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AGRONOMIC,PHYSIOLOGICAL,AND MOLECULARVARIATIONS AMONG SELECTED RICE GENOTYPES UNDER NORMAL AND SALINE SOIL CONDITIONS

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ABSTRACT

Salinity is a crucial abiotic stress that severely limits rice growth and production, particularly under the current severe climate changes. Consequently, cultivation of new salt-tolerant rice genotypes is one of the best strategies to sustain rice production. This study aimed to evaluate the physiological and agronomic performance of diverse rice genotypes under both normal and saline soil conditions, identify promising and salinity-tolerant rice genotypes, and assess the molecular genetic diversity among the evaluated genotypes using Sequence Tagged Microsatellite Site (STMS) markers. Seventeen rice genotypes were evaluated at Sakha Agricultural Research Station, which represents normal soil conditions, and at the El-Sirw Agricultural Research Station, which represents saline soil conditions, during 2023 and 2024 growing seasons. The obtained results indicated highly significant variation among the years, environments, genotypes and their interactions for most studied traits. Salinity stress substantially decreased relative water content (RWC), plant height, spikelet fertility percentage, grain yield, and its attributes. Conversely, it significantly increased malondialdehyde (MDA) content, proline content, and antioxidant enzyme activities (APX and SOD) compared to normal conditions. The genotypes Giza178, L1, L6, and L4 recorded the highest values of RWC, proline content, APX, and SOD activity under salinity stress conditions, respectively, reflecting their enhanced physiological adaptability and resilience to salinity. Additionally, the genotypes L10, Sakha Super-301, Sakha Super300, had the highest grain yield under normal conditions, while L4, GZ1368-S-5-4 and Giza178 exhibited the highest grain yield under salinity stress conditions. In contrast, the lowest grain yield was recorded in the genotypes L8, L3, and L7 under both conditions. Moreover, the genotypes Giza178, L10, Sakha Super300, GZ1368, and L4 exhibited the highest stress tolerance index (STI) and yield index (YI), indicating their potential as salt-tolerant genotypes. Consequently, these tolerant genotypes could be utilized in the future rice breeding program for enhancing grain yield under salinity stress conditions. The molecular analysis with 16 STMS markers revealed detection of 272 total amplified fragments representing 45 alleles across the tested materials. The detected alleles ranged from 1 allele for RM223 to 4 alleles in RM10852, RM8094and RM 10772with an average of ٢٫٨ alleles per locus. The polymorphic information content (PIC) ranged from 0 for RM223 (monomorphic marker), to 0.73 for RM8094.The nearby position of tolerant genotypes (Giza 178, GZ1368and Sakha Super 300) in cluster analysis proves the ability of STMS molecular markers to identify salt tolerant genotypes that co-linear with most studied parameters and indices. The study demonstrates the power of STMS markers in detecting molecular diversity of the tested genotypes and the existence of considerable amount of diversity.

Key words: ***Rice, Soil salinity, Physiological traits, Grain yield, Tolerance indices, STMS markers.***

INTRODUCTION

Rice (*Oryza sativa* L.) is a fundamental crop for global food security, acting as a key dietary staple for more than half of the world's population (Sackey *et al* 2025). It serves as an excellent source of carbohydrates, calories, essential minerals, vitamins, and proteins (Abid *et al* 2024), making it a vital component of food security worldwide. The global population is projected to reach 9.7 billion by 2050. Hence, it is crucial to boost global rice production to address food security challenges (Li *et al* 2024). Salinity is a significant abiotic stress challenge that greatly impacts rice production globally (Zhang *et al*2021). It is estimated that 20% of cultivated land and 33% of irrigated land globally face high salinity, a situation further worsened by the impacts of climate change (Shrivastava and Kumar 2014). With the rising percentage of salt-affected lands, sustaining rice production to feed the growing population will become increasingly challenging (Zayed*et al* 2024). Therefore, developing salt-tolerant rice genotypes is crucial for ensuring global food security, especially in response to the challenges posed by climate change.

Rice is among the most salt-sensitive crops (Ganie *et al* 2019); however, its cultivation is recommended during soil reclamation processes due to its high-water requirements, which facilitate the leaching of salts into deeper soil layers (Chhabra and Chhabra 2021). The drastic effects of salinity on the growth and physiology of rice are especially pronounced during its seedling and reproductive stages (Singh *et al* 2021). Salinity stress leads to both ionic and osmotic stresses, causing adverse effects such as membrane disruption, metabolic imbalance, and oxidative damage (Munns *et al* 2020). Additionally, it impairs water absorption, reducing cell expansion and stomatal conductance, which negatively impacts photosynthesis, biomass accumulation, and grain yield. (Shabala and Munns 2017). Soil salinity adversely affects rice yield by decreasing tiller numbers, delaying panicle initiation, lowering pollen fertility, and reducing grain weight per plant (Guha *et al* 2025). These reductions stem from ion toxicity, and nutrient deficiencies due to saline conditions. Additionally, excess sodium generates reactive oxygen species (ROS), causing oxidative damage and potentially resulting in programmed cell death (Liang *et al* 2024). To mitigate oxidative stress caused by ROS, plants activate antioxidant defenses, including superoxide dismutase (SOD), and ascorbate peroxidase (APX). SOD converts superoxide radicals into hydrogen peroxide, which APX then detoxify to prevent damage (Kibria *et al* 2017). Salinity stress also increases proline accumulation, which stabilizes cell membranes and enhances salinity stress tolerance (Koc *et al* 2024).

Molecular markers are vital for identifying salinity tolerant rice genotypes, enabling efficient selection and breeding of resilient genotypes that can thrive in saline soils conditions(Ramadan *et al* 2020). It assists breeders in assessing genetic variations and selecting lines with specific genomic regions for salt tolerance through marker-assisted selection. These markers offer greater accuracy, consistency, and repeatability compared to morphological and biochemical markers, and they can be applied across different growth stages and methodologies (Salem *et al* 2024). Among molecular markers Sequence Tagged Microsatellite Site (STMS), or microsatellite markers, are particularly advantageous due to their co-dominant inheritance, multi-allelic nature, high abundance, broad genome coverage, high in formativeness, and low DNA requirement (Joshi *et al* 2024). STMS markers have demonstrated a strong capability in assessing genetic diversity and elucidating genetic relationships among rice genotypes (Mukta *et al* 2024). The objectives of the current study were to 1) Evaluate the physiological and agronomic performance of diverse rice genotypes under normal and soil salinity stress conditions. 2) Identify superior and salinity-tolerant rice genotypes 3) Assess the molecular genetic diversity among the evaluated genotypes using STMS markers.

MATERIALS AND METHODS

Plant Material and Experimental design

Seventeen diverse rice genotypes, including twelve newly developed advanced rice lines and four Egyptian cultivars were used in this study. The name, pedigree and type of the studied rice genotypes are listed in Table 1. The advanced lines were collected from F_8 generation in the Sakha Research Station breeding program of Rice Research Department following a pedigree selection scheme based on agronomic performance.

The seventeen rice genotypes were evaluated under normal and salinity stress conditions during the 2023 and 2024 growing summer seasons at Sakha Agricultural Research Station, Kafr El-Sheikh Governorate as normal soil condition and at the El-Sirw Agricultural Research Station, Damietta Governorate asa saline soil conditions. The physical and chemical soil properties of both locations are presented in Table 2. At each location, the seeds of each genotype were sown on May 1st during both seasons. After thirty days, the seedlings were individually transplanted into the permanent field in seven rows. Each row measured 5 meters in length and consisted of 25 hills, spaced 20 cm apart. The applied experimental design was a randomized complete block design (RCBD), with three replications. All recommended agricultural practices for the permanent rice field were followed at each location.

Table 1. Name, and parentage of the evaluated rice genotypes.

Name	Parentage	Type
L1	GZ-5603/ Yun Len 4	Japonica
L2	GZ-6910 / Nanjing-15	Japonica
L3	IRAT-112/ Giza -177	Japonica
L4	Giza-177 / KEHWA -4	Japonica
L5	Sakha -101 / IR-60080	Japonica
L6	Giza-178 / 2X-788	Indica/Japonica
L7	GZ-6522/ IR-69923	Indica/Japonica
L8	Giza-177 / IRAT-170	Indica/Japonica
L9	Sakha 101 / IR-12L355	Indica/Japonica
L10	GZ 6522-15-1-1-13 / BL -1	Indica/Japonica
L10	Giza 178 / IR-43	Indica/Japonica
L11	IET-1444 / IR 65844	Indica/Japonica
Giza177	Giza-171/Yamji No.1//Pi-No.4	Japonica
Giza178	Giza -175/ Milyang49	Indica/Japonica
Sakha102	GZ4096-7-1/GZ4120-2-5-2 (Giza177)	Japonica
GZ1368-S-5-4	IR1615-31 / BG90-2	Indica/Japonica
Sakha Super301	Not available	Japonica
Sakha Super300	PTGMS 38 × EJGSR-2	Japonica

Table 2. Soil properties of the two locations during the 2023 and 2024 growing seasons

Location	Sakha		El-Sirw	
Season	**2023**	**2024**	**2023**	**2024**
Soil properties				
pH (1:2.5)	**8.3**	**8.4**	**8.4**	**8.5**
Ec (ds.m^{-1})	**3.1**	**3.3**	**8.63**	**8.05**
Organic matter%	**1.35**	**1.36**	**1.06**	**1.0**
Available P, mg/kg	**12.4**	**13.0**	**11.7**	**12.3**
Available Ammonium (ppm)	**19.3**	**19.9**	**17.0**	**17.4**
Available Nitrate (ppm)	**16.6**	**16.0**	**14.2**	**14.7**
Available Potassium (ppm)	**300**	**305**	**245**	**263**
Anions (meq/L)				
CO3-	**-**	**-**	**-**	**-**
HCO3	**5.4**	**5.5**	**11.6**	**10.3**
SO4-	**11.3**	**11.5**	**33.4**	**30.5**
CL-	**14.7**	**15.6**	**40.9**	**39.5**
Cations(meq/L)				
Ca+Mg	**13.2**	**14.6**	**40.4**	**37.4**
Na+	**16.6**	**17.1**	**45.3**	**43.1**
K+	**0.8**	**0.95**	**0.40**	**0.31**

Measured traits

A. Physiological Measurements

1. Relative Water Content (RWC%)

Relative water content (RWC) was determined following the method described by Barrs and Weatherley (1962), using the formula:

RWC (%) = [(FW – DW)/(TW – DW)] × 100

where:FW is fresh weight, DW is dry weight, and TW is turgid weight.

2. Malondialdehyde (MDA) content

A fresh leaf sample (0.1 g) was homogenized in 1.5 mL of trichloroacetic acid (TCA) on ice. The homogenate was then centrifuged at 12,000 rpm for 10 minutes at 4°C to obtain the supernatant. An aliquot of this supernatant was mixed with thiobarbituric acid (TBA) reagent and heated in a boiling water bath for 30 minutes, which allowed MDA to react with TBA. After cooling and further centrifugation, the absorbance of the resulting solution was measured at 532 nm using a spectrophotometer. The concentration of MDA was then calculated using a standard curve, following the method by Heath and Packer (1968).

3. Proline Content

The concentration of proline was measured in micrograms per gram of fresh weight using a spectrophotometer, as described by Bates *et al* (1973).

4. Antioxidant Enzymes Activity (APX and SOD)

Fresh leaves samples were ground in liquid nitrogen and then homogenized in 2 ml of extraction buffer, comprised of 100 mM potassium phosphate (pH 7.8), 0.1 mM EDTA, and 10 mM ascorbic acid. The resulting homogenate was centrifuged at 13,000g for 15 minutes at 4°C and used to determine different enzyme activities. APX activity was quantified at 290 nm following the methodology established by Ma and Cheng (2004). Using the approach of Beauchamp and Fridovich (1971), the SOD activity was determined at 560 nm.

B. Agronomic characters

Data collections were taken on the following traits; plant height (cm), number of panicle plant, panicle length (cm), spikelet fertility (%), 1000-grain weight (g), and grain yield (t/ha) as recommended according to standard evaluation system of rice (IRRI, 2016).

Data analysis

The collected data were analyzed using analysis of variance (ANOVA) procedures, as described by Snedecor and Cochran (1989), utilizing the M Stat-C statistical software package. The combined analysis was done whenever homogeneity of variance was detected. The least significant difference (LSD) values were calculated at the 5% and 1% probability levels. Stress tolerance indices were calculated to identify salt - tolerant genotypes. Geometric mean productivity (GMP) was calculated according to Fernandez (1992) using the following equation $GMP = \sqrt{\mathrm{Ys} \times \mathrm{Yp}}$.

Yield index (YI) was calculated as outlined by Gavuzzi *et al* (1997) using the following equation, $\mathrm{YI}=\frac{\mathrm{Ys}}{\bar{\mathrm{Y}}\mathrm{s}}$. Mean productivity (MP) was calculated according to Rosielle and Hamblin (1981) using the following equation $\mathrm{MP}=\frac{\mathrm{Y_s}+\mathrm{Y_p}}{2}$. Stress tolerance index (STI) was calculated following Fernandez (1992) using the following equation $\mathrm{STI}=\frac{\mathrm{Y_s}\times\mathrm{Y_p}}{(\bar{\mathrm{Y}}_\mathrm{p})^2}$

Yield stability index (YSI) = Ys/Yp and Relative stress index (RSI) = $Y_s/Y_p/Y_{ms}/Y_{mp}$, were calculated according to Bouslama and Schapaugh (1984)where Y_s is the grain yield of each genotype under salinity stress conditions, Y_p is the grain yield of each genotype under normal conditions, and $\bar{Y}_s$ and $\bar{Y}_p$ are the means of all evaluated genotypes under salinity stress and normal conditions, respectively.

Molecular analyses

DNA Extraction

Genomic DNA was extracted from young leaves of the seventeen rice genotypes using a modified CTAB extraction protocol (Murray and Thompson, 1980). DNA quality and quantity were assessed using a Nano Drop 2000 spectrophotometer (Thermo Scientific, Bremen, Germany). The integrity of the DNA was verified by electrophoresis on 1% agarose gel.

PCR Amplification and Gel Electrophoresis

Sixteen Sequence Tagged Microsatellite Site (STMS markers) associated with salinity tolerance in rice were utilized in this study. The sequences of the applied primers are detailed in Table 3. PCR reactions were performed in 15 µL volumes, each containing 1.5 µL of template DNA, 1 µL of both forward and reverse SSR primers, 7.5 µL of ROVALAB 2× Red PCR Master Mix, and 4.5 µL of dd H_2O. Amplification was carried out using a PerkinElmer Gene Amp PCR System 2400 with the following thermal profile: initial denaturation at 94 °C for 5 minutes; 35 cycles of denaturation at 94 °C for 1 minute, annealing at 55–60 °C (based on primer Tm) for 30 seconds, and extension at 72 °C for 1 minute; followed by a final extension at 72 °C for 7 minutes. PCR products were resolved on 3% agarose gels in 0.5× TAE buffer, stained with ethidium bromide

(0.5 µg/mL), and visualized using a Biometra Biodoc Analyze system. Band sizes were estimated against a 50 bp DNA ladder (MBI Fermentas).

Table 3. The applied Sequence Tagged Microsatellite Site (STMS) markers.

Marker	Chromosome No.	Repeat motif	Forward Sequence	Reverse Sequence
RM10793	**1**	**(ATAG)7**	**GACTTGCCAACTCCTTCAATTCG**	**TCGTCGAGTAGCTTCCCTCTCTACC**
RM562	**1**	**(AAG)13**	**CACAACCCACAAACAGCAAG**	**CTTCCCCCAAAGTTTTAGCC**
RM10852	**1**	**(ATAG)5**	**GAATTTCTAGGCCATGAGAGC**	**AACGGAGGGAGTATATGTTAGCC**
RM11463	**1**	**(AG)18**	**ACGAGCACTACAGCACACATGC**	**AATGCTGCAACCTCTTCTTCTCC**
RM219	**9**	**(CT)17**	**CGTCGGATGATGTAAAGCCT**	**CATATCGGCATTCGCCTG**
RM493	**1**	**(CTT)9**	**TAGCTCCAACAGGATCGACC**	**GTACGTAAACGCGGAAGGTG**
RM9	**1**	**(GA)15GT (GA)2**	**GGTGCCATTGTCGTCCTC**	**ACGGCCCTCATCACCTTC**
RM242	**9**	**(CT)26**	**GGCCAACGTGTGTATGTCTC**	**TATATGCCAAGACGGATGGG**
RM8094	**1**	**(AT)31**	**AAGTTTGTACACATCGTATACA**	**CGCGACCAGTACTACTACTA**
RM212	**1**	**(CT)24**	**CCACTTTCAGCTACTACCAG**	**CACCCATTTGTCTCTCATTATG**
RM277	**12**	**(GA)11**	**CGGTCAAATCATCACCTGAC**	**CAAGGCTTGCAAGGGAAG**
RM10745	**1**	**(TATG)9**	**TGACGAATTGACACACCGAGTACG**	**ACTTCACCGTCGGCAACATGG**
RM10764	**1**	**(AT)28**	**AGATGTCGCCTGATCTTGCATCG**	**GATCGACCAGGTTGCATTAACAGC**
RM140	**1**	**(CT)12**	**TGCCTCTTCCCTGGCTCCCCTG**	**GGCATGCCGAATGAAATGCATG**
RM10772	**1**	**(CTT)16**	**GCACACCATGCAAATCAATGC**	**CAGAAACCTCATCTCCACCTTC**
RM223	**1**	**(CT)25**	**GAGTGAGCTTGGGCTGAAAC**	**GAAGGCAAGTCTTGGCACTG**

SSR data analysis

The amplified bands for each STMS marker were scored based on the presence or absence of bands, creating a binary data matrix represented as (0) and (1). The data generated from the STMS analysis were analyzed using the Jaccard similarity coefficient (Jaccard, 1908). The resulting similarity coefficients were used to construct a dendrogram using the Unweighted Pair Group Method with Arithmetic Average (UPGMA) employing NTSys 2.1 program (Rohlf *et al* 2000). The polymorphic information content (PIC) for each primer was calculated to estimate its allelic variation as follows: PIC = 1- $\sum_{j=1}^{n} Pij^2$ where Pij is the frequency of the ith allele for marker j with the summation extending over n alleles, calculated for each marker (Anderson *et al* 1993)**.**

RESULTS AND DISCUSSIONS

1. Analysis of variance

The analysis of variance (Table 4) showed that the mean squares due to years (Y) were significant for all the traits studied, except panicle length. This suggests notable variations between the two years for all the traits studied. Furthermore, the mean squares of environments (E) were highly significant for all the studied traits, indicating that the performance of tested genotypes varied significantly between normal and salinity stress conditions. These results agree with those obtained by Zeng and Shannon (2000), Li *et al* (2023) and Zheng *et al*(2023).

Mean squares due to genotypes (G) were highly significant for all studied traits. This indicates the wide diversity among the genetic materials used in the present study. Additionally, the interactions between genotypes and environments (G × E) were significant for all the studied traits, suggesting that the tested genotypes varied from one environment to another and ranked differently from normal to salinity conditions. These results align with those found by Meng *et al*(2021) and Ghazy *et al*(2023).

The genotypes × years (G × Y) interaction showed significant effects on most studied traits, suggesting that the ranking of the evaluated genotypes varied across years. The three-way interaction genotype ×

environment × year (G × E × Y) was significant for all studied traits, except number of panicles per plant. This indicates that the performance of each genotype varied from one year to another within different environments.

Table 4. Combined analysis of variance of all the studied traits across years, environments and genotypes.

SOV	df	Mean squares					
		RWC (%)	MDA (µmol/g FW)	ProC (mg g^{-1} FW)	APX (Unit mg/ protein)	SOD (Unit mg/ protein)	Plant height (cm)
Years (Y)	**1**	**975.47****	**1058.56****	**2.91****	**5.67****	**253.35****	**186.40***
Rep/Y	**4**	**5.166**	**3.493**	**0.03**	**0.75**	**2.177**	**12.563**
Environments (E)	**1**	**3576.00****	**1984.20****	**103.74****	**851.33****	**4913.14****	**24180.59****
Y × E	**1**	**32.73****	**106.50****	**0.75****	**18.17****	**28.12****	**175.47****
Error a	**4**	**0.93**	**1.93**	**0.02**	**0.66**	**1.51**	**4.47**
Genotypes	**16**	**270.39****	**56.84****	**0.87****	**51.29****	**175.83****	**417.56****
G × Y	**16**	**62.58****	**13.93****	**0.10****	**56.54****	**46.90****	**84.64****
G × E	**16**	**25.25****	**22.67****	**0.39****	**6.91****	**15.29****	**51.53****
G × Y × E	**16**	**10.62****	**11.73****	**0.05****	**2.02****	**8.61****	**39.65****
Pooled Error (Eb)	**128**	**2.74**	**1.24**	**0.01**	**0.57**	**0.90**	**4.49**

SOV	df	Mean squares					
		No. of panicles per plant	Panicle length (cm)	Number of filled grains /panicle	Spikelet fertility (%)	1000-grain weight (g)	Grain yield (t ha^{-1})
Years (Y)	**1**	**15.82***	**5.80**	**687.43***	**216.42****	**187.35****	**7.53***
Rep/Y	**4**	**٢.28**	**٣.47**	**85.4١**	**٢.7٢**	**1.283**	**0.68**
Environments (E)	**1**	**1381.43****	**836.53****	**149155.88****	**13677.47****	**1818.64****	**1402.17****
Y x E	**1**	**40.91***	**2.08**	**127.25**	**4.76**	**0.28**	**21.62****
Error a	**4**	**2.28**	**1.65**	**59.25**	**٢.٦3**	**0.91**	**0.25**
Genotypes	**16**	**30.95****	**19.72****	**4104.67****	**337.02****	**89.62****	**8.60****
G x Y	**16**	**4.80****	**9.59****	**693.68****	**20.28****	**19.92****	**2.57****
G x E	**16**	**9.73****	**14.22****	**2328.34****	**118.94****	**11.49****	**3.86****
G x Y x E	**16**	**3.21**	**6.55****	**395.25****	**13.27****	**5.68****	**2.55****
Pooled Error (Eb)	**128**	**2.02**	**1.60**	**54.02**	**2.47**	**1.49**	**0.39**

***, **Significant at 0.05 and 0.01 levels of probability, respectively.RWC= Relative water content; MDA= Malondialdehyde; Proc= Proline content; APX= Ascorbate peroxidase and SOD = Superoxide dismutase.**

2. Mean performance

2.1. Interaction between environments and genotypes

Mean performance of all the studied traits under normal and salinity stress conditions across the two years are presented in Table 5. The interaction between assessed environments (normal and salinity conditions) and evaluated genotypes significantly affected all the studied traits. Salinity stress significantly reduced relative water content (RWC) in all tested genotypes compared to non-saline conditions, highlighting the detrimental effect of salinity on leaf water retention. These findings are consistent with Hossen *et al* (2022) and Ubaidillah *et al* (2024), who reported that salinity stress resulted in a significant reduction in the RWC of rice plants. There were notable variations in the RWC among genotypes under normal or salinity stress treatments. Under normal conditions, Sakha Super301, L10, Sakha Super 300, L4 and Giza-178 exhibited the highest RWC, indicating superior water retention, while L8 recorded the lowest. In contrast, under salinity stress, Giza178, Sakha Super-301, L10and L4 maintained the highest values, whereas L1 showed the lowest. Malondialdehyde (MDA) isa key indicator of oxidative damage caused by salinity stress. Salinity stress significantly increased MDA content compared to normal conditions. The genotypes L8, L7, L5, and Giza177 accumulated the highest MDA content under salinity stress, indicating severe oxidative damage and heightened sensitivity to salinity. In contrast, L2, Sakha Super-300, and GZ-1368displayed the lowest MDA levels, suggesting greater tolerance to salt-induced oxidative stress. Salinity stress led to a significant increase in proline content in all evaluated genotypes compared to normal conditions, highlighting its crucial role in improving salt tolerance in rice. Proline enhances salinity tolerance by protecting cell membranes, reducing oxidative stress, and maintaining cellular functions under salt stress (Ghosh *et al* 2022). Significant variation was detected among genotypes in proline content under saline and non-saline environments. Under normal conditions, L1, L5 and L10 exhibited the highest proline content, indicating their natural tendency to accumulate proline in non-stress environments.

Table 5. Mean performance of all evaluated genotypes for all studied characters under normal (N) and saline soil (S) conditions combined across the two seasons.

Genotypes	RWC (%)		MDA (µmol/g FW)		ProC (mg g^{-1} FW)		APX (Unit mg/ protein)		SOD (Unit mg/ protein)		Plant height (cm)	
	N	S	N	S	N	S	N	S	N	S	N	S
L1	76.61	61.23	6.45	14.18	0.92	2.67	8.13	11.67	4.98	11.44	102.03	83.82
L2	78.25	71.28	5.69	11.58	0.25	1.30	6.78	14.17	7.65	17.16	110.33	82.40
L3	79.07	70.45	10.58	15.45	0.47	2.66	12.98	15.58	7.75	17.37	112.27	86.97
L4	82.55	74.83	10.02	15.58	0.19	1.98	10.08	16.45	11.27	23.63	113.65	86.08
L5	75.86	68.00	9.59	17.87	0.72	2.07	11.40	14.77	11.62	20.95	116.67	98.45
L6	78.90	72.42	11.18	15.50	0.59	2.21	12.13	17.37	13.73	23.49	114.57	88.42
L7	78.90	72.48	7.24	18.17	0.28	1.70	11.90	15.15	12.57	21.88	109.75	86.32
L8	68.33	62.50	7.53	20.42	0.38	1.42	8.59	10.42	7.49	14.41	111.75	82.43
L9	81.97	73.17	9.94	14.27	0.60	1.66	7.84	12.07	2.47	10.77	116.83	97.50
L10	84.22	76.67	9.79	16.83	0.70	1.88	7.94	11.31	6.76	21.50	116.00	95.02
L11	74.67	67.33	6.63	14.05	0.35	1.69	9.08	12.61	6.96	12.88	101.33	79.00
Giza 177	79.65	65.33	15.37	17.07	0.49	2.30	11.05	14.85	11.53	22.02	101.17	83.93
Giza 178	82.50	76.83	9.12	13.06	0.72	2.30	12.64	16.45	14.12	23.05	98.33	81.87
Sakha 102	68.83	64.38	5.42	11.35	0.43	1.66	11.78	15.31	11.08	21.80	110.17	88.77
GZ1368	81.67	73.17	8.92	12.18	0.56	2.40	10.35	17.10	11.08	22.92	101.67	81.60
Sakha Super 301	85.87	76.68	5.88	12.72	0.62	1.52	14.42	17.02	12.43	24.85	114.83	97.50
Sakha Super 300	84.21	72.92	6.88	11.99	0.65	1.74	12.28	16.53	11.83	22.05	112.33	93.45
LSD 0.05	1.89		1.27		0.13		0.86		1.08		2.42	
LSD 0.01	2.50		1.68		0.18		1.14		1.43		3.20	

Table 5. Cont.

Genotypes	No. of panicles per plant		Panicle length (cm)		Number of filled grains /panicle		Spikelet fertility (%)		1000-grain weight (g)		Grain yield (t ha-1)	
	N	S	N	S	N	S	N	S	N	S	N	S
L1	20.99	12.90	26.79	16.38	192.00	91.25	91.19	66.17	30.83	24.33	10.15	3.41
L2	18.40	13.25	22.58	20.92	130.17	115.77	91.99	75.17	33.12	23.50	9.41	5.03
L3	15.55	12.54	22.00	17.70	115.25	90.83	84.67	75.70	29.33	23.75	8.31	4.44
L4	19.89	14.83	27.08	21.60	209.61	132.25	93.17	83.89	34.07	29.20	10.69	5.42
L5	15.83	13.10	24.33	19.37	153.06	109.85	90.15	68.25	33.28	26.72	9.19	5.20
L6	15.06	12.13	22.63	19.57	141.60	110.63	81.73	70.59	30.17	24.00	10.03	5.08
L7	18.33	12.87	20.63	18.45	167.54	96.70	80.81	65.27	29.63	22.55	8.71	3.64
L8	14.58	12.17	24.46	18.28	132.50	104.00	83.33	63.17	23.00	19.17	7.76	3.10
L9	17.92	14.72	24.29	19.43	187.26	94.10	93.96	67.67	33.58	23.58	10.40	4.51
L10	22.17	15.77	23.13	21.38	209.78	129.23	96.07	82.00	34.00	26.17	11.37	5.33
L11	19.17	14.57	23.88	20.03	164.88	96.47	93.58	67.74	28.52	22.97	10.49	4.52
Giza177	18.50	11.42	24.08	18.72	142.17	100.38	94.00	70.87	28.83	24.27	9.63	3.42
Giza178	21.92	15.50	22.96	21.23	165.24	126.13	92.00	82.03	24.33	21.30	10.44	6.45
Sakha102	19.42	12.17	20.92	18.58	150.50	103.67	92.03	75.34	29.62	23.13	9.85	3.49
GZ1368	20.67	13.47	21.17	17.00	130.50	119.77	92.67	85.17	24.17	20.97	9.54	6.58
Sakha Super301	18.92	13.10	23.17	19.38	183.57	116.77	94.10	81.20	28.42	23.75	11.02	4.16
Sakha Super300	19.33	13.65	21.42	18.62	202.00	120.47	94.33	81.17	30.17	24.20	11.16	5.23
LSD 0.05	1.62		1.44		8.39		1.79		1.39		0.71	
LSD 0.01	2.15		1.91		11.09		2.37		1.84		0.94	

RWC= Relative water content; MDA = Malondialdehyde; Proc = Proline content; APX= Ascorbate peroxidase and SOD = Superoxide dismutase.

In contrast, under salinity stress conditions, L1, L3, and GZ-1368 recorded the highest proline content, demonstrating their stronger ability to adapt to salinity through enhanced proline production. Salinity stress significantly increased the activity of ascorbate peroxidase (APX) and superoxide dismutase (SOD) in all evaluated rice genotypes. However, substantial variations were detected among the assessed genotypes studied for APX and SOD activities under normal and stress conditions. The highest APX activity was observed in the genotypes L3 and Sakha Super301 under normal conditions, while the lowest was recorded in L2 and L9.

Under salinity stress, the highest APX activity was found in L6 and GZ-1368, whereas L8 exhibited the lowest activity. Similarly, the highest SOD activity was shown by Giza178 and Sakha Super-301 under normal conditions, whereas Sakha Super301, L4, and L6 displayed the highest activity under salinity stress. In contrast, L9 and L1 had the lowest SOD activity under both conditions. The observed increase in antioxidant activity under salinity stress aligns with the previous studies which demonstrated enhanced ROS-scavenging capacity in salt-stressed plants (Kibria *et al* 2017; Abdelaziz *et al* 2018; Kumar *et al* 2024, Mekawy*et al* 2024). This indicates the essential role of antioxidant systems in enhanced salinity tolerance of rice plants. Salinity stress significantly impacted plant height across all tested genotypes, resulting in noticeable reductions compared to non-saline conditions. This finding highlights the detrimental effects of salinity on plant growth and development. Salinity reduces plant height by limiting nutrient uptake due to osmotic stress, restricting cell expansion, and disrupting metabolic processes that are essential for plant growth (Munns and Tester, 2008 and Ghadirnezhad Shiade *et al* 2023).Substantial variations in plant height were observed among the assessed genotypes. The tallest plants belonged to the L5 and L9 genotypes, while the shortest plants were recorded for the L11 genotype under both normal and stress conditions. The results in Table 5 indicated that salinity stress caused a significant reduction in the number of panicles per plant across all evaluated genotypes compared to normal conditions. The genotypes L10, Giza178 produced the highest number of panicles per plant under normal conditions. Under salinity stress, L4, L10, Giza178 exhibited the greatest number of panicles per plant. In contrast, L3, L6, and L8 displayed lower values of panicles per plant. Likewise, significant reductions in panicle length were noted under salt stress conditions. Under normal conditions, the highest panicle lengths were observed in lines L1 and L4, while line L7 exhibited the lowest values. In contrast, under salinity stress, lines L10 and L4 demonstrated the greatest panicle lengths, whereas line L1 had the lowest. Likewise, the number of filled grains /panicle was significantly affected by salinity stress, and the genotypes exhibited different performances under normal and stress conditions. The genotypes L10, L4, and Sakha Super300 recorded the highest number of filled grains per panicle under normal conditions. In contrast, under salinity stress, L4, Giza178, and L10 demonstrated the greatest number of filled grains. Meanwhile, L3 consistently had the lowest counts in both conditions. The spikelet fertility percentage decreased significantly under salinity stress compared to normal conditions, and the genotypes demonstrating varying performances in both environments. The genotypes: L10, Sakha Super301 and Sakha Super-300, exhibited the highest fertility under normal conditions. While L4, Giza178, and GZ-1368 demonstrated had the highest fertility under stress conditions.Conversely, genotypes L7 and L8 consistently displayed the lowest fertility across both conditions. Likewise, salinity stress caused a significant reduction in 1000-grain weight, with varying responses among genotypes. The heaviest 1000-grain weight was observed in genotypes L4, L10, and L9 under normal conditions, while L5, L4, and L10 exhibited the heaviest weights under salinity stress. In contrast, genotype L8 displayed the lightest 1000-grain weight across both environments. Salinity stress significantly impacted grain yield across all tested genotypes, resulting in noticeable reductions compared to normal conditions. It varied from 7.76 to 11.37 t /ha (average of 9.89 t/ha) under normal conditions, and from 3.١ to 6.58 t/ha (average of4.65 t/ha) under salinity stress conditions. The highest grain yield under normal conditions was assigned for the genotypes; L10, Sakha Super301, Sakha Super300, while under salinity stress conditions, the highest grain yield was detected by L4, GZ-1368 and Giza178. In contrast, the lowest grain yield was noted in the genotypes L8, L3, and L1 under both conditions. Generally, the results indicated that grain yield and its components significantly decreased under salinity stress conditions compared to normal conditions. These results are in harmony with those reported by Zayed *et al* (2023), Zheng *et al* (2023) and Huanhe *et al*(2024). The observed decline in rice grain yield under salinity stress could be attributed to reduced spikelet fertility resulting from impaired pollen viability and stigma receptivity (Rodríguez Coca *et al* 2023). Furthermore, salt stress induces ion toxicity and osmotic stress, which limits nutrient translocation and grain filling (Zheng *et al* 2021). Additionally, oxidative stress from ROS accumulation damages cellular structures, further compromising seed development and ultimately reducing grain yield (Challabathula *et al* 2022).

2.2. Interaction between years, environments, and genotypes

Mean performance of all the studied traits for the interaction between years, environments and genotypes are presented in Table 6. The interaction effect between the three factors was significant for all studied traits, except number of panicles per plant. The highest relative water content (RWC) was obtained by L9 and Sakha Super-301 in the first season under normal and salinity stress conditions, respectively. However, in the second season, L10 exhibited the highest RWC under both conditions. The lowest malondialdehyde (MDA) content was detected in Sakha Super-301 and Sakha-102 in the first season under normal and salinity stress treatments, respectively, while Giza177 and L7 had the highest levels. In the second season, L2 and GZ-1368 recorded the lowest MDA content under normal and salinity stress conditions, respectively. Meanwhile, L8 exhibited the highest MDA content under salinity stress, and Giza-177 showed the highest value under normal conditions. Regarding proline content, L1, L5 and Giza178 accumulated the highest proline levels under normal conditions, while L1 and L3 showed maximal proline content under salinity stress in both seasons. The highest APX activity was observed in the genotypes Sakha Super301 and L3 in the first season under normal and salinity stress conditions, respectively. However, in the second season, Giza178 exhibited the highest APX activity under both conditions. Concerning SOD activity, the highest levels in the first season were shown by Giza177 and Sakha Super-301, while in the second season, Giza178 and

L6 exhibited the highest activity under normal and salinity stress conditions, respectively.

Table 6. Mean performance of all evaluated genotypes for all studied characters under normal (N) and saline soil (S) conditions during the two growing seasons.

Genotype	RWC (%)				MDA (µmol/g FW)				ProC (mg g^{-1} FW)			
	2023		2024		2023		2024		2023		2024	
	N	S	N	S	N	S	N	S	N	S	N	S
L1	75.00	62.67	78.21	59.80	5.23	12.37	7.67	16.00	0.91	2.86	0.93	2.47
L2	82.50	73.00	74.00	69.57	4.55	9.67	6.83	13.50	0.31	1.43	0.19	1.18
L3	78.80	71.67	79.33	69.23	10.17	14.33	11.00	16.57	0.40	2.95	0.55	2.37
L4	86.10	78.67	79.00	71.00	7.70	14.83	12.33	16.33	0.26	2.21	0.12	1.74
L5	79.37	72.67	72.34	63.33	7.45	13.00	11.73	22.73	0.82	2.44	0.61	1.69
L6	84.80	76.67	73.00	68.17	9.35	14.33	13.00	16.67	0.55	2.35	0.64	2.07
L7	82.47	77.33	75.33	67.63	5.98	15.33	8.50	21.00	0.40	2.01	0.16	1.40
L8	69.67	64.33	67.00	60.67	5.38	13.67	9.67	27.17	0.31	1.57	0.45	1.28
L9	87.00	76.00	76.94	70.33	6.22	12.33	13.67	16.20	0.73	1.88	0.47	1.44
L10	80.00	74.33	88.44	79.00	8.92	13.33	10.67	20.33	0.80	1.77	0.59	1.98
L11	79.00	73.80	70.33	60.87	5.83	8.33	7.43	19.77	0.56	2.02	0.15	1.37
Giza-177	80.17	66.00	79.13	64.67	13.00	10.73	17.73	23.40	0.74	2.46	0.24	2.15
Giza-178	81.67	76.67	83.33	77.00	8.00	10.45	10.23	15.67	0.59	2.30	0.85	2.30
Sakha-102	69.67	66.50	68.00	62.27	4.50	7.70	6.33	15.00	0.49	1.78	0.37	1.54
GZ-1368	84.00	74.33	79.33	72.00	8.17	11.02	9.67	13.33	0.64	2.59	0.48	2.20
Sakha Super-301	85.83	80.83	85.90	72.53	4.00	11.00	7.77	14.43	0.60	1.60	0.63	1.44
Sakha Super-300	86.37	78.20	82.04	67.63	5.33	8.82	8.43	15.17	0.80	2.00	0.49	1.48
LSD 0.05	2.67				1.79				0.19			
LSD 0.01	3.53				2.37				0.25			

Table 6. Cont.

Genotype	APX (Unit mg/ protein)				SOD (Unit mg/ protein)				Plant height (cm)			
	2023		2024		2023		2024		2023		2024	
	N	S	N	S	N	S	N	S	N	S	N	S
L1	9.17	11.00	7.10	12.33	5.23	10.17	4.73	12.70	103.40	86.13	100.67	81.50
L2	8.50	15.00	5.06	13.33	10.13	22.80	5.17	11.52	113.67	83.70	107.00	81.10
L3	12.77	14.20	13.20	16.97	5.40	11.87	10.10	22.87	114.20	88.10	110.33	85.83
L4	9.29	16.33	10.87	16.57	10.40	24.00	12.13	23.27	112.97	85.57	114.33	86.60
L5	8.97	11.93	13.83	17.60	12.47	21.17	10.77	20.73	116.33	99.67	117.00	97.23
L6	11.90	16.73	12.37	18.00	15.43	23.00	12.03	23.97	115.80	80.33	113.33	96.50
L7	11.17	13.00	12.63	17.30	15.67	23.00	9.47	20.77	107.50	81.00	112.00	91.63
L8	9.80	11.23	7.37	9.60	11.33	17.80	3.64	11.03	116.67	78.67	106.83	86.20
L9	11.47	15.30	4.20	8.84	3.93	12.27	1.00	9.28	117.33	96.43	116.33	98.57
L10	10.64	13.61	5.24	9.01	11.37	24.00	2.14	19.00	116.33	97.33	115.67	92.70
L11	14.27	15.70	3.88	9.52	8.83	13.77	5.08	12.00	99.00	68.50	103.67	89.50
Giza-177	11.83	15.67	10.27	14.03	15.87	23.20	7.20	20.83	101.67	83.67	100.67	84.20
Giza-178	9.50	12.47	15.77	20.44	13.77	23.00	14.47	23.10	99.00	80.47	97.67	83.27
Sakha-102	9.17	14.00	14.38	16.62	13.37	21.70	8.78	21.90	104.67	81.17	115.67	96.37
GZ-1368	8.23	14.53	12.47	19.67	11.03	23.67	11.13	22.17	100.67	81.20	102.67	82.00
Sakha Super-301	14.73	16.17	14.10	17.87	14.83	27.87	10.03	21.83	113.33	95.17	116.33	99.83
Sakha Super-300	10.20	14.03	14.37	19.03	11.50	21.53	12.17	22.57	110.67	94.40	114.00	92.50
LSD 0.05	1.22				1.53				3.42			
LSD 0.01	1.61				2.02				4.52			

Table 6. Contd.

Genotype	No. of panicles per plant				Panicle length (cm)				Number of filled grains/panicle			
	2023		2024		2023		2024		2023		2024	
	N	S	N	S	N	S	N	S	N	S	N	S
L1	18.35	13.77	23.63	12.03	26.50	15.63	27.08	17.13	195.00	80.50	189.00	102.00
L2	18.33	14.67	18.47	11.83	22.33	20.33	22.83	21.50	144.67	128.53	115.66	103.00
L3	16.33	13.60	14.77	11.48	21.67	14.47	22.33	20.93	119.33	88.33	111.17	93.33
L4	18.90	15.67	20.87	14.00	26.67	21.20	27.50	22.00	210.00	130.57	209.21	133.93
L5	16.85	14.57	14.80	11.63	23.83	17.87	24.83	20.87	155.34	118.27	150.79	101.43
L6	15.05	12.80	15.07	11.47	21.67	18.37	23.58	20.77	151.80	121.00	131.40	100.27
L7	18.67	12.93	18.00	12.80	20.67	19.60	20.58	17.30	146.00	106.13	189.09	87.27
L8	15.17	12.97	14.00	11.37	23.33	15.63	25.58	20.93	125.00	102.33	140.00	105.67
L9	17.67	15.00	18.17	14.43	23.58	21.30	25.00	17.57	189.33	106.57	185.19	81.63
L10	20.00	15.53	24.33	16.00	23.50	21.77	22.75	21.00	197.33	113.63	222.23	144.83
L11	19.00	15.13	19.33	14.00	23.33	21.77	24.42	18.30	168.00	81.83	161.75	111.10
Giza-177	18.33	11.60	18.67	11.24	22.75	19.60	25.42	17.83	143.00	102.43	141.33	98.33
Giza-178	21.17	15.37	22.67	15.63	24.00	22.20	21.92	20.27	168.15	117.90	162.33	134.37
Sakha-102	19.67	12.40	19.17	11.94	22.17	19.00	19.67	18.17	156.67	124.87	144.33	82.47
GZ-1368	18.83	14.00	22.50	12.94	20.50	17.00	21.83	17.00	131.67	122.20	129.33	117.33
Sakha Super-301	18.17	13.43	19.67	12.77	22.08	20.40	24.25	18.37	186.12	128.53	181.03	105.00
Sakha Super-300	19.67	13.47	19.00	13.84	22.33	19.37	20.50	17.87	208.00	129.27	196.00	111.67
LSD 0.05	NS				2.04				11.87			
LSD 0.01	NS				2.70				15.68			

Table 6. Contd.

Genotype	Spikelet fertility (%)				1000-grain weight (g)				Grain yield (t ha^{-1})			
	2023		2024		2023		2024		2023		2024	
	N	S	N	S	N	S	N	S	N	S	N	S
L1	92.52	66.00	89.87	66.33	32.70	25.77	28.97	22.90	11.31	3.35	8.99	3.46
L2	91.67	73.33	92.31	77.00	31.67	24.00	34.57	23.00	10.46	3.51	8.36	6.54
L3	85.00	75.85	84.33	75.54	30.00	26.50	28.67	21.00	9.07	4.22	7.55	4.67
L4	94.00	83.10	92.33	84.67	36.13	30.70	32.00	27.70	11.53	4.41	9.84	6.43
L5	92.09	74.00	88.20	62.50	34.00	26.10	32.57	27.33	10.07	4.58	8.31	5.82
L6	83.81	74.50	79.66	66.67	29.67	22.17	30.67	25.83	9.34	3.19	10.72	6.97
L7	82.85	66.00	78.77	64.55	31.00	24.10	28.27	21.00	8.80	3.84	8.62	3.44
L8	83.00	62.67	83.67	63.67	23.33	20.33	22.67	18.00	8.55	2.58	6.96	3.63
L9	93.90	73.33	94.02	62.00	35.20	28.30	31.97	18.87	10.34	5.26	10.46	3.75
L10	97.33	82.67	94.81	81.33	35.33	27.33	32.67	25.00	12.14	6.48	10.59	4.17
L11	94.16	68.00	93.00	67.47	27.93	20.60	29.10	25.33	10.17	4.42	10.80	4.62
Giza-177	95.00	74.33	93.00	67.41	29.67	26.03	28.00	22.50	9.50	3.38	9.76	3.45
Giza-178	92.33	81.67	91.67	82.40	23.67	21.10	25.00	21.50	10.40	6.43	10.48	6.47
Sakha-102	93.17	75.02	90.89	75.67	30.93	24.27	28.30	22.00	10.20	3.45	9.51	3.53
GZ-1368	94.33	86.00	91.00	84.33	25.67	22.27	22.67	19.67	9.39	6.41	9.70	6.74
Sakha Super-301	94.54	83.33	93.66	79.07	29.83	24.67	27.00	22.83	11.47	3.26	10.57	5.06
Sakha Super-300	95.00	81.67	93.67	80.67	34.00	26.23	26.33	22.17	11.63	5.38	10.69	5.09
LSD 0.05	2.54				1.97				1.01			
LSD 0.01	3.35				2.60				1.34			

NS = non-significant. RWC = Relative water content; MDA = Malondialdehyde; Proc = Proline content; APX = Ascorbate peroxidase and SOD = Superoxide dismutase.

For plant height, L9 under normal and L5 under stress conditions showed the maximum plant height in the first season, while L11 was the shortest under both conditions. In the second season, L5 and Sakha Super-301 were the tallest, whereas L1 and L2 were the shortest under normal and salinity stress conditions, respectively. In terms of panicle length, in the first season, L4 produced the longest panicles under normal conditions, while Giza178 performed best under salinity stress. In the second season, L4 achieved the maximum panicle length under both normal and salinity stress conditions.

The highest number of filled grains per panicle were observed in L4 and Sakha Super300 under both normal and salinity stress conditions during the first season. However, in the second season, L4 and L10 recorded the highest values under normal conditions, while L10 and Giza178 had the greatest numbers under salinity stress. The genotypes L10 and Sakha Super-300 exhibited the highest fertility percentages under normal conditions in the first season, while Sakha Super-301 and GZ-1368 showed the highest values under salinity stress. In the second season, L10 and L9 recorded the highest fertility percentages under normal conditions, whereas L4 and GZ-1368 performed best under salinity stress. The heaviest 1000-grain weight in the first season was noted in L10 and L4 under normal conditions, and in L9 and L4 under salinity stress. In the second season, L2 and L10 exhibited the highest 1000-grain weight under normal conditions, while L5 and L4 showed the greatest weight under salinity stress. The highest grain yield in the first season was achieved by L10 under normal conditions and by Giza-178 under salinity stress. While, in the second season, L11 and GZ-1368 recorded the highest grain yield under normal and stress conditions, respectively.

3. Stress tolerance indices

Tolerance indices, including mean productivity (MP), geometric mean productivity (GMP), stress tolerance index (STI), yield index (YI), yield stability index (YSI) and relative stability index (RSI) were calculated based on grain yield under both normal and stress conditions, to identify salt tolerant genotypes (Table 7).

Table 7. Stress tolerance indices for the seventeen genotypes under normal and salinity conditions.

Genotype Code	Yp	Ys	MP	GMP	HM	STI	YI	YSI	RSI
L1	10.15	3.41	6.78	5.88	5.10	1.25	0.35	0.73	0.34
L2	9.41	5.02	7.22	6.87	6.55	0.88	0.48	1.08	0.53
L3	8.31	4.44	6.38	6.07	5.79	0.88	0.38	0.96	0.53
L4	10.68	5.42	8.05	7.61	7.19	0.93	0.59	1.17	0.51
L5	9.19	5.20	7.20	6.91	6.64	0.82	0.49	1.12	0.57
L6	10.03	5.08	7.56	7.14	6.74	0.93	0.52	1.09	0.51
L7	8.71	3.64	6.18	5.63	5.13	1.10	0.32	0.78	0.42
L8	7.76	3.10	5.43	4.90	4.43	1.13	0.25	0.67	0.40
L9	10.40	4.51	7.46	6.85	6.29	1.07	0.48	0.97	0.43
L10	11.37	5.33	8.35	7.78	7.26	1.00	0.62	1.15	0.47
L11	10.49	4.52	7.51	6.89	6.32	1.07	0.48	0.97	0.43
Giza-177	9.63	3.42	6.53	5.74	5.05	1.22	0.34	0.74	0.36
Giza-178	10.44	6.45	8.45	8.21	7.97	0.72	0.69	1.39	0.62
Sakha-102	9.85	3.49	6.67	5.86	5.15	1.22	0.35	0.75	0.35
GZ-1368	9.54	6.58	8.06	7.92	7.79	0.59	0.64	1.42	0.69
Sakha Super-301	11.02	4.16	7.59	6.77	6.04	1.17	0.47	0.90	0.38
Sakha Super-300	11.16	5.23	8.20	7.64	7.12	1.00	0.60	1.13	0.47

Yp, mean grain yield under normal conditions, Ys, mean grain yield under salinity stress conditions, MP, mean productivity; GMP, geometric mean productivity; HM, harmonic mean; STI, stress tolerance index; YI, yield index; YSI, yield stability index; RSI, Relative Stress Index.

The genotypes Giza178, L10, and GZ-1368 demonstrated the highest mean productivity (MP) and geometric mean productivity (GMP), indicating their superior performance under both environments. In contrast, L8 exhibited the lowest MP and GMP, reflecting its weak productivity. The genotypes Giza178, L10, Sakha Super-300, GZ-1368, and L4 had the highest stress tolerance index (STI) and yield index (YI), hence, they could be considered as salt-tolerant genotypes. Thereupon, these tolerant genotypes could be utilized in the future rice breeding programs for boosting grain yield under salinity stress conditions. Conversely, L8 and L7 showed the lowest STI and YI, accordingly, they are considered salt-sensitive genotypes. The genotypes GZ-1368, L5 and Giza-178 ranked highest in both yield stability index (YSI) and relative stability index (RSI), reflecting their excellent yield stability and superior performance under salinity stress. In contrast, L1 ranked lowest, indicating strong sensitivity and poor adaptability to salinity stress conditions. These results are in line with those reported by Anshori *et al* (2021); Chattopadhyay *et al* (2021) and Sogir *et al* (2024). They applied stress tolerance indices to identify the tolerant and sensitive rice genotypes.

4. Molecular analysis

A total of 16 STMS markers were used to access the diversity of tested materials at molecular level. These markers are known to be linked to salinity tolerance genes. Fig (1) shows the banding patterns of some of the tested STMS markers that show a clear polymorphism among tested genotypes. The results obtained here showed significant amount of diversity among the tested genotypes. Table (8) shows summary of molecular analysis of 17 rice genotypes using STMS markers. The results revealed detection of 272 total amplified fragments representing 45 alleles across the tested materials. The detected alleles ranged from 1 allele for RM223 to 4 alleles in RM10852, RM8094and RM 10772. Moreover, the number of polymorphic alleles ranged from 0 for RM223 to 4 in RM10852, RM8094and RM 10772. The polymorphic information content ranged from 0 for RM223 (monomorphic marker), to 0.73 for RM8094. The banding patterns were then used to calculate the similarity matrix among the tested genotypes (Table 9). The results showed that the most similar genotypes pairs were Line 9 and line 10 with 0.94 similarity index followed by Sakha 102 and Giza 177 as well as line 10 and line 11 with similarity of 0.88. On the other hand the most diverse pair of genotypes line 1 and each of line 10 and line 11 with only 0.11 similarity%. These results are in full coherence with genetic background of the tested genotypes. GZ-1368and Sakha 101 share a common ancestor and both are pure japonica genotypes, Giza 177 and Sakha 102 are also close to each other since Giza 177 is the male parent for Sakha 102 and both are pure japonica varieties. Also both line 10 and 11 are indica/japonica genotypes. On the other hand the Japonica line (line 1) showed maximum variation with the indica/japonica lines 10 and 11 since they have completely different genetic background. The similarity matrix index was then used to construct dendrogram explaining the phylogenic relationships among the 17 tested genotypes. The dendrogram illustrated in Fig (2) confirms the existence of considerable amount of variability among tested genotypes. The results showed also some coherence with salinity tolerance mechanisms operating in tolerant genotypes and also coherence with salinity tolerance index. The clustering of Giza 178 and GZ1368-S-5-4 nearby each other on the dendrogram with their relative high yield under salt stress as well as high salinity tolerance index (STI).represents a good example of coherence between molecular analysis with STMS markers and salinity tolerance. However, other genotypes like Line 4 that shows also high yield and high STI values but cluster faraway from Giza 178 and GZ13٦٨that clearly suggest different salt tolerant mechanisms in line 4 since this line belongs to japonica background. Also, Sakha super 300 that had high STI value, suggesting different mechanisms of salt tolerant pure japonica from that of indica/japonica genotypes. Results showed also that the salt sensitive checks Giza 177 and Sakha 102 were clustered together. These results demonstrates the power of using STMS markers in assessing genetic variability at the molecular level and the relative coherence of salinity tolerance linked markers for clustering salt tolerant genotypes. The complexity of salt tolerant mechanisms operating in rice genotypes makes it difficult to cluster all tolerant genotypes together in one cluster.

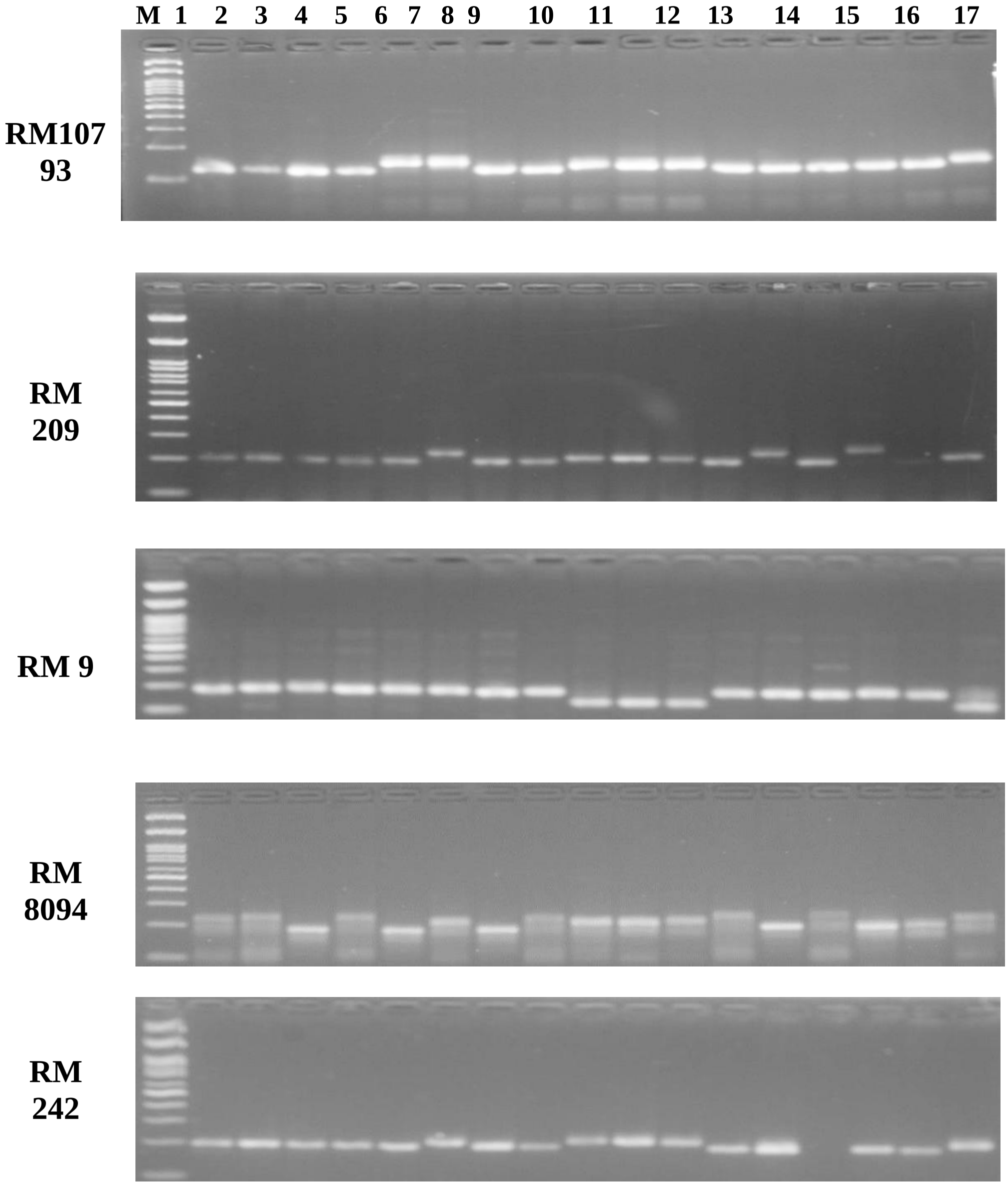

Fig. 1. Banding patterns of some tested STMS markers, M, 100 bp ladder, 1-17, tested rice genotypes as listed in Table (1).

Table 8. Summary of Molecular analysis for tested genotypes using STMS markers.

STMS marker	# of amplified bands	# of amplified alleles	# of polymorphic alleles	Polymorphism %	PIC value
RM10793	17	3	3	100	0.60
RM562	17	2	2	100	0.49
RM10852	17	4	4	100	0.46
RM11463	17	3	3	100	0.66
RM219	17	3	3	100	0.66
RM493	17	3	3	100	0.46
RM9	17	3	3	100	0.65
RM242	17	3	3	100	0.46
RM8094	17	4	4	100	0.73
RM212	17	3	3	100	0.60
RM277	17	2	2	100	0.21
RM10745	17	2	2	100	0.36
RM10764	17	3	3	100	0.63
RM140	17	2	2	100	0.36
RM10772	17	4	4	100	0.67
RM223	17	1	0	0	0
Total	272	45	44		
Average	17	2.8	2.75	93.75	0.5

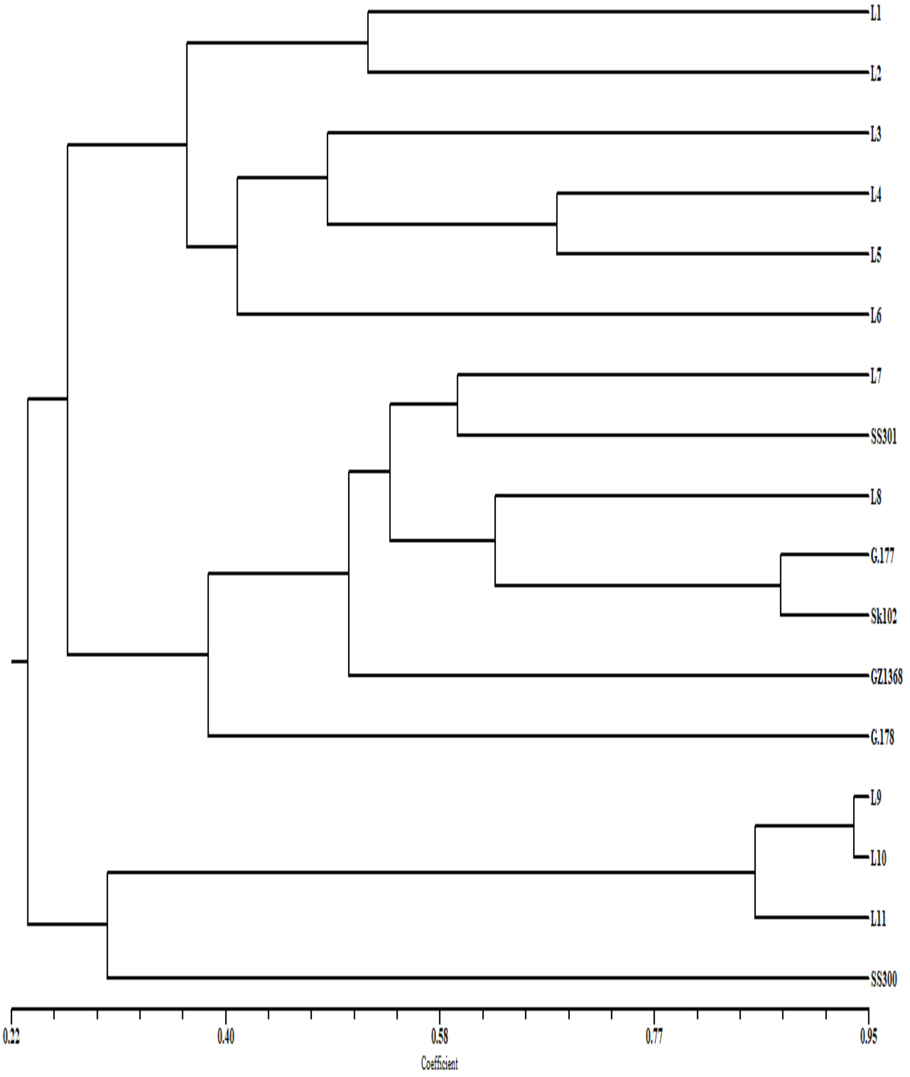

Fig 2. Dendrogram explaining the genetic relationships among tested genotypes using STMS markers employing UPGMA method.

Table 9. Similarity matrix among tested rice genotypes based on STMS markers.

	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	L11	G177	G178	Sk 102	GZ 1368	SS 301	SS 300
L1	**1.00**																
L2	0.52	**1.00**															
L3	0.39	0.52	**1.00**														
L4	0.33	0.52	0.45	**1.00**													
L5	0.33	0.33	0.52	0.68	**1.00**												
L6	0.19	0.33	0.39	0.39	0.45	**1.00**											
L7	0.14	0.33	0.33	0.52	0.45	0.39	**1.00**										
L8	0.23	0.28	0.28	0.39	0.39	0.39	0.60	**1.00**									
L9	0.11	0.19	0.35	0.29	0.29	0.41	0.24	0.24	**1.00**								
L10	0.10	0.19	0.33	0.28	0.28	0.39	0.23	0.23	0.94	**1.00**							
L11	0.10	0.14	0.28	0.28	0.28	0.33	0.28	0.19	0.82	0.88	**1.00**						
G177	0.14	0.14	0.14	0.28	0.28	0.23	0.52	0.68	0.19	0.19	0.23	**1.00**					
G178	0.19	0.23	0.28	0.28	0.28	0.28	0.39	0.39	0.24	0.28	0.28	0.39	**1.00**				
Sk102	0.15	0.07	0.07	0.20	0.20	0.20	0.43	0.58	0.16	0.15	0.20	0.88	0.30	**1.00**			
GZ1368	0.33	0.23	0.23	0.33	0.39	0.33	0.45	0.45	0.19	0.19	0.23	0.52	0.45	0.58	**1.00**		
SS301	0.23	0.23	0.28	0.28	0.33	0.23	0.60	0.60	0.15	0.14	0.19	0.60	0.39	0.50	0.52	**1.00**	
SS300	0.14	0.07	0.14	0.14	0.19	0.33	0.28	0.28	0.29	0.28	0.33	0.28	0.23	0.36	0.33	0.33	**1.00**

The results obtained here reflects STMS hyper variability and their high resolution power. The nearby position of tolerant genotypes (Giza 178, GZ1368-S-5-4 and Sakha Super 300) in cluster analysis proves the ability of STMS molecular markers to identify salt tolerant genotypes that co-linear with most studied parameters and indices. The findings are likely to expedite breeding new salt tolerant cultivars by involving parents from diverse molecular clusters with different salt tolerance mechanisms and in a full correspondence with that of Sanjay *et al* (2010). Among the potential salt tolerant lines, Line 4, 5, 6, 9, 10 and 11. These lines represent Japonica (Lines 4, 5) and Indica Japonica (lines 6, 9, 10 and 11) they clustered on both sides of tolerant genotypes (Fig. 1) and possibly have different tolerance mechanisms operating that led to their clustering a part in the dendrogram. Notably Line 10 was noticed for better performance in RWC and had higher values in MP, GMP, STI, YI indices. Line 6 had high antioxidant activities. The results demonstrate the feasibility to develop diverse salt tolerant genotypes through breeding with salt tolerant donors. Similar findings were also reported by Anupam *et al* (2017), Adak *et al* (2020) and Sahoo *et al* (2020). The results obtained suggests that line 9, 10 and 11 might have the same tolerance mechanism as they tend to cluster together near by the tolerant check Giza 178. Hazman *et al* (2025) concluded that Giza 178 accumulates more K^+ and Ca^{++} ions and hence maintain hemostasis and lower Na/K ratio. This may imply that the GZ1368-S-5-4 might have the same mechanisms and this might held true for the nearby lines 9, 10 and 11. The other salt tolerant lines on the other side of the dendrogram may have other mechanisms operating since the fall a part from Giza178 and GZ1368-S-5-4. These findings are important in developing salt tolerance breeding strategies for rice and further investigations are required to disclose the key genes operating in those different japonica and indica/japonica lines.

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التباينات المحصوليه والفسيولوجيه والجزيئيه لتراكيب وراثيه منتخبه من الارز تحت ظروف الأراضى الطبيعيه والأراضى الملحيه

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قسم بحوث الأرز– معهد بحوث المحاصيل الحقلية– مركز البحوث الزراعية – مصر

تعد الملوحة أحد الإجهادات البيئية التى تؤثر سلبا على نمو و انتاج محصول الارز خاصه فى ظل التغيرات المناخيه الحاليه. لذلك فإن استنباط و زراعة تراكيب وراثيه جديدة من الأرز متحملة للملوحة يُعد من أفضل الاستراتيجيات للحفاظ على إنتاج الأرز واستدامته. تهدف هذه الدراسة إلى تقييم الأداء الفسيولوجي

والمحصولى لمجموعة منتخبه من سلالات الأرز تحت ظروف الاراضى العادية والملحية، و ذلك للتعرف على افضل السلالات المبشره و المتحملة للملوحة، بالإضافة إلى تقييم التنوع الوراثي الجزيئي بين السلالات تحت الدراسه باستخدام الدلائل الجزيئيه (STMS). تم تقييم سبعة عش رتركيبًا وراثيًا من الأرز في محطة البحوث الزراعية بسخا التي تمثل ظروف الاراضى العادية، وفي محطة البحوث الزراعية بالسرو التي تمثل ظروف الاراضى الملحية، وذلك خلال موسمي النمو ٢٠٢٣ و ٢٠٢٤. أظهرت النتائج وجود فروق عالية المعنوية بين السنوات، والبيئات، والتراكيب الوراثية، والتفاعل فيما بينها لمعظم الصفات تحت الدراسه. أظهرت النتائج أن إجهاد الملوحة أدى إلى انخفاض ملحوظ في محتوى الورقه النسبى من الماء النسبي، إرتفاع النبات، ونسبة الخصوبة، وكذلك محصول الحبوب و معظم مكوناته. بينما حدث ارتفاع معنوي في كلا من محتوى المالونديالدهيد، ومحتوى البرولين، وكذلك في نشاط إنزيمي مضادات الاكسده (APX و SOD) مقارنة بالظروف العادية. سجّلت التراكيب الوراثية Giza178 و L1 وL6 و L4 أعلى القيم لصفات محتوى الورقه النسبى من الماء، ومحتوى البرولين، ونشاط إنزيمي APX وSOD على التوالي تحت ظروف الاراضى الملحيه، مما يعكس قدرتها الفسيولوجية العالية على التكيف مع الملوحة وتحملها. أظهرت التراكيب L10 وSakha Super-301 وSakha Super-300 أعلى القيم لصفه محصول الحبوب وبعض مكوناته تحت الظروف العاديه، في حين سجلت التراكيب L4 و GZ1368 وGiza178 أعلى القيم لصفه محصول الحبوب تحت ظروف الاراضى الملحيه. وعلى النقيض، سجلت التراكيب L8 وL3 و L7 أقل القيم لصفه محصول الحبوب تحت كلا من ظروف الاراضى العادية و الملحية. أظهرت التراكيب الوراثية Giza178 و L10 وSakha Super300 و GZ1368 و L4أعلى القيم لدليل تحمل الملوحه (STI) ودليل المحصول (YI) وبالتالى تعتبر هذه التراكيب متحمله للملوحه ويمكن الاستفادة من هذه التراكيب في برامج تربيةالأرز المستقبلية لتحسين صفه محصول الحبوب تحت ظروف الاراضى الملحيه. أظهرت نتائج التحليل الجزيئي باستخدام ١٦ معلماً جزيئياً متنوع STMS و المرتبطة بتحمل الملوحة، الحصول على ٢٧٢ حزمة DNA متعددة الشكل المظهرى، مما يعكس كفاءة هذه المعلمات في الكشف عن التنوع الجزيئي بين التراكيب الوراثية المستخدمه. تروواح عدد الأليلات من ٢ الى٤ بمتوسط ٢,٨ اليل لكل موقع. كما تراوحت قيمة محتوى المعلومات متعددة الأشكال المظهريه (PIC) من ٠ للمعلم الجزيئي RM223 إلى ٠,٧٣ للمعلم الجزيئي RM8094. أظهر التحليل العنقودي تقارب مواقع التراكيب الوراثيه المتحملة للملوحة Giza178 وGZ1368 وSakha Super-300 مما يدل على كفاءة معلمات STMS الجزيئيه في تمييز التراكيب الوراثيه المتحملة للملوحة والتى يمكن الاستفادة منها مستقبلاً في برامج تربية وتحسين الأرز.

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