normal and saline conditions.

MATERIALS AND METHODS

The experiment was carried out using line x tester mating design, during 2011 and 2012 rice growing seasons at the Lysimeter and the Experimental Farm of Rice Research and Training Center (RRTC), Sakha, Kafr El-Sheikh, Egypt. The experimental material of the present study comprised thirteen lines, namely, IEET1444, Gz 1368-S-5-4, BG 34-8, Agami M1, Giza 182 and Gaori (tolerant genotypes for salinity), Wab 880SG-33, Suweon 345 and Yabani lulu (moderately tolerant to salinity), and Wab 880-p1, Giza 177, Sakha 106 and Sakha 105 (sensitive genotypes to salinity); and three testers namely, Sakha 104 and Giza 178 (tolerant genotypes to salinity) and Sakha 102 (sensitive genotype to salinity) with diverse pure and elite genotypes of rice. The parents were selected on the basis of different genetic and geographical origin. The testers used for this study were selected according to their subcontinent origin and adaption to Egyptian locality and their yield potential was up to the mark (The lines were originated from RRTC, Egypt). In 2011, the thirteen lines and three testers were grown at RRTC farm in three successive dates of planting with ten days intervals in order to overcome the differences in flowering time between parents. At flowering time, hybridization between the parents was done, 30 days old seedlings of each parent were individually transplanted in the permanent field in seven rows following the technique proposed by Jodon (1938) to produce their F₁ using line x tester mating design.

In 2012 season, seeds of the line x tester F₁ Hybrids and their parents were sown in dry seedbed. After thirty days from sowing, seedlings of each F₁ hybrids and their parents were transplanted under normal and saline soil conditions in Lysimeter at randomized complete block design experiment with three replications. Each replicate comprised 5 row for each F₁ cross and 20 x 20cm apart was maintained between rows and seedlings. All agricultural practices such as sowing date, fertilizer application and weed control were applied as recommended. Irrigation and drainage cycle were accurately controlled in normal and saline conditions. The saline soil conditions were adjusted to 4000 ppm (S1) and 6000 ppm (S2), in addition, the normal soil conditions were irrigated by pumping water. The mean value of electrical conductivity (EC) of irrigation water is 0.77 mmhos/cm for normal, otherwise, 6.9 and 10.6 mmhos/cm at 25^o C for the two levels of saline soil condition, respectively. The water was artificially salinized by applying sodium chloride (NaCl) and calcium chloride (CaCl₂). The Lysimeter plot is concrete beds (1m width x 2m length) filled with soil to 100 cm depth in three layers, i.e., 60 cm clay at surface layer, 20 cm sand at the middle layer and 20 cm gravel at bottom layer. Data were collected for vegetative, yield and its components

traits; number of days to 50% heading, plant height (cm), number of panicles/plant, number of filled grains/ panicle, sterility %, 1000- grain weight (g), salinity tolerance index and grain yield /plant (g) according to the standard evaluation system of IRRI (1996).

Combining ability analysis was done using line x tester. The variances for general combining ability and specific combining ability were tested against their respective error variances derived from ANOVA reduced to mean level. Significance test for GCA and SCA effects were performed using T-test. The following variance components were estimated based on the expectations of mean squares according to Kempthorne (1957).

RESULTS AND DISCUSSION

Estimates of general and specific combining ability effects

General combining ability effects:

The estimates of general combining ability effects consider an important indicator of the potential of parental lines for generating superior breeding populations. A negligible or negative combining ability effect indicates a poor ability to transfer its genetic superiority to hybrids. The largest significant positive values have the largest effects. On the other hand, the largest significant negative values have the smallest effects, except in case of sterility %, duration (days) and plant height traits. Obviously, under normal conditions, Table 1 indicated that the line Giza 177 and the tester Sakha 102 were the best general combiners for earliness, plant height and 1000- grain weight. While, Gaori was the best general combiners for plant height, number of filled grains per panicle and sterility%. In addition, Suweon 345 rice line was a good general combiner for increasing number of panicles/plant, 1000- grain weight, number of filled grains/panicle, sterility% and grain yield/plant. While, Wab 880SG-33 and Wab 880- p1 were the best general combiners for 1000- grain weight. The results revealed that among the studied parents, Gz 1368-S-5-4 followed by Suweon 345 and Giza 178 were the best general combiners for grain yield /plant. However, some parents with high mean values exhibited low GCA effects. Hence, both performances *per se* and GCA effects should be taken into account for parental selection.

It is obvious that none of the parents were found to be good combiners for all the studied traits. Hence, it would be desirable to have multiple crosses involving the parents, viz., IEET 1444, Giza 178, Wab 880SG-33, Suweon 345, Gaori and Gz 1368-S-5-4 for practicing a selection in the segregating generations to isolate superior genotypes under normal conditions.

On the other hand, under level S1 of salinity condition, results in the Table 1 show that lines, Sakha106, Wab 880SG-33, Wab 880-p1 and IEET1444 and tester, Sakha 102 were the best general combiners for earliness. While, Gaori, Yabani lulu, Giza 177and Wab 880-p1 were the best general combiners for plant height. In addition, the genotype IEET 1444 was good general combiners for improving number of panicles per plant, salinity

tolerance index and grain yield/plant. While, Wab 880SG-33 was the best general combiner for 1000- grain weight and number of filled grains per panicle. The results revealed that among the studied parents, Suweon 345 followed by Wab 880SG-33 and Yabani lulu were the best general combiners for sterility%. Moreover, IEET1444 and Gz1368-S-5-4 were the best general combiners for grain yield/plant. Regarding the level (S2) of salinity condition, results in Table (1) exhibited that Sakha 106 and IEET1444 were the best general combiners for earliness.

Table 1: Estimates of general combining ability effects for yield and its related traits for parental genotypes.

Genotypes	Days to 50% heading			Plant height (cm)		
	N	S1	S2	N	S1	S2
L ₁ - Wab 880SG-33	1.92	-3.92**	-1.05	11.08**	3.89**	-6.72**
L ₂ - Wab 880-p1	-2.08	-5.70**	-4.05**	12.74**	-3.89**	-2.05
L ₃ - IEET 1444	0.03	-5.92**	-5.39**	-4.59**	0.22	2.62
L ₄ - Gaori	-2.63	1.08	1.28	-19.92**	-17.11**	-14.05**
L ₅ - Giza 177	-7.74**	3.30*	-6.05**	-11.26**	-6.22**	-5.39**
L ₆ - Giza 182	3.59**	0.74	-2.27	-3.92**	-3.11*	-1.05
L ₇ - Sakha 106	-5.08**	-6.70**	-10.39**	-13.92**	2.56	2.62
L ₈ - Sakha 105	-4.41**	5.30**	-0.72	-14.81**	-2.11	-1.39
L ₉ - Suweon 345	1.26	1.74	2.62	9.19**	-2.11	-3.39*
L ₁₀ - Gz 1368-S-5-4	-0.08	-2.81*	2.95*	11.41**	8.89**	9.95**
L ₁₁ - BG 34-8	6.92**	5.08**	8.39**	19.74**	19.22**	18.28**
L ₁₂ - Agami M1	5.26**	3.74**	6.39**	6.86**	9.89**	11.28**
L ₁₃ - Yabani lulu	3.03*	4.08**	8.28**	-2.59	-10.11**	-10.72**
S.E (g _i)	1.33	1.40	1.41	1.32	1.35	1.37
S.E (g _i -g _j)	1.88	1.97	1.99	1.87	1.90	1.93
L.S.D 0.05	2.66	2.8	2.82	2.64	2.7	2.74
0.01	3.54	3.72	3.75	3.51	3.59	3.64
T ₁ - Sakha 102	-8.67**	-6.03*	-4.77	-5.64*	-1.80	-0.59
T ₂ - Sakha 104	9.85**	5.21	6.54*	4.59	-4.93	-6.13*
T ₃ - Giza 178	-1.18	0.82	-1.77	1.05	6.74*	6.72*
S.E (g _i)	2.76	2.91	2.93	2.75	2.80	2.85
S.E (gt-g _j)	0.90	0.95	0.96	0.90	0.91	0.93
LS D at 0.05	5.52	5.82	5.86	5.5	5.6	5.7
at 0.01	7.34	7.74	7.79	7.32	7.45	7.58

Table 1 : Cont.

Genotypes	No. of panicles/plant			1000-grain weight (g)		
	N	S1	S2	N	S1	S2
L ₁ - Wab 880SG-33	-8.21**	-2.46	-1.00	0.40**	0.36*	0.38*
L ₂ - Wab 880-p1	-0.55	-0.46	1.00	0.22**	0.09	0.12
L ₃ - IEET 1444	5.45**	4.54**	5.33**	-0.21**	0.01	-0.19
L ₄ - Gaori	-3.88*	-0.46	-2.33	-0.17**	-0.11	0.09
L ₅ - Giza 177	-2.55	-3.46*	-3.00*	0.13**	0.20	0.03
L ₆ - Giza 182	-2.44	1.87	0.67	0.04	0.07	0.22
L ₇ - Sakha 106	-3.55**	-2.46	-3.33*	0.15**	0.13	0.02
L ₈ - Sakha 105	1.45	-1.80	-1.00	-0.01	0.06	0.06
L ₉ - Suweon 345	10.45**	0.54	1.33	0.17**	0.06	0.07
L ₁₀ - Gz 1368-S-5-4	4.45**	4.21**	4.33**	-0.04	-0.04	-0.02
L ₁₁ - BG 34-8	1.12	3.87**	2.00	-0.41**	-0.50**	-0.40*
L ₁₂ - Agami M1	-1.21	-0.13	0.00	-0.24**	-0.12	0.11
L ₁₃ - Yabani lulu	-0.55	-3.80**	-4.00**	-0.04	-0.19	-0.48**
S.E (g _i)	1.28	1.32	1.30	0.03	0.16	0.17
S.E (g _{r-g})	1.82	1.87	1.84	0.04	0.22	0.25
L.S.D 0.05	2.56	2.64	2.60	0.06	0.32	0.34
0.01	3.40	3.51	3.5	0.08	0.43	0.45
T ₁ - Sakha 102	-3.73	-2.03	-0.74	0.15*	0.41	0.10
T ₂ - Sakha 104	-2.01	-4.41	-2.97	0.07	0.27	0.13
T ₃ - Giza 178	5.74*	6.44*	3.72	-0.22**	-0.69*	-0.23
S.E (g _i)	2.67	2.75	2.71	0.07	0.33	0.36
S.E (gt-g)	0.87	0.90	0.88	0.02	0.11	0.12
LS D at 0.05	5.34	5.5	5.4	0.14	0.66	0.72
at 0.01	7.10	7.32	7.2	0.19	0.88	0.96

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

Abbreviations: N, normal conditions, S1, first level of salinity (4000ppm), S2, second level of salinity (6000ppm)

Table 1 : Cont.

No. Genotype	No. of filled grains/panicle			salinity index	
	N	S1	S2-	S1	S2
L ₁ - Wab 880SG-33	-9.46**	26.34**	16.92**	-1.37	-1.58
L ₂ - Wab 880-p1	24.54**	-3.21*	-9.20**	-6.30**	-2.63*
L ₃ - IEET 1444	7.21**	10.79**	3.58*	15.96**	7.99**
L ₄ - Gaori	44.54**	-13.99**	-14.42**	-7.22**	-1.17
L ₅ - Giza 177	-26.13**	5.23**	1.14	-3.92**	0.38
L ₆ - Giza 182	-0.13	-1.10	5.14**	-0.25	-2.12
L ₇ - Sakha 106	-28.13**	17.12**	-1.64	-0.09	2.22*
L ₈ - Sakha 105	6.87**	1.79	10.03**	-4.77**	-0.33
L ₉ - Suweon 345	28.54**	13.12**	12.36**	-10.32**	-5.79**
L ₁₀ - Gz 1368-S-5-4	7.21**	-1.88	11.69**	-8.11**	-5.09**
L ₁₁ - BG 34-8	-73.80**	-31.33**	-11.20**	11.43**	6.32**
L ₁₂ - Agami M1	6.54**	-3.77*	-3.53*	6.19**	-2.87*
L ₁₃ - Yabani lulu	12.21**	-19.10**	-20.86**	8.76**	4.66**
S.E (g _i)	1.45	1.53	1.56	1.04	1.08
S.E (g _{r-g})	2.05	2.17	2.20	1.48	1.52
L.S.D 0.05	2.9	3.06	3.12	2.08	2.16
0.01	3.86	4.07	4.15	2.77	2.87
T ₁ - Sakha 102	-13.72**	-11.38**	-6.86*	4.75*	5.71*
T ₂ - Sakha 104	2.28	-2.12	-5.48	-3.76	-4.06
T ₃ - Giza 178	11.44**	13.50**	12.34**	-0.99	-1.65
S.E (g _i)	3.02	3.19	3.24	2.17	2.24
S.E (gt-g)	0.99	1.04	1.06	0.71	0.73
LS D at 0.05	6.04	6.38	6.48	4.34	4.48
at 0.01	8.03	8.49	8.62	5.77	5.96

*and ** significant at 0.05 and 0.01 probability levels, respectively. Abbreviations: N, normal conditions, S1, first level of salinity (4000ppm), S2, second level of salinity (6000ppm)

Table 1: Cont.

Genotype	Sterility %			Grain yield/ plant (g)		
	N	S1	S2	N	S1	S2
L ₁ - Wab 880SG-33	-11.29**	-12.19**	-15.54**	2.79	0.71	-0.07
L ₂ - Wab 880-p1	-6.51**	-5.63**	2.68	-13.47***	-6.29**	-3.10*
L ₃ - IEET 1444	6.03**	1.17	4.54**	-0.52	12.30**	6.26**
L ₄ - Gaori	-18.28**	1.90	11.29**	-6.33**	-5.14**	-1.13
L ₅ - Giza 177	-2.73	-6.69**	-4.71**	-5.79**	-500**	-0.16
L ₆ - Giza 182	-3.46*	6.65**	10.11**	5.53**	-0.32	-1.96
L ₇ - Sakha 106	-4.46**	-7.21**	-0.55	-10.49**	-1.80	-0.16
L ₈ - Sakha 105	-7.36**	-0.60	-10.28**	6.43**	-1.10	1.98
L ₉ - Suweon 345	-10.53**	-15.31**	-20.90**	17.37**	-4.08*	-3.54*
L ₁₀ - Gz 1368-S-5-4	5.71**	7.89**	3.56*	37.35**	5.53**	3.96**
L ₁₁ - BG 34-8	40.04**	29.27**	18.59**	-19.32**	1.16	-0.62
L ₁₂ - Agami M1	14.24**	8.33**	2.59	-3.01	4.68**	-3.92**
L ₁₃ - Yabani lulu	-1.41	-7.58**	-1.39	-10.53**	1.35	2.47
S.E (g)	1.38	1.55	1.48	1.52	1.68	1.36
S.E (g/g)	1.95	1.20	2.10	2.15	2.37	1.93
L.S.D 0.05	2.76	3.1	2.96	3.04	3.36	2.72
0.01	3.67	4.12	3.94	4.04	4.47	3.62
T ₁ - Sakha 102	-4.13	7.37*	-6.34*	-19.85**	-7.86*	-5.75*
T ₂ - Sakha 104	6.21*	-2.06	2.63	9.22**	-1.06	1.17
T ₃ - Giza 178	-2.08	-5.31	3.71	10.63**	8.91*	4.58
S.E (g)	2.87	3.24	3.09	3.17	3.49	2.84
S.E (gt-g)	0.94	1.06	1.01	1.03	1.14	0.93
LS D at 0.05	5.74	6.48	6.18	6.34	6.98	5.68
at 0.01	7.63	8.62	8.22	8.43	9.28	7.55

*and ** significant at 0.05 and 0.01 probability levels, respectively. Abbreviations: N, normal conditions, S1, first level of salinity (4000 ppm), S2, second level of salinity (6000 ppm).

While, Gaori was the greatest general combiner for plant height. In addition, the genotype, IEET1444 was good general combiners for improving number of panicles per plant, salinity tolerance index and grain yield/plant. While, Wab 880SG-33 was the best general combiner for 1000-grain weight and number of filled grains per panicle. The results revealed that among the studied parents, Suweon 345 followed by Wab 880SG-33 and Sakha 105 were the best general combiners for sterility%. Moreover, IEET1444 and Gz1368-S-5-4 were the best general combiners for grain yield /plant. Similar results were obtained previously by Shehata, (2004), Verma and Srivastava (2004), Soroush and Moumeni (2006). El Abd *et al.* (2007), Viswanathan Satheesh and Thiyagarajan (2008) and Muthuramu *et al.*, (2010) and El-Naem (2010).

Specific combining ability effects:

High specific combining ability effects were caused by the dominance and interaction or epistatic effects (non-fixable genes) that existed between the crossed parents. The same can be used as an index to determine the usefulness of a particular cross-combination in the exploitation of heterosis. As shown in Table 2, under normal conditions, 18 crosses out of 39 cross combinations possessed significant desirable SCA effects for number of days to 50% heading, the highest estimated negative value (-14.18) was recorded in Suweon 345 x Sakha 104 rice hybrid followed by Gaori x Sakha 104

(-12.96) and BG 34-8 X Giza 178 (-11.82). Furthermore, the hybrids, Giza 182 x Giza 178 and Suweon 345 x Sakha 102 were the best cross combinations to improve shortness of plant height.

Table 2: Estimates of specific combining ability effects for yield and its related traits in f1 crosses

Genotypes	Days to 50% heading			Plant height (cm)		
	N	S1	S2	N	S1	S2
Wab 880 SG -33 x Sakha 102	-2.33**	9.03**	9.77**	-2.69**	-7.86**	1.26
Wab 880SG -33 x Sakha 104	8.15**	-7.21**	-7.54**	1.08	15.27**	-0.21
Wab 880SG -33 x Giza 178	-5.82**	-1.82*	-2.23**	1.62*	-7.40**	-1.05
Wab 880-p1 x Sakha 102	2.67**	12.47**	11.77**	6.64**	-3.09**	-6.41**
Wab 880-p1 x Sakha 104	2.15**	-12.43**	-7.54**	-2.59**	6.04**	1.13
Wab 880-p1 x Giza 178	-4.82**	-0.04	-4.23**	-4.05**	-2.96**	5.28**
IEET 1444 x Sakha 102	1.56*	9.03**	7.10**	14.97**	14.80**	7.92**
IEET 1444 x Sakha 104	-1.62*	-0.21	1.80*	2.74**	9.93**	11.46**
IEET 1444 x Giza 178	0.07	-8.82**	-8.90**	-17.72**	-24.74**	-19.39**
Gaori x Sakha 102	11.22**	-2.97**	-2.56**	8.31**	-3.86**	-2.41**
Gaori x Sakha 104	-12.96**	-11.21**	-14.87**	-4.92**	-4.74**	-4.87**
Gaori x Giza 178	1.74*	14.18**	17.44**	-3.39**	8.60**	7.28**
Giza 177 x Sakha 102	0.33	-11.53**	-2.23**	-1.36	-2.09**	0.92
Giza 177 x Sakha 104	-4.18**	-2.43**	2.46**	-1.59*	-4.62**	-9.54**
Giza 177 x Giza 178	3.85**	13.96**	-0.23	2.95**	6.71**	8.62**
Giza 182 x Sakha 102	-3.00**	-3.64**	-5.01**	2.31**	11.14**	4.59**
Giza 182 x Sakha 104	7.49**	15.13**	13.02**	20.08**	9.27**	19.13**
Giza 182 x Giza 178	-4.49**	-11.49**	-8.01**	-22.39**	-20.40**	-23.72**
Sakha 106 x Sakha 102	0.67	0.80	-3.90**	2.31**	-1.53	-4.08**
Sakha 106 x Sakha 104	-1.85*	4.57**	7.46**	-8.92**	-7.40**	-10.54**
Sakha 106 x Giza 178	1.18	-5.38**	-3.56**	6.62**	8.93**	14.62**
Sakha 105 x Sakha 102	2.00*	-8.53**	3.44**	2.20**	-0.86	-3.08**
Sakha 105 x Sakha 104	-2.51**	-1.43	0.13	-0.70	-10.74**	-9.54**
Sakha 105 x Giza 178	0.51	9.96**	-3.56**	-1.50	11.60**	12.62**
Suweon 345 x Sakha 102	-4.67**	-4.64**	-8.90**	-18.80**	-3.86**	3.92**
Suweon 345 x Sakha 104	-14.18**	-8.87**	-7.21**	-10.70**	-9.74**	-8.54**
Suweon 345 x Giza 178	18.85**	13.51**	16.10**	29.50**	13.60**	4.62**
Gz 1368-S-5-4 x Sakha 102	-0.33	1.58	-2.23**	-4.03**	-1.86*	-0.41
Gz 1368-S-5-4 x Sakha 104	10.15**	13.35**	11.46**	6.74**	3.27**	11.13**
Gz 1368-S-5-4 x Giza 178	-9.82**	-14.93**	-9.23**	-2.72**	-1.40	-10.72**
BG 34-8 x Sakha 102	-3.33**	10.03**	4.66**	-0.36	-6.20**	-3.74**
BG 34-8 x Sakha 104	15.15**	7.80**	6.68**	14.41**	17.93**	9.80**
BG 34-8 x Giza 178	-11.82**	-17.82**	-11.34**	-14.05**	-11.74**	-6.05**
Agami M1 x Sakha 102	-2.67**	-0.64	-3.34**	-4.47**	7.14**	5.26**
Agami 1 x Sakha 104	3.82**	4.13**	0.68	-2.37**	-7.74**	-5.21**
Agami M 1 x Giza 178	-1.15	-3.49**	2.66**	6.84**	0.60	-0.05
Yabani lulu x Sakha 102	-2.11**	-10.97**	-8.56**	-5.03**	-1.86*	-3.74**
Yabani lulu x Sakha 104	-9.62**	-1.21	-6.54**	-13.26**	-16.74**	-4.21**
Yabani lulu x Giza 178	11.74**	12.18**	15.10**	18.28**	18.60**	7.95**
S.E (S _{ij})	0.77	0.81	0.81	0.76	0.78	0.79
S.E (S _{ij} - S _{kl})	1.08	1.14	1.15	1.08	1.10	1.12
LS D at 0.05	1.54	1.62	1.62	1.52	1.56	1.58
at 0.01	2.05	2.15	2.15	2.02	2.07	2.10

*and ** significant at 0.05 and 0.01 probability levels, respectively. Abbreviations: N, normal conditions, S1, first level of salinity (4000ppm), S2, second level of salinity (6000ppm)

While, Suweon 345 x Sakha 102 and Sakha 105 x Giza 178 were the best cross combinations for improving number of panicles per plant. In addition, Sakha 106 x Sakha 102 and Agami M1 x Giza 178 were the greatest cross combinations for 1000- grain weight. The results indicated that among the studied crosses, BG 34-8 x Giza 178 the best cross combination for number of filled grains/panicle, sterility% and grain yield /plant. Moreover, Wab 880SG-33 x Sakha 104 was the best cross combination for grain yield /plant under normal conditions. The superiority of these crosses may be due to complementary and duplicate type of gene interactions. Hence, these hybrids are expected to produce desirable segregates and could be exploited successfully in breeding programs.

On the other side, under level (S1) of salinity conditions, the cross combination BG34-8 x Giza178 the best cross combinations for number of days to 50% heading, number of filled grains/panicle and sterility%. While, the best cross combinations for plant height were IEET 1444 x Giza 178, Giza 182 x Giza 178 and Yabani lulu x Sakha 104. The cross combinations, Suweon 345 x Giza 178, IEET1444 x Sakha 104 and Agami M1 x Giza 178 showed higher positive SCA effect for number of panicles/plant. Four crosses namely, Wab 880SG-33 x Sakha 104, Yabani lulu x Giza 178, Suweon 345 x Sakha 102 and BG34-8 x Sakha 102 exhibited highly significant and positive SCA effects for 1000- grain weight. The results indicated that among the studied crosses, IEET1444 x Sakha 104 was the best cross combinations for salinity tolerance index and grain yield /plant. The crosses which gave the highest values of these traits could be used in breeding program for improving these traits. Similar findings were reported earlier by El Abd *et al.* (2003), Verma and Srivastava (2004), Dhakar and vinit (2006), Hariprasanna *et al.* (2006), El-Naem (2010) and Negm (2011).

In case of, the level (S2) of salinity condition, 21 out of the 39 hybrid combinations showed significant, highly significant and negative SCA effects for No. of days to 50% heading. Giza 182 x Giza 178 was the best cross combination for sterility%, number of filled grains/panicle and plant height. The best specific combinations for number of filled grains/panicle and number of panicles/plant was Suweon 345 x Giza 178. Three crosses namely, Yabani lulu x Sakha 102, Sakha 106 x Sakha 104 and IEET1444 x Sakha 104 exhibited highly significant and positive SCA effects for 1000-grain weight.

The cross combination, BG 34-8 x Giza 178 showed higher SCA effects for number of filled grains/panicle and sterility%. Results in the Table 2 indicated that significant and highly significant positive estimates of specific combining ability were illustrated for 9 crosses for salinity tolerance index, these estimates varied from 1.39 to 16.84 % for Gaori x Sakha 104, IEET1444 x Sakha 104, respectively. Ten crosses showed significant and highly significant desirable SCA effects for grain yield /plant, highest estimated values were recorded in IEET1444 x Sakha 104 (10.18) followed by Wab880SG-33 x Sakha 104 (5.10) and Sakha 105 x Giza 178 (3.71).

Table 2 : Cont.

Genotypes	No. of panicles/plant			1000-grain weight (g)		
	N	S1	S2	N	S1	S2
Wab 880 SG -33 x Sakha 102	2.06**	-2.31**	1.08	-0.03	-0.13	0.16
Wab 880SG -33 x Sakha 104	-0.66	4.08**	0.31	-0.03	0.37**	0.17
Wab 880SG -33 x Giza 178	-1.40	-1.77*	-1.39	0.06**	-0.24*	-0.34**
Wab 880-p1 x Sakha 102	-0.61	-1.31	0.08	0.02	-0.27**	-0.05
Wab 880-p1 x Sakha 104	-4.33**	4.08**	3.31**	0.08**	0.12	0.06
Wab 880-p1 x Giza 178	4.93**	-2.77**	-3.39**	-0.09**	0.15	0.00
IEET 1444 x Sakha 102	2.39**	3.69**	3.74**	0.04	0.07	-0.10
IEET 1444 x Sakha 104	-2.33**	7.08**	5.97**	0.10**	0.22*	0.31**
IEET 1444 x Giza 178	-0.07	-10.77**	-9.72**	-0.14**	-0.29**	-0.22*
Gaori x Sakha 102	-4.27**	-1.31	-1.59*	0.00	-0.25**	-0.24*
Gaori x Sakha 104	2.01**	-3.92**	-1.36	0.27**	0.13	0.05
Gaori x Giza 178	2.27**	5.23**	2.95**	-0.27**	0.13	0.19
Giza 177 x Sakha 102	-2.61**	-1.31	-1.92*	0.00	0.10	-0.06
Giza 177 x Sakha 104	1.68*	2.08**	2.31**	-0.03	-0.02	-0.13
Giza 177 x Giza 178	0.93	-0.77	-0.39	0.03	-0.08	0.19
Giza 182 x Sakha 102	0.28	0.36	2.41**	0.09**	0.11	0.14
Giza 182 x Sakha 104	3.90**	5.74**	3.64**	-0.01	0.09	0.00
Giza 182 x Giza 178	-4.18**	-6.10**	-6.05**	-0.08**	-0.19*	-0.14
Sakha 106 x Sakha 102	-2.61**	-2.31**	-3.59**	0.34**	-0.17	-0.62**
Sakha 106 x Sakha 104	0.68	-0.92	0.64	-0.15**	0.24*	0.52**
Sakha 106 x Giza 178	1.93*	3.23**	2.95**	-0.19**	-0.07	0.09
Sakha 105 x Sakha 102	-7.61**	2.03**	2.08**	-0.26**	-0.12	-0.11
Sakha 105 x Sakha 104	-1.33	-0.59	-1.69*	0.10**	0.13	-0.04
Sakha 105 x Giza 178	8.93**	-1.44	-0.39	0.16**	-0.01	0.14
Suweon 345 x Sakha 102	16.39**	-5.31**	-4.26**	-0.24**	0.34**	0.08
Suweon 345 x Sakha 104	-14.33**	-6.92**	-6.03**	0.26**	-0.41**	-0.17
Suweon 345 x Giza 178	-2.07**	12.23**	10.28**	-0.02	0.08	0.09
Gz 1368-S-5-4 x Sakha 102	-2.61**	5.03**	4.74**	0.07**	0.08	0.09
Gz 1368-S-5-4 x Sakha 104	3.68**	-0.59	-1.03	-0.07**	0.01	-0.12
Gz 1368-S-5-4 x Giza 178	-1.07	-4.44**	-3.72**	-0.01	-0.09	0.02
BG 34-8 x Sakha 102	-1.27	1.36	1.08	0.24**	0.30**	0.14
BG 34-8 x Sakha 104	3.01**	0.74	2.31**	-0.30**	-0.41**	-0.25*
BG 34-8 x Giza 178	-1.74*	-2.10**	-3.39**	0.06**	0.12	0.11
Agami M1 x Sakha 102	1.06	0.36	-2.92**	-0.13**	0.01	0.14
Agami 1 x Sakha 104	4.34**	-7.26**	-4.69**	-0.17**	-0.16	-0.30**
Agami M 1 x Giza 178	-5.40**	6.90**	7.62**	0.30**	0.14	0.17
Yabani lulu x Sakha 102	-0.61	1.03	-0.92	-0.13**	-0.07	0.42**
Yabani lulu x Sakha 104	3.68**	-3.59**	-3.69**	-0.07**	-0.29*	-0.13
Yabani lulu x Giza 178	-3.07**	2.56**	4.62**	0.20**	0.35**	-0.30**
S.E (S _{ij})	0.74	0.76	0.75	0.02	0.09	0.10
S.E (S _{ij} - S _{ki})	1.05	1.08	1.06	0.03	0.13	0.14
LS D at 0.05	1.48	1.52	1.50	0.04	0.18	0.2
at 0.01	1.97	2.02	2.00	0.05	0.24	0.27

*and ** significant at 0.05 and 0.01 probability levels, respectively. Abbreviations: N, normal conditions, S1, first level of salinity (4000ppm), S2, second level of salinity (6000ppm)

Table 2 : Cont.

Genotype	No. of filled grains/panicle			Salinity index	
	N	S1	S2	S1	S2
Wab 880 SG -33 x Sakha 102	3.39*	0.38	-14.92**	-0.41	-0.65
Wab 880SG -33 x Sakha 104	40.39**	49.79**	26.03**	1.42*	0.70
Wab 880SG -33 x Giza 178	-43.77**	-50.16**	-11.12**	-1.01	-0.05
Wab 880-p1 x Sakha 102	10.39**	-13.40*	4.53**	-12.27**	-2.53**
Wab 880-p1 x Sakha 104	3.39*	18.68**	25.15**	20.89**	6.08**
Wab 880-p1 x Giza 178	-13.77**	-5.27**	-29.68**	-8.62**	-3.55**
IEET 1444 x Sakha 102	7.72**	-26.07**	-17.92**	-19.40**	-9.40**
IEET 1444 x Sakha 104	-28.28**	46.01**	14.37**	33.15**	16.84**
IEET 1444 x Giza 178	20.56**	-19.94**	3.55**	-13.75**	-7.44**
Gaori x Sakha 102	10.39**	2.38**	6.09**	-4.67**	-0.60
Gaori x Sakha 104	-36.62**	4.45**	11.70**	-0.24	1.39*
Gaori x Giza 178	26.23**	-6.83**	-17.79**	4.92**	-0.79
Giza 177 x Sakha 102	14.05**	8.49**	21.53**	-8.27**	-2.95**
Giza 177 x Sakha 104	37.05**	6.56**	-11.52**	-0.33	-1.66**
Giza 177 x Giza 178	-51.10**	-15.05**	-10.01**	8.60**	4.61**
Giza 182 x Sakha 102	-19.95**	-12.51**	-7.47**	14.62**	3.98**
Giza 182 x Sakha 104	-47.95**	-8.44**	-1.52	-9.47**	-4.16**
Giza 182 x Giza 178	67.90**	20.95**	8.99**	-5.15**	0.19
Sakha 106 x Sakha 102	-6.95**	18.60**	9.64**	-4.90**	0.96
Sakha 106 x Sakha 104	39.05**	2.68**	-1.41	0.93	-1.69**
Sakha 106 x Giza 178	-32.10**	-21.27**	-8.23**	3.97**	0.74
Sakha 105 x Sakha 102	37.05**	4.60**	10.31**	4.03**	4.47**
Sakha 105 x Sakha 104	22.05**	-6.99**	-2.41**	-5.12**	-4.60**
Sakha 105 x Giza 178	-59.10**	2.39**	-7.90**	1.09	0.13
Suweon 345 x Sakha 102	14.39**	9.60**	3.31**	-3.53**	1.45*
Suweon 345 x Sakha 104	-1.62	-31.66**	-13.74**	-4.85**	-0.11
Suweon 345 x Giza 178	-12.77**	22.06**	10.44**	8.38**	-1.34*
Gz 1368-S-5-4 x Sakha 102	-48.28**	-12.07**	-2.69**	7.25**	0.36
Gz 1368-S-5-4 x Sakha 104	-12.28**	-34.33**	-20.74**	-4.47**	-0.63
Gz 1368-S-5-4 x Giza 178	60.56**	46.39**	23.44**	-2.78**	0.28
BG 34-8 x Sakha 102	-17.28**	-18.96**	-24.80**	11.15**	6.26**
BG 34-8 x Sakha 104	-80.28**	-38.21**	-24.86**	-5.35**	0.56
BG 34-8 x Giza 178	97.56**	57.17**	49.66**	-5.80**	-6.82**
Agami M1 x Sakha 102	-39.62**	33.82**	3.86*	19.85**	1.58*
Agami 1 x Sakha 104	69.39**	-7.44**	1.15	-11.10**	-1.94**
Agami M 1 x Giza 178	-29.77**	-26.39**	-5.01**	-8.74**	0.36
Yabani lulu x Sakha 102	34.72**	5.15**	8.53**	-3.44**	-2.91**
Yabani lulu x Sakha 104	-30.44**	-4.05**	-6.34**	-15.46**	-10.78**
S.E (S _{ij})	0.84	0.89	0.90	0.60	0.62
S.E (S _{ij} - S _{kl})	1.19	1.25	1.27	0.85	0.88
LS D at 0.05	1.68	1.78	1.8	1.2	1.24
at 0.01	2.23	2.37	2.39	1.60	1.65

*and ** significant at 0.05 and 0.01 probability levels, respectively. Abbreviations: N, normal conditions, S1, first level of salinity (4000ppm), S2, second level of salinity (6000ppm)

Table 2 : Cont.

Genotypes	Sterility %			Grain yield/plant (g)		
	N	S1	S2	N	S1	S2
Wab 880 SG -33 x Sakha 102	-1.42	-3.31**	7.90**	-6.21**	-2.44*	-1.39
Wab 880SG -33 x Sakha 104	-3.22**	-8.05**	-13.77**	28.48**	9.52**	5.10**
Wab 880SG -33 x Giza 178	4.64**	11.36**	5.88**	-22.26**	-7.08**	-3.71**
Wab 880-p1 x Sakha 102	16.66**	4.19**	-4.12**	15.91**	-2.08*	1.25
Wab 880-p1 x Sakha 104	-4.09**	-3.97**	-15.44**	-8.20**	9.92**	2.30**
Wab 880-p1 x Giza 178	-12.58**	-0.22	19.56**	-7.71**	-7.85**	-3.55**
IEET 1444 x Sakha 102	-0.03	13.27**	13.80**	6.77**	-11.63**	-5.44**
IEET 1444 x Sakha 104	13.99**	9.50**	2.93**	-8.91**	20.47**	10.18**
IEET 1444 x Giza 178	-13.97**	-22.77**	-16.73**	2.15*	-8.83**	-4.74**
Gaori x Sakha 102	0.60	-11.62**	-23.23**	7.64**	-0.05	0.81
Gaori x Sakha 104	0.93	1.84*	4.31**	-1.73	-0.89	0.80
Gaori x Giza 178	-1.53	9.78**	18.92**	-5.91**	0.94	-1.61*
Giza 177 x Sakha 102	-11.09**	-10.53**	-16.56**	8.80**	-1.93	-0.27
Giza 177 x Sakha 104	-13.25**	-17.42**	0.25	4.61**	0.87	-0.18
Giza 177 x Giza 178	24.34**	27.95**	16.32**	-13.41**	1.07	0.44
Giza 182 x Sakha 102	-15.92**	14.75**	16.49**	-11.56**	4.66**	0.77
Giza 182 x Sakha 104	32.53**	15.53**	6.51**	19.40**	-1.25	-0.58
Giza 182 x Giza 178	-16.61**	-30.28**	-23.01**	-7.84**	-3.41**	-0.19
Sakha 106 x Sakha 102	-11.74**	-13.85**	-16.66**	-6.56**	-5.70**	-2.17**
Sakha 106 x Sakha 104	-16.37**	-15.44**	-4.87**	-2.09*	0.30	-0.74
Sakha 106 x Giza 178	28.11**	29.29**	21.53**	8.65**	5.40**	2.91**
Sakha 105 x Sakha 102	-7.43**	-4.98**	-1.76*	-10.79**	-0.50	0.24
Sakha 105 x Sakha 104	-8.65**	-8.75**	-6.78**	-5.93**	-5.07**	-3.94**
Sakha 105 x Giza 178	16.08**	13.73**	8.54**	16.73**	5.57**	3.71**
Suweon 345 x Sakha 102	-5.77**	-12.67**	-5.27**	-10.89**	-2.95**	0.69
Suweon 345 x Sakha 104	-6.63**	-4.15**	-5.73**	3.67**	-5.62**	0.01
Suweon 345 x Giza 178	12.40**	16.82**	11.7**	7.23**	8.58**	-0.70
Gz 1368-S-5-4 x Sakha 102	23.60**	9.33**	7.17**	-19.97**	3.57**	-1.11
Gz 1368-S-5-4 x Sakha 104	2.19*	21.24**	19.46**	-7.41**	-6.30**	-2.36**
Gz 1368-S-5-4 x Giza 178	-25.79**	-30.57**	-26.62**	27.38**	2.73**	3.47**
BG 34-8 x Sakha 102	13.12**	23.86**	31.03**	7.30**	4.18**	3.04**
BG 34-8 x Sakha 104	32.21**	32.05**	28.59**	-28.95**	-10.36**	-4.44**
BG 34-8 x Giza 178	-45.34**	-55.91**	-59.62**	21.65**	6.18**	1.41
Agami M1 x Sakha 102	14.49**	6.08**	16.68**	4.75**	11.49**	1.90*
Agami 1 x Sakha 104	-21.26**	-15.91**	-20.10**	-1.06	-5.98**	-1.48
Agami M 1 x Giza 178	6.77**	9.83**	3.42**	-3.70**	-5.51**	-0.42
Yabani lulu x Sakha 102	-15.08**	-14.52**	-25.46**	14.81**	3.39**	1.68*
Yabani lulu x Sakha 104	-8.40**	-6.47**	4.65**	8.13**	-5.61**	-4.67**
Yabani lulu x Giza 178	23.48**	20.99**	20.81**	-22.94**	2.22*	2.99**
S.E (S _{ij})	0.80	0.90	0.86	0.88	0.97	0.79
S.E (S _{ij} - S _{ki})	1.13	1.27	1.21	1.24	1.37	1.11
LS D at 0.05	1.6	1.8	1.72	1.76	1.94	1.58
at 0.01	2.13	2.39	2.29	2.34	2.58	2.10

*and ** significant at 0.05 and 0.01 probability levels, respectively. Abbreviations: N, normal conditions, S1, first level of salinity (4000ppm), S2, second level of salinity (6000ppm)

These results indicated that most of these crosses could be utilized for improving grain yield trait in rice breeding program The results obtained here concerning general and specific combining ability effects could indicate that the excellent crosses which showed desirable SCA effects were obtained from crossing good by good, good by low and low by

low combiners. Consequently, it could be concluded that GCA effects of the parental varieties were generally unrelated to the specific combining ability effects of their respective crosses. This conclusion was also reported by Sedeek (2006) and Chakraborty *et al.* (2010).

Estimation of genetic parameters and heritability:

The estimates of, phenotypic variance ($\sigma^2 P$), genotype variance ($\sigma^2 G$), environmental variance ($\sigma^2 E$), dominance genetic variance ($\sigma^2 D$), additive genetic variance ($\sigma^2 A$), broad sense heritability (h^2b %), narrow sense heritability (h^2n %), GCA to Sca ratio are presented in Table 3.

It is evident from Table 3 that the dominance genetic variance was greater than additive genetic variance for all the studied traits. The highest estimated values of environmental variance were recorded for number of filled grains/panicle followed by number of days to 50% heading under normal and two saline soil conditions. On the other hand, high estimates of broad sense heritability coupled with high genetic advance were noted for number of filled grains/panicle and sterility% under all conditions, revealing substantial contribution of additive genetic variance in phenotypic expression, and indicating the effectiveness of selection in early generations to improve these traits. Falconer and Mackay (1996) demonstrated that the lower narrow sense heritability was caused by low additive effects and high dominant gene action. These results are in harmony with the combining ability analysis. Low estimate values of narrow sense heritability were exhibited for all the studied traits under all studied conditions, On the contrary, the lowest values were observed for number of filled grains/panicle and sterility% .

Table 3 : Genetic parameters for some vegetative, yield and its components traits under normal and saline (S1, S2) soil conditions.

Genetic Parameters	Days to 50% heading			Plant height (cm)		
	N	S1	S2	N	S1	S2
Phenotypic Variance	98.17	81.54	115.23	205.28	184.48	141.62
Genetic Variance	92.47	75.23	108.78	199.61	178.54	135.41
Environment Variance	5.70	6.31	6.45	5.67	5.94	6.21
Dominance Variance	81.10	71.81	105.46	172.61	167.79	124.71
Additive Variance	11.37	3.42	3.32	27.00	10.75	10.70
Broad sense of Heritability	94.19	92.27	94.40	97.24	96.78	95.61
Narrow sense of Heritability	11.58	4.19	2.88	13.15	5.83	7.55
Genetic Advance	1922.55	1716.27	2087.50	2869.93	2707.89	2343.95
Ratio of gca Var. to sca Var.	1.14	1.05	1.03	1.16	1.06	1.09

Abbreviations: N, normal conditions, S1, first level of salinity (4000ppm),S2, second level of salinity (6000ppm)

Moreover, the ratio of GCA and SCA variances was greater than unity for all the traits studied that revealed the preponderance of additive gene action and additive x additive type of gene interaction in the inheritance of such traits. Hammoud (2004) who found that narrow sense heritability estimates were lower than of broad sense for most characters studied indicating the importance of non-additive genetic variance in the inheritance of vegetative characters, subsequently selection procedures are preferred in the late generation.

Table 3 : Cont.

Genetic Parameters	No. of panicles/plant			1000-grain weight (g)		
	N	S1	S2	N	S1	S2
Phenotypic Variance	39.83	34.66	27.36	0.07	0.1	0.11
Genetic Variance	37.48	31.91	25.06	0.04	0.06	0.08
Environment Variance	2.35	2.75	2.30	0.03	0.04	0.03
Dominance Variance	35.38	31.33	24.93	0.03	0.05	0.06
Additive Variance	2.10	0.58	0.13	0.01	0.01	0.01
Broad sense of Heritability	94.11	92.06	91.60	63.84	60.58	72.09
Narrow sense of Heritability	5.27	1.66	0.48	17.90	8.58	11.91
Genetic Advance	1223.43	1116.55	987.04	34.64	39.40	48.70
Ratio of gca Var. to sca Var.	1.06	1.02	1.01	1.39	1.17	1.20

Abbreviations: N, normal conditions, S1, first level of salinity (4000ppm), S2, second level of salinity (6000ppm)

Table 3 : Cont.

Genetic Parameters	No. of filled grains/panicle			Salinity index	
	N	S1	S2	S1	S2
Phenotypic Variance	2474.19	724.16	431.55	193.9	47.31
Genetic Variance	2466.77	702.65	422.43	188.78	42.93
Environment Variance	7.42	21.51	9.12	5.12	4.38
Dominance Variance	2453.19	681.99	410.13	187.03	41.58
Additive Variance	13.58	20.66	12.30	1.75	1.35
Broad sense of Heritability	99.70	97.03	97.89	97.36	90.74
Narrow sense of Heritability	0.55	2.85	2.85	0.90	2.86
Genetic Advance	10215.96	5378.87	4188.95	2792.76	1285.75
Ratio of gca Var. to sca Var.	1.01	1.03	1.03	1.01	1.03

Abbreviations: N, normal conditions, S1, first level of salinity (4000ppm), S2, second level of salinity (6000ppm)

Table 3 : Cont.

Genetic Parameters	Sterility %			Grain yield/ plant (g)		
	N	S1	S2	N	S1	S2
Phenotypic Variance	477.22	318.7	357.11	366.14	65.81	16.38
Genetic Variance	475.02	316.28	355.21	363.82	63.00	14.52
Environment Variance	2.20	2.42	1.90	2.32	2.81	1.86
Dominance Variance	466.93	313.26	342.76	288.82	61.90	14.18
Additive Variance	8.09	3.03	12.46	75.00	1.10	0.34
Broad sense of Heritability	99.54	99.24	99.47	99.37	95.74	88.63
Narrow sense of Heritability	1.69	0.95	3.49	20.48	1.67	2.08
Genetic Advance	4479.38	3649.66	3872.16	3916.77	1599.80	739.03
Ratio of gca Var. to sca Var.	1.02	1.01	1.04	1.26	1.02	1.02

Abbreviations: N, normal conditions, S1, first level of salinity (4000ppm), S2, second level of salinity (6000ppm)

The results suggest that improvement in these traits may be obtained via heterosis breeding or by single plant selection in early generations following hybridization or intermitting of selected segregates through recurrent selection. Similar results were observed previously by Verma and Srivastava (2004), Bagheri *et al.* (2005), Saxena *et al.* (2005), Manickavelu *et al.* (2006) Pradhan *et al.* (2006) and Sharma *et al.* (2007).

Estimates of phenotypic correlation coefficients.

Phenotypic correlation coefficients among all possible pairs of the studied characters are presented in Tables 4-6. The results in table 4

revealed that days to 50% heading was significantly and positive associated with each of plant height, 1000-grain weight and grain yield/plant . On the contrary, highly significant negative estimated of phenotypic correlation coefficients was observed between days to 50% heading and sterility % under normal conditions. Plant height was significantly correlated with sterility%. While, Ganapathy *et al.* (2007), reported that Plant height was positively and significantly correlated with grain yield/plant.

Table 4: Estimates of phenotypic correlation coefficients between grain yield/plant and its components under normal conditions.

Characters	1	2	3	4	5	6
1- Days to 50% heading	-					
2- Plant height (cm)	0.233*	-				
3- No. of panicles /plant	0.138	0.098	-			
4- No. of filled grains /plant	0.163	-0.133	0.103	-		
5-1000-grain weight (g)	0.202*	0.063	-0.310**	-0.242*	-	
6- Sterility (%)	-0.199*	0.381**	0.133	-0.317**	-0.074	-
7- Grain yield/plant (g)	0.214*	0.075	0.329**	0.278**	0.402**	-0.069

*, ** Significant and highly significant at 0.05 and 0.01 levels of probability, respectively.

On the other hand, under the first level of salinity conditions significant or highly significant positive estimated of phenotypic correlation coefficients were obtained between days to 50% heading and each of plant height and salinity index. On the other hand, significant or highly significant positive estimated of phenotypic correlation coefficients obtained between plant height and number of panicles per plant, salinity index, sterility % and grain yield per plant. In the same time, number of panicle/plant gave significant and positive correlation with each of salinity index and sterility % with values (0.226) and (0.236), respectively. Moreover, highly significant positive correlation coefficient was recorded between number of filled grains per panicle and salinity index (Table 5).

Table 5: Estimates of phenotypic correlation coefficients between grain yield/plant and its components under level S1 conditions.

Characters	1	2	3	4	5	6	7
1- Days to 50% heading	-						
2- Plant height (cm)	0.207*	-					
3- No. of panicles /plant	0.144	0.386**	-				
4- No. of filled grains /plant	-0.087	0.152	0.082	-			
5-1000-grain weight (g)	0.094	0.068	-0.050	0.087	-		
6- Salinity index (%)	0.289**	0.287**	0.226*	0.389**	0.040	-	
7- Sterility (%)	-0.032	0.195*	0.236*	-0.232*	0.039	-0.022	-
8- Grain yield/plant (g)	0.063	0.312**	0.396**	0.409**	0.305**	0.049	-0.444**

*, ** Significant and highly significant at 0.05 and 0.01 levels of probability, respectively.

Moreover, highly significant positive estimated of phenotypic correlation coefficients were obtained between days to 50% heading and 1000- grain weight. While, highly significant positive estimated of phenotypic correlation coefficients obtained between plant height and number of panicles per plant, salinity index under S2 conditions (Table 6). Highly significant positive

estimates of phenotypic correlation coefficients were obtained between no. of panicles/plant with grain yield /plant under all conditions. These findings were in close agreement with those reported earlier by Abd-Allah (2000) and Abd El-Lattef *et al.* (2008).

Table 6: Estimates of phenotypic correlation coefficients between grain yield/plant and its components under level S2 conditions.

Characters	1	2	3	4	5	6	7
1- Days to 50% heading	-						
2- Plant height (cm)	0.131	-					
3- No.of panicles /plant	0.090	0.382**	-				
4- No. of filled grains /plant	-0.178	0.101	0.172	-			
5-1000-grain weight (g)	0.264**	0.078	-0.053	0.032	-		
6- Salinity index (%)	0.126	0.244**	0.185	0.437**	-0.053	-	
7- Sterility (%)	-0.176	0.080	0.160	-0.016	-0.088	-0.035	-
8- Grain yield/plant (g)	-0.044	0.155	0.252**	0.387**	0.316**	0.135	-0.255**

*, ** Significant and highly significant at 0.05 and 0.01 levels of probability, respectively.

Highly significant positive correlation coefficient was recorded between number of filled grains per panicle and grain yield/plant under all conditions. Regarding to 1000-grain weight, results emphasizes that it was positively and highly significantly phenotypically correlated with grain yield/plant under all conditions.

These results were in harmony with those of Abd-Allah (2000) and Abd El-Lattef *et al.* (2008). They reported that 1000-grain weight was positive correlated with grain yield/plant. In addition to, negative and highly significant correlation coefficient was recorded between this trait and grain yield per plant under level S1, S2 conditions. Abd-Allah (2000) illustrated that sterility % was negatively associated with grain yield/plant under both conditions.

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دراسات على القدرة على التألف للمحصول ومكوناته في الأرز باستخدام نظام السلالة X الكشف تحت ظروف الأراضي الملحية.

محمود سليمان سلطان¹، مامون احمد عبدالمنعم¹، حماده محمد حسن² و الحسيني محمد ضاهر²

1- قسم المحاصيل ، كلية الزراعة ، جامعة المنصورة ، مصر .
2- قسم بحوث الأرز ، معهد بحوث المحاصيل الحقلية ، مركز البحوث الزراعية ، الجيزة، مصر

تمت دراسة القدرة العامة والخاصة على التألف وتقدير المكونات الوراثية باستخدام تسعة وثلاثون هجيناً وستة عشر تراكيب وراثية من الأرز (ثلاثة عشر منها كأمهات و ثلاثة سلالات كشافة كآباء) لدراسة السلوك الوراثي لصفات عدد الأيام الى 50% طرد، طول النبات، عدد الحبوب الممتلئة/دالية، عدد الداليات/ نبات ، وزن الحبة، معامل تحمل الملوحة، النسبة المئوية للعقم و محصول حبوب النبات الفردي وذلك بهدف انتخاب أفضل التراكيب الوراثية تحت الظروف العادية والملحية. وذلك باستخدام تصميم اختبار السلالة X الكشف أثناء موسمي 2011 و2012 بالليزوميتر والمزرعة البحثية لمركز البحوث والتدريب في الأرز – سخا – كفر الشيخ – مصر

كانت القدرة العامة والقدرة الخاصة على التألف معنوية و فائقة المعنوية لكل الصفات المدروسة حيث كانت القدرة العامة على التألف عالية المعنوية وسالبة وذلك لصفة عدد الأيام حتى 50% طرد للصنفين سخا 102 و جيزة 177 تحت ظروف الأراضي العادية بينما كانت القدرة العامة على التألف عالية المعنوية وسالبة لصفة عدد الأيام حتى 50% طرد وذلك للصنف سخا 106 تحت كلا ظرفي الملوحة . كان الصنف جوري أفضل الأباء لصفة طول النبات تحت كل الظروف بالإضافة إلى انه كان أفضل الأباء لصفة عدد الحبوب الممتلئة / الدالية والنسبة المئوية للعقم تحت الظروف العادية. كما أظهر الصنف أى إى تى 1444 قدرة عامة على التألف عالية المعنوية لصفات عدد الداليات / نبات ومعامل تحمل الملوحة و محصول النبات الفردي تحت كلا ظرفي الملوحة. كان الصنف واب 880 إس جى 33 أفضل الأباء قدرة على التألف لصفات وزن الحبة تحت كل الظروف وعدد الحبوب الممتلئة تحت كلا ظرفي الملوحة. كما كان الصنف سون345 أفضل الأباء لصفات عدد الداليات / نبات تحت الظروف العادية والنسبة المئوية للعقم تحت كلا ظرفي الملوحة. هذا وقد وجد أن الهجن أى إى تى X سخا 104 و واب880 إس جى-33 X سخا 104 و جى زد1368- إس-5-4 X جيزة 178 كانت أفضل التراكيب الوراثية لمعظم الصفات المدروسة حيث كانت قدرتها الخاصة على التألف عالية المعنوية في الإتجاه المرغوب تحت كل الظروف (العادية والملحية) سجلت أعلى القيم لكل من التباين المظهري والوراثي لصفات عدد الحبوب الممتلئة/دالية، النسبة المئوية للعقم موضحة إمكانية التحسين الوراثي في هاتين الصفتين. كما كانت درجة التوريث بمعناها الواسع عالية مقرونة بارتفاع التحسين الوراثي لصفات عدد الحبوب الممتلئة/دالية، النسبة المئوية للعقم و طول النبات، موضحة أهمية التباين الجيني المضيف في وراثته هذه الصفات وعليه فإن الانتخاب المباشر فى الأجيال الإنعزالية المبكرة يكون أكثر فاعلية لتحسين هذه الصفات تحت كل الظروف. كما سجلت النتائج أن محصول الحبوب قد تلازم تلازماً قوياً وموجباً مع كل من عدد الداليات / نبات وعدد الحبوب الممتلئة/دالية ووزن الحبة تحت كل الظروف (العادية والملحية).

قام بتحكيم البحث

كلية الزراعة – جامعة المنصورة
مركز البحوث الزراعية

أ.د / عادل محمد سلامه
أ.د / عبد المعطى بسيونى العبد