Genetic Divergence of Some Rice Genotypes Under Normal and Saline soil Conditions

Hadifa, A. A. ; Mervet M. A. Osman and M. M. Abdelhameed
Rice Research Section, Field Crops Research Institute, Agricultural Research Center.

This article was CHECKED against plagiarism using TurnitIn software

ABSTRACT

The present study was carried out at the Experimental Farm of Sakha Agricultural Research Station,Sakha,Kafr EL-Sheikh Governorate and El-Sirw Agriculture Research Station, Dammietta Governorate, Egypt, during 2016 and 2017 growing seasons to study the inheritance of some growth traits, yield and its components under normal and saline soil conditions and to study the relationship between some growth characters and yield and its components by estimating correlation coefficient between studied characters.Results showed that location mean squares were found to be highly significant for all growth characters and yield and its attributes, indicating wide differences between the stress and non-stress conditions.Salinity condition has a negative effect on all studied traits for all genotypes compared with that of normal conditions.The interactions of genotypes,parents and crosses with locations (Sakha and El-Sirw) were detected to be highly significant for grain yield and its component except for harvest index, indicating that the genotypes behaved differently from non-stress to stress conditions.The parents Giza 178 and GZ9057 recorded the highest mean values of grain yield under normal and saline conditions as well as their combined data,while the parent Sakha106 gave the lowest mean value under the same conditions.Grain yield/plant was highly significant positively correlated with each of plant height, number of tillers/ plant, 1000-grain weight, panicle length, number of filled grains/panicle and harvest index.The results revealed that the studied genotypes were expected to similarly a broad spectrum of variability and confirmed the detected significant among these parents. Euclidean distance was ranged from 17.59 between (GZ6296 and Sakha 106) to 71.23, between (Giza 178 and Sakha 105) under stress conditions.

Keywords: Rice, Genetic divergence, Normal, saline conditions

INTRODUCTION

Rice is the most important food crop in the world since it is the staple food for more than 50% of the world population. Rice is considered the most popular and important field crop in Egypt for several reasons: as a staple food after wheat for the Egyptian population,as a second exporting crop after cotton,as a land reclamation crop for improving the productivity of the saline soils widely spread in North Delta and coastal area, and finally it is a social crop in which all farmers family member could gain money during its growing season.Salinity is the most widespread and prevalent problem in the irrigated agriculture.Genetic improvement for salt tolerance in major crops has become an urgent task in dealing with salinity problems in agricultural production.In traditional plant breeding for salt tolerance,overall agronomic characters such as seedling growth, survival and grain yield are usually the main selection criteria.Unfortunately, very limited success has been achieved from the previous efforts in plant breeding selecting on these characters for salt tolerance (Flowers and Yeo, 1997).The low success of breeding rice (Oryza sativa L.) for salt tolerance is at least partially,due to the low selection efficiency using overall agronomic traits, lack of effective evaluation methods for salt tolerance among genotypes, and the complexity of salinity tolerance phenotypes among genotypes. Differential salinity sensitivity at various growth stages is one of the factors affecting salt tolerance phenotypes. Generally, rice vegetative growth is moderately sensitive to salinity at young seedling stages and less sensitive at reproductive stages (Flowers and Yeo, 1981and Lutts el al., 1995). Early reproductive stage and panicle initiation are the most salinity sensitive growth stages affecting the formation of yield components and grain yield. On the other hand, rice plant is more tolerant to salinity at germination stage as compared with other rice stages (Heenan *et al.*, 1988).The objectives of the present investigation are to study the inheritance of some growth characters,yield and its components under normal and saline soil conditions and to study the relationship between some growth characters and yield and its components by estimating correlation coefficient between the mentioned characters.

MATERIALS AND METHODS

The present study was carried out at the Experimental Farm of Sakha Agricultural Research Station,Kafrelsheikh and EL-Sriw Agricultural Research Station,Damietta, during 2016 and 2017 seasons. In 2016 growing season, grains from each of the parental genotypes (Table 1) was sown at a various planting dates in order to overcome the differences in time of heading,all possible parental combinations without reciprocal were made among the six genotypes producing 15 crosses. In 2017 season,30 days old seedling of the parents and their 15 F1 hybrids were individually transplanted in randomized complete block design with three replications, at two locations Sakha as a normal soil and El-Sirw as a saline soil. Each replicate consisted of three rows of each parent and F1 cross. The rows were five meters long with 20 cm between rows and comprised 25 hills each of a single plant/hill. All agronomic practices were done as recommended with rice crop during growing seasons of the study.The data were recorded on an individual plant basis for parents and F1 generation.

Table 1. Name, pedigree and origin of evaluated Egyptian parental genotypes.

No.	parent	Pedigree	Types	Reaction to salinity
1	GZ1368-5-S-4	IR 1615 X BY 94	Indica	Tolerance
2	GZ9057-6-1-3-2	GZ 1368 X GZ 6296	Indica/Japonica	Tolerance
3	Giza 178	Giza 175/ Milyang 49	Indica/Japonica	Tolerance
4	GZ6296-12-1-2-1-1	AC 1225 × Hua lien 202	Indica/Japonica	Sensitive
5	Sakha 105	GZ 5581× GZ 4316	Japonica	Sensitive
6	Sakha 106	Giza 177 × Hexi 30	Japonica	Moderate

Soil analysis:

Four sites (from 1-4) were randomly chosen within El-Sirw Agricultural Research Station to represent the area under study.The chemical analysis was carried out using the soil extract 1:5 to estimate the soluble anions, cations and salinity level according to Black *et al.*(1965) .Some chemical characters of soil and water of the experimental site at Sakha and El-Sirw location in 2016 season are given in Table 2.The following traits were measured i.e., number of days to heading (days),plant height (cm),flag leaf area (cm2)

,number of tillers per plant, number of panicles/plant, 1000-grain weight, panicle length, number of filled grains/panicle, spikelets fertility(%),grain yield/plant and harvest index(%) according to IRRI (1996). Salinity tolerance index % (SI) for each character was calculated by the formula of Dwivedi *et al.* (1991) as follows:-

$$\text{Salinity Index} = \frac{\text{Value of each character under saline situation}}{\text{Value of each character under normal situation}} \times 100$$

Table 2. Soil chemical analyses of experiment sites.

Location	Ece ds.m-1	Anions(meq.L-1)				Cations(meq.L-1)				micronutrients (ppm)		
		CO3=	HCO3-	Cl-	SO4--	Ca++	Mg++	K+	Na+	Fe	Mn	Zn
Sakha	3.33	--	5.56	9.04	18.33	10.01	5.00	16.30	1.88	4.55	3.10	1.50
El Sirw	6.79	--	8.0	27.0	25.1	9.0	12.0	4.0	38.7	--	--	--

Estimates of phenotypic Correlation:

The relationship among the important characters under this study were assessed statistically through simple correlation as reported by Gomez and Gomez (1984), using SPSS (Statistical Package for Social Sciences) version 10 for windows.The phenotypic correlation coefficients (rp) between all possible pairs of the characters were estimated by rising the combined data of the two environments by using the Gomez and Gomez (1984).

Multivariate technique:

Multivariate technique was used to asses the similarities among varied genotypes to evaluate morphological parameters contributing the variation.Principal components analysis were used according to Hair *et al.* (1987).This analysis was calculated from a matrix bases on correlation between the contributed traits from all genotypes. The principal components of the contributed traits were expressed as given value, latent roots, and manifested in principal component analysis was also plotted in a joint plot diagram.Hierarchical clustering procedure was carried out using word's minimum method, which minimize within group sum of squares a cross all partitions.The procedure used a method performing a disjoint cluster analysis in the basis of Eaclidean distances as out lined.The principal components (PC) associated with all genotypes were expressed as Eigen value and manifested Eigen vector for all the studied characters in each PC axis.Results from principal components analysis and cluster analysis were presented in graphical

and dendrogram presentations.These computations were performed by using SPSS computer procedure.

RESULTS AND DISCUSSION

1. Growth characters:
Variation and interaction:

Results indicated that location mean squares were found to be highly significant for all growth characters studied, indicating that over all wide differences between the stress and non-stress conditions table 3.Genotypes, parents and their F1 crosses variance were found to be highly significant for all growth characters studied in both locations and their combined data indicating that over all wide environments differences among these populations.Parent vs crosses mean squares,as an indications to average heterosis over all crosses,were found to be highly significant for all growth characters under investigation at the salinity level and their combined data. Also, this indicating that the average heterosis over all crosses of these traits was inconsistent from environment to the other.The interaction of genotypes, parents and crosses with locations (Sakha and El-Sirw) were detected to be significant and highly significant for growth traits studied except for plant height, indicating that the genotypes behaved differently from non-stress to stress conditions.The interaction of parent vs crosses with environments were highly significant for all studied traits.Such results indicated that the tested genotypes varied from each other, and ranked differently from location to another (normal to saline soil)

Table 3. Observed mean square from analysis of variance for growth traits under normal (Sakha), saline soil (EL-Sirw) and their combined data.

S.O.V	d.f		Days to heading (day)			Plant height (cm)			Flag leaf area (cm2)			Number of tillers / plant		
	Sin	com	N	S	comb	N	S	comb	N	S	comb	N	S	comb
Replications		2	5.33	15.19		19.50	5.3		6.644	0.778		0.57	0.25	
Location		1		171.5**			8769.34**			7364.96**			1582.45*	
Rep. / Location		4		6.69**			10.85			3.71			0.13	
(Genotypes)	20	20	53.50**	45.70**	95.7**	700.60**	540.18**	1112.68**	110.38**	71.65**	124.66**	28.26**	28.95**	48.41**
Parents	5	5	59.60**	71.60**	125.4**	150.48**	177.07**	312.27**	33.10**	57.88**	29.42**	30.38**	44.01**	70.07**
Crosses	14	14	47.95**	37.90**	83.83**	716.72**	462.90**	1095.1	88.92**	80.73**	131.30**	10.55**	20.59**	22.32**
Parent vs crosses	1	1	100.80**	26.00**	113.4**	3225.5**	1607.46**	4693.53**	797.28**	13.21**	507.86**	265.66**	70.81**	305.38**
(Genotypes x Location)		20		3.5**			67.59**			57.37**			8.81**	
Parents x Location		5		5.8**			15.28			61.56**			4.32*	
Crosses x Location		14		2.03**			84.57**			38.35**			8.82**	
Parent vs cross x Location		1		12.6**			139.46**			302.62**			31.08**	
Error	40	80	0.78	2.06	0.72	3.95	2.64	3.30	9.00	1.45	5.23	1.36	1.50	1.53

*, ** significant and highly significant at 0.05 and 0.01 probability levels, respectively. N=normal soil (Sakha location), S=salinity soil (El-Sirw), comb= combined data.

Mean performance:

The mean performance of growth characters i.e.days to heading, plant height, flag leaf area and number of tillers / plant in both environments and their combined are presented in Table (4).The results of number of days to heading suggested that dominant effect was variable and depends on the cross itself. Some crosses were tended towards the early parents, while the others were found to be closed to the late parents. However the two parents involved, indicating presence of partial or no dominance effect. For days to heading, the desirable mean values towards the earliness were obtained from parent GZ9057, the crosses (GZ9057 × GZ6296), (Giza178 × GZ 6296) and (GZ9057 × Giza178) ranged from 117 to 121 days under both environments and their combined data.The results in Table 4 indicated that salinity conditions had a negative effect on the days to heading, where it decreased under saline soil (El-Sirw) for all genotypes as compared with that normal soil (Sakha).Concerning plant height, the parents GZ9057 and GZ6296, the crosses (GZ9057 × Giza178), (GZ9057 × GZ6296) and (Giza178 × GZ6296) recorded the desirable mean values towards dwarfing for this trait at the two locations and their combined data.Highly significant reduction in plant height under stress condition in the most of rice genotypes studied. The differences in plant height among rice genotypes may be due to mainly genetic background of genotypes environmental effect and nature of soil. These results are in agreement with those reported by Purendu *et al.*(2004). With respect to flag leaf area, the crosses (GZ9057 × Sakha 105) and (GZ6296 × Sakha 105) gave the highest values (56.45 and 52.60 cm2), respectively, while the parent Sakha 105 and the cross (GZ9057 × Giza178) recorded the lowest values (34.21 and 34.84 cm2) respectively, under normal soil. The rice genotype Giza 178, the crosses (GZ1368 × Giza 178) and (GZ9057 × GZ6296) gave the highest values of flag leaf area (25 and 25.76cm2) respectively, under saline soil.On the other hand, the crosses (GZ9057 × Sakha 106) and (GZ1368 × Sakha 106) gave the lowest values of flag leaf area (15.91 and 18.74 cm2), respectively under the same condition. On the other side, the parents Giza 178 and GZ9057 gave

the highest values of flag leaf area (30.95 and 32.83 cm2), respectively under combined analysis, while the crosses (GZ9057 × Sakha 105) and (GZ6296 × Sakha 105) recorded the highest values (39.26 and 37.14 cm2), respectively under the same condition. Generally, the flag leaf area reduced significantly when the rice genotypes grown under saline soil indicating that the adverse effect of salinity on the genotypes and their traits.For number of tillers/plant among parents, Giza 178 showed the highest mean value under normal and saline soil as well as their combined data (30, 26 and 28), respectively. While, Sakha 106 gave the lowest values for no. of tillers/plant under the same conditions, (21, 16 and 19), respectively. The crosses (GZ1368 × Giza 178) and (GZ9057 × GZ6296) showed the highest values under both environments and their combined data Table 4.Whereas, the lowest mean values belonged to (GZ 9057 × Sakha 106) under normal and saline conditions and their combined data (27, 16 and 21), respectively.For the vegetative characters, the results related to salinity effects showed that flowering was delayed due to salinity effect as a result of slowed elongation of the panicle and supporting tissues Lafitte *et al.* (2004). Vegetative stage under salinity is relation to timing of plant growth and developing. Also, plant height was affected by salt stress that caused plant dwarfness than normal condition (Kamoshita *et al*. 2008). Salinity stress resulted in reduction of number of tillers / plant due to plant weakness growth. Flag leaf area is an important trait for photosynthesis and salinity stress reduces it and reflects on the photosynthesis processes. Results in Table 4 showed that most favorable combiners for vegetative characters under salinity stress were GZ9057, Giza 178 and GZ6296. Regarding to the behavior towards the salinity stress we expected that GZ9057 will be the worst parent under salinity condition but if we considered that GZ9057 has some of desirable vegetative traits such as days to heading, plant height and number of tillers per plant and these traits gave the superiority to be the first of the ranking and Giza 178 had the same pattern. Concerning, (GZ9057 × GZ6296) and (Giza 178 × GZ6296) were the most superior crosses for vegetative traits under salinity conditions.

Table 4. Mean performance of growth traits for six parents and their F1 crosses in both environments and their combined data.

NO	Genotypes	Days to heading(day)			Plant height (cm)			Flag leaf area (cm2)			Number of tillers/plant		
		N	S	Comb.	N	S	Comb.	N	S	Comb.	N	S	Comb.
1	GZ1368	131	130	131	114.53	87.33	108.85	37.50	19.20	28.35	26	19	23
2	GZ9057	123	121	122	97.20	91.83	92.27	43.87	21.78	32.83	25	22	23
3	Giza 178	135	131	133	103.66	80.16	97.75	35.89	26.00	30.95	30	26	28
4	GZ6296	125	123	124	97.76	91.21	88.97	38.25	17.00	27.63	25	17	21
5	Sakha 105	126	120	123	107.33	95.10	99.27	34.21	17.11	25.66	23	17	20
6	Sakha 106	126	121	124	111.33	87.33	103.22	39.34	15.78	27.56	21	16	19
	Over all parents	128	124	126	105.30	91.47	98.39	38.18	19.48	28.83	25	20	22
7	GZ1368 x GZ9057	133	129	131	123.66	109.33	116.50	47.54	20.00	33.77	31	20	26
8	GZ1368 x Giza 178	126	126	126	119.33	102.33	110.83	45.83	25.00	35.42	31	25	28
9	GZ1368 x GZ6296	132	128	130	124.99	102.33	113.67	41.49	20.33	30.91	28	20	24
10	GZ1368 x Sakha 105	127	125	126	144.44	115.10	129.77	48.98	23.33	36.16	31	23	27
11	GZ1368x Sakha 106	127	125	126	141.21	125.99	133.61	49.10	18.74	33.92	28	19	24
12	GZ9057 x Giza 178	121	119	120	104.99	93.55	99.28	34.84	22.00	28.42	32	22	27
13	GZ9057 x GZ6296	120	119	120	91.10	82.99	87.05	46.48	25.67	36.08	32	26	29
14	GZ9057 x Sakha 105	124	123	124	125.66	107.77	116.72	56.45	22.07	39.26	27	22	25
15	GZ9057 x Sakha 106	121	120	121	119.22	111.33	115.28	47.83	15.91	31.87	27	16	21
16	Giza 178 x GZ6296	120	117	119	95.99	73.55	84.77	37.68	19.67	28.68	29	20	24
17	Giza 178 x Sakha 105	127	125	126	117.55	106.33	111.94	47.58	24.20	35.89	27	24	25
18	Giza 178 x Sakha 106	122	120	121	117.44	88.553	103.00	47.97	24.67	36.32	29	25	28
19	GZ6296 x Sakha 105	123	119	123	135.66	116.86	126.26	52.60	21.67	37.14	30	22	26
20	GZ6296 x Sakha 106	126	125	126	138.55	111.66	125.11	42.53	21.67	32.10	31	22	26
21	Sakha 105 x Sakha 106	124	121	123	117.32	92.053	104.69	43.79	22.44	33.12	28	22	25
	Over all cresses	116	114	115	121.14	102.65	111.90	46.05	21.82	33.94	29	22	26
	Over all genotypes	122	119	121	111.68	94.88	103.38	43.80	21.15	32.48	27	21	24
	L.S.D. 0.05	0.72	1.17	0.69	1.62	1.33	1.48	2.45	0.98	1.87	0.95	1.00	1.01
	L.S.D. 0.01	1.41	2.30	1.36	3.18	2.60	2.91	4.80	1.93	3.66	1.87	1.96	1.98

N=normal soil (Sakha location), S=salinity soil (El-Sirw), comb= combined data.

2. Yield and its component:
Variation and interaction:

Results indicated that location mean squares were found to be highly significant for all yield and its component traits, indicating over all differences between the stress and non-stress conditions table5.Genotypes, parents and their F1 crosses mean squares were found to be highly significant for all grain yield and its components in both locations and their combined data indicating that over all wide differences among these population. Parent vs. crosses mean squares, as an indications to average heterosis over all crosses, were found to be highly significant also for all yield characters under investigation at the two environments and their combined data. This indicating that the average heterosis over all crosses of these traits

was inconsistent from environment to the other. The interaction of genotypes, parents and crosses with locations (Sakha and El-Sirw) were detected to be highly significant for grain yield and its component studied traits except for harvest index, indicating that the genotypes behaved differently from non-stress to stress conditions. The interaction of parent vs crosses with environments was highly significant for all studied yield characters except for harvest index. Such results indicated that the tested genotypes varied from each other, and ranked differently from location to another (normal to saline soils). The current results are in agreement with the results of EL-Mowafy (2001), EL-Refaee (2002) but Negm (2011).foun that mean square values of parent vs crosses were insignificant for 1000-grain weight.

Table 5.Observed mean square from analysis of variance for grain yield and its components traits under normal (Sakha), saline soil (EL-Sirw) and their combined data.

S.O.V	d.f		Number of panicles/plant			1000-grain weight (g)			Panicles length (cm)			Number of filled grains/panicle		
	sin	Com	N	S	comb	N	S	comb	N	S	comb	N	S	comb
Replications		2	0.54	4.02		1.20	1.89		0.03	0.17		4.67	1.86	
Location		1			1370.56**			194.88**			412.86**			46482.10**
Rep. / Location		4			6.99			1.54			0.10			3.28
(Genotypes)	20	20	24.39**	18.05**	43.69**	58.38**	35.45**	85.14**	17.89**	13.27**	26.69**	1880.20**	1765.10**	3121.17**
Parents	5	5	22.92**	65.19**	80.07**	37.19**	27.33**	63.36**	10.67**	5.34**	10.99**	560.32**	2064.60**	2188.06**
Crosses	14	14	10.72**	11.44**	19.08**	52.83**	27.26**	68.20**	13.52**	12.27**	21.43**	2455.80**	1767.60**	3668.56**
Parent vs crosses	1	1	223.15**	125.04**	206.32**	242.05**	190.68**	431.20**	115.2**	66.93**	178.86**	425.00**	234.10**	123.10**
(Genotypes x Location)		20			6.46*			8.69**			4.47**			524.15**
Parents x Location		5			8.04**			1.17**			5.02**			436.82**
Crosses x Location		14			3.09			11.88**			4.37**			584.83**
Parent vs cross x Location		1			45.73**			1.53**			3.25**			111.20**
Error	40	80	2.10	1.52	2.90	0.22	0.54	0.38	0.62	0.31	0.46	48.28	33.34	40.81

*, ** significant and highly significant at 0.05 and 0.01 probability levels, respectively. N=normal soil (Sakha location), S=salinity soil (El-Sirw), comb= combined data.

Table 5. Cont.

S.O.V	d.f		Spikelet fertility %			Harvest index%			Grain yield/plant (g)			Salinity index %
	sin	com	N	S	comb	N	S	comb	N	S	comb	comb
Replications		2	25.99	0.87		1.63	0.19		6.92	1.97		15.29
Location		1			3019.97**			353.07**			15101.80**	-
Rep. / Location		4			1.81			0.91			4.45	-
(Genotypes)	20	20	447.66**	708.50**	964.83**	49.16**	54.04**	102.14**	348.90**	263.95**	514.41**	326.80**
Parents	5	5	23.98	101.89**	68.50*	12.50**	10.94**	22.96**	115.30**	34.86**	128.53**	42.34
Crosses	14	14	462.27**	755.30**	924.48**	62.31**	69.30**	130.27**	285.08**	177.46**	329.79**	353.60**
Parent vs crosses	1	1	2012.40**	3037.40**	5423.09**	48.37**	55.97**	104.21**	2410.50**	2620.20**	5028.49**	1374.00**
(Genotypes x Location)		20			220.43**			1.06			98.44**	-
Parents x Location		5			57.37**			0.48			21.62**	-
Crosses x Location		14			293.09**			1.34			132.75**	-
Parent vs cross x Location		1			18.48**			0.14			22.18	-
Error	40	80	1.78	1.81	1.60	0.78	0.70	0.74	8.51	6.92	7.719	33.96

*, ** significant and highly significant at 0.05 and 0.01probability levels, respectively. N=normal soil (Sakha location), S=salinity soil (El-Sirw), comb= combined data.

Mean performance:

The mean performance of the yield and its components varied from combination to other table 6.The parent Giza 178 and GZ9057 recorded the highest mean values of yield and yield components under normal and saline conditions as well as their combined data, while the parent Sakha106 gave the lowest mean value of them under the same conditions. On the other hand, the crosses (GZ9057 × GZ6296), (GZ1368 × Giza178) , (GZ1368 × Sakha 105) and (Giza178 × Sakha 106) gave the highest mean values of number of panicles/plant under both environments and their combined under normal conditions all entries showed mean values higher than under saline soil for this trait. For 1000-grain weight (g) among parents GZ1368 and GZ6296 showed the highest mean value under normal

and saline soil as well as their combined data. On the other side, Giza 178 gave the lowest values for 1000-grain weight (g) under the same conditions, which values were (22.50 , 20.67 and 21.58, respectively), the crosses (GZ6269 × Sakha 106), (Sakha 105 × Sakha 106), (Giza178 × Sakha 106), (GZ9057 × GZ6296) and (GZ1368 × Sakha 106) showed the highest values under both environments and their combined data (Table 6).The lowest mean values belong to (GZ 1368× Giza178) under normal and saline conditions and their combined data(22.03 ,21.30 and 21.67, respectively).Regarding panicle length, among parents GZ 1368 and Giza 178 showed the highest mean value under normal and saline soil as well as their combined data.On contrary, Sakha 105 gave the lowest values for panicle length under the same conditions,which values were

(21.50, 19.67 and 20.58, respectively).The crosses (GZ6296 × Sakha 106), (GZ1368 × Giza 178), (GZ1368× GZ9057) and (GZ1368 × GZ6296) showed the highest mean values under both environments and their combined data Table 6. The lowest mean values of (Giza 178 × Sakha 106) under normal and saline conditions and their combined data (25.44, 18.83 and 22.14 respectively).With respect to number of filled grains/panicle , Giza 178 showed the highest mean value under normal and saline soil as well as their combined data (153, 146 and 150, respectively).The crosses (GZ9057 × Giza 178), (GZ1368 × GZ6296), (GZ6296 × Sakha 106) and (GZ1368 × Giza 178) gave the highest values, while the parent Sakha 105 recorded the lowest mean values of filled grain/panicle(138,95 and 116 in normal, saline and combined data, respectively). While the cross (GZ9057 × Sakha 106) recorded the lowest values (93, 64 and 79 grains, respectively) under normal and saline soil as well as their combined. For spikelet fertility %, the desirable mean values were obtained from parents Sakha 106, Sakha 105 and GZ6296 and the crosses(GZ9057 × GZ6296), (GZ1368 × GZ6296) and (GZ9057 × Giza178) and ranged from 90.55% to 97.57 under both environments and their combined data. The results in Table (6) indicated that salinity conditions have negative effect on the spikelet fertility %, where it decreased under saline soil (El-Sirw) for all genotypes compared with normal soil.Sinha (198 Zayed *et al.* (2017) 6).Under normal and soil salinity found that spikelets sterility was highly affected by soil salinity in all evaluated rice genotypes.Concerning harvest index, the parents Sakha 106 and Sakha 105 and the crosses (GZ6296 × Sakha 106), (Giza178 × GZ6296) and (GZ1368× GZ6296)   recorded the desirable mean values for this trait at the two locations and their combined data. There was highly significant reduction in harvest index under stress conditions in the most of studied rice genotypes studied. For grain yield/plant, the desirable mean values were obtained from parents

Giza 178 and GZ1368 and the crosses (GZ1368 × GZ6296), (Giza178 × GZ6296) and (GZ1368 × GZ9057), and ranged from 51 to 74 (g) under both environments and their combined data. Hassan (2003) and Zayed *et al* (2016) indicated that increasing salinity levels caused significantly reduction in spikelets sterility, panicle weight, 1000-grain weight and grain yield per plant.Regarding to salinity index%, the crosses GZ6296 x Sakha106, GZ1368 x Sakha106 and GZ9057 x Sakha106 gave the highest values (82, 77 and 74%, respectively) under normal soil at Sakha ,while the cross as Sakha105 x Sakha106 and GZ9057 x Giza 178 recorded the lowest values (41.33and 49.04%) of harvest index under the same condition. Zayed *et al.* (2017) reported that an average salinity can reduce rice grain yields, which was quite lower than current guidelines indicating that salinity affects rice yield at or above 3.0 dSm-1. Salinity had negative impacts on a number of yield components, including stand establishment, numbers of panicles and spikelets per plant. Khatun *et al.* (1995) studied the effects of salinity on the reproductive stage of rice genotypes also reported that salinity reduced the number of productive tillers, number of fertile florets panicle-1, grain weight and the grain yield. Effects on grain yield were more severe than on vegetative growth. There was genotypic variation in the response of these characters to salinity.Regarding to the behavior towards the salinity stress we expected that Giza 178 and Sakha 105 was the worst under salinity condition but if we considered that Giza 178 has some of desirable yield and its component traits such as number of panicles / plant, panicle length (cm) and no. of filled grains / panicle and those traits gave it the superiority to be in the first of the ranking, in the same trend Giza 178 was behaved.Concerning, (GZ6296 × Sakha 106) and (GZ1368 × GZ 6296) were the most superior crosses for grain yield and its components traits under salinity conditions In fact, for the previous two crosses that gave the highest mean values under salinity stress.

Table 6. Mean performance of grin yield components traits for six parents and their F1 crosses in both environments and their combined data.

NO	Genotypes	Number of panicles/plant			1000-grain weight (g)			Panicle length (cm)			Number of filled grains/panicle		
		N	S	Comb.	N	S	Comb.	N	S	Comb.	N	S	Comb.
1	GZ1368	25	18	21	30.97	29.03	30.00	26.78	21.55	24.17	161	131	146
2	GZ9057	23	20	22	25.73	24.83	25.28	24.67	19.89	22.28	167	131	149
3	Giza 178	28	23	26	22.50	20.67	21.58	23.00	22.66	22.83	153	146	150
4	GZ6296	23	16	19	32.13	28.53	30.33	22.33	19.33	20.83	137	100	119
5	Sakha 105	22	16	19	28.20	26.07	27.13	21.50	19.67	20.58	137	78	107
6	Sakha 106	20	15	18	28.83	26.40	27.62	23.17	19.67	21.42	138	95	116
	Over all parents	23	19	21	28.06	25.92	26.99	23.58	20.46	22.02	149	113	131
7	GZ1368 x GZ9057	28	18	23	32.53	28.27	30.40	27.67	24.55	26.11	154	116	135
8	GZ1368 x Giza 178	30	23	27	22.03	21.30	21.67	29.77	24.55	27.16	167	131	149
9	GZ1368 x GZ6296	26	18	22	34.30	29.93	32.12	25.66	24.33	25.00	170	141	155
10	GZ1368 x Sakha 105	29	22	26	28.27	27.37	27.82	29.77	23.66	26.72	169	103	136
11	GZ1368x Sakha 106	26	19	22	32.60	31.63	32.12	28.89	23.55	26.22	154	96	125
12	GZ9057 x Giza 178	30	21	25	31.60	28.10	29.85	24.55	23.22	23.89	204	145	175
13	GZ9057 x GZ6296	31	23	27	34.13	31.63	32.88	24.17	20.33	22.25	163	122	142
14	GZ9057 x Sakha 105	26	20	23	32.73	29.53	31.13	25.50	23.55	24.53	112	86	99
15	GZ9057 x Sakha 106	25	16	21	36.40	29.27	32.83	27.22	21.44	24.33	93	64	79
16	Giza 178 x GZ6296	27	20	23	31.90	28.77	30.33	23.77	20.67	22.22	165	79	122
17	Giza 178 x Sakha 105	25	21	23	26.50	30.47	28.48	27.55	24.00	25.78	137	120	128
18	Giza 178 x Sakha 106	29	22	26	33.37	32.77	33.07	25.44	18.83	22.14	102	83	93
19	GZ6296 x Sakha 105	26	20	23	38.57	31.00	34.78	27.44	24.33	25.89	142	107	125
20	GZ6296 x Sakha 106	29	20	24	37.10	33.87	35.48	27.89	24.67	26.28	153	137	145
21	Sakha 105 x Sakha 106	27	21	24	33.97	32.70	33.33	23.22	19.44	21.33	144	105	125
	Over all cresses	28	20	24	32.40	29.77	31.09	26.57	22.74	24.66	158	116	137
	Over all genotypes	26	19	23	31.16	28.67	29.92	25.71	22.09	23.90	153	115	134
	l.s.d 0.05	2.32	1.97	2.73	0.75	1.18	0.98	1.26	0.89	1.09	11.12	9.24	10.22
	l.s.d 0.01	3.05	2.60	3.59	0.98	1.55	1.30	1.66	1.17	1.43	14.64	12.16	13.46

N=normal soil (Sakha location), S=salinity soil (El-Sirw), comb= combined data.

Table 6. cont.

NO	Genotypes	Spikelet fertility %			Harvest index			Grain yield/plant (g)			Salinity index%
		N	S	Comb.	N	S	Comb.	N	S	Comb.	
1	GZ1368	97.12	81.22	89.19	35.05	31.93	33.49	52.66	30.33	41.50	57.72
2	GZ9057	94.33	79.26	86.80	34.19	31.22	32.71	58.33	35.00	46.67	60.03
3	Giza 178	90.55	88.18	89.36	37.38	33.32	35.35	55.27	30.00	42.64	54.31
4	GZ6296	97.41	90.51	93.96	38.44	34.33	36.39	49.27	28.00	38.64	57.12
5	Sakha 105	93.42	91.41	91.92	38.55	34.90	36.73	40.50	25.00	32.75	61.70
6	Sakha 106	97.61	94.19	95.90	39.15	36.34	37.75	53.48	27.33	40.41	51.38
	Over all parents	95.20	87.38	91.19	37.10	33.67	35.40	51.59	29.28	40.44	57
7	GZ1368 x GZ9057	96.44	57.57	77.01	44.26	39.90	42.08	69.16	51.76	60.47	74.86
8	GZ1368 x Giza 178	94.16	61.28	77.72	37.52	33.27	35.39	65.55	44.00	54.78	67.37
9	GZ1368 x GZ6296	93.66	91.36	92.51	43.39	41.05	42.22	73.72	52.70	63.21	71.75
10	GZ1368 x Sakha 105	79.34	67.40	73.29	38.94	36.01	37.48	63.33	41.66	52.50	65.74
11	GZ1368x Sakha 106	71.26	88.27	79.77	32.38	28.58	30.48	62.33	48.00	55.17	77.05
12	GZ9057 x Giza 178	97.57	90.55	94.56	39.37	38.40	38.89	90.51	44.33	67.43	49.04
13	GZ9057 x GZ6296	95.24	94.51	94.87	35.52	32.73	34.13	66.94	48.40	57.67	72.46
14	GZ9057 x Sakha 105	65.23	58.49	61.86	35.27	32.15	33.71	57.33	32.13	44.73	56.01
15	GZ9057 x Sakha 106	65.57	54.76	60.17	36.00	31.06	33.53	45.33	33.66	39.50	74.37
16	Giza 178 x GZ6296	94.13	87.74	90.93	47.60	44.17	45.88	70.95	51.66	61.31	72.89
17	Giza 178 x Sakha 105	75.71	61.58	68.65	35.13	31.15	33.14	67.66	45.00	56.33	67.43
18	Giza 178 x Sakha 106	67.13	56.27	61.70	33.47	30.18	31.83	57.99	39.80	48.90	68.48
19	GZ6296 x Sakha 105	77.58	64.33	70.96	42.53	39.05	40.79	60.00	41.70	50.85	69.54
20	GZ6296 x Sakha 106	70.51	56.00	63.26	44.42	41.55	42.99	62.00	51.03	56.52	82.34
21	Sakha 105 x Sakha 106	92.88	87.91	82.73	40.17	37.14	38.66	66.38	27.43	46.91	41.33
	Over all cresses	81.67	69.57	76.67	39.06	35.76	37.41	65.28	43.55	54.42	67.38
	Over all genotypes	85.52	74.66	80.82	38.51	35.16	36.84	61.11	39.21	50.16	64.42
	L.S.D. 0.05	2.14	1.66	2.15	1.41	1.33	1.37	4.67	4.21	4.45	9.33
	L.S.D. 0.01	2.81	2.19	2.83	1.86	1.76	1.81	6.15	5.54	5.85	12.28

N=normal soil (Sakha location), S=salinity soil (El-Sirw), comb= combined data.

Phenotypic correlation coefficients:

High yield at the salinity conditions has been attributed to the salinity tolerance nature of the genotypes association analysis reveals that the relationship between the various independent yield contributing characters with the dependent variable of interest, the grain yield. Also, yield improvement in salinity conditions is difficult without understanding the association of secondary and putative traits of salinity tolerance with grain yield. In the present study the association has been done to identify the nature of association among important yield contributing vegetative, yield and its component traits of salinity tolerance with grain yield in F1 generation of rice. Observation values were recorded on 16 yield contributing and salinity tolerance characters viz, days to heading, plant height, flag leaf area, number of tillers/plant, number of panicles/plant,1000-grain weight,panicle length,no. of filled grains/panicle, harvest index and grain yield /plant. Data in Table (7) showed that grain yield/plant was highly significant positive correlated with each of plant height, number of tillers/ plant, 1000-grain weight, panicle length, number of filled grains/panicle and harvest index. As for number of filled grains/panicle gave highly significant positive correlation coefficient with number of days to heading (days) (0.536) and number of tillers per plant (0.472). In the same time, grain yield had significant correlation with number of of panicles/plant (0.411).For panicle length, results showed that highly significant positive correlation coefficient between this trait and number of days to heading with value (0.532) and gave significant with plant height (0.724), flag leaf area (0.360).Flag leaf area is concerned, positive significant and highly significant correlation coefficient estimates were found between this trait and number of days to heading and plant height with values 0.397 and 0.438, respectively.For plant height only number of days to heading showed significant positive correlation coefficient with plant height with value (0.405).Similar findings were obtained by Negm,(2011).

Table 7. Estimates of correlation coefficients between all studies traits under salinity stress conditions.

	P.H	F.L.A	N.T	N.P	1000.G	P.L	N.F.G	S.F	H.I	H.P	M.P	H.R	G.L	G.W	G.Y
D.H	0.405**	0.397**	0.165	0.223	-0.282*	0.532**	0.536**	-0.154	-0.062	0.433**	-0.18	0.417**	-0.279*	-0.256*	0.079
P H		0.438**	-0.077	-0.067	0.214	0.724**	-0.027	-0.508**	-0.074	0.380**	0.176	0.072	-0.176	-0.243	0.397**
F.L.A			-0.015	-0.094	0.096	0.360**	-0.097	-0.568**	-0.082	0.414**	0.02	0.04	-0.133	-0.283*	0.123
N.T				0.811**	-0.071	0.251*	0.472**	-0.202	-0.123	0.114	0.054	0.044	0.114	-0.285*	0.388**
N.P					-0.225	0.219	0.411**	-0.1	-0.059	0.156	-0.013	-0.058	0.016	-0.304*	0.167
1000.G						-0.015	-0.232	-0.163	0.118	-0.042	0.12	-0.319*	-0.052	0.09	0.392**
P.L							0.431*	-0.411**	0.242	0.324*	0.065	0.228	-0.202	-0.554**	0.578**
N.F.G								0.17	0.176	0.228	-0.144	0.374**	-0.036	-0.23	0.394**
S.F									0.114	-0.416**	-0.105	-0.019	-0.037	0.370**	-0.211
H.I										-0.179	-0.082	-0.213	-0.035	0.384**
H.P											0.026	0.124	-0.021	-0.065	0.038
M.P												-0.307*	0.128	-0.13	0.245
H.R													-0.027	-0.053	-0.003
G.L														-0.051	0.024
G.W															-0.574**

D.H.	Number of Days to heading (day)	N.T	Number of tillers per plant.	P.L	Panicle length (cm).	H.I.	Harvest index (HI %).	H.R	Head rice percentage.		G.Y	Grain yield per plant (g).
P.H.	Plant height (cm).	N.P	Number of panicles/plant .	N.F.G	Number of filled grains/panic	H.P	Hilling percentage	G.L.	Grain length			
F.L.A	Flag leaf area (cm²).	1000.G	1000-grain weight (g).	S.F.	Spikelets fertility (%).	M.P.	Milling percentage .	G.W.	Grain width			

7- Multivariate analysis and genetic divergence of rice genotypes under stress conditions:

Genetic divergence studies on rice have been revealed some interesting features of differentiation and adaptability. Such analysis can provide useful additional information, studying interrelationships of genotypes and giving graphical assessment of genetic variability. The present approach for studying genetic divergence in rice based on vegetative traits, yield and its components of the parents and F1 hybrids under salinity stress conditions. These information could be useful in identifying optimal breeding strategies for rice improvement.

A-Multivariate analysis:

Multivariate techniques which used principal components analysis were performed on sixteen agronomic traits to extract important component to obtain the initial factor solution using some values. These values could measure the explained variance associated with each factor and variable (Hair *et al*., 1987).In an analysis with sixteen variable traits as well as sixteen axes were existed. However, only those traits which exhibited high multivariate variations were considered for stress conditions. The relative magnitude of the coefficient of each traits relating to the first five principal components from the component analysis can often provide an interpretation for each component axis Table 8. The sign of the coefficient is irrelevant, and in fact arbitrary, though negatively correlated traits will generally have opposite sign on the given axis. Though clear guidelines do not exist to determine the significance of a trait coefficient, on role of thumb is to treat coefficient < 0.5 as having a large enough effect to be considered important (Hair *et al*., 1987). Each trait was an important source of variation, at least, one principal component axis. Some traits may have greater importance in determining plant phenotypes than others (Brown,1991).The principal components analysis Table 8 showed that panicle length (cm) , number of days to heading , grain yield per plant, and spikelets fertility (%).As most of these traits deal with yield and its components traits which correlated with yield. Thus, we have essentially a component, or an axis, dealing with yield traits (weight axis), and giving negative loading with axis.This trend was changed in the PC2 axis since earliness traits i.e. number of panicles/ plant, 1000-grain weight (g) and number of filled grains/ panicle. An inter-correlation is implied among traits with high coefficients on the same axis, all these traits had positive loading with axis. Similarly for PC3, number of tillers per plant followed by milling exhibited the largest coefficients on this axis with positive loadings.The rest PC axes deals with harvest index, PC4, and grain length, PC5 Table 8. Zulqarnain *et al* (2013) reported that yield per plant by plant height and delay in heading time was a primary source of variation on the first PC axis with the largest coefficient. Span length had the largest coefficient in the second axis. However, Sinha and Mishra (2013) found that the most important traits were panicle length and 100 grain weight in the PC1, 50% heading (days) for PC2 and grain length (mm) for PC3.Each component score is a linear combination of the trait similar to an index,the maximal amount of variance is shown on the first PC and second maximal on the second PC, etc.Thus the two dimensional distance between genotypes might reflect a summary of differences based on all traits measured to the extent that the first two PC axes, are effective in capturing the combined variance of all traits (Hair *et al*.,1987).Therefore, the first two PC axes were used for presentation of the six parents and 15 F1 hybrids as shown in Fig. 1. It is clear that the first PC axis separated most F1 hybrids with some original parents. However PC2 axis separated most parental genotypes. In this connection Abdel-Salam *et al*. (2010) separated nine parents into 6 groups by using principal components analysis.

Table 8. Principal component factor analysis of traits associated with 21 rice genotypes under salinity stress conditions.

Variable	PC axis					
	PC1	PC2	PC3	PC4	PC4	Communality
Number of Days to heading (days).	0.707	0.266	-.502	0.043	-.101	0.835
Plant height (cm).	0.622	-.541	-.216	0.039	-.004	0.727
Flag leaf area (cm2).	0.528	-.481	-.316	-.177	-.111	0.654
Flag leaf area (cm2).	0.482	0.448	0.573	-.298	-.330	0.958
Number of tillers per plant.	0.441	0.573	0.469	-.252	-.358	0.934
Number of panicles/plant.	-.087	-.625	0.274	0.206	-.345	0.634
1000-grain weight (g).	0.878	-.120	0.02	0.302	0.104	0.888
Panicle length (cm).	0.532	0.646	0.079	0.218	0.059	0.757
Number of filled grains/panicle.	-.564	0.493	0.005	0.347	0.1	0.692
Spikelets fertility (%).	0.041	0.008	0.141	0.823	0.077	0.704
Harvest index (HI %).	0.633	-.099	-.336	-.398	0.018	0.682
Grain yield per plant (g).	0.099	-.411	0.544	-.190	0.275	0.587
Milling percentage.	0.417	0.461	-.466	0.072	0.402	0.771
Head rice percentage.	-.151	0.022	0.351	-.508-	0.634	0.806
Grain length	-.668	0.072	-.338	-.042	-.219	0.615
Grain width	0.556	-.212	0.566	0.411	0.166	0.871
Eigen value	4.335	2.632	2.232	1.794	1.124	12.117
Var %	27.094	16.449	13.951	11.21	7.026	75.73
Comulative%	27.09%	43.54%	57.49%	68.70%	75.73%	75.73%

b- Hierarchical clustering analysis:

This procedure, which using disjoint cluster analysis on the basis of Euclidean distance, provides visual idea about variability's presented in the studied rice genotypes, in addition to assuring the continued genetic improvement.

Diversity among parental genotypes:

The estimates of Euclidean dissimilarity coefficient between the six parental genotypes corresponding to the 15 possible comparisons are given in Table 9. These estimated that treated as Chi-square values, showed that about 80 of values were significant. These results indicated that the studied genotypes were expected to similarly a broad spectrum of variability and confirmed the detected significant among these parents. Euclidean distance were ranged from 17.59 between (GZ6296 and Sakha 106) to 71.23, between (Giza 178 and Sakha 105) under stress conditions. In this regard, these results are in agreement with Chakravarthi and

Naravaneni (2006) they reported low similarity coefficient between Japonica type and Indica type's genotypes, and Kanawapee *et al*. (2011) they reported relatively high level of similarity between closely related genotypes. Genetic divergence based on Euclidean distance between the six parental genotypes are presented in Fig. 2. All genotypes clearly grouped into four major clusters. The first cluster represents Sakha 105, Sakha 106 and GZ6296 as salt sensitive cluster in most of the characters, but showed the GCA in the number of filled grains / panicles. On the other hand clusters 3 and 4 include the parents Giza178 and GZ9057. They were superior for plant height, number of panicles/plant, number of filled grains/panicles and spikelets fertility %. Cluster analysis provided with a complete view of the variation present among the six rice genotypes and it might be used for the plant breeders for the genetic improvement of rice under saline soil. El-Malky *et al*. (2007) reported that the ability of SSR makers to divide the genotypes into two groups, one included the Indica genotypes and the other included the Japonica genotypes. Also, Zeng *et al*., (2004) found that, all genotypes clearly grouped into two major branches in the dendrogram with less than 10% similarity based on Jaccard similarity index, one branch represented the subspecies Japonica rice and the other branch represented the subspecies Indica or the hybrids between Japonica rice and Indica rice.Machado *et al*.(2002) noticed that in order to obtain the best combination, choose parents which have greatest genetic divergence. However, not only the genetic divergence might be used to choose parents for crossing, but also the performance of parents and their F1,s. as well as GCA and SCA effects are more informative than performance El-Mansy 2014).It is interesting to note that crossing genotypes from genetically distant clustered populations may result in the expression of more heterosis in F1 generation and wider genetic variability in the selected on the basis of large inter cluster distance for isolating useful recombinants in the segregating generations under salinity stress conditions.

Divergence between parental genotypes and their F1 progenies:

Based on relative dissimilarity among the genotypes the 21 rice genotypes (15 F1 hybrids and six parents) were grouped into eight major clusters as presented in Fig. 3. The relative distribution of parental genotypes and their F1 heterozygous in dendrogram reflects a broad parallelism between divergence distance and principal component analysis as well as general and specific combining ability. Cluster 1 contained two F1

hybrids. Both of them between closely related parents and gave desirable significant values for spikelets fertility% traits, GZ9057 and Sakha 105 as a common parent with Giza 178 and Sakha 106 under stress conditions. Cluster 2 contained one F1 genotype having divergent distance with other genotypes and clusters. This genotype was the best hybrid for SCA effect for grain yield. The parents in this hybrid were distantly related parents. Most combinations which had good specific combining ability were having one or two parents of either good × good or good × poor general combiner for example, the cross combinations (Giza 178× GZ6296) surpassed all crosses for most earliness character. The crosses which included one good and one poor general combiners, could produce desirable transgressive sergeants if fixable gene complexes (additive) in good combiners and complementary epistatic effect in poor combiners acted in the same direction to maximize the desirable attributes. Cluster 3 consisted of three genotypes. Three of them were parental. The genotypes in such cluster were the best GCA for spikelets fertility% trait. In contrast cluster 4 contained two F1 hybrid. On the other hand, cluster 5 consisted of five genotypes (two F1 hybrids and three parents). Cluster 6 and cluster 7 contained one F1 genotype having divergent distance with other genotypes and cluster 8 consisted of six F1 hybrids. Agrama *et al*., (2007) studied association mapping of yield and its components in rice cultivars. Cluster Analysis grouped 92 accessions in eight clusters according to geographic region. Rashid *et al*. (2008), Akter *et al*., (2009), Seetharam *et al*., (2009) and Vanniarajan *et al*., (2012).

Data in Table 10 showed that the largest intra cluster distance between clusters 2, 6 and 7 also cluster 1and cluster 3 and cluster 8closely related. The distribution pattern of the F1 heterozygous were more or less influenced by their parents as expected on the basic of close affinity between the parents and their F1 progenies.It is evident that crossing of distantly related parents may give hybrids which surpassed their parents in most trait and should produce higher variance in segregating generation rather than crossing between nearly related parents, which agree with AI-Akheder (2007) and EI-Mansy *et al* (2014).Grouping of genotypes by multivariate methods in the study is of practical value for the rice breeder. Representative genotypes may be chosen from the particular groups for hybridization programs with other approved cultivars.This will aid in identification, selection and combining genotypes to obtain important characters in one line with a broad genetic base.
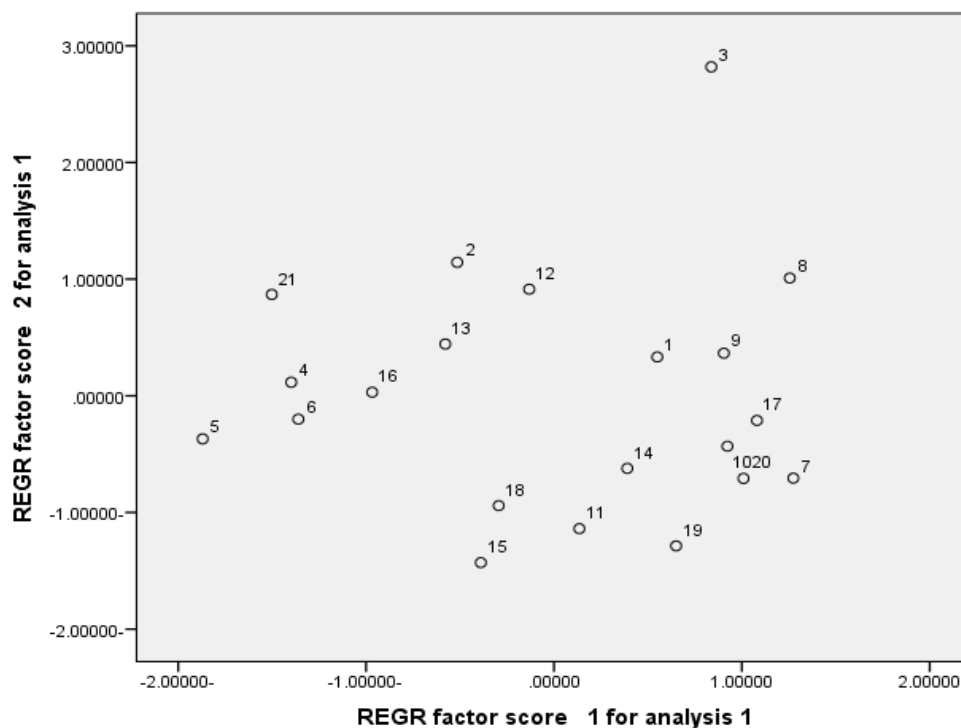
Table 9. Euclidean dissimilarity coefficients among six parental rice genotypes under salinity stress conditions.

| Case	Euclidean Distance					
	1:GZ1368	2:GZ9057	3:Giza 178	4:GZ6296	5:Sakha 105	6:Sakha 106
1:GZ1368		23.381	26.922	40.963	57.332	42.428
2:GZ9057			23.963	35.266	55.824	41.487
3:Giza 178				50.85	71.23	55.622
4:GZ6296					25.771	17.587
5:Sakha 105						18.547
6:Sakha 106						

Table 10. Inter and intra cluster distance among eight clusters under salinity stress condition

Cluster	1	2	3	4	5	6	7	8
1	11.300	56.301	58.139	69.642	36.895	45.743	26.436	38.776
2		0.000	29.688	28.671	36.86	51.952	78.046	44.524
3			14.400	23.101	46.822	55.082	79.796	35.647
4				8.900	55.525	56.502	90.186	41.2
5					16.900	42.68	51.312	48.956
6						0.000	51.585	40.996
7							0.000	57.801
8								15.420

Fig. 1. Representation of 21 rice genotypes of the first two PC axes of principal component analysis under salinity stress conditions.
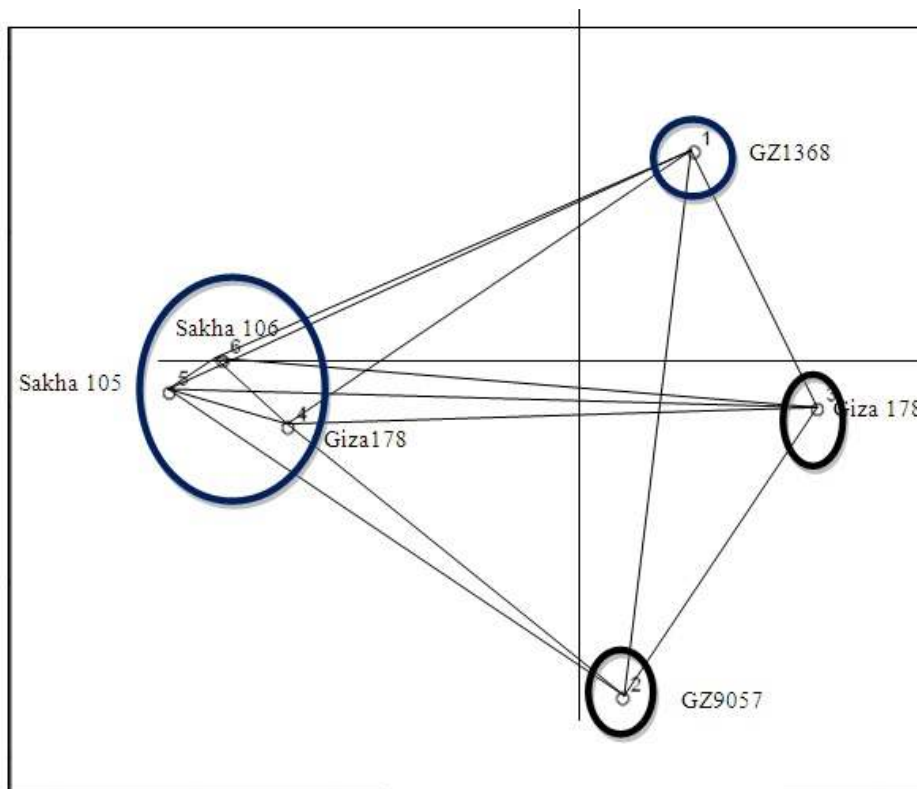
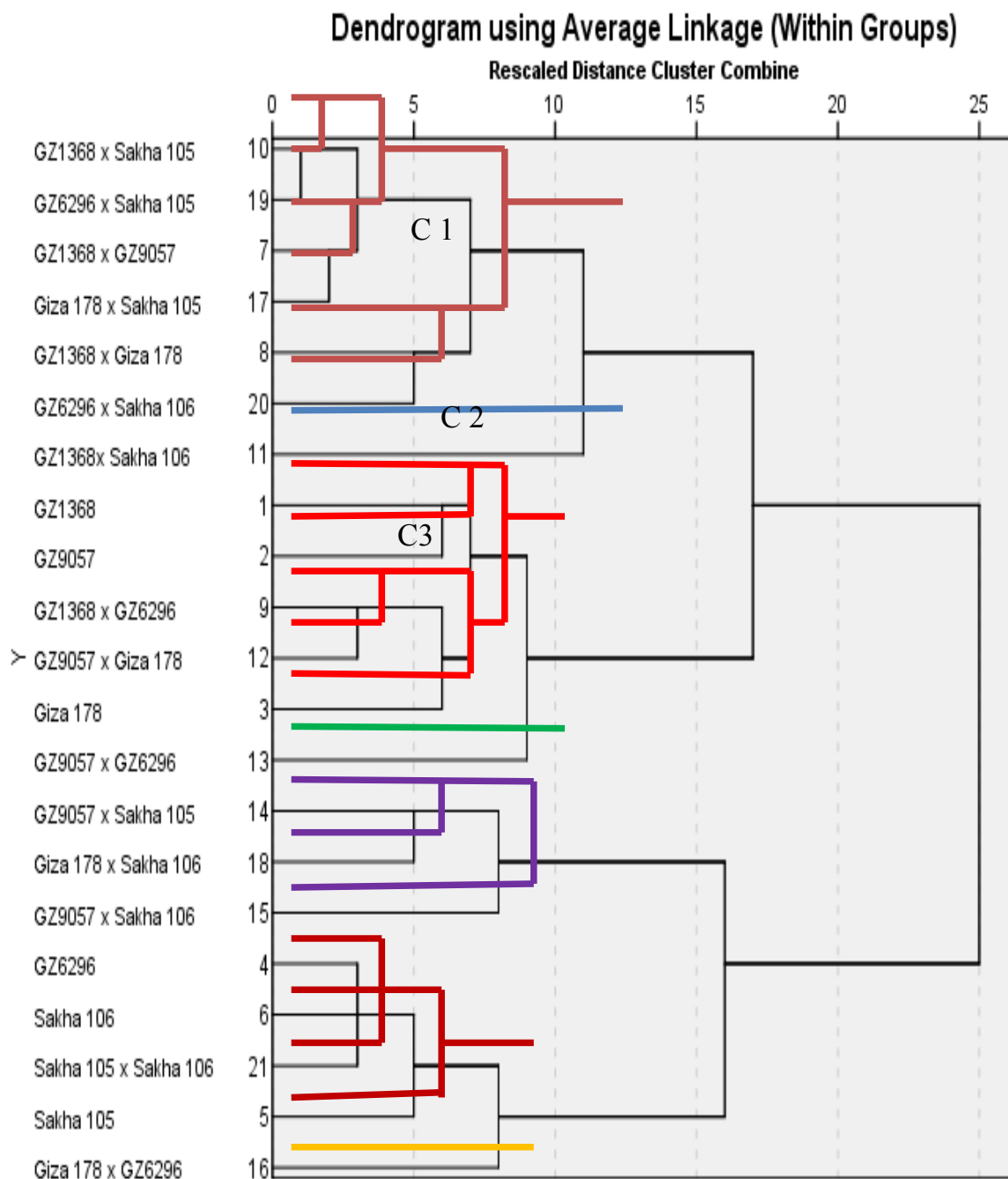**Fig.2.Dendrogram presentation of 6 rice parental genotypes based on dissimilarity coefficients.**

Fig. 3. Result of hierarchical cluster analysis based on dissimilarity coefficient among 21 rice genotypes under salinity stress conditions.

REFERENCES

Abd El-Salam, M.E.; Y.M.El-Mansy and Rokia, M. Hassan (2010). The relative importance of characters affectinh genetic divergence in cotton.J. Agric.Kafr El-Sheikh Univ., 36(1):44-63.

Agrama H.A, G.C.Eizenga and W.Yan (2007). Association mapping of yield and its components in rice cultivars. Mol. Breed., 19: 341-356.

AI-Akheder, A.A.A.(2007). Genetic divergence and association with heterosis in cotton Egypt.J. Genet. Cytology. (2): 1-10.

Akter, A., M.J. Hasan, A.K. Paul, M.M.Motalib and M.K. Hossain (2009). Selection of parent for improvement of restorer line in rice (Oryza sativa L.). SAARC J. Agri., 7(2): 43-50.

Black, C.D., L.E. Evans, J.L. Ensminger and F.E. Clark (1965). Methods of soil Analysis. Part 1 and Part 11. Amer. Soc of Agron. In publisher, Madison-Wisconsin, U.S.A.

Brown. M. S.(1991). Principal component and cluster analysis of cotton cultivars variability across the US cotton Betl. Crop. Sci., 31:915-921.

Chakravarthi, B. K. and R. Naravaneni (2006). SSR marker based DNA fingerprinting and diversity study in rice (Oryza sativa L.). African Journal of Biotechnology, 5(9): 684-688.

Dwivedi, K.N.,C.N .Chaubey and N.R .Gupta .(1991) Study of saline-alkali soil resistance in rice (Oryza sativa L).Oryza .267-265 :(28)

El-Malky, M. M. (2007). Combining ability and genetic analysis of some quantitative characters in rice. Proc. 5th Conf. Egypt. J. Plant breed. 11: 581-592.

El-Mansy Y.M., M.E.Abdel-Salam and B. M. Ramdan.(2014). Multivariate analysis of genetic divergence and combining abilityin G. barbadense L.j.Agric. res. Kafr El-Seikh Univ.40(1).

El-Mowafi, H. F. (2001). Study on heterosis in hybrid rice under Egyptian condition. Egypt. J. Appl. Sci., 16(2): 52-63.

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

Flowers, T.J. and A.R. Yeo (1997). Breeding for salt resistance in plants. In: P.K. Jaiwal, P.R. Sing & A. Gulaati (Eds.), Strategies for Improving Salt Tolerance in Higher Plants. Science Publishers. Inc., Enfield, New Hampshire, p. 247-264.

Flowers, T.J. and A.R. Yeo. (1981). Variability in the resistance of sodium chloride salinity within rice varieties. New Phytol. 88: 363-373.

Gomez, K.A. and A.A. Gomez, (1984). Statistical Procedures for Agricultural Research. 2nd ed. Jahn Wiley Sons, New York, USA.

Hair. J. F.; Jr.F. E.Andrson and R.l. Tatham (1987). Multivariate data analysis with reading. Mac. Millan Pub. Co., New York.

Hassan, A.L.A. (2003). Breeding studies for salt tolerance in rice. M.Sc. Thesis, Fac. of Agric., Tanta University, Kafr El-Sheikh, Egypt.

Heenan, D.P., L.G. Lewin, and D.W. McCaffery.(1988). Salinity tolerance in rice varieties at different growth stages. Aust. J. Exp. Agric. 28:343-349.

IRRI (1996). International Rice Research Descriptors for Rice. Los Banos, Laguna, Philippines. 52p.

Kamoshita, A., R. Chandra, N. Manikanda, and S. fukai (2008). Phenotypic and genotypic analysis of drought-resistance traits for development of rice cultivar adapted to rainfed environments. Field crops Res., 109 109:1-23.

Kanawapee, N.; J. Sanitchon; P. Srihaban and P. Theerakulpisut(2011). Genetic diversity analysis of rice cultivars (Oryza sativa, L.) differing in salinity tolerance based on RAPD and SSR markers. Electronic Journal of Biotechnology, 14(6): 1-17.

Khatun, S.;C.A. Rizzo and T.J. Flowers (1995). Genotypic variation in the effect of salinity on fertility in rice. Plant and Soil,173(2): 239-250

Lafitte, H.R.; A. Ismail and J. Bennet (2004). Abiotic stress tolerance to rice for Asia: progress and the future, in New Directions for a Diverse Planet: Proceedings of the 4th International Crop Science Congress, ed. By Fischer, T., Turner, N.; Angus, J.; McIntyre, L.; Robertson, M.; Borrell, A. *et al*., Brisbane, Australia.

Lutts, J.M Kinet, J. Bouharmont (1995). Changes in plant response to NaCl during development of rice (Oryza sativa L.) varieties differing in salinity resistance. Journal of Experimental Botany, 46 (12): 1843-1852.

Machado, C. F.; G. H. S. Munes and D. F. Ferreria (2002). Genetic divergence among genotypes using multivariate technique. Ciencia Rural, 32(2):251-258.

Negm, M.E.A.A.(2011). Genetical studies on some physiological characters of salinity tolerance in rice. M.Sc. Thesis, Fac. of Agric., Kafr El-Sheikh Uni., Egypt.

Purnendu, G.; M.A. Mannan; P.S. Pal; M.M. Hossain and S. Parvin (2004). Effect of salinity on some yield attributes of rice. Pakistan J. of Biological Sci., 7(5): 760-762.

Rabbani MA, Z.H. Pervaiz and M.S. Masood (2008). Genetic diversity analysis of traditional and improved cultivars of Pakistani rice (Oryza sativa L.) using RAPD markers. Elect J. Biotech., 11(3): 1-10.

Rashid, M., A.A. Cheema and M. Ashraf (2008). Numerical analysis of variation among basmati rice (Oryza sativa.) mutants. Pakistan. J. Bot., 40(6): 2413-2417.

Seetharam K, S, Thirumeni and K. Paramasivam (2009). Estimation of genetic diversity in rice (Oryza sativa.) genotypes using SSR markers and morphological characters. Afr. J. Biotech., 8(10): 2050-2059

Sinha and P.k .Mishra (2013). Morphologybased multivariate analysis of phenotypic diversity of landraces of rice (Oryza sativa L.) of Bankura district of West Bengal. J.of Crop and Weed, 9(2):115-121(2013).

Sinha, T.S. (1986). Varietal evaluation of rice genotypes in coastal saline soil. Inter. Rice. Res. Newsletter, 11(3): 12-13.

Vanniarajan ,C.,K.K .Vinod and Y. Pereira (2012). Molecular evaluation of genetic diversity and association studies. J. Genet., 91: 9-19.

Zayed,B.A.,O.A.M.Ali andS.A.Hamoud(2016)Physiological and genetic performance of some rice genotypes grown in medium and high salinity soils.Menoufia,J.of Plant Prod.,(1):155-175.

Zayed, B.A., R.A. EL-Namaky., M.M.A.Osman and M.E.Negm (2017). Inheritance some of physio-morphological characteristics, yield and its components under salinity conditions. The 11th Interaction Plant Breeding Conference 17-18 October. Crop Science Department, Faculty of Agriculture, Kafrelsheikh Univ., Egypt.

Zeng, L., T. R. Kwon; X. Liu; C. Wilson; C. M. Grieve and G. B. Gregorio (2004). Genetic diversity analyzed by microsatellite markers among rice (Oryza sativa, L.) genotypes with different adaptations to saline soils. Plant Sci., 166: 1275–1285.

Zulqarnain Haider1, 2, Abdul Razaq2, Asrar Mehboob2, Saleem ur Rehman2, Aftab Iqbal3, Aamir Hussain2, Usman Saeed1, Muhammad Tahir Naveed1, Samta Zia1, Zahid Mahmood1 and Khalid Mehmood2(2013). Comparison of associations among yield and yield components in Rice (Oryza sativa L.) under simulated drought stress condition using multivariate statistics. International J. of Scientific & Engineering Research, 4, Issue 8, August-2013 329 ISSN 2229-5518.

التنوع الوراثى بين بعض اصناف الارز تحت ظروف الارض العادية والملحية

عادل عطية حديفة ، مرفت محمد عوض الله عثمان و محمد محمد عبدالحميد

قسم بحوث الارز .معهد بحوث المحاصيل الحقلية .مركز البحوث الزراعية

اقيمت تجربتان فى المزارع البحثية بمحطة بحوث سخا ومحطة بحوث السرو خلال موسمى 2016 و 2017 وذلك لدراسه وراثه بعض صفات النمو والمحصول ومكوناته تحت ظروف الاراضى العاديه والملحيه وكذلك دراسه العلاقه بين صفات النمو والمحصول ومكوناته وكذا درجه التباعد بين التراكيب الوراثيه المستخدمه.اظهرت نتائج تحليل التباين لتاثير الموقع وجود اختلافات عالية المعنوية لكل صفات النموصفات المحصول ومكوناته مما يدل على وجود مدى واسع من الاختلافات بين ظروف التربة العادية والملحية على نبات الارز. كانت التربة الملحية لها تاثير سلبى على كل الصفات المدروسة لكل الاصناف مقارنة بالتربة العادية.التفاعلات بين التراكيب الوراثية والمواقع فى سخا والسرو لوحظ انها كانت ذات تاثير عالى المعنوية لمحصول الحبوب ومكوناته ما عدا دليل الحصاد مما يوضح ان هذه التراكيب الوراثية تسلك سلوكا مختلفا تحت ظروف الاراضى العادية والمحلية.سجلت الاصناف جيزة 178 و جى زد 9057 اعلى محصول حبوب تحت ظروف الاراضى العادية والملحية بينما الصنف سخا 106 اعطى اقل محصول حبوب تحت نفس الظروف. اظهر محصول الحبوب ارتباط معنوى وموجب مع كلا من طول النبات وعدد الفروع بالنبات ووزن الالف حبة و طول السنبلة وعدد الحبوب الممتلئة بالسنبلة ومعامل الحصاد. اظهرت النتائج ان التراكيب الوراثية تحت الدراسة وجود مدى واسع من الاختلافات فيما بينهم وكانت المسافة 17,59 بين جى زد 6296 و سخا 106 و 23,71 بين جيزة 178 و سخا 105 تحت ظروف الملوحة على اساس الصفات المورفولوجية.لذلك توصى الدراسه بزراعه الصنف جيزه178 والسلاله جى زد9057 تحت ظروف الاراضى الملحيه.