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## Characterization of some Agronomic Traits and Salinity Tolerance Indices Under Normal and Saline Soil Conditions in Rice

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### ABSTRACT

Salinity is one of the major factors responsible for crop yield losses in the world. Genetic improvement for salt tolerance becomes an urgent task to cope with the salinity rice problem. In order to evaluate the presence of variability for desirable traits and correlations under both normal and salinity stress conditions, thirty genotypes of rice were evaluated in the two successive rice seasons of 2020 and 2021. The results showed highly significant for all studied traits for the genotype (G), and L x G. The heaviest panicle and highest number of spikelets per panicle were recorded for the promising lines, RGA-2, RGA-3, RGA-4 and RGA-14. Under normal location, RGA-2, RGA-3, RGA-6, RGA-9 and RGA-14 revealed the high yielding, while under saline location, RGA-13 and RGA-14 showed the highest yields compared with the salinity tolerance check Giza178. The salinity yield indices, SSI and TOL gave the same trend approximately for thirty genotypes, whereas, the salinity susceptible genotypes resulted in the highest values, while the salinity tolerance genotypes recorded the lowest values. Using mean performances and salinity tolerance indices for the screening of salinity tolerant genotypes exhibited that Giza178, Giza179, RGA-2, RGA-3, RGA-4, RGA-11, RGA-13, RGA-14 and RGA-15 were tolerant to salinity stress.

**Keywords:** Rice, agronomic traits, salinity tolerance indices, correlation coefficient



### INTRODUCTION

Over half of the world's population is fed by one of the most important staple food crops, rice (*Oryza sativa* L.) (Ricepedia, 2020; USDA, 2020). By 2050, production must be doubled in order to feed the world's population of more over 9 billion people (Ray *et al.*, 2013; Arbelaez *et al.*, 2015; Saraswathipura *et al.*, 2022). One of the main abiotic factors limiting agricultural productivity worldwide is abiotic stress, such as salinity (Zhu, 2016). 10% of Earth's land affected by soil salinization, a problem that affects agriculture globally and results from natural accumulation over extended periods of time (Rengasamy, 2002; Hassani *et al.*, 2021). However, secondary salinization is a result of agricultural activity: More than 20% of irrigated soils are impacted, primarily as a result of irrigation water that contains trace quantities of sodium chloride (Tester and Davenport, 2003; Cuevas *et al.*, 2019). The main component of breeding programs for broadening the gene pool of rice and other crops is genetic variability for agronomic traits. To maintain high rice productivity levels, genetic diversity is necessary (Tripathi *et al.*, 2013; Temesgen Begna, 2022). One of the most important objectives for rice breeders is usually increasing grain yield. As a result, many studies have concentrated on the improvement and inheritance of agronomical traits for high production of yield (Samonte *et al.*, 1998; Khan *et al.*, 2015). In addition to genotype, environment, and genotype x environment (G x E) affect on variation for a particular agronomic trait. The interactions between varieties and environment highlight the need for the development of varieties that should be selected for specific growing environments (Fehr, R.F.1987; Katsenios *et al.*, 2021). Plant breeders frequently aim to produce broadly-adapted cultivars for a wide range of

environments. However, it is frequently impossible to identify high yield varieties in all environments. In order to benefit specific adaptations, breeders often develop varieties for a particular environment (Annicchiarico, P. (2002); Samonte *et al.*, 2005; Ewing *et al.*, 2019). Rice grain yield is the result of a combination of different yield components, such as the panicle number plant<sup>-1</sup>, the filled grain number panicle<sup>-1</sup>, and the weight of grain yield panicle<sup>-1</sup> (Yoshida, 1983). The selection of high yield genotypes with salinity tolerance can help you in selecting best genotypes having salinity tolerance. (Yadav and Bhatnagar, 2001; Anwaar *et al.*, 2020). These indices are developed using a mathematical relationship between yield under water-stressed and non-stressed conditions. Some researchers (Golabadi *et al.*, 2006; Azizi Chakherchaman *et al.*, 2009; Majidi *et al.*, 2011) suggested selection based on principal component analysis (PCA). One of the best methods for reducing the numerous observed variables' dimensions to a smaller intrinsic dimensionality of independent variables is PCA (Johnson & Wichern, 2007). There is a need to identify selection indices able to distinguish high yielding rice varieties in stress environments to improve rice yield and its stability. Thus, the purpose of this study was to: I) Identify high yield rice varieties suitable for normal and salinity environments II) Evaluate the efficiency of different salinity tolerance indices for screening of salt tolerance rice genotypes.

### MATERIALS AND METHODS

The experimental research was carried out in two locations, Sakha, Kafrelsheikh as normal location and El-Sirw Station as saline location during 2020 and 2021. In this study, we used thirty rice genotypes involving two check varieties, Giza178 and Giza177 as salinity tolerant and

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sensitive checks. The desired traits were assessed, the genetic parameters and correlations for traits for thirteen rice genotypes were estimated under normal and salinity stress conditions. Before cultivation, soil samples were collected from (0-30 cm) depth of both locations (normal and saline) to determine the physical and chemical properties of the soil Table (1). A Randomized Complete Block Design (RCBD) with three replications was done. All the recommended cultural procedures for rice were used when the genotypes were grown in seven rows, each row were five meters long and had individual plants that were 20 x 20 cm. Days to maturity (days), plant height (cm), number of panicles plant<sup>-1</sup>, panicle weight (g), number of spikelets panicle<sup>-1</sup>, 1000-grain weight (g), spikelet fertility (%), and grain yield (t ha<sup>-1</sup>) were studied. Grain yield were estimated based from the fifth inner rows in the middle of each plot. To estimate the agronomic traits, ten plants were taken randomly from each plot. All studied traits were measured and documented using the IRRRI standard evaluation system (SES) (IRRI, 2016) for data collection. According to formula suggested by Burton (1952) and (Johnson et al., 1955), genetic parameters were computed.

**Statistical Analysis:**

By the IRRISTAT program for pooled data, the data were subjected to analysis of variance (Steel et al., 1996) to determine the significant differences among genotypes for all studied characters. A combined analysis of variance for the two years was carried out for the yield and nailed components. The data were analyzed using Gene's program. Cluster and

principal component analysis were performed by cluster program.

**Table 1. Some chemical and physical properties of experimental locations.**

Properities	Normal soil (Sakha)		Saline soil (El-Sirw)	
	2020	2021	2020	2021
pH	7.9	8.1	8.4	8.3
ECe dS.m <sup>-1</sup>	2.3	2.5	8.3	8.0
O.M. %	1.15	1.2	1.15	1.2
Available N, mg kg <sup>-1</sup>	32	31	29	30
Available P, mg kg <sup>-1</sup>	13	12	10	11
Available K, mg kg <sup>-1</sup>	420	410	400	380
Soluble cations meq. L <sup>-1</sup>	-	-	-	-
Ca <sup>++</sup>	5.0	5.2	9.0	8.0
Mg <sup>++</sup>	3.0	4.0	10.9	10.0
K <sup>+</sup>	0.3	0.40	0.5	0.7
Na <sup>+</sup>	14.7	15.5	63.0	65.0
Soluble anions meq. L <sup>-1</sup>	-	-	-	-
CO <sub>3</sub> --	-	-	-	-
HCO <sub>3</sub>	3.0	4.0	9.60	8.64
CL-	16.0	16.2	63.5	60.6
SO <sub>4</sub> --	4.0	5.2	10.33	11.33
Available micronutrients ppm	-	-	-	-
Fe <sup>++</sup>	5.7	5.2	5.23	5.95
Zn <sup>++</sup>	1.12	1.21	0.90	1.01
Mn <sup>++</sup>	4.7	4.3	4.60	4.5

**Stress Tolerance Indices**

Salinity tolerance indices for each genotype were calculated using the following formulas in Table 2:

**Table 2. The indices of salinity tolerance used in this study**

No	Salinity tolerance indices	Equation	Reference
1	Abiotic tolerance index (ATI)	$ATI = [(Y_p - Y_s) / (\bar{Y}_p / \bar{Y}_s)] * [\sqrt{1}]$	Moosavi et al. (2008)
2	Stress susceptibility index (SSI)	$SSI = \frac{1 - (\frac{Y_s}{Y_p})}{1 - (\frac{\bar{Y}_s}{\bar{Y}_p})}$	Fischer and Maurer (1978)
3	Tolerance index (TOL)	$TOL = Y_p - Y_s$	Rosielle and Hambling (1981)
4	Stress susceptibility percentage index (SSPI)	$SSPI = [ \frac{Y_p - Y_s}{2(Y_p)} ] * 100$	Moosavi et al. (2008)
5	Stress tolerance index (STI)	$STI = \frac{(Y_s)(Y_p)}{(\bar{Y}_p)^2}$	Fernandez (1992)
6	Yield stability index (YSI)	$YSI = \frac{Y_s}{Y_p}$	Bouslama and Schapaugh (1984)
7	Yield index (YI)	$YI = \frac{Y_s}{\bar{Y}_s}$	Gavuzzi et al. (1997)
8	Relative salinity index (RSI)	$RSI = [Y_s / Y_p] / [\bar{Y}_s / \bar{Y}_p]$	Fischer et al. (1979)
9	Stress non-stress production index (SNPI)	$SNPI = [\sqrt[3]{(Y_p + Y_s) / (Y_p - Y_s)}] *$	Moosavi et al. (2008)
10	Harmonic mean (HM)	$HM = \frac{2(Y_p \cdot Y_s)}{Y_p + Y_s}$	Jafari et al. (2009)
11	Geometric mean productivity (GMP)	$GMP = \sqrt{(Y_s)(Y_p)}$	Fernandez (1992) and Kristin et al., (1997)

where Y<sub>p</sub> = the mean yield of the genotype under non-stress conditions, Y<sub>s</sub> = the mean yield of the genotype under stress conditions,  $\bar{Y}_p$  = the mean yield of all genotypes under non-stress conditions, and  $\bar{Y}_s$  = the mean yield of all genotypes under stress conditions.

**RESULTS AND DISCUSSION**

**Analysis of variance:**

The variance analysis for years, locations, genotypes, interactions and combined analysis are presented in Table 3. For all evaluated traits, highly significant differences were identified among genotypes under both of normal and saline locations. Non-significant differences were observed between

the two years for all evaluated traits under normal location except for number of panicles plant<sup>-1</sup> which gave highly significant differences, while highly significant differences were recorded between the two years for the days to maturity, plant height, number of panicles plant<sup>-1</sup>, panicle weight and grain yield under saline location. In addition, with the exception of days to maturity, there were highly significant

differences between normal and saline sites (Sakha and El-Sirw). The combined analysis exhibited highly significant between the genotype and location (G x L) for all studied traits. Also, the combined analysis (Year x Location) interaction was highly significant for days to maturity, panicle weight and grain yield. Genotype x Location interaction indicates that environment effects on studied traits of rice genotypes during environments are clearly different. These results are in harmony with results obtained by (Sharifi, *et al* 2017; Jaruchai, *et al* 2018). These findings suggested that the genotypes tested differed from one another and scored

differently depending on location (normal to saline soil). This study's findings are consistent with Radanielson *et al.*, 2018; Steppuhn and Asay (2005). According to Ren *et al.*, 2005 and Platten *et al.*, 2013, variability in rice genotypic response to salinity is linked to the genotype ability to exclude Na<sup>+</sup> from the shoot (Radanielson *et al.*, 2018). Acosta-Pech *et al.*, (2017); Mafouasson *et al.*, 2018; Al-Naggar *et al.*, 2016; and Badu-Apraku *et al.*, 2015 stated significant differences in maize agronomic characters related environmental and genotypic impacts.

**Table 3. Analysis of variance for grain yield and agronomic traits under normal (Sakha) and saline (EL Sirw) locations and combined analysis.**

Source of variance	d.f	DM (days)			PH(cm)			NPP			PnW (g)		
		NL	SL	COM	NL	SL	COM	NL	SL	COM	NL	SL	COM
Years(Y)	1	1.61ns	36.23**	13.03**	9.66ns	265.6**	188.31*	31.33**	50.26**	80.43**	0.05ns	3.51**	1.37*
Location (L)	1	-	-	4.56 ns	-	-	27471.1**	-	-	6604.6**	-	-	623.5**
Replicates	2	0.52	2.13	1.05	54.93	13.03	21.19	1.52	4.87	2.26	0.15	0.07	0.14
Genotypes(G)	29	162.0**	114.4**	266.58**	1226.6**	1360.3	2484.7**	163.0**	30.28**	92.94**	42.41**	18.31**	56.23**
G x Y	29	1.58**	0.21ns	1.08 ns	7.47ns	0.84	3.91ns	4.54	0.65ns	3.23ns	0.3ns	0.01ns	0.15ns
G x L	29	-	-	9.87**	-	-	102.15**	-	-	100.38**	-	-	4.3**
Y x L	1	-	-	29.18**	-	-	87ns	-	-	1.12ns	-	-	2.19**
G x Y x L	29	-	-	0.72 ns	-	-	4.4ns	-	-	1.86ns	-	-	0.15ns
Error	232	0.81	0.69	0.75	11.25	5.16	8.2	5.17	1.06	3.11	0.33	0.05	0.19
Mean		125.42	125.6	125.53	114.89	97.42	106.15	21.74	13.17	17.46	6.83	4.19	5.51
C.V (%)		0.72	0.66	0.69	10.46	2.33	2.7	10.46	7.8	10.11	8.54	5.56	7.9
S O V	d.f	NS/Pn			SpF (%)			1000-Gw (g)			GY (t/ha)		
		NL	SL	COM	NL	SL	COM	NL	SL	COM	NL	SL	COM
Years(Y)	1	532.2ns	995.4ns	1491.66ns	0.13ns	33.71ns	18.79ns	0.3ns	4.01ns	3.24ns	0.01 ns	17.84**	11.97**
Location (L)	1	-	-	586414.7**	-	-	13678.7**	-	-	727.18**	-	-	4686.58**
Replicates	2	458.4	622.8	434.34	34.51	42.44	19.75	0.11	1.92	0.82	0.44	0.12	0.25
Genotypes(G)	29	99529**	36425**	123305**	96.12	529.9**	317.75**	25.89**	29.55	48.94**	5.09**	4.32	14.56**
G x Y	29	126.7ns	25.94ns	81.55ns	0.3ns	0.76ns	0.4ns	0.46ns	0.17ns	0.32ns	0.01ns	0.01ns	0.12ns
G x L	29	-	-	12649.6**	-	-	308.26**	-	-	6.5**	-	-	4.82**
Y x L	1	-	-	35.96ns	-	-	15.03ns	-	-	1.06ns	-	-	6.3**
G x Y x L	29	-	-	71.1ns	-	-	0.66ns	-	-	0.31ns	-	-	0.11ns
Error	232	549.9	147.8	348.88	4.06	10.75	7.4	0.53	0.4	0.46	0.28	0.04	0.22
Mean		282.75	202	242.39	88.41	76.08	82.24	25.94	23.1	24.52	11.13	4.71	8.32
C.V (%)		8.3	6.02	7.71	2.28	4.31	3.31	2.82	2.73	2.78	4.73	4.04	5.68

Y= Year, L= Location and G = genotype, \*and \*\* are significant and highly significant at 0.05 and 0.01 probability, respectively. DM: number DM: days to maturity, PH: plant height, NPP: number of panicle plant<sup>-1</sup>, PW: panicle weight, NSP: number of spikelets panicle<sup>-1</sup>, SF: spikelet fertility (%); 1000-GW: 1000-grain weight, GY: grain yield

**Mean performance of combined analysis:**

Tables 4 and 5 showed the mean performance of 28 rice genotypes, salinity tolerant check (Giza178), and salinity sensitive check (Giza177). For all studied traits, the results revealed a substantial range among the tested genotypes. Data of days to maturity, plant height, number of panicles plant<sup>-1</sup> and panicle weight for tested genotypes and check varieties under normal and saline conditions are showed in table 4.

There are no significant differences in the days to maturity among the studied genotypes, the days to maturity for all studied genotypes ranged between 118.08 to 136.67 days. Regarding plant height, all genotypes were shorter under saline location compared with the normal location. Giza178 and GZ10598-9-1-5-1 were the shortest plant under normal location (94.03 and 94.17) respectively, while Giza182 was the shortest plant under saline location (75.43 cm). The combined analysis demonstrated that tested varieties showed wide variation in the plant height ranging between (86.80 and 139.9 cm), the rice variety Giza182 was the shortest plant height 86.8 cm. Although some promising lines showed high stature more than 130cm, non-lodging were observed among tested lines, these were due to a strong stem of most of tested rice genotypes, (Fig. 1-E and D). Concerning, number of panicles plant<sup>-1</sup> and panicle weight, all tested genotypes revealed highly significant under normal location compared with saline location. Giza179, Giza178 and GZ10590-1-3-3-2 gave the highest panicles plant<sup>-1</sup> under normal location with mean value, 30.03, 29.77 and 29.17,

respectively. In the same time, RGA-13 and Giza179 gave the highest number of panicle plant<sup>-1</sup> under saline location, 17.97 and 17.17, respectively. The combined analysis revealed that Giza 178, Giza179, GZ10590-1-1-3-9-1 and GZ10590-1-3-3-2, recorded highest values compared with other tested lines with mean values 21.49, 23.60, 21.62 and 22.65, respectively. In the same time, panicle weight values under normal location were higher than the saline location for the checks and all tested genotypes. The promising lines RGA-2 and RGA-3 gave the highest panicle weight under normal (10.30, 10.77) and saline locations (7.07, 6.97 g), respectively. RGA-5 gave heavy panicle weight under normal location (10.60 g), the combined analysis promising lines, RGA-2, RGA-3 and RGA -4 recorded the heaviest panicle and highest number of spikelets panicle<sup>-1</sup> (8.68g and 390.14, 8.87g and 376.67, 8.46g and 407.00) respectively. Although, some promising lines gave a low number of panicles plant<sup>-1</sup>, they showed heavy panicles and large number of grains panicle<sup>-1</sup> compared with cultivated rice varieties and check varieties. The salinity has an impact on the performance of the plant height, number of panicles plant<sup>-1</sup> and panicle weight. Salinity hindered plant growth by lowering the rate of CO<sub>2</sub> uptake, leaf growth, leaf cells enlargement, dry weight accumulation, and relative growth (Hussain *et al.*, 2017). Saline stress reduced tiller number, grain filling, thousand grain weight, and biomass and harvest index (De Leon *et al.*, 2015).

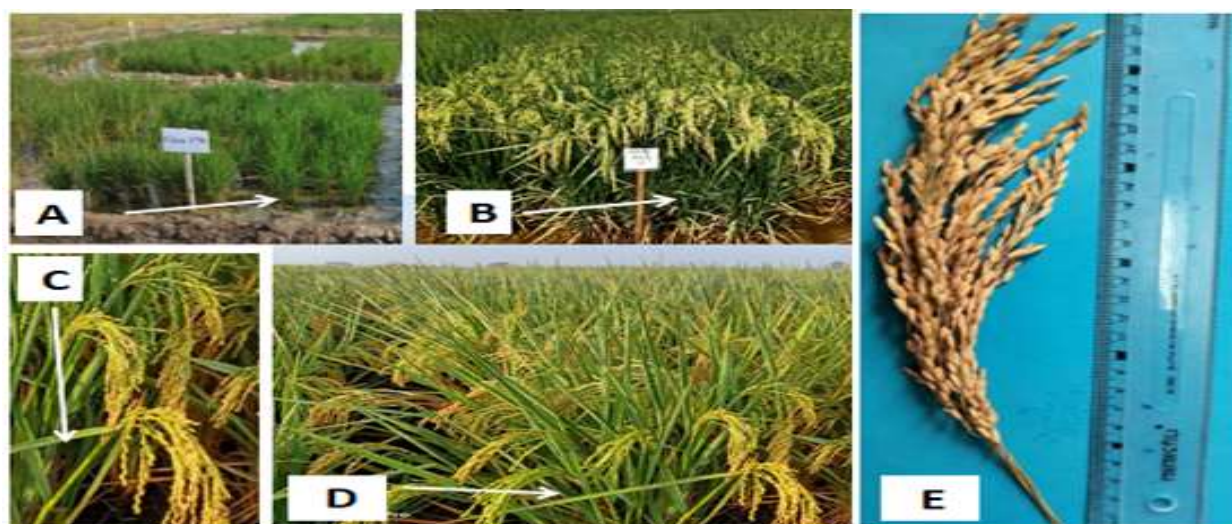


Figure 1. A) salinity effect of rice genotypes, B) plant height under normal locations, C and D strong stem and large panicle, E) huge number of spikelet panicle<sup>-1</sup>

Table 4. Days to maturity, plant height, number of panicle plant<sup>-1</sup> and panicle weight as affected by the interaction between genotypes and locations

Genotype	DM (days)			PH (cm)			NPP		PW (g)			
	NL	SL	Com	NL	SL	Com	NL	Com	NL	SL	Com	
Giza 177	121.00	120.92	120.96	100.00	76.33	88.17	27.50	8.83	18.17	2.68	2.25	2.47
Giza 178	130.83	133.25	132.04	94.03	80.51	87.27	29.77	13.22	21.49	3.52	2.38	2.95
Giza 179	120.00	120.92	120.46	99.00	80.30	89.65	30.03	17.17	23.60	3.87	2.47	3.17
Sakha 106	119.33	121.25	120.29	104.00	94.14	99.07	27.10	11.67	19.38	3.77	2.03	2.90
Giza 182	127.67	125.92	126.79	98.17	75.43	86.80	28.97	12.46	20.71	3.53	2.43	2.98
GZ10590-1-1-3-9-1	119.33	123.67	121.50	96.50	84.18	90.34	28.60	14.65	21.62	3.90	2.71	3.30
GZ10590-1-3-3-2	120.33	122.33	121.33	98.17	83.20	90.68	29.17	16.13	22.65	5.77	2.89	4.33
GZ10598-9-1-5-1	118.50	122.50	120.50	94.17	82.91	88.54	27.57	11.78	19.68	3.23	2.30	2.77
GZ11332-2-2-2	118.83	121.92	120.38	105.17	77.24	91.20	27.67	11.33	19.50	5.17	2.84	4.00
RGA-1	119.67	122.17	120.92	123.33	107.76	115.55	19.43	12.61	16.02	9.97	5.73	7.85
RGA-2	119.50	118.08	118.79	115.67	100.38	108.03	15.00	10.34	12.67	10.30	7.07	8.68
RGA-3	126.00	124.08	125.04	114.87	104.70	109.78	15.23	11.61	13.42	10.77	6.97	8.87
RGA-4	125.83	123.92	124.88	119.38	115.08	117.23	16.83	13.80	15.32	9.97	6.96	8.46
RGA-5	131.33	129.08	130.21	126.37	113.77	120.07	15.77	14.28	15.03	10.60	6.11	8.35
RGA-6	132.50	131.50	132.00	129.00	117.78	123.39	19.07	14.13	16.60	7.43	4.40	5.92
RGA-7	136.67	135.92	136.29	146.67	123.54	135.10	17.27	12.59	14.93	9.13	4.97	7.05
RGA-8	134.67	133.08	133.88	126.00	105.66	115.83	17.27	13.29	15.28	7.80	5.28	6.54
RGA-9	128.67	127.25	127.96	125.50	108.64	117.07	17.83	13.88	15.86	6.87	5.02	5.94
RGA-10	126.00	126.50	126.25	124.83	99.59	112.21	17.93	15.21	16.57	7.52	6.20	6.86
RGA-11	127.00	127.08	127.04	120.83	94.08	107.46	17.07	12.17	14.62	9.40	5.98	7.69
RGA-12	135.33	134.92	135.13	147.00	132.80	139.90	15.70	13.22	14.46	9.43	6.28	7.86
RGA-13	125.83	125.25	125.54	118.67	99.94	109.30	19.32	17.97	18.64	7.37	4.42	5.89
RGA-14	125.67	124.75	125.21	123.17	98.50	110.83	17.75	16.27	17.01	9.63	5.84	7.74
RGA-15	125.50	125.75	125.63	123.30	101.42	112.36	18.50	14.75	16.63	9.77	5.47	7.62
RGA-16	124.67	125.42	125.04	122.67	109.67	116.17	18.80	13.05	15.93	8.33	3.39	5.86
RGA-17	124.33	123.25	123.79	119.67	96.77	108.22	21.60	14.25	17.93	6.27	3.56	4.91
RGA-18	123.67	124.08	123.88	111.87	97.01	104.44	25.50	9.95	17.73	5.60	2.69	4.15
RGA-19	120.83	122.83	121.83	116.83	100.03	108.43	20.48	8.40	14.44	5.10	2.67	3.88
RGA-20	125.33	124.75	125.04	99.33	82.45	90.89	22.87	14.46	18.66	4.53	2.42	3.48
RGA-21	127.67	126.92	127.29	102.50	78.72	90.61	26.57	11.70	19.13	3.53	2.10	2.82
LSD 0.05	1.21	1.12	1.16	4.51	3.05	3.78	3.05	1.39	2.22	0.77	0.30	0.54
LSD 0.01	1.71	1.58	1.64	6.37	4.31	5.34	4.32	1.96	3.14	1.09	0.42	0.76

NL=normal location, SL=saline location, DM: days to maturity, PH: plant height, NPP: number of panicle plant<sup>-1</sup>, PW: panicle weight.

In terms of the number of spikelets panicle<sup>-1</sup>, spikelet fertility percentage, 1000 grain weight, and grain yield weight as affected by the interaction between genotypes and locations are presented in table 5. Under saline conditions, the number of spikelets plant<sup>-1</sup> and spikelet fertility% decreased. All tested genotypes and check varieties have low values of number of spikelets per panicle and spikelet fertility% under saline location compared with the normal location. RGA-2 and RGA-4 gave the highest number of spikelets panicle<sup>-1</sup> in normal conditions (458.87 and 499.07) respectively. RGA-2, RGA-3 and RGA-14 recorded the highest number of spikelets panicle<sup>-1</sup> under saline location (321.42, 335.4 and 321.6) respectively. Giza178 revealed high spikelet fertility%

under normal and saline locations (95.83% and 88.1%) respectively. Giza177 (sensitive check), Sakha106, RGA-19, RGA-20 and RGA-21, show low spikelet fertility% under saline location (60.42, 58.06, 57.53, 66.1 and 62.21) respectively. The combined analysis shows that most tested genotypes show high spikelet fertility% more than 72%. Giza178 and RGA-1 recorded highest spikelet fertility%, with mean value (91.96 and 89.14) respectively.

Regarding 1000-grain weight and grain yield, all tested genotypes and check varieties exhibited high value under normal location compared with saline location. Among tested genotypes, RGA-19 and RGA-20 recorded the highest values under normal and saline locations (30.07, 29.83. and 27.73,

27.03) respectively. However, Giza178 and RGA-13 were recorded the lowest value of 1000-grain weight under saline location (20.04 and 20.92 g) respectively. The combined analysis revealed that the 1000- grain weight of tested genotypes ranged between 20.04 and 28.9 (g), the promising lines RGA-19 and RGA-20 recorded the highest value of 1000 grain weight (28.9 and 28.43) respectively. Concerning grain yield, promising lines, RGA-2, RGA-3, RGA-4, RGA-6, RGA-9 and RGA14 revealed the highest grain yield under normal location (12.23, 12.18, 12.27, 12.18, 12.15 and 12.40 t ha<sup>-1</sup>) respectively. While under saline condition, the lines RGA-13 and RGA-14 showed the highest yield among (6.89

and 6.7 t ha<sup>-1</sup>) compared with the salinity tolerance check, Giza178 (5.17 t ha<sup>-1</sup>). It has been discovered that excessive salt concentrations have a significant effect on physiological and biochemical processes in plants, resulting in lower yield production and eventual death (D'antonio & Meyerson, 2002). Djaman *et al.*, 2019 reported that soil salinity had a substantial impact on rice yield, with hot and dry seasons yielding 20% more than wet seasons. Salinity had highly significant effect on grain yield, plant height, seed weight plant<sup>-1</sup>, panicle weight, and number of spikelets panicle<sup>-1</sup>, according to Zeng and Shannon (2000).

**Table 5. Number of spikelets panicle<sup>-1</sup>, spikelet fertility%, 1000-grain weight and grain weight as affected by the interaction between genotypes and locations.**

Genotypes	NSP			SF (%)			1000-Gw(g)			GY (t ha <sup>-1</sup> )		
	NL	SL	Com	NL	SL	Com	NL	SL	Com	NL	SL	Com
Giza 177	119.63	109.15	114.39	91.18	62.42	76.80	27.53	22.97	25.25	9.37	3.31	6.34
Giza 178	167.40	137.28	152.34	95.83	88.10	91.96	22.07	18.02	20.04	10.10	5.17	7.64
Giza 179	158.53	128.83	143.68	88.62	86.52	87.57	27.33	21.23	24.28	9.87	5.26	7.57
Sakha 106	131.40	111.53	121.47	95.63	58.06	76.85	28.30	24.85	26.58	10.02	3.13	6.57
Giza 182	140.20	127.35	133.78	87.55	77.18	82.37	23.47	22.10	22.78	10.23	3.63	6.93
GZ10590-1-1-3-9-1	143.97	122.73	133.35	91.72	76.63	84.17	25.13	24.26	24.70	10.42	4.62	7.52
GZ10590-1-3-3-2	243.67	171.33	207.50	94.13	80.19	87.16	23.70	20.43	22.07	10.52	4.91	7.71
GZ10598-9-1-5-1	123.37	114.85	119.11	86.90	68.35	77.62	27.70	24.14	25.92	10.65	3.83	7.24
GZ11332-2-2-2	184.90	152.18	168.54	90.08	68.63	79.36	26.30	20.58	23.44	10.73	4.43	7.58
RGA-1	362.00	252.20	307.10	93.58	84.72	89.15	25.43	24.63	25.03	10.65	5.28	7.96
RGA-2	458.87	321.42	390.14	87.20	82.71	84.96	24.80	23.23	24.02	12.23	5.11	8.67
RGA-3	417.93	335.40	376.67	85.03	69.95	77.49	27.13	21.68	24.40	12.18	5.48	8.83
RGA-4	499.07	314.93	407.00	84.88	79.46	82.17	26.07	23.94	25.00	12.27	5.27	8.77
RGA-5	474.40	265.67	370.03	84.25	83.20	83.73	26.02	24.28	25.15	11.43	4.65	8.04
RGA-6	281.53	210.58	246.06	78.15	66.49	72.32	26.20	23.78	24.99	12.18	4.47	8.33
RGA-7	343.20	212.22	277.71	87.57	75.94	81.76	28.23	23.85	26.04	11.42	4.51	7.96
RGA-8	325.47	270.48	297.98	82.33	79.51	80.92	25.10	21.01	23.05	12.13	4.50	8.32
RGA-9	276.53	240.25	258.39	85.62	81.39	83.51	25.73	24.36	25.05	12.15	5.09	8.62
RGA-10	312.87	270.80	291.83	86.57	85.14	85.86	25.97	23.68	24.82	12.03	4.92	8.48
RGA-11	440.87	304.77	372.82	89.30	87.47	88.38	23.17	20.10	21.63	11.48	5.17	8.33
RGA-12	347.67	260.85	304.26	87.63	84.65	86.14	26.00	24.80	25.40	12.12	4.63	8.37
RGA-13	444.27	251.95	348.11	86.73	83.50	85.12	22.37	19.48	20.92	11.73	6.89	9.31
RGA-14	446.40	321.60	384.00	89.38	83.39	86.39	23.30	20.23	21.77	12.40	6.70	9.55
RGA-15	435.00	252.47	343.73	89.47	87.63	88.55	24.12	23.16	23.64	11.57	5.38	8.47
RGA-16	326.67	147.33	237.00	92.15	79.32	85.74	24.92	22.76	23.84	12.00	4.91	8.46
RGA-17	276.93	140.68	208.81	82.88	66.05	74.47	25.47	24.60	25.03	10.63	4.18	7.41
RGA-18	180.33	162.03	171.18	87.32	69.86	78.59	28.40	25.18	26.79	11.07	4.03	7.55
RGA-19	175.20	138.08	156.64	88.17	57.53	72.85	30.07	27.73	28.90	10.25	3.93	7.09
RGA-20	134.07	113.83	123.95	89.08	66.10	77.59	29.83	27.03	28.43	9.98	4.31	7.14
RGA-21	110.08	98.02	104.05	93.32	62.21	77.76	28.33	24.84	26.59	10.05	3.64	6.85
LSD 0.05	31.50	16.33	23.91	2.71	4.41	3.56	0.98	0.86	0.92	0.71	0.29	0.50
LSD 0.01	44.54	23.09	33.81	3.83	6.23	5.03	1.38	1.21	1.30	1.00	0.40	0.70

NL=normal location, SL=saline location, NSP: number of spikelets panicle<sup>-1</sup>, SF: spikelet fertility (%); 1000-GW: 1000-grain weight, GY: grain yield.

The combined analysis revealed a high difference among the tested genotypes in grain yield. For the check varieties, Giza178 showed grain yield (7.64 t ha<sup>-1</sup>), compared with Giza177 (6.34 t ha<sup>-1</sup>), while, the salinity decreased grain yield of Giza177. In general, the grain yield ranged between 6.34 and 9.55 t ha<sup>-1</sup>, the promising lines RGA-13 and RGA-14 had the highest grain yield, 9.31 and 9.55 t ha<sup>-1</sup>. This conclusion supported the use of a stress tolerance index to reflect genotypes behavior under stress and normal conditions (Benmahammed *et al.*, 2010; El-Hashash *et al.*, 2018). Selection based on just yield is ineffective, whereas selection based on yield and its components is more efficient. It suggested that genotypes respond differently when the plant is subjected to normal or stress conditions. The various response of genotypes to different environments was presented by the substantial diverse of the genetic background among the tested genotypes (Nafisah *et al.*, 2022). In rice, salinity stress affects many yield components (Shannon, 2000). During salt stress, however, some plants can exhibit stunted growth, chlorosis, interveinal chlorosis, and necrosis (Acosta-Motos *et al.*, 2017). Tiller numbers plant<sup>-1</sup> are a key yield component in rice since

the value of the trait can predict the ultimate yield (Xue *et al.*, 2008). Both genetic and environmental factors influence tiller establishment (Hussien *et al.*, 2014).

**Heritability and Genetic parameter:**

Genetic parameters of grain yield and agronomic characters for tested genotypes and two check varieties are presented in Table 6. For a better understanding of the pattern of variation, the phenotypic variance was divided into genotypic and environmental variances. For all studied traits, genotypic variance was greater than environmental variance, while, the phenotypic coefficient of variation (PCV) was close to the genotypic coefficient of variation (GCV). Broad-sense heritability estimates for all traits were relatively high, implying a significant genetic advance associated with breeding for grain yield and agronomic characters. High heritability, along with high genetic advance, was also observed for floret opening duration, indicating that this trait was simply inherited, requiring only a few major genes and most likely having additive gene effects. This result shows the possibility of genetic gains as a result of selection for these traits in such promising rice lines.

**Table 6. Genetic parameters of grain yield and agronomic traits of tested genotypes and two varieties checks**

Genetic Parameters	DM (days)	PH (cm)	NPP	PW (g)	NSP	SF (%)	1000 -Gw	GY (tha <sup>-1</sup> )
Genetic Variance ( $\sigma^2_G$ )	265.83	825.5	29.94	18.68	40985.4	103.45	16.16	2.42
Phenotypic Variance ( $\sigma^2_P$ )	266.58	833.7	33.05	18.87	41334.3	110.85	16.62	2.58
Environmental Variance ( $\sigma^2_E$ )	0.75	8.2	3.11	0.19	348.8	7.4	0.46	0.16
Genetic Coefficient of Variance (GCV%)	211.77	777.67	171.48	339.02	16908.87	125.79	65.91	30.56
Phenotypic Coefficient of Variance (PCV%)	212.36	785.40	189.29	342.47	17052.81	134.79	67.78	32.58
Heritability in broad sense ( $H^2$ ) %	99.72	99.02	90.59	98.99	99.16	93.32	97.23	93.80
Genetic advance (GA)	335.87	591.87	112.72	89.03	4170.44	209.52	82.81	32.05

DH: days to maturity, PH: plant height, NPP: number of panicle plant<sup>-1</sup>, PW: panicle weight, NSP: number of spikelets panicle<sup>-1</sup>, SF: spikelet fertility (%); 1000-GW: 1000-grain weight, GY: grain yield

For the most characteristics, the results also indicated significant genetic variability among the tested genotypes which agreed with previous research (El-Namaky 2018). Broad-sense heritability estimates for all characteristics were relatively high, indicating that superior genotypes selection based on phenotypic performance could be very effective (Singh *et al* 1996). The high heritability estimates along with high genetic advance should allow for genotype selection. Low heritability estimates along with low genetic advance exhibited a non-additive type of gene action and significant genotype × environment interaction affecting the expression of characteristics (Hossain *et al* 2016).

**Comparison of genotypes based on tolerance indices**

The grain yield was used to estimate tolerance indices such as ATI, SSI, TOL, SSPI, STI, YSI, YI, RSI, SNPI, HM and GMP in all genotypes, Table 7. The data show that the salinity yield indices SSI, TOL and SSPI gave the highest values for the salinity susceptible genotypes, while the salinity tolerance genotypes recorded the lowest values. Otherwise, the salinity yield indices ATI, STI, YSI, YI, RSI, SNPI, HM and GMP gave the lowest values for the salinity susceptible genotypes as well as the salinity tolerance genotypes were recorded the highest values. To screen genotypes to salinity

conditions, the use of tolerance indices such as SSI, STI, GMP, TOL, YI, HM, SDI, DI, RSI, and YSI has been extensively studied (Singh *et al.*, 2015; Mahdy *et al.*, 2021; Mirela *et al.*, 2022). The results were in agreement with results obtained by Sanchez *et al.*, 2020; Kumar *et al.*, 2014 and Kondhia *et al.*, 2015.

Based on ATI, STI, YSI, YI, RSI, SNPI, HM and GMP, it can be inferred that the checks (Giza178), the variety Giza179 and the genotypes, RGA-13 and RGA-14 were tolerant to salinity stress, while the genotypes (GZ10590-1-1-3-9-1, GZ10590-1-3-3-8, GZ10598-9-1-5-1, RGA-1, RGA-2, RGA-20) were categorized as semi-tolerant genotypes. The more stress tolerance of a genotype was indicated by fewer numerical rate of SSI. Yadav and Bhatnagar (2001) reported the use of SSI in combination with yield value under stressed conditions for identifying drought tolerant/susceptible genotypes. Fernández (1992) showed that the selected genotypes performed poorly under non-stressed condition and TOL index was efficient in improving yield under stressed condition. several criteria have been proposed to select genotypes based on their behavior in an environment under conditions with or without stress (Sanchez *et al.*, 2020; Naghavi *et al.*, 2013).

**Table 7. Salinity tolerance indices for studied genotypes**

Genotype	ATI	SSI	TOL	SSPI	STI	YSI	YI	RSI	SNPI	HM	GMP
Giza 177	14.27	1.12	6.06	27.22	0.25	0.35	0.70	0.83	5.98	4.89	5.57
Giza 178	15.08	0.85	4.93	22.14	0.42	0.51	1.10	1.21	9.40	6.84	7.23
Giza 179	14.04	0.81	4.60	20.68	0.42	0.53	1.12	1.26	9.63	6.86	7.21
Sakha 106	16.32	1.19	6.89	30.96	0.25	0.31	0.66	0.74	5.70	4.76	5.59
Giza 182	17.04	1.12	6.61	29.69	0.30	0.35	0.77	0.84	6.55	5.35	6.09
GZ10590-1-1-3-9-1	17.02	0.96	5.79	26.03	0.39	0.44	0.98	1.05	8.31	6.40	6.94
GZ10590-1-3-3-2	17.05	0.92	5.61	25.19	0.42	0.47	1.04	1.10	8.85	6.69	7.19
GZ10598-9-1-5-1	17.05	0.88	5.38	24.15	0.45	0.50	1.12	1.17	9.55	7.06	7.50
GZ11332-2-2-2	23.84	1.01	7.13	32.01	0.50	0.42	1.08	0.99	9.17	7.21	7.91
RGA-1	23.18	0.95	6.70	30.11	0.54	0.45	1.16	1.06	9.86	7.56	8.17
RGA-2	23.81	0.99	7.00	31.45	0.52	0.43	1.12	1.01	9.46	7.37	8.04
RGA-3	20.93	1.03	6.78	30.48	0.43	0.41	0.99	0.96	8.35	6.61	7.29
RGA-4	24.09	1.10	7.72	34.67	0.44	0.37	0.95	0.87	8.05	6.54	7.38
RGA-5	20.98	1.05	6.91	31.05	0.42	0.39	0.96	0.93	8.10	6.46	7.17
RGA-6	23.87	1.09	7.63	34.28	0.44	0.37	0.96	0.88	8.11	6.57	7.39
RGA-7	23.50	1.01	7.06	31.72	0.50	0.42	1.08	0.99	9.14	7.17	7.86
RGA-8	23.17	1.03	7.12	31.97	0.48	0.41	1.04	0.97	8.83	6.98	7.69
RGA-9	20.59	0.95	6.32	28.37	0.48	0.45	1.10	1.06	9.30	7.13	7.70
RGA-10	23.74	1.07	7.49	33.65	0.45	0.38	0.98	0.90	8.32	6.70	7.49
RGA-11	20.66	0.93	6.19	27.82	0.50	0.46	1.14	1.10	9.68	7.34	7.88
RGA-12	23.03	1.02	7.09	31.84	0.48	0.41	1.04	0.97	8.82	6.97	7.68
RGA-13	18.43	0.72	4.84	21.75	0.65	0.59	1.46	1.39	12.86	8.68	8.99
RGA-14	21.99	0.80	5.70	25.61	0.67	0.54	1.42	1.28	12.28	8.70	9.11
RGA-15	18.21	1.05	6.45	28.98	0.36	0.39	0.89	0.93	7.52	6.00	6.67
RGA-16	18.40	1.02	6.31	28.34	0.38	0.41	0.94	0.97	7.95	6.27	6.89
RGA-17	19.89	1.10	7.04	31.61	0.36	0.36	0.86	0.86	7.26	5.91	6.68
RGA-18	16.98	1.07	6.32	28.38	0.33	0.38	0.84	0.91	7.07	5.69	6.35
RGA-19	18.44	1.11	6.82	30.66	0.33	0.36	0.81	0.85	6.90	5.63	6.38
RGA-20	15.76	0.99	5.68	25.51	0.35	0.43	0.91	1.02	7.73	6.02	6.56
RGA-21	16.41	1.11	6.41	28.79	0.30	0.36	0.77	0.86	6.57	5.35	6.05

ATI= Abiotic tolerance index SSPI= Stress susceptibility percentage index STI= Stress tolerance index SSI= Stress susceptibility index SNPI= Stress non-stress production index YSI= Yield stability index TOL= Tolerance index GMP= Geometric mean productivity YI= Yield index RSI= Relative Salinity index HM= Harmonic mean

**Correlation among salinity tolerance indices:**

Correlation analysis among salinity tolerance indices used for determining the best genotypes in Table 8. The

salinity tolerance indices, ATI exhibited positive and significant correlations with TOL, SSPI, STI, YI, SNPI, HM and GMP. These findings demonstrated that these criteria were more effective in identifying high-yielding cultivars

under different conditions. As a result, these indices might distinguish group genotypes from other genotypes. Fernandez (1992) classified the genotypes based on their performance into four groups under stress and non-stress conditions: (Group A): genotypes that uniform superiority in both stress and nonstress conditions, (Group B): genotypes that perform well only in non-stress conditions, (Group C): genotypes that

perform relatively well only in stress conditions, and (Group D): genotypes that perform poorly in both stress and non-stress conditions. According to Fernandez (1992), the best selection index is the relationships among yield under stress condition (Ys), yield at non-stress condition (Yp) and STI (Stress tolerance index) which distinguished genotypes of Group A from others.

**Table 8. Correlation coefficient among salinity tolerance indices**

Tolerance indices	ATI	SSI	TOL	SSPI	STI	YSI	YI	RSI	SNPI	HM
SSI	0.11ns									
TOL	0.73**	0.76**								
SSPI	0.73**	0.76**	1.00**							
STI	0.59**	-0.72**	-0.11ns	-0.11ns						
YSI	-0.11ns	-1.00**	-0.76**	-0.76**	0.72**					
YI	0.35*	-0.89**	-0.39*	-0.39*	0.96**	0.89**				
RSI	-0.11ns	-1.00**	-0.76**	-0.76**	0.72**	1.00**	0.89**			
SNPI	0.32*	-0.90**	-0.41**	-0.41*	0.95**	0.90**	1.00**	0.90**		
HM	0.49**	-0.81**	-0.23ns	-0.23ns	0.99**	0.81**	0.99**	0.81**	0.98**	
GMP	0.61**	-0.72**	-0.09ns	-0.09ns	1.00**	0.72**	0.95**	0.72**	0.94**	0.99**

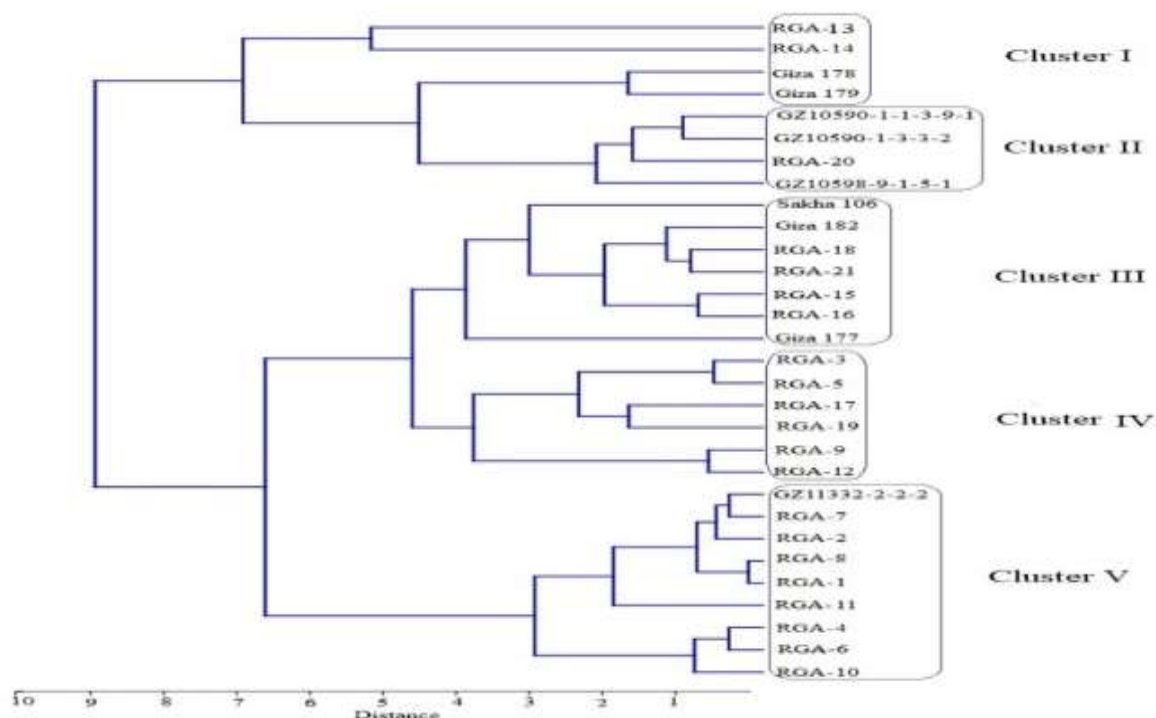
ns: no.significance, \*and \*\*significant and highly significant at 5% and 1% probability, respectively

SSI, TOL and SSPI indices were highly positive significant with each other in screening salinity tolerant genotypes, showing that they are identical. Singh *et al.*, (2017) reported that under normal and stress conditions, SSI showed a high correlation with grain yield. Under both conditions, negative relation between SSI and grain yield indicated that selection on the basis of this index decreases grain yield in favorable conditions but increases it in salinity stress conditions (Khalili *et al.*, 2016). TOL has a highly significant positive correlation with ATI, SSI and SSPI, as well as significantly and negatively correlation with YSI, YI, RSI and SNPI. The salinity tolerance indices including; STI with YSI, YI, RSI, SNPI, HM, GMP& YSI with YI, RSI, SNPI, HM, GMP& YI with RSI, SNPI, HM, GMP& RSI with SNPI & SNPI with HM and HM with GMP were significantly and positively correlated with each other. Based on correlation analysis of grain yield in both conditions and for both years, the ATI, STI, YSI, YI, RSI, SNPI, HM and GMP indices were identified to be the best criteria for identifying the

salinity-tolerant genotypes in rice. These results were earlier corroborated by Rahimi *et al.*, 2013.

**Cluster Analysis**

Cluster analysis showed that the genotypes were divided into five clusters, based on the studied traits in normal and salinity conditions, the genotypes number in each cluster were; 4, 4, 7, 6 and 9 genotypes, respectively (Fig. 2). The genotypes of the first cluster recorded the best values for tolerance indices, grain yield and most studied traits under normal and saline locations. While, the genotypes of the third cluster showed the lowest values for tolerance indices, grain yield and the most studied traits under salinity conditions, while clusters; 2, 4 and 5 show moderate values. The genotypes, RGA-13 and RGA-14 were discriminated as the most salinity tolerant using cluster analysis based on studied traits. As a result, they are recommended for using as parents in breeding program to improve salinity tolerance. This means that the tested genotypes have high to moderate diversity. These results are in agreed with results obtained by Kumar *et al.*, 2014 and Iqbal *et al.*, 2018.



**Figure 2. Dendrogram from cluster analysis based on salinity tolerance indices of rice genotypes under normal and stress conditions.**

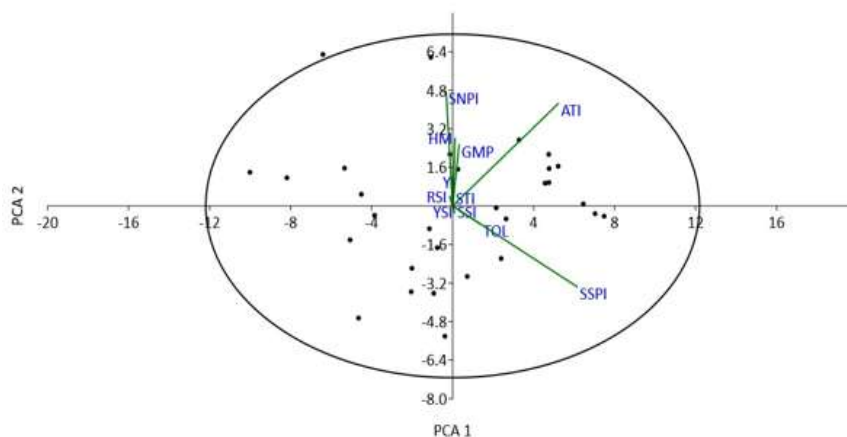
**Principal Component Analysis (PCA):**

Principal component analysis transforms the number of associated variables into a smaller number of variables known as principal components, which simplifies complex data. Principal component analysis was used to analyze the association between rice genotypes and salinity tolerance indices, which condenses eleven indices into only two components (PCA1 and PCA2). The first two main PCAs extracted contained more than one eigenvalue (Eigen value >1). On the other hand, the other PCAs registered eigenvalues less than one (Eigen value < 1). PC1 and PC2 eigenvalues were 21.49 and 7.35, respectively (Table 9). The cumulative variance of PCA1 and PCA2 explained 99.87% of the total variation between salinity stress indices. These findings are consistent with those of Rahimi et al., (2013) and Baghyalakshmi et al., (2016) in rice. The first principal component analysis (PCA) contributed 74.42% of the total variation with ATI, SSI, TOL, SSPI, STI, YSI, YI, RSI, SNPI, HM and GMP. Thus, the first component is yield potential and salinity tolerance, whereas the second PCA explained 25.45% of the total variability. This argument is supported by biplot analysis in Fig. 2. The relationships (similarities and dissimilarities) among various indices are graphically displayed in a biplot of PCA1 and PCA2. The biplot analysis revealed a positive correlation between yield indices due to acute angles between the corresponding vectors in this context. According to biplot analysis, SNPI, HM, GMP, ATI, STI, RSI, YI and YSI had a highly positive correlation with each other, implying that selection based on these indices will increase grain yield in both locations. A highly positive correlation was discovered between the SSI, TOL and SSPI, indicating that they are closely related in genotypes ranking. On the other hand, the SSI, TOL and SSPI indices were negatively linked with the indices SNPI, HM, GMP, ATI, STI, RSI, YI and YSI. Perfect positive correlations were found between salinity tolerance indices, STI and ATI as well as among YSI, RSI, YI and HM,

indicating that they rank the same genotypes. The results of principal components through biplot analysis provide useful information in data analysis and confirm correlation analysis. These findings were consistent with those of Rahimi et al.,(2013) and Baghyalakshmi et al., (2016). According to Khalili et al., (2016), the biplot graph revealed ten genotypes with high PCA1 and low PCA2 scores that were nearly located to the best drought tolerance indices (STI, MP, GMP, SI), implying that cultivars selection with high PCA1 and PCA2 were more suitable for normal and stress conditions (Marley and Khedr 2017). Similarly, Sanchez et al., 2020; Kaya et al., (2002) found that genotypes with greater PCA1 and lower PCA2 values have better grain yields (stable genotypes), whereas genotypes with low PCA1 and high PCA2 values have lower yields (unstable genotypes). Furthermore, the first axis (PCA1) can be identified as having potential yield and being stress tolerant, whereas the second component can be identified as being a component susceptible to stress with having low grain yield production in a stressed environment (Khodarahmipour et al., 2011).

**Table 9. Eigen value, percent of variance and cumulative variance obtained from PCA for salinity tolerance indices of thirty genotypes.**

Tolerant indices	PC 1	PC 2
ATI	0.64	0.52
SSI	0.01	-0.03
TOL	0.17	-0.09
SSPI	0.75	-0.41
STI	0.00	0.04
YSI	-0.01	0.02
YI	0.00	0.07
RSI	-0.02	0.05
SNPI	-0.04	0.58
HM	0.01	0.34
GMP	0.04	0.31
Eigenvalue	21.49	7.35
% Variance	74.42	25.45
Cumulative variance	74.42	99.87



**Figure 3. principal component analysis using salinity tolerant indices, ●: genotypes**

**CONCLUSION**

This study concluded that highly significant differences were observed among genotypes under both normal and saline locations. All test rice genotypes were affected by salinity stress for grain yield and other agronomic traits. For all studied traits, genotypic variance was greater than environmental variance and the phenotypic coefficient of

variation (PCV) was close to the genotypic coefficient of variation (GCV). Broad-sense heritability estimates for all traits were relatively high, implying a significant genetic advance associated with breeding for grain yield and agronomic characters. The combined analysis for promising lines RGA-13 and RGA-14 showed high performances under salinity condition compared with salinity tolerant check



Giza178. Based on ATI, STI, YSI, YI, RSI, SNPI, HM and GMP, it can be inferred that the checks (Giza178), the variety Giza179 and the genotypes, RGA-13 and RGA-14 were tolerant to salinity stress. Therefore, they are recommended to be used as parents for improvement of salinity tolerance in breeding programs

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## تقييم بعض الصفات المحصولية ودلائل تحمل الملوحة تحت ظروف الأراضي العادية والملحية في الأرز

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### المخلص

الملوحة هي أحد العوامل الرئيسية المسؤولة عن خسائر محاصيل الحبوب في العالم. لقد أصبح التحسين الوراثي لتحمل الملوحة مهم لحل مشكلة ملوحة الأرز. تم زراعة ثلاثون تركيباً وراثياً من الأرز في موسمين متتاليين 2020 و 2021 لتقييم التباين والارتباط بين الصفات المرغوبة تحت ظروف التربية العادية والتربة المالحة. كانت التركيب الوراثية (G) والتفاعل بين المواقع والتركيب الوراثي L x G عالي المعنوية لجميع الصفات المدروسة. لقد سجلت السلالات المباشرة RGA-2 و RGA-3 و RGA-4 و RGA-14 أعلى قيم لوزن السنبله وأكبر عدد من الحبوب بالسنبله. كما أعطت السلالات RGA-2 و RGA-3 و RGA-6 و RGA-9 و RGA-14 أعلى محصول حبوب تحت ظروف الأراضي العادية، بينما أعطت السلالات RGA-13 و RGA-14 أعلى محصول حبوب تحت ظروف الأراضي الملحية مقارنة بالصفة المتحمل للملوحة جيزه 178. أعطت دلائل تحمل الملوحة TOL و SSI ونفس الاتجاه تقريباً للثلاثين تركيباً وراثياً، حيث أعطت التركيب الوراثية الحساسه للملوحة أعلى القيم بينما أعطت التركيب الوراثية المتحملة للملوحة أقل القيم. أظهر فحص التركيب الوراثية المتحملة للملوحة باستخدام المتوسطات ودلائل تحمل الملوحة أن الأصناف جيزه 178 و جيزه 179 و التركيب الوراثية Giza 178 و Giza 179 و RGA-2 و RGA-3 و RGA-4 و RGA-11 و RGA-13 و RGA-14 و RGA-15 كلت متحملة لإجهاد الملوحة.