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# Genotypic Differences in Agro-Physiological, Yield and Yield-Related Traits Responses to Saline Field Environment for Rice Genotypes through Line x Tester Analysis

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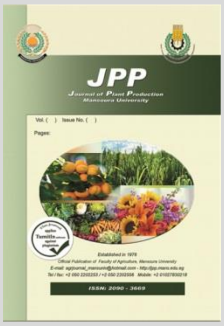


## ABSTRACT

Rice is confronted with various abiotic stress factors during growth due to the challenges presented by global climate change, which poses a major risk to overall productivity and development. Salinity is considered the most serious abiotic stress that significantly affects yield stability among all other factors. Twenty-four hybrids generated from the combination of six lines with four new introgression testers were assessed along with their respective parents for the extent of physiological and yield potential-related traits under saline field conditions. A wide range of variability was observed among genotypes, the magnitude of SCA variance was higher than the GCA variance for all the traits, revealing the predominance of non-additive gene action. The promising line GZ 10101-5-1-1-1 was identified as a potential good combiner genotype for peroxidase, superoxide dismutase, proline, malondialdehyde, and hydrogen peroxide contents. Furthermore, it was found that Giza 178, Sakha 104, AR 278-41-1-1-6-3, and IHL 296 were effective general combiners for improving grain yield. Three cross combinations Giza 178/IHL 180, Sakha 104/IHL 296, and Sakha 109/IHL 185 exhibited favorable SCA effects for antioxidant enzyme activity. The cross-combination Sakha 104/IHL 249 was considered a good specific combiner for yield and certain yield-related traits. The highly positive significant heterobeltiosis was observed for antioxidant enzyme activity, malondialdehyde, and hydrogen peroxide concentrations by the cross-combination AR 278-41-1-1-6-3/IHL 185. In addition, the hybrid combinations Giza 178/IHL 296, Sakha 104/IHL 180, and Sakha 104/IHL 296 were found to have highly significant heterobeltiosis effects for yield and related traits under a saline field environment.

***Keywords***: Rice, salinity, heterobeltiosis, yield.

## INTRODUCTION

Rice (*Oryza sativa* L.) is a staple crop that provides about half of the world's population with essential nutrients such energy, calcium, iron, thiamin, folate, carbs, and pantothenic acid (Mahanta *et al.,* 2023). Over 400 million people globally, including those from South America, Asia, and Africa, suffer from chronic hunger; to alleviate this issue, food production must rise by 38% in 30 years (WHO, 2020). As the world's population grows and their wide nutritional needs are met, it is becoming more and more important to improve grain production and quality standards (Hanafiah *et al.,* 2020; Mohapatra and Sahu, 2022). Improving the rate at which land resources are used is a key tactic to boost food production. An estimated 1.0 billion hectares, or more than 7% of the world's total land area, are impacted by salt (Hopmans *et al.,* 2021). In addition, the 20th century saw a 12–22 cm rise in sea levels worldwide (Walthall *et al.,* 2013). In Egypt, where 50% of the planted rice area is damaged by salt, rice production is severely constrained and needs to be improved (Zayed *et al.,* 2019). Increasing the pace at which land resources are utilized is a crucial strategy for boosting food production.

The sensitivity of rice to salt stress is modest. Soil salt levels beyond the critical threshold of 3.0 dS/m negatively impact grain yield characteristics, including grain yield, seed set rate, 1000-grain weight, effective panicle numbers, panicle length, and grain number per panicle (Mumtaz *et al.,* 2018). A 50% reduction in rice grain production was observed when the soil electrical conductivity (EC) was 6.0 dS/m (Djaman *et al.,* 2020). Although research indicates that the effective panicle number was more susceptible to saline stress than other features, it is unclear how much salinity influences the yield components (Gerona *et al.,* 2019). Additionally, during the seedling and reproductive phases, rice is more susceptible to salt stress than other features (Ali *et al.,* 2013). However, the reproductive stage has little to do with the seedling stage's ability to withstand salt (Mohammadi *et al.,* 2014).

Rice yield potential has frequently been enhanced using of morphological and yield-associated traits as the basis for the assessment of phenotypic variability. In addition to other traits including plant height, tillering ability, total biomass production, and photosynthetic efficiency, the yield of rice is correlated with multiple component traits, such as panicle number per unit area, filled grains per panicle, and 1000-grain weight (Xing and Zhang, 2010; Huang *et al.,* 2013; Li *et al.,* 2014; Zayed *et al.,* 2024). The accumulation of salts have a direct impact on crucial morpho-physiological traits and yield-related factors, such as photosynthesis, height of the plant, root length, number of tillers, length of panicles, the quantity of spikelets per panicle, grain filling, and overall biomass. Consequently, this leads to a notable decrease in yield (Zayed *et al.,* 2024). When a salt-sensitive plant is

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subjected to salinity stress, it's growing and productivity will significantly decrease.

In the basal area, glutathione reductase (GR) may inhibit the generation of $O_2$ under saline conditions. Conversely, the apical region can scavenge $O_2$ by increasing the activity of superoxide dismutase (SOD), although the activity of H2O2 scavenging enzymes such as APX and CAT diminishes under salinity (Yamane *et al.,* 2009).

Proline stands out as the primary endogenous osmolyte among osmolytes, accumulating in response to various abiotic stressors, including salinity (Slama *et al.,* 2015). Research has demonstrated that the overexpression of the regulatory enzyme 1-pyrroline-5-carboxylate synthetase (P5CS), which is involved in proline biosynthesis, enhances the salinity tolerance of plants (Székely *et al.,* 2008; Chen *et al.,* 2013). Furthermore, increased proline accumulation has been linked to improved salinity tolerance in plants (Goudarzi and Pakniyat, 2009). Plant morphology and physiological changes are important to study, but it's also important to compare how different cultivar species affect a plant's response. Limited progress has been made in developing salt-tolerance rice varieties due to the lack of genetic resources with high salinity tolerance and reliable salinity-tolerance genes with large effects (Ganapati *et al.,* 2022). The current study aims to assess how various rice genotypes and their hybrids react to environments abundant in salinity. We focused on the effects of agro-physiological, antioxidant enzyme activity, yield, and yield-related traits to provide information for selecting new parental lines for successful breeding. This information will be useful for further mining of breeding strategies for improving salinity tolerance in rice.

## MATERIALS AND METHODS

### Plant material and growth conditions

The present investigation was conducted at the experimental research farm of the Rice Research Department, Sakha, Kafr El-Sheikh, and El-Sirw Agricultural Research Station experimental farm, Damietta, Egypt during the two rice-growing seasons of 2023 and 2024. The experimental material composed of ten parental genotypes and twenty-four $F_1$ crosses in accordance with the line x tester mating design (Kempthrone, 1957). Six rice genotypes; Giza 178, Sakha 104, Sakha 108, Sakha 109, GZ 10101-5-1-1-1, and AR 278-41-1-1-6-3 used as lines whereas the remaining four genotypes consisted of new introgression with a wide genetic background; IHL 180, IHL 185, IHL 249 and IHL 296 used as testers (Table 1). During the 2023 rice-growing season, the parental genotypes were cultivated on three separate planting dates, spaced 14 days apart, to address variations in flowering times. Thirty-day-old seedlings from each parent were transplanted individually into the field, arranged in five rows. Each row measured 5 meters in length and contained 25 hills, with a uniform spacing of 20 centimeters between them. A hybridization process among the parents was carried out during the flowering period, resulting in the production of twenty-four $F_1$ crosses in the summer of that same season.

During the 2024 rice cultivation season, all F1 hybrids and their parental lines were cultivated, with seedlings being transplanted 30 days post-sowing. This was conducted using a randomized complete block design featuring three replicates, situated within the saline conditions of the El-Sirw Agricultural Research Station. Each hybrid was planted in three rows, each measuring 2 meters in length, alongside rows of parental varieties. A standard spacing of 20 centimeters was maintained between both the rows and the hills. All recommended agricultural practices for rice production in salt-affected soils were implemented at the experimental site.

**Table 1. The parentage and type of parental studied rice genotypes**

| NO | Genotype | Parentage | Type |
|---|---|---|---|
| 1 | Giza 178 | Giza 175/Milyang 49 | indica/japonica |
| 2 | Sakha 104 | GZ 4096-8-1/GZ 4100-9-1 | japonica |
| 3 | Sakha 108 | Sakha 101/HR 5824-B-3-2-3//Sakha 101 | japonica |
| 4 | Sakha 109 | Sakha 101/Sakha 105 | japonica |
| 5 | GZ 10101-5-1-1-1 | Sakha 103/IRI 385 | japonica |
| 6 | AR 278-41-1-1-6-3 | Introduced | indica/japonica |
| 7 | IHL 180 | Sakha 103/Chujing 28//Yunjing 29 | japonica |
| 8 | IHL 185 | Sakha 103/Chujing 28//Yunjing 29 | japonica |
| 9 | IHL 249 | Sakha 103/L-80//Yunjing 37 | japonica |
| 10 | IHL 296 | Sakha 106/L-80//Yunjing 37 | japonica |

**L-80: *Oryza rufipogon*/Hexi 35**

### Experimental soil properties

Soil samples were randomly taken before land preparation at a 0-20 cm depth from the soil surface, mixed, then transported to the laboratory, dried, and ground to fine particles. The chemical analysis used soil extract 1:5 to assess the soluble anions and cations. The soil EC and pH were measured using pH and EC meters in a 1:5 soil water solution. The soil analysis was determined based on the methods of Chapman and Parker (1961); The findings regarding the chemical properties of the soil are displayed in Table 2.

**Table 2. The chemical soil properties**

| pH (1:2.5 soil water | ECe (1:5 soil water | Soluble cations (meq. $L^{-1}$) (soil paste): | | | | Soluble anions (meq. $L^{-1}$) (soil paste): | | |
|---|---|---|---|---|---|---|---|---|
| suspension) | extraction) | $Ca^{++}$ | $Mg^{++}$ | $K^{+}$ | $Na^{+}$ | $HCO_3^{-}$ | $Cl^{-}$ | SO4⁻⁻ |
| 8.33 | 8.52 | 7.91 | 4.84 | 2.62 | 65.94 | 7.96 | 64.53 | 8.82 |

### Measurement of antioxidant enzyme activity

Catalase activity was assessed using the technique outlined by Bergmeyer (1970). Fresh leaves weighing 0.2 g were pulverized in liquid nitrogen and subsequently homogenized in 2 ml of extraction buffer, which consisted of 100 mm potassium phosphate (pH 7.8), 0.1 mm EDTA, and 10 mm ascorbic acid. The resulting homogenate was then centrifuged at 13,000g for 15 minutes at a temperature of 4°C. The catalase (CAT) activity was evaluated in the supernatant at a wavelength of 240 nm, based on the rate of hydrogen peroxide ($H_2O_2$) consumption. Peroxidase (POX) activity was quantified at 420 nm following the methodology established by Kar and Mishra (1976). The activity of superoxide dismutase (SOD) was measured at 560 nm in accordance with the procedure described by Beauchamp and Fridovich (1971).

### Leaf proline content

Leaf samples weighing 0.3 g were immersed in 3% sulphosalicylic acid and subjected to centrifugation for 20 minutes at 3000g. Subsequently, 2 ml of the resulting supernatant was combined with 2 ml of ninhydrin reagent and 2 ml of glacial acetic acid. The concentration of proline was quantified in micrograms per gram of fresh weight using a spectrophotometer, following the procedure outlined by Bates *et al.* (1973).

**Determination of $H_2O_2$ and Lipid peroxidation contents**

Fresh leaf tissue weighing 0.1 g was subjected to extraction using 3 mL of TCA (0.1% w/v) in an ice bath, followed by centrifugation at 12,000 g for 15 minutes. Subsequently, 0.5 mL of the resulting supernatant was combined with 0.5 mL of 10 mM potassium phosphate buffer (pH 7.0) and 1 mL of 1 M potassium iodide (KI). The absorbance of the supernatant was measured at a wavelength of 390 nm. The concentration of hydrogen peroxide ($H_2O_2$) was quantified using a standard curve as described by Velikova *et al.* (2000) and was expressed in mmol $g^{-1}$ FW. Additionally, lipid peroxidation was assessed by measuring the malondialdehyde (MDA) content, utilizing an extinction coefficient of 155 mM $cm^{-1}$. The estimation of MDA was performed following the methodology outlined by Heath and Packer (1968).

**Leaf stomatal conductance (gs) and transpiration rate measurement**

The stomatal conductance (gs) was measured (units; mol $m^{-2}$ $s^{-1}$) at the heading stage via a portable photosynthesis measurement system (Li-Cor, Lincoln, NE, USA) according to Hubbard *et al.,* (2001). Transpiration rate ($H_2O$ $m^{-2}$ $s^{-1}$) was taken using the LI-COR Biosciences device (Nebraska, USA) at photosynthetically active radiation (PAR) 600e1200 nm and measured at 09:00e11:30. Finally, relative water content (RWC) was quantified according to Bastam *et al.,* (2013) using the formula:

$$RWC = \frac{FW\text{-}DW}{TW\text{-}DW} \times 100$$

**Agro-morphological, yield and yield-related parameters**

Five plants were randomly chosen from each replication, and biometric measurements were taken for nine specific traits: days to flowering (days), plant height (cm), number of tillers per plant, number of panicles per plant, panicle length (cm), panicle weight (g), spikelet fertility percentage, 1000-grain weight (g), and grain yield per plant (g). Upon reaching maturity, the counts of filled grains and sterile spikelets within the panicle were recorded. Spikelet fertility is defined as the proportion of filled grains relative to the total number of spikelets.

**Statistical analysis**

Under salt-affected soil, line x tester analysis, described by Kempthrone (1957) and Singh and Chaudhary (1977), was used to assess general combining ability (GCA) effects for parents and specific combining ability (SCA) effects for each cross combination. Additive and dominant types of gene action and heritability were estimated. The heterosis was determined for each cross-over better parent (Mather and Jinks, 1982). According to formula of Wyanne *et al.,* (1970) the LSD values were computed to assess the significance of the heterobeltiosis effects.

## RESULTS AND DISCUSSION

**Analysis of variance**

The analysis of variance revealed substantial differences among genotypes, parents, crosses, lines, and the interaction between lines and testers concerning all antioxidative activities and physiological traits examined, as detailed in (Table 3A). Notable variations were observed between parents and crosses, with significant and highly significant differences for all traits studied, except for leaf-free proline content, which showed no significant difference. Additionally, significant differences in transpiration rates were identified through the analysis. Moreover, the analysis of variance indicated highly significant differences among genotypes, crosses, and the interaction between parents and crosses, as well as lines and testers, for all morphological, yield, and yield-related traits, as presented in (Table 3B).

The notable mean square values observed among the parental lines and their crosses indicated a substantial range of heterosis performance across all examined traits.

**Table 3A. Mean square (ANOVA) for antioxidative activities and physiological traits of rice genotypes**

| Source of variance | Df | CAT | POX | SOD | Leaf free proline | MDA | Leaf $H_2O_2$ | Stomatal conductance | Transpiration rate | RWC (%) |
|---|---|---|---|---|---|---|---|---|---|---|
| Replications | 2 | 1.93 | 0.37 | 1.62 | 0.017 | 0.09 | 0.933 | 0.0003 | 0.16 | 2.98 |
| Genotypes | 33 | 64.61** | 10.39** | 47.45** | 0.122** | 39.60** | 38.732** | 0.0117** | 25.70** | 438.58** |
| Parents | 9 | 55.91** | 18.91** | 100.46** | 0.166** | 59.88** | 86.406** | 0.0262** | 64.31** | 414.19** |
| Crosses | 23 | 27.87** | 6.69** | 11.23** | 0.109** | 33.22** | 13.946** | 0.0059** | 9.54** | 431.37** |
| Parents vs Crosses | 1 | 987.86** | 18.80** | 403.50** | 0.018 | 3.82* | 179.742** | 0.0131** | 49.91** | 823.72** |
| Lines | 5 | 39.51** | 7.53** | 16.57** | 0.229** | 21.99** | 26.953** | 0.0158** | 13.67** | 698.15** |
| Testers | 3 | 16.23** | 7.73** | 10.13** | 0.117** | 69.45** | 5.684** | 0.0010** | 5.12** | 137.72** |
| Lines x Testers | 15 | 26.32** | 6.20** | 9.67** | 0.067** | 29.72** | 11.263** | 0.0036** | 9.05** | 401.18** |
| Error | 66 | 1.51 | 0.37 | 0.78 | 0.008 | 0.87 | 0.978 | 0.0001 | 0.46 | 1.04 |

**CAT: Catalase (mmol $min^{-1}$ $g^{-1}$ protein), POX: Peroxidase (mmol $min^{-1}$ $g^{-1}$ protein), SOD: Superoxide dismutase (mmol $min^{-1}$ $g^{-1}$ protein), Proline (µg $g^{-1}$ FW), MDA: Malondialdehyde (mmol $g^{-1}$ FW), $H_2O_2$: Hydrogen peroxide (mmol $g^{-1}$ FW), Stomatal conductance (mmol $m^{-2}$ $s^{-1}$), Leaf transpiration rate (mmol $H_2O$ $m^{-2}$ $s^{-1}$), RWC: Relative water content. Which * Significant at 0.05 level and ** Significant at 0.01 level**

**Table 3B. Mean square (ANOVA) for morphological, yield and yield-related traits of rice genotypes**

| Source of variance | Df | Days to flowering (day)) | Plant height (cm) | No of tillers | No of panicles | Panicle length (cm) | Panicle weight (g) | Spikelets fertility (%) | 1000-grain weight (g) | Grain yield $plant^{-1}$ (g) |
|---|---|---|---|---|---|---|---|---|---|---|
| Replications | 2 | 1.85 | 13.79 | 2.75 | 0.52 | 0.22 | 0.010 | 0.51 | 0.72 | 0.25 |
| Genotypes | 33 | 68.42** | 445.15** | 56.65** | 53.28** | 9.49** | 0.528** | 1179.10** | 13.77** | 152.57** |
| Parents | 9 | 58.09** | 101.05** | 28.30** | 31.20** | 3.39** | 0.793** | 115.84** | 18.87** | 84.22** |
| Crosses | 23 | 74.84** | 440.41** | 62.77** | 53.21** | 10.13** | 0.442** | 1457.31** | 10.77** | 115.98** |
| Parents vs Crosses | 1 | 13.74** | 3651.07** | 171.04** | 253.78** | 49.79** | 0.130** | 4349.67** | 36.77** | 1609.3** |
| Lines | 5 | 256.86** | 1634.48** | 227.68** | 189.73** | 29.33** | 0.835** | 5987.67** | 9.88** | 361.07** |
| Testers | 3 | 70.13** | 283.79** | 17.76** | 22.66** | 2.58** | 0.858** | 115.63** | 30.61** | 90.88** |
| Lines x Testers | 15 | 15.11** | 73.70** | 16.80** | 13.81** | 5.24** | 0.228** | 215.52** | 7.10** | 39.30** |
| Error | 66 | 0.76 | 5.10 | 1.33 | 0.73 | 0.68 | 0.017 | 5.74 | 0.55 | 2.33 |

*** Significant at 0.05 level and ** Significant at 0.01 level**

Furthermore, the significant mean squares associated with the lines and testers underscored the dominance of additive genetic variance for these traits. Prior research has highlighted both additive and non-additive gene effects on yield and associated yield component traits in rice (Rahimi *et al.,* 2010). These results are consistent with the findings of Abo-Yousef *et al.* (2020) and Negm *et al.* (2023), who also reported significant variations in physiological, biochemical, agro-morphological yield, and yield-related traits among the parents and their crosses. Additionally, the pronounced differences in the interaction between lines and testers for these traits suggested that non-additive genetic variances or dominance play a crucial role in all these traits, with specific combining ability being largely responsible for their expression. A multitude of studies have established that dominant gene action is prevalent for most rice yield traits (Ganapati *et al.,* 2020; Ghidan and Khedr, 2021; El-Agoury *et al.,* 2023).

**Mean performance**

**Antioxidative and physiological activities**

The mean performance of the genotypes for antioxidative activities and physiological studied traits was found significant indicating the differences among the parental lines and their twenty-four $F_1$ crosses as shown in Table 4A. Among the parental lines, a desirable content was measured in the genotype Giza 178 for enhanced catalase (CAT) activity, whereas significantly decreased the concentration of malondialdehyde (MDA), hydrogen peroxide ($H_2O_2$) in the leaf and recorded the highest mean value of relative water content (RWC) among the parental genotypes. The variety Sakha 108 recorded maximum peroxidase (POX) and superoxide dismutase (SOD) activities than the other parental genotypes. The results also revealed a significant leaf-free proline accumulation and stomatal conductance increase for all the parental genotypes under a saline field environment with the maximum content observed in the new introgression lines IHL 180, IHL 296, and IHL 185, respectively.

Regarding the hybrid combinations, the hybrid Giza 178/IHL 180 showed the highest mean values regarding CAT content followed by the combination Sakha 108/IHL 180. Whereas, the highest POX values were produced by the combination GZ 10101-5-1-1-1/IHL 249 While the hybrid GZ 10101-5-1-1-1/IHL 185 exhibited the highest mean values of 23.607 for SOD activity among the studied hybrids.

**Table 4A. Mean values of lines, testers, and hybrids concerning antioxidative activities and physiological traits**

| Genotype | CAT | POX | SOD | Leaf free proline | MDA | Leaf H2O2 | Stomatal conductance | Transpiration rate | RWC (%) |
|---|---|---|---|---|---|---|---|---|---|
| Giza 178 | 18.49 | 16.85 | 22.830 | 1.710 | 16.833 | 11.180 | 0.578 | 14.49 | 83.333 |
| Sakha 104 | 17.77 | 17.96 | 21.090 | 1.574 | 17.430 | 11.773 | 0.543 | 15.36 | 82.510 |
| Sakha 108 | 17.22 | 18.99 | 24.610 | 1.423 | 19.283 | 15.490 | 0.525 | 13.98 | 77.700 |
| Sakha 109 | 16.88 | 17.93 | 20.987 | 1.350 | 22.320 | 14.923 | 0.493 | 14.40 | 65.220 |
| GZ 10101-5-1-1-1 | 10.90 | 14.90 | 13.027 | 1.490 | 19.763 | 12.773 | 0.548 | 19.99 | 66.700 |
| AR 278-41-1-1-6-3 | 7.84 | 11.84 | 10.747 | 1.410 | 27.277 | 26.920 | 0.527 | 23.12 | 51.123 |
| IHL 180 | 8.89 | 12.89 | 11.700 | 1.949 | 28.280 | 23.333 | 0.589 | 24.19 | 54.907 |
| IHL 185 | 9.54 | 13.54 | 12.317 | 1.373 | 26.310 | 21.420 | 0.654 | 26.16 | 60.243 |
| IHL 249 | 9.52 | 13.52 | 10.830 | 1.938 | 27.463 | 21.050 | 0.436 | 22.29 | 58.073 |
| IHL 296 | 9.70 | 13.70 | 10.090 | 1.837 | 25.980 | 19.457 | 0.775 | 16.53 | 56.373 |
| Giza 178/IHL 180 | 24.36 | 15.04 | 21.360 | 1.487 | 20.320 | 12.440 | 0.537 | 17.40 | 78.667 |
| Giza 178/IHL 185 | 22.51 | 15.69 | 20.590 | 1.823 | 23.647 | 11.800 | 0.498 | 16.66 | 75.427 |
| Giza 178/IHL 249 | 19.61 | 14.71 | 18.987 | 2.023 | 26.763 | 10.533 | 0.541 | 18.10 | 67.157 |
| Giza 178/IHL 296 | 18.94 | 14.45 | 19.347 | 1.667 | 20.467 | 14.627 | 0.571 | 15.43 | 60.560 |
| Sakha 104/IHL 180 | 12.10 | 14.32 | 18.257 | 1.303 | 18.773 | 15.573 | 0.517 | 20.76 | 90.463 |
| Sakha 104/IHL 185 | 14.23 | 15.43 | 18.397 | 1.627 | 30.250 | 16.510 | 0.566 | 18.81 | 85.083 |
| Sakha 104/IHL 249 | 20.46 | 18.08 | 18.803 | 1.330 | 21.363 | 15.017 | 0.539 | 17.46 | 61.743 |
| Sakha 104/IHL 296 | 17.60 | 17.44 | 19.350 | 1.397 | 23.693 | 18.057 | 0.594 | 16.40 | 77.290 |
| Sakha 108/IHL 180 | 23.07 | 15.15 | 15.697 | 1.387 | 19.683 | 13.860 | 0.539 | 17.08 | 76.373 |
| Sakha 108/IHL 185 | 19.83 | 16.10 | 22.173 | 1.703 | 23.067 | 19.293 | 0.539 | 19.73 | 85.223 |
| Sakha 108/IHL 249 | 20.48 | 15.98 | 18.743 | 1.667 | 21.120 | 16.597 | 0.571 | 20.65 | 91.983 |
| Sakha 108/IHL 296 | 18.63 | 15.39 | 20.953 | 1.437 | 25.083 | 11.660 | 0.504 | 15.27 | 54.580 |
| Sakha 109/IHL 180 | 17.58 | 16.61 | 21.560 | 1.757 | 22.737 | 16.917 | 0.587 | 15.49 | 67.563 |
| Sakha 109/IHL 185 | 22.57 | 18.62 | 23.380 | 1.447 | 30.193 | 15.750 | 0.589 | 15.32 | 55.620 |
| Sakha 109/IHL 249 | 19.37 | 17.06 | 18.763 | 1.553 | 18.493 | 14.080 | 0.618 | 16.48 | 68.557 |
| Sakha 109/IHL 296 | 19.39 | 15.74 | 18.553 | 1.663 | 22.697 | 15.333 | 0.584 | 18.25 | 76.453 |
| GZ10101-5-1-1-1/IHL180 | 22.14 | 16.57 | 22.220 | 1.650 | 21.240 | 13.587 | 0.576 | 15.59 | 57.783 |
| GZ10101-5-1-1-1/IHL185 | 21.44 | 18.28 | 23.607 | 1.673 | 20.490 | 12.877 | 0.580 | 16.11 | 55.327 |
| GZ10101-5-1-1-1/IHL249 | 22.45 | 19.05 | 20.950 | 1.777 | 22.443 | 14.977 | 0.555 | 16.69 | 63.247 |
| GZ10101-5-1-1-1/IHL296 | 14.29 | 14.07 | 21.877 | 1.815 | 16.470 | 14.373 | 0.471 | 17.40 | 61.987 |
| AR27841-1-1-63/IHL180 | 16.56 | 15.02 | 22.707 | 1.673 | 21.090 | 14.813 | 0.503 | 18.39 | 77.403 |
| AR27841-1-1-63/IHL185 | 22.00 | 14.09 | 18.977 | 1.897 | 24.437 | 18.243 | 0.444 | 21.56 | 85.590 |
| AR27841-1-1-63/IHL249 | 17.78 | 16.87 | 20.520 | 1.907 | 25.053 | 16.437 | 0.486 | 17.34 | 62.110 |
| AR27841-1-1-63/IHL296 | 20.75 | 17.93 | 18.737 | 1.577 | 24.483 | 14.693 | 0.494 | 18.05 | 88.333 |
| LSD 0.05 | 2.01 | 0.99 | 1.446 | 0.149 | 1.521 | 1.615 | 0.018 | 1.11 | 1.665 |
| LSD 0.01 | 2.66 | 1.32 | 1.917 | 0.198 | 2.017 | 2.141 | 0.023 | 1.47 | 2.207 |

**CAT: Catalase (mmol $min^{-1}$ $g^{-1}$ protein), POX: Peroxidase (mmol $min^{-1}$ $g^{-1}$ protein), SOD: Superoxide dismutase (mmol $min^{-1}$ $g^{-1}$ protein), Proline (µg $g^{-1}$ FW), MDA: Malondialdehyde (mmol $g^{-1}$ FW), $H_2O_2$: Hydrogen peroxide (mmol $g^{-1}$ FW), Stomatal conductance (mmol $m^{-2}$ $s^{-1}$), Leaf transpiration rate (mmol $H_2O$ $m^{-2}$ $s^{-1}$), RWC: Relative water content**

Giza 178/IHL 249 showed the highest maximum values of leaf-free proline accumulation (2.023) compared with other parental genotypes and a highly decreased concentration of leaf $H_2O_2$ among the hybrids. For lipid peroxidation content (MDA), the combination GZ 10101-5-1-1-1/IHL 296 revealed a desirable decreased content among the studied genotypes. As for stomatal conductance and transpiration rate, the cross combinations Sakha 109/IHL 249 and AR 278-41-1-6-3/IHL 185 reported the highest mean values, respectively. Additionally, regarding the RWC, the hybrid Sakha 108/IHL 249 showed the maximum mean performance values of 91.983 followed by the combination Sakha 104/IHL 180 compared with other parental genotypes under the saline field.

Salinity stress has a considerable negative impact on rice biomass, as well as on shoot and root lengths and seed germination rates, ultimately hindering plant growth (Luo *et al.,* 2022). Furthermore, the detrimental effects on plant growth and biomass are more severe under salt stress compared to normal conditions. This phenomenon may be attributed to elevated levels of $Na^+$, MDA, and $H_2O_2$, which compromise chloroplast membrane integrity and lead to the degradation of the protein-pigment-lipid complex (Mushtaq *et al.,* 2022). The data presented in the aforementioned Table illustrate the activities of antioxidant enzymes such as CAT, POX, and SOD in various rice genotypes. In this context, Abdallah *et al.* (2020) noted that an increase in antioxidant enzyme activity can serve as an indicator of heightened reactive oxygen species (ROS) production, which stimulates protective mechanisms aimed at mitigating oxidative damage resulting from plant responses to stress. The current findings are corroborated by the research conducted by Zayed *et al.* (2023) and Khan *et al.* (2024).

During the flowering stage, the accumulation of proline in the initial leaves and developing panicles of the examined genotypes was assessed to explore a possible correlation with tolerance. Salt stress notably elevated proline levels in the first leaves across all genotypes, with a marked increase observed in the salt-tolerant varieties. It has been extensively documented that proline serves as a protective function against oxidative damage induced by NaCl in various plant species (Bhusan *et al.,* 2016). Proline is recognized for its role in safeguarding subcellular structures and facilitating osmotic adjustment during stress conditions (Rao *et al.,* 2013). Additionally, proline exhibits multifunctional properties, including protection against oxidative damage (Hoque *et al.,* 2008). The obtained results align with previous findings that indicate tolerant genotypes synthesize higher levels of proline when subjected to salt stress (Zayed *et al.,* 2023 and 2024). In this investigation, the concentrations of malondialdehyde (MDA) and hydrogen peroxide ($H_2O_2$) displayed significant variability among the rice genotypes under salinity stress, with the parental genotype Giza 178, followed by Sakha 104, demonstrating lower levels of MDA and $H_2O_2$ among the parental lines. In contrast, the salt-sensitive rice cultivars exhibited increased levels of hydrogen peroxide ($H_2O_2$) and malondialdehyde (MDA) under salinity stress. MDA serves as an indicator of biological membrane damage, as it is the primary byproduct of the degradation of unsaturated fatty acids resulting from oxidative stress at 200 mM NaCl (Abu-Muriefah, 2015).

**Agro-morphological, yield and yield-related traits**

As seen in Table 4B, the most favorable mean values for the traits of days to flowering and plant height are the lowest. The parental lines Sakha 109 and Sakha 104 recorded the lowest mean values of 93.67 days and 81.33 cm for flowering and plant height traits among lines and testers, respectively. The most $F_1$ hybrid combinations coveted mean values towards earliness were obtained from GZ10101-5-1-1-1/IHL 249 which gave the lowest mean values of 93.00 days to flowering trait. While the hybrid combination Sakha 109/IHL 249 had the lowest mean values among all the studied genotypes for plant height trait under saline field. Concerning the tillers number, panicles number, and panicle length traits, the parental variety Giza 178 among lines and testers recorded the highest mean values of 23.64, 20.93, and 20.17 cm, respectively. Conversely, the hybrid combination Giza 178/IHL 185 exhibited the highest mean values of 33.11 and 31.14 for the number of tillers and panicles number traits compared to other genotypes studied. For grain yield plant$^{-1}$ the hybrid combination Sakha 104/IHL 296 exhibited the highest mean value (51.54 g). For the panicle length trait, the hybrids Giza 178/IHL 180 and Sakha 104/IHL 180 gave the highest mean values of 22.83 cm.

Regarding the panicle weight, the new line IHL 185 recorded the highest mean values of 2.94 g among lines and testers. In comparison, the combination Sakha 104/IHL 180 showed the highest mean values of 3.50 g under the saline effect among all the studied genotypes for the same trait. For the spikelets fertility percentage, the two parental genotypes, AR 278-41-1-1-6-3 and Giza 178 recorded the highest mean values of 90.41 and 89.16%, respectively. In this concern, the two hybrid combinations Sakha 104/IHL 249 and GZ 10101-5-1-1-1/IHL 249 recorded the highest mean values of 95.34 and 93.53%, respectively. As regards the 1000-grain weight traits, the mean values of the parental genotypes among lines and testers showed that Sakha 108 and Sakha 109 exhibited the highest 1000-grain weight with mean values of 26.74 and 25.87 g, respectively. In the meantime, the hybrid combination GZ 10101-5-1-1-1/IHL 185 gave the highest 1000-grain weight (27.89 g) for the same trait. For grain yield plant$^{-1}$, among lines and testers, the new introgression line IHL 249 recorded the highest mean values of 40.77 g. The highest mean values were observed in the hybrid combination Sakha 104/IHL 296 with mean values of 51.54 g, followed by the mean value of 50.88 g for the hybrid combination Sakha 104/IHL 249.

In this research, genotypes that exhibit salt tolerance demonstrated superior yields in comparison to those that are susceptible to salt. A primary goal for rice breeders is to create varieties that possess high salinity tolerance, significant yield potential, and other favorable agronomic characteristics. The findings from the experiment indicated a reduction in yield and yield-related traits, which directly or indirectly influence yield, including plant height, tiller count, panicle count, and panicle length. The new introgression parental line IHL 249 and the cross-combination Sakha 104/IHL 296 displayed the least impact from salinity stress regarding grain yield per plant, while more pronounced negative effects of salinity were noted in other genotypes. The observed decline in growth may be attributed to the accumulation of toxic NaCl in the soil surrounding the roots, leading to an imbalance in nutrient uptake by the seedlings, which aligns with previous studies (Efisue and Igoma, 2019; Negm *et al.,* 2023; Zheng *et al.,* 2023; Zayed *et al.,* 2024).

**Table 4B. Mean values of lines, testers, and hybrids concerning morphological, yield and yield-related traits of rice genotypes**

| Genotype | Days to flowering (day) | Plant height (cm) | No of tillers | No of panicles | Panicle length (cm) | Panicle weight (g) | Spikelets fertility (%) | 1000-grain weight (g) | Grain yield plant$^{-1}$ (g) |
|---|---|---|---|---|---|---|---|---|---|
| Giza 178 | 99.33 | 91.33 | 23.64 | 20.93 | 20.17 | 2.68 | 89.16 | 18.87 | 40.52 |
| Sakha 104 | 101.00 | 81.33 | 18.05 | 16.56 | 18.83 | 2.66 | 86.74 | 25.74 | 35.05 |
| Sakha 108 | 104.67 | 84.33 | 16.78 | 15.61 | 18.50 | 2.63 | 84.09 | 26.74 | 32.55 |
| Sakha 109 | 93.67 | 84.00 | 17.78 | 15.00 | 18.33 | 2.58 | 84.94 | 25.87 | 30.14 |
| GZ 10101-5-1-1-1 | 96.33 | 90.00 | 12.89 | 12.19 | 17.83 | 2.76 | 84.50 | 25.80 | 26.84 |
| AR 278-41-1-1-6-3 | 101.67 | 98.67 | 16.56 | 12.94 | 18.17 | 4.19 | 90.41 | 20.66 | 38.48 |
| IHL 180 | 104.00 | 97.33 | 16.46 | 12.80 | 18.17 | 2.72 | 85.57 | 22.60 | 26.24 |
| IHL 185 | 107.67 | 85.00 | 19.17 | 16.06 | 16.00 | 2.94 | 74.40 | 24.11 | 33.61 |
| IHL 249 | 103.67 | 90.00 | 21.94 | 21.05 | 18.67 | 2.67 | 85.77 | 24.11 | 40.77 |
| IHL 296 | 106.33 | 92.67 | 20.30 | 18.94 | 19.17 | 2.26 | 70.78 | 23.96 | 37.89 |
| Giza 178/IHL 180 | 100.67 | 109.33 | 27.67 | 25.67 | 22.83 | 2.39 | 46.67 | 23.48 | 45.38 |
| Giza 178/IHL 185 | 100.67 | 114.67 | 33.11 | 31.14 | 19.50 | 2.97 | 55.43 | 23.96 | 50.09 |
| Giza 178/IHL 249 | 101.00 | 105.33 | 28.17 | 26.00 | 22.33 | 1.83 | 31.41 | 24.53 | 43.80 |
| Giza 178/IHL 296 | 103.00 | 122.33 | 27.75 | 24.78 | 22.17 | 2.49 | 39.29 | 25.52 | 50.76 |
| Sakha 104/IHL 180 | 111.00 | 108.67 | 19.11 | 17.36 | 22.83 | 3.50 | 77.82 | 22.49 | 46.16 |
| Sakha 104/IHL 185 | 103.67 | 104.00 | 20.72 | 19.22 | 20.33 | 3.43 | 87.99 | 26.59 | 45.99 |
| Sakha 104/IHL 249 | 103.67 | 90.00 | 24.78 | 23.28 | 17.33 | 2.99 | 95.34 | 26.98 | 50.88 |
| Sakha 104/IHL 296 | 110.67 | 100.67 | 21.13 | 19.91 | 21.17 | 2.90 | 77.85 | 21.91 | 51.54 |
| Sakha 108/IHL 180 | 105.67 | 97.00 | 16.30 | 15.00 | 20.50 | 2.66 | 68.91 | 21.65 | 31.53 |
| Sakha 108/IHL 185 | 103.33 | 103.33 | 16.89 | 16.11 | 21.67 | 3.31 | 62.93 | 27.56 | 37.83 |
| Sakha 108/IHL 249 | 103.00 | 101.33 | 16.38 | 15.22 | 20.33 | 2.95 | 79.89 | 24.76 | 35.30 |
| Sakha 108/IHL 296 | 106.33 | 96.00 | 17.20 | 16.79 | 21.50 | 2.51 | 81.91 | 23.42 | 34.30 |
| Sakha 109/IHL 180 | 99.00 | 91.67 | 19.13 | 16.17 | 17.83 | 3.28 | 90.19 | 24.62 | 38.06 |
| Sakha 109/IHL 185 | 98.00 | 91.33 | 15.46 | 14.31 | 18.67 | 2.74 | 71.07 | 27.02 | 31.60 |
| Sakha 109/IHL 249 | 93.67 | 79.33 | 21.56 | 20.72 | 17.83 | 2.49 | 87.31 | 25.64 | 44.17 |
| Sakha 109/IHL 296 | 94.67 | 92.67 | 20.86 | 17.66 | 18.17 | 2.86 | 86.57 | 27.50 | 44.36 |
| GZ 10101-5-1-1-1/IHL 180 | 98.33 | 95.67 | 17.67 | 16.86 | 17.50 | 3.09 | 88.81 | 22.84 | 34.49 |
| GZ 10101-5-1-1-1/IHL 185 | 96.00 | 96.00 | 18.94 | 17.33 | 19.17 | 2.96 | 88.65 | 27.89 | 42.64 |
| GZ 10101-5-1-1-1/IHL 249 | 93.00 | 88.00 | 20.50 | 19.11 | 18.00 | 3.05 | 93.53 | 27.39 | 43.47 |
| GZ 10101-5-1-1-1/IHL 296 | 93.67 | 96.00 | 17.50 | 16.78 | 16.83 | 2.99 | 93.01 | 27.09 | 41.79 |
| AR 278-41-1-1-6-3/IHL 180 | 102.67 | 128.00 | 19.50 | 18.11 | 20.00 | 2.98 | 41.86 | 25.75 | 44.22 |
| AR 278-41-1-1-6-3/IHL 185 | 103.67 | 115.67 | 27.00 | 24.33 | 19.67 | 3.44 | 34.58 | 26.23 | 49.71 |
| AR 278-41-1-1-6-3/IHL 249 | 95.67 | 116.00 | 20.17 | 19.67 | 20.67 | 2.65 | 49.39 | 24.88 | 42.34 |
| AR 278-41-1-1-6-3/IHL 296 | 103.67 | 119.33 | 21.28 | 20.58 | 21.17 | 2.83 | 32.90 | 24.23 | 49.82 |
| LSD 0.05 | 1.43 | 3.69 | 1.88 | 1.40 | 1.35 | 0.21 | 3.91 | 1.21 | 2.49 |
| LSD 0.01 | 1.89 | 4.89 | 2.49 | 1.85 | 1.79 | 0.28 | 5.19 | 1.60 | 3.31 |

*** Significant at 0.05 level and ** Significant at 0.01 level**

### Variances assessment of combining ability

### General combining ability (GCA) effects

The general combining ability effects of antioxidative and physiological activities are exhibited in Table 5A. Among the studied lines and testers under a saline field environment, the parental line Giza 178 was observed to have good GCA effects and desirable direction for CAT activity and leaf $H_2O_2$ concentration, followed by the parental line Sakha 108, and the new line IHL 185 which recorded highly significant and positive GCA effects for CAT activity. The parental line Sakha 109 exhibited a good general combiner under saline conditions among the lines for POX activity and stomatal conductance. While among testers in the same conditions, the new introgression line IHL 249 showed a highly positive desirable effect for the POX activity, Leaf proline content, and stomatal conductance. For leaf proline content, parental line AR 278-41-1-1-6-3 exhibited a good general combiner followed by GZ 10101-5-1-1-1 and Giza 178 among the lines. On the contrary, the negative effects are desirable for MDA. Among the studied lines and testers, GZ 10101-5-1-1-1 followed by the genotype Sakha 108 recorded significant positive GCA effects. The parental line Giza 178, Sakha 109, GZ 10101-5-1-1-1 and IHL 296 recorded a desirable effect and best general combiners for transpiration rate. The genotype Sakha 104 followed by AR 278-41-1-1-6-3 were identified as good general combiners for RWC among the lines while among the testers the new line IHL 180 followed by the new line IHL 185 showed a highly positive desirable effect.

For the genetic worth of parents, the general combing ability effects of morphological, yield and yield-related traits were consolidated in Table 5B. The negative estimates of GCA effects are desirable for earliness and medium dwarf plant height. Among the studied lines and testers under saline environments, the parental lines GZ 10101-5-1-1-1 and Sakha 109 were observed to have good GCA effects and desirable direction for days to flowering and plant height traits, followed by the parental line Sakha 108 and Sakha 104 for plant height trait, which recorded significant and negative GCA effects. While, among testers in the same conditions the new introgression line IHL 249 showed a high negative desirable general combiner effect for both days to flowering and plant height traits. Concerning the number of tillers plant$^{-1}$ and number of panicles plant$^{-1}$, the parental genotypes Giza 178, IHL 249 and IHL 185 were the best general combiners for both traits. For panicle length, parental line Giza 178, Sakha 108 and Sakha 104 exhibited a good general combiner saline field among the lines and testers. The parental promising line GZ 10101-5-1-1-1 had highly significant GCA effects for panicle weight, spikelets fertility percentage, and 1000-grain weight traits among the lines. In the same direction, the new genotype IHL 185 of the testers was identified as a good general combiner among testers for panicle weight, and 1000-grain weight while the new introgression line IHL 249 a potential parent also had the highly significant GCA effect of spikelets fertility percentage trait under saline conditions. Furthermore, the new introgression line IHL 296 was good combiner for grain yield plant$^{-1}$

**Table 5A. General combining ability for antioxidative activities and physiological traits of parental lines genotypes**

| Genotype | CAT | POX | SOD | Leaf free proline | MDA | Leaf $H_2O_2$ | Stomatal conductance | Transpiration rate | RWC (%) |
|---|---|---|---|---|---|---|---|---|---|
| Giza 178 | 1.85** | -1.18** | -0.12 | 0.12** | 0.13 | -2.57** | -0.0053 | -0.62** | -1.40** |
| Sakha 104 | -3.41** | 0.16 | -1.49** | -0.22** | 0.85** | 1.37** | 0.0122** | 0.84** | 6.79** |
| Sakha 108 | 1.00** | -0.50** | -0.80** | -0.09** | -0.43* | 0.43 | -0.0034 | 0.67** | 5.18** |
| Sakha 109 | 0.22 | 0.85** | 0.38 | -0.03 | 0.86** | 0.60* | 0.0527** | -1.13** | -4.81** |
| GZ 10101-5-1-1-1 | 0.57 | 0.84** | 1.98** | 0.09** | -2.51** | -0.97** | 0.0038 | -1.07** | -12.27** |
| AR 278-41-1-1-6-3 | -0.23 | -0.18 | 0.05 | 0.13** | 1.10** | 1.13** | -0.0601** | 1.32** | 6.50** |
| LSD 0.05 | 0.71 | 0.35 | 0.51 | 0.05 | 0.54 | 0.57 | 0.0062 | 0.39 | 0.59 |
| LSD 0.01 | 0.94 | 0.47 | 0.68 | 0.07 | 0.71 | 0.76 | 0.0083 | 0.52 | 0.78 |
| IHL 180 | -0.20 | -0.70** | 0.11 | -0.09** | -2.03** | -0.39 | 0.0014 | -0.07 | 2.85** |
| IHL 185 | 0.93** | 0.21 | 1.00** | 0.06** | 2.68** | 0.83** | -0.0058* | 0.51** | 1.86** |
| IHL 249 | 0.52 | 0.81** | -0.73** | 0.07** | -0.13 | -0.31 | 0.0100** | 0.27 | -2.72** |
| IHL 296 | -1.24** | -0.32* | -0.39* | -0.04* | -0.52* | -0.13 | -0.0056* | -0.72** | -1.99** |
| LSD 0.05 | 0.54 | 0.27 | 0.39 | 0.04 | 0.41 | 0.43 | 0.0047 | 0.30 | 0.44 |
| LSD 0.01 | 0.71 | 0.35 | 0.51 | 0.05 | 0.54 | 0.57 | 0.0063 | 0.39 | 0.59 |

**CAT: Catalase (mmol min$^{-1}$ g$^{-1}$ protein), POX: Peroxidase (mmol min$^{-1}$ g$^{-1}$ protein), SOD: Superoxide dismutase (mmol min$^{-1}$ g$^{-1}$ protein), Proline (µg g$^{-1}$ FW), MDA: Malondialdehyde (mmol g$^{-1}$ FW), $H_2O_2$: Hydrogen peroxide (mmol g$^{-1}$ FW), Stomatal conductance (mmol m$^{-2}$ s$^{-1}$), Leaf transpiration rate (mmol $H_2O$ m$^{-2}$ s$^{-1}$), RWC: Relative water content. Which * Significant at 0.05 level and ** Significant at 0.01 level**

**Table 5B. General combining ability for morphological, yield and yield-related traits of rice genotypes**

| Genotype | Days to flowering (day) | Plant height (cm) | No of tillers | No of panicles | Panicle length (cm) | Panicle weight (g) | Spikelets fertility (%) | 1000-grain weight (g) | Grain yield plant$^{-1}$ (g) |
|---|---|---|---|---|---|---|---|---|---|
| Giza 178 | 0.31 | 10.32** | 7.98** | 7.22** | 1.79** | -0.466** | -26.11** | -0.79** | 4.58** |
| Sakha 104 | 6.22** | -1.76* | 0.24 | 0.27 | 0.50* | 0.319** | 15.45** | -0.67** | 5.72** |
| Sakha 108 | 3.56** | -3.18** | -4.51** | -3.89** | 1.08** | -0.032 | 4.11** | -0.82** | -8.19** |
| Sakha 109 | -4.69** | -13.85** | -1.95** | -2.46** | -1.79** | -0.043 | 14.48** | 1.03** | -3.38** |
| GZ 10101-5-1-1-1 | -5.78** | -8.68** | -2.55** | -2.15** | -2.04** | 0.136** | 21.70** | 1.14** | -2.33** |
| AR 278-41-1-1-6-3 | 0.39 | 17.15** | 0.79* | 1.00** | 0.46 | 0.086* | -29.62** | 0.11 | 3.60** |
| LSD 0.05 | 0.50 | 1.303 | 0.66 | 0.49 | 0.48 | 0.076 | 1.38 | 0.43 | 0.88 |
| LSD 0.01 | 0.67 | 1.728 | 0.88 | 0.66 | 0.63 | 0.101 | 1.83 | 0.57 | 1.17 |
| IHL 180 | 1.86** | 2.46** | -1.30** | -1.48** | 0.33 | 0.096** | -0.26 | -1.69** | -2.95** |
| IHL 185 | -0.14 | 1.57** | 0.82** | 0.74** | -0.08 | 0.257** | -2.53** | 1.38** | 0.05 |
| IHL 249 | -2.69** | -5.93** | 0.73** | 1.00** | -0.50** | -0.229** | 3.51** | 0.54** | 0.40 |
| IHL 296 | 0.97** | 1.90** | -0.25 | -0.25 | 0.25 | -0.124** | -0.72 | -0.22 | 2.50** |
| LSD 0.05 | 0.38 | 0.99 | 0.50 | 0.37 | 0.36 | 0.057 | 1.05 | 0.32 | 0.67 |
| LSD 0.01 | 0.51 | 1.31 | 0.67 | 0.50 | 0.48 | 0.076 | 1.39 | 0.43 | 0.88 |

*** Significant at 0.05 level and ** Significant at 0.01 level**

The nature and magnitude of combining ability effects provide guidelines for identifying better parents and their utilization. Our findings are consistent with earlier research indicating that different parental genotypes exhibited varying responses to salinized environments concerning physiological, antioxidative, and yield processes (Negm *et al.,* 2023; Zayed *et al.,* 2023). It could be noticed from the results mentioned above that none of the parents possessed beneficial genes for all traits under investigation. Therefore, multiple crossings among these parents would be desirable to obtain superior recombinants with desired traits in addition to grain yield. Furthermore, they could be beneficial contributors in a program involving hybridization or multiple crossings to produce high-yielding hybrid varieties, or in the process of choosing transgressive segregates to create pure line varieties through background selection. Hence, simultaneous improvement for yield, yield component, and other associated traits are possible and very important for enhancing yield potential in rice under salt-stress environments.

**Specific combining ability (SCA) effects**

Estimates of SCA effects of the $F_1$ crosses for antioxidative and physiological activities were presented in Table 6A. Nine hybrid combinations exhibited significant and highly desirable SCA effects on CAT activity. In addition, eight hybrids were found to be substantial desirable SCA effects on POX activity, while for SOD, seven crosses gave significant and highly significant positive SCA effects. Three hybrid combinations Sakha 109/IHL 185, Sakha 104/IHL 296, and Giza 178/IHL 180 were good specific combiners for antioxidative activities such as CAT, POX, and SOD under saline stress conditions. For leaf proline content, four hybrid combinations showed significant and highly significant desirable SCA effects, the highest significant SCA effects in the desired direction were exhibited by the combination Sakha 109/IHL 180. Furthermore, it was found that nine crosses were additionally highly and negatively significant desirable SCA effects on MDA concentration. For leaf $H_2O_2$ concentration, five hybrid combinations were found to have the desired SCA effects. Under saline conditions, the two cross-combinations GZ 10101-5-1-1-1/IHL 185 and Giza 178/IHL 185 are good specific combiners for both MDA and $H_2O_2$ concentrations. Six hybrid combinations exhibited significant and highly desirable positive SCA effects on stomatal conductance, and six crosses were found to be significant desirable and highly significant negative SCA effects on transpiration rate. In addition, it was observed that twelve hybrid combinations recorded highly desirable significant SCA effects for RWC percent. None of the additional crosses, except for Sakha 108/IHL 249, showed significant desirable SCA effects for stomatal conductance, and RWC under a saline field environment.

**Table 6A. Specific combining ability for antioxidative activities and physiological traits of the hybrid combinations genotypes**

| Hybrid | CAT | POX | SOD | Leaf free proline | MDA | Leaf $H_2O_2$ | Stomatal conductance | Transpiration rate | RWC (%) |
|---|---|---|---|---|---|---|---|---|---|
| Giza 178/IHL 180 | 3.21** | 0.77* | 1.18* | -0.17** | -0.45 | 0.48 | -0.001 | 0.57 | 5.36** |
| Giza 178/IHL 185 | 0.23 | 0.50 | -0.48 | 0.01 | -1.83** | -1.38* | -0.033** | -0.75 | 3.12** |
| Giza 178/IHL 249 | -2.26** | -1.07** | -0.36 | 0.20** | 4.09** | -1.50* | -0.006 | 0.93* | -0.57 |
| Giza 178/IHL 296 | -1.18 | -0.20** | -0.34 | -0.04 | -1.81** | 2.40** | 0.040** | -0.75 | -7.90** |
| Sakha 104/IHL 180 | -3.79** | -1.30** | -0.56 | -0.02 | -2.72** | -0.33 | -0.038** | 2.47** | 8.96** |
| Sakha 104/IHL 185 | -2.79** | -1.10** | -1.30* | 0.15** | 4.05** | -0.61 | 0.018** | -0.06 | 4.58** |
| Sakha 104/IHL 249 | 3.84** | 0.96** | 0.83 | -0.16** | -2.03** | -0.96 | -0.025** | -1.16** | -14.18** |
| Sakha 104/IHL 296 | 2.74** | 1.44** | 1.03* | 0.02 | 0.69 | 1.90** | 0.046** | -1.24** | 0.63 |
| Sakha 108/IHL 180 | 2.77** | 0.20 | -3.81** | -0.07 | -0.53 | -1.11 | -0.001 | -1.04** | -3.52** |
| Sakha 108/IHL 185 | -1.59* | 0.23 | 1.78** | 0.09 | -1.85** | 3.11** | 0.007 | 1.03* | 6.33** |
| Sakha 108/IHL 249 | -0.54 | -0.48 | 0.08 | 0.04 | -0.99 | 1.56** | 0.023** | 2.20** | 17.67** |
| Sakha 108/IHL 296 | -0.63 | 0.05 | 1.95** | -0.07 | 3.37** | -3.56** | -0.028** | -2.19** | -20.47** |
| Sakha 109/IHL 180 | -1.94** | 0.30 | 0.88 | 0.24** | 1.24* | 1.78** | -0.009 | -0.83* | -2.34** |
| Sakha 109/IHL 185 | 1.92** | 1.40** | 1.82** | -0.22** | 3.99** | -0.60 | 0.001 | -1.58** | -13.28** |
| Sakha 109/IHL 249 | -0.88 | -0.75* | -1.07* | -0.13* | -4.91** | -1.13 | 0.014** | -0.18 | 4.23** |
| Sakha 109/IHL 296 | 0.90 | -0.95** | -1.63** | 0.10 | -0.31 | -0.06 | -0.005 | 2.58** | 11.39** |
| GZ 10101-5-1-1-1/IHL 180 | 2.26** | 0.28 | -0.06 | 0.01 | 3.11** | 0.02 | 0.029 | -0.79* | -4.66** |
| GZ 10101-5-1-1-1/IHL 185 | 0.43 | 1.07** | 0.44 | -0.12* | -2.35** | -1.90** | 0.040** | -0.85* | -6.12** |
| GZ 10101-5-1-1-1/IHL 249 | 1.85* | 1.25** | -0.49 | -0.03 | 2.41** | 1.34* | 0.001 | -0.03 | 6.38** |
| GZ 10101-5-1-1-1/IHL 296 | -4.55** | -2.60** | 0.10 | 0.13* | -3.17** | 0.55 | -0.069** | 1.67** | 4.39** |
| AR 278-41-1-1-6-3/IHL 180 | -2.51** | -0.25 | 2.36** | 0.01 | -0.65 | -0.85 | 0.020** | -0.38 | -3.81** |
| AR 278-41-1-1-6-3/IHL 185 | 1.80* | -2.11** | -2.26** | 0.07 | -2.01** | 1.37* | -0.032** | 2.21** | 5.37** |
| AR 278-41-1-1-6-3/IHL 249 | -2.01** | 0.09 | 1.01 | 0.07 | 1.42* | 0.70 | -0.005 | -1.76** | -13.53** |
| AR 278-41-1-1-6-3/IHL 296 | 2.72** | 2.27** | -1.11** | -0.14** | 1.24* | -1.23* | 0.018** | -0.07 | 11.96** |
| LSD 0.05 | 1.42 | 0.70 | 1.02 | 0.11 | 1.08 | 1.14 | 0.012 | 0.78 | 1.18 |
| LSD 0.01 | 1.88 | 0.93 | 1.36 | 0.14 | 1.43 | 1.51 | 0.017 | 1.04 | 1.56 |

**CAT: Catalase (mmol $min^{-1}$ $g^{-1}$ protein), POX: Peroxidase (mmol $min^{-1}$ $g^{-1}$ protein), SOD: Superoxide dismutase (mmol $min^{-1}$ $g^{-1}$ protein), Proline (µg $g^{-1}$ FW), MDA: Malondialdehyde (mmol $g^{-1}$ FW), $H_2O_2$: Hydrogen peroxide (mmol $g^{-1}$ FW), Stomatal conductance (mmol $m^{-2}$ $s^{-1}$), Leaf transpiration rate (mmol $H_2O$ $m^{-2}$ $s^{-1}$), RWC: Relative water content. Which * Significant at 0.05 level and ** Significant at 0.01 level**

The specific combining ability of the twenty-four crosses for the morphological, yield and yield components traits are presented in Table 6B. Six cross combinations showed highly significant and negative significant desirable SCA effects for days to flowering. Furthermore, it was discovered that six hybrids had negative and highly significant desirable SCA effects on plant height. For plant height, number of tillers plant$^{-1}$, and number of panicles plant$^{-1}$ traits, the cross-combination Sakha 104/IHL 249 is an excellent specific combiner under the same saline condition. In contrast, the hybrid combination AR 278-41-1-1-6-3/IHL 185 is a good specific combiner with highly significant desirable SCA effects for the traits of plant height, number of tillers plant$^{-1}$, number of panicles number plant$^{-1}$, and panicle weight. For the number of tillers plant$^{-1}$ and panicles plant$^{-1}$ traits, four hybrid combinations were found to be positive significant and highly significant SCA effects. For panicle length, two hybrid combinations showed positive and highly significant SCA effects while the panicle weight trait exhibited positive significant and highly significant SCA effects by eight hybrid combinations. Eight crosses were found to have positive and significant SCA effects for spikelets fertility percentage. The 1000-grain weight trait exhibited positive and highly significant SCA effects by six-hybrid combinations. According to the data above, the hybrid combinations Giza 178/IHL 185, Sakha 108/IHL 185, Sakha 109/IHL 249, GZ 10101-5-1-1-1/IHL 249 and AR 278-41/IHL 185 showed a highly significant and desired SCA effect for grain yield$^{-1}$. A good specific combiner with highly desirable SCA effects for the traits of spikelet fertility percentage, 1000-grain weight, and grain yield plant$^{-1}$ under saline stress conditions is the hybrid combination Sakha 104/IHL 249.

According to numerous study findings, hybrid combinations involving at least one parent with a high GCA, mean performance and desirable SCA estimates would be considered favorable allele combinations. Undoubtedly, a high SCA indicates a high heterotic response, however, this could also be attributed to the parents' relative performance to that of their hybrids. With the same heterotic effect, the SCA may be less, where the mean performance of the parents was higher, but this estimate may also be biased (Jaiswal and Patel, 2018). This suggested that the selection of cross combinations based on a heterotic response would be more realistic rather than based on SCA effects. In addition, most cross-combinations involved high/low or average/low gene interactions that substantiate the non-additive gene action activity for the expression of these traits. The findings of Selvaraj *et al.,* (2011); Devi *et al.,* (2017); Ghidan *et al.,* (2019); Abo-Yousef *et al.,* (2020); Ghidan and Khedr, (2021); Negm *et al.,* (2023) Claimed similar results these results.

**Table 6B. Specific combining ability for morphological, yield and yield-related traits of rice genotypes**

| Hybrid | Days to flowering (day) | Plant height (cm) | No of tillers | No of panicles | Panicle length (cm) | Panicle weight (g) | Spikelets fertility (%) | 1000-grain weight (g) | Grain yield plant$^{-1}$ (g) |
|---|---|---|---|---|---|---|---|---|---|
| Giza 178/IHL 180 | -2.53** | -6.04** | -0.20 | 0.25 | 0.79 | -0.125 | 3.73** | 0.80 | 0.83 |
| Giza 178/IHL 185 | -0.53 | 0.18 | 3.11** | 3.51** | -2.13** | 0.296** | 14.76** | -1.79** | 2.53** |
| Giza 178/IHL 249 | 2.36** | -1.65 | -1.73* | -1.89** | 1.13 | -0.364** | -15.30** | -0.37 | -4.11** |
| Giza 178/IHL 296 | 0.69 | 7.51** | -1.18 | -1.86** | 0.21 | 0.193* | -3.20* | 1.36** | 0.75 |
| Sakha 104/IHL 180 | 1.89** | 5.38** | -1.02 | -1.10* | 2.08** | 0.201** | -6.67** | -0.31 | 0.47 |
| Sakha 104/IHL 185 | -3.44** | 1.60 | -1.54* | -1.46** | 0.00 | -0.029 | 5.77** | 0.72 | -2.70** |
| Sakha 104/IHL 249 | -0.89 | -4.90** | 2.62** | 2.34** | -2.58** | 0.009 | 7.08** | 1.95** | 1.84* |
| Sakha 104/IHL 296 | 2.44** | -2.07 | -0.06 | 0.22 | 0.50 | -0.181* | -6.18** | -2.37** | 0.39 |
| Sakha 108/IHL 180 | -0.78 | -4.88** | 0.91 | 0.69 | -0.83 | -0.295** | -4.24** | -1.00* | -0.26 |
| Sakha 108/IHL 185 | -1.11* | 2.35 | -0.62 | -0.41 | 0.75 | 0.198* | -7.95** | 1.83** | 3.04** |
| Sakha 108/IHL 249 | 1.11* | 7.85** | -1.04 | -1.55** | -0.17 | 0.321** | 2.97* | -0.12 | 0.16 |
| Sakha 108/IHL 296 | 0.78 | -5.32** | 0.75 | 1.27* | 0.25 | -0.224** | 9.22** | -0.71 | -2.94** |
| Sakha 109/IHL 180 | 0.81 | 0.46 | 1.18 | 0.43 | -0.63 | 0.340** | 6.67** | 0.11 | 1.46 |
| Sakha 109/IHL 185 | 1.81** | 1.01 | -4.61** | -3.64** | 0.63 | -0.358** | -10.18** | -0.55 | -8.00** |
| Sakha 109/IHL 249 | 0.03 | -3.49** | 1.58* | 2.51** | 0.21 | -0.121 | 0.02 | -1.09* | 4.22** |
| Sakha 109/IHL 296 | -2.64** | 2.01 | 1.86** | 0.70 | -0.21 | 0.139 | 3.50* | 1.53** | 2.31* |
| GZ 10101-5-1-1-1/IHL 180 | 1.22* | -0.71 | 0.32 | 0.82 | -0.71 | -0.029 | -1.93 | -1.77** | -3.16** |
| GZ 10101-5-1-1-1/IHL 185 | 0.89 | 0.51 | -0.53 | -0.92 | 1.38** | -0.318** | 0.18 | 0.21 | 2.00* |
| GZ 10101-5-1-1-1/IHL 249 | 0.44 | 0.01 | 1.12 | 0.59 | 0.63 | 0.253** | -0.98 | 0.55 | 2.47** |
| GZ 10101-5-1-1-1/IHL 296 | -2.56** | 0.18 | -0.91 | -0.49 | -1.29** | 0.093 | 2.73 | 1.01* | -1.31 |
| AR 278-41-1-1-6-3/IHL 180 | -0.61 | 5.79** | -1.18 | -1.09* | -0.71 | -0.092 | 2.44 | 2.17** | 0.65 |
| AR 278-41-1-1-6-3/IHL 185 | 2.39** | -5.65** | 4.19** | 2.92** | -0.62 | 0.211** | -2.58 | -0.42 | 3.14** |
| AR 278-41-1-1-6-3/IHL 249 | -3.06** | 2.18 | -2.55** | -2.00** | 0.79 | -0.098 | 6.20** | -0.93* | -4.59** |
| AR 278-41-1-1-6-3/IHL 296 | 1.28* | -2.32 | -0.46 | 0.16 | 0.54 | -0.020 | -6.06** | -0.82 | 0.79 |
| LSD 0.05 | 1.01 | 2.61 | 1.33 | 0.99 | 0.95 | 0.152 | 2.77 | 0.85 | 1.76 |
| LSD 0.01 | 1.34 | 3.46 | 1.76 | 1.31 | 1.26 | 0.201 | 3.67 | 1.13 | 2.34 |

*** Significant at 0.05 level and ** Significant at 0.01 level**

### Evaluation of heterobeltiosis

The heterotic responses of hybrids over heterobeltiosis for antioxidative and physiological activities are presented in Table 7A. The cross combinations Sakha 109/IHL 185, GZ 10101-5-1-1-1/IHL 185, and AR 278-41-1-1-6-3/IHL 185 showed the highly significant and desirable positive SCA effect heterobeltiosis in the study of antioxidant enzyme activity and leaf-free proline accumulation.

**Table 7A. Heterobeltiosis estimates for antioxidative activities and physiological traits of the hybrid combinations genotypes**

| Hybrid | CAT | POX | SOD | Leaf free proline | MDA | Leaf $H_2O_2$ | Stomatal conductance | Transpiration rate | RWC (%) |
|---|---|---|---|---|---|---|---|---|---|
| Giza 178/IHL 180 | 31.75** | -10.76** | -6.44** | -23.71** | 20.71** | 11.27** | -8.89** | 20.11** | -5.60** |
| Giza 178/IHL 185 | 21.74** | -6.90** | -9.81** | 6.63** | 40.48** | 5.55** | -23.81** | 14.95** | -9.49** |
| Giza 178/IHL 249 | 6.06** | -12.74** | -16.83** | 4.40** | 58.99** | -5.78** | -6.46** | 24.89** | -19.41** |
| Giza 178/IHL 296 | 2.42* | -14.26** | -15.26** | -9.26** | 21.58** | 30.83** | -26.37** | 6.46** | -27.33** |
| Sakha 104/IHL 180 | -31.90** | -20.28** | -13.43** | -33.12** | 7.71** | 32.28** | -12.17** | 35.11** | 9.64** |
| Sakha 104/IHL 185 | -19.94* | -14.08** | -12.77** | 3.35** | 73.55** | 40.23** | -13.41** | 22.41** | 3.12** |
| Sakha 104/IHL 249 | 15.10** | 0.65 | -10.84** | -31.37** | 22.57** | 27.55** | -0.80** | 13.65** | -25.17** |
| Sakha 104/IHL 296 | -0.99 | -2.93** | -8.25** | -23.96** | 35.93** | 53.37** | -23.31** | 6.75** | -6.33** |
| Sakha 108/IHL 180 | 33.93** | -20.21** | -36.22** | -28.84** | 2.07** | -10.52** | -8.55** | 22.17** | -1.71* |
| Sakha 108/IHL 185 | 15.15** | -15.21** | -9.90** | 19.67** | 19.62** | 24.55** | -17.49** | 41.13** | 9.68** |
| Sakha 108/IHL 249 | 18.91** | -15.82** | -23.84** | -14.00** | 9.52** | 7.14** | 8.89** | 47.69** | 18.38** |
| Sakha 108/IHL 296 | 8.17** | -18.96** | -14.86** | -21.78** | 30.08** | -24.73** | -34.92** | 9.25** | -29.76** |
| Sakha 109/IHL 180 | 4.15** | -7.40** | 2.73** | -9.85** | 1.87* | 13.36** | -0.28** | 7.55** | 3.59** |
| Sakha 109/IHL 185 | 33.70** | 3.85** | 11.40** | 5.37** | 35.27** | 5.54** | -9.89** | 6.39** | -14.72** |
| Sakha 109/IHL 249 | 14.73** | -4.87** | -10.59** | -19.85** | -17.14** | -5.65** | 25.51** | 14.42** | 5.12** |
| Sakha 109/IHL 296 | 14.85** | -12.23** | -11.59** | -9.44** | 1.69* | 2.75** | -24.69** | 26.74** | 17.22** |
| GZ 10101-5-1-1-1/IHL 180 | 103.15** | 11.23** | 70.57** | -15.33** | 7.47** | 6.37** | -2.15** | -22.02** | -13.37** |
| GZ 10101-5-1-1-1/IHL 185 | 96.73** | 22.69** | 81.22** | 12.30** | 3.68** | 0.81 | -11.22** | -19.42** | -17.05** |
| GZ 10101-5-1-1-1/IHL 249 | 106.00** | 27.90** | 60.82** | -8.32** | 13.56** | 17.25** | 1.28** | -16.52** | -5.18** |
| GZ 10101-5-1-1-1/IHL 296 | 31.11** | -5.53** | 67.94** | -1.18** | -16.66** | 12.53** | -39.27** | 5.24** | -7.07** |
| AR 278-41-1-1-6-3/IHL 180 | 86.35** | 16.58** | 94.07** | -14.16** | -22.68** | -36.51** | -14.54** | -20.46** | 40.97** |
| AR 278-41-1-1-6-3/IHL 185 | 130.65** | 4.06** | 54.07** | 34.52** | -7.12** | -14.83** | -32.13** | -6.76** | 42.07** |
| AR 278-41-1-1-6-3/IHL 249 | 86.83** | 24.81** | 89.47** | -1.62** | -8.15** | -21.92** | -7.72** | -22.21** | 6.95** |
| AR 278-41-1-1-6-3/IHL 296 | 113.88** | 30.90** | 74.35** | -14.16** | -5.76** | -24.48** | -36.30** | 9.17** | 56.69** |
| LSD 0.05 | 2.005 | 0.994 | 1.446 | 0.149 | 1.52 | 1.61 | 0.018 | 1.11 | 1.665 |
| LSD 0.01 | 2.659 | 1.319 | 1.917 | 0.198 | 2.02 | 2.14 | 0.023 | 1.47 | 2.207 |

**CAT: Catalase (mmol min$^{-1}$ g$^{-1}$ protein), POX: Peroxidase (mmol min$^{-1}$ g$^{-1}$ protein), SOD: Superoxide dismutase (mmol min$^{-1}$ g$^{-1}$ protein), Proline (µg g$^{-1}$ FW), MDA: Malondialdehyde (mmol g$^{-1}$ FW), $H_2O_2$: Hydrogen peroxide (mmol g$^{-1}$ FW), Stomatal conductance (mmol m$^{-2}$ s$^{-1}$), Leaf transpiration rate (mmol $H_2O$ m$^{-2}$ s$^{-1}$), RWC: Relative water content. Which * Significant at 0.05 level and ** Significant at 0.01 level**

Twenty hybrid combinations revealed significant and highly desirable effects over heterobeltiosis for CAT activity. In contrast, four hybrid combinations showed heterobeltiosis effects for POX and six hybrid combinations for SOD activity were desirable. Negative heterosis was desirable for MDA and leaf $H_2O_2$ concentrations, the negative and highly significant heterobeltiosis were found in the five cross combinations Sakha 109/IHL 249, AR 278-41-1-1-6-3/IHL 180, AR 278-41-1-1-6-3/IHL 185, AR 278-41-1-1-6-3/IHL 249 and AR 278-41-1-1-6-3/IHL 296. Six of the hybrid combinations exhibited the most serious negative heterobeltiosis for transpiration rate. The positive and highly significant heterobeltiosis for the stomatal conductance were found in the three cross combinations Sakha 109/IHL 249, Sakha 108/IHL 249 and GZ 10101-5-1-1-1/IHL 249. Twelve hybrid combinations were found to be highly significant and desirable positive heterobeltiosis effects for RWC percentage.

Heterobeltiosis morphological, yield and yield-related traits are presented in Table 7B. Negative heterobeltiosis was desirable for days to flowering and plant height but positive Heterobeltiosis was desirable for the remaining studied traits. The negative and highly significant heterobeltiosis for the days to flowering and plant height were found in the cross-combinations AR278-41-1-1-6-3/IHL 249 and Sakha 109/IHL 249 whereas two hybrid combinations exhibited negative significant heterobeltiosis effects desirable for days to flowering trait. For the number of tillers plant$^{-1}$ and the number of panicles plant$^{-1}$, highly significant and positive heterobeltiosis was exhibited in thirteen hybrid combinations. In addition, regards panicle length out of 24 cross combinations, seventeen hybrid combinations recorded positive, highly significant heterobeltiosis effects. It was observed that the hybrid combinations Giza 178/IHL 180 and Sakha 104/IHL 296 showed a highly significant and desirable positive heterobeltiosis effect in the study of number of tillers plant$^{-1}$, the number of panicles plant$^{-1}$ and panicle length traits under saline field conditions. Whereas, the cross combinations Sakha 104/IHL 185, Sakha 104/IHL 249, and Sakha 109/IHL 180 exhibited a highly significant heterobeltiosis effect for tillers number plant$^{-1}$ and the number of panicles plant$^{-1}$ under the same conditions.

**Table 7B. Heterobeltiosis estimates for morphological, yield and yield-related traits of rice genotypes**

| Hybrid | Days to flowering (day) | Plant height (cm) | No of tillers | No of panicles | Panicle length (cm) | Panicle weight (g) | Spikelets fertility (%) | 1000-grain weight (g) | Grain yield plant$^{-1}$ (g) |
|---|---|---|---|---|---|---|---|---|---|
| Giza 178/IHL 180 | 1.34 | 19.71** | 17.03** | 22.63** | 13.22** | -12.14** | -47.66** | 3.91** | 12.01** |
| Giza 178/IHL 185 | 1.34 | 34.90** | 40.06** | 48.77** | -3.31** | 1.25** | -37.83** | -0.65 | 23.62** |
| Giza 178/IHL 249 | 1.68* | 17.04** | 19.15** | 23.50** | 10.74** | -31.69** | -64.78** | 1.75** | 7.44** |
| Giza 178/IHL 296 | 3.69** | 33.94** | 17.39** | 18.38** | 9.92** | -6.93** | -55.94** | 6.49** | 25.27** |
| Sakha 104/IHL 180 | 9.90** | 33.61** | 5.87** | 4.85** | 21.24** | 28.67** | -10.28** | -12.65** | 31.70** |
| Sakha 104/IHL 185 | 2.64** | 27.87** | 8.12** | 16.09** | 7.96** | 16.91** | 1.44 | 3.30** | 31.23** |
| Sakha 104/IHL 249 | 2.64** | 10.66** | 12.93** | 10.56** | -7.96** | 11.63** | 9.91** | 4.80** | 24.82** |
| Sakha 104/IHL 296 | 9.57** | 23.77** | 4.06** | 5.09** | 10.43** | 9.21** | -10.25** | -14.90** | 36.03** |
| Sakha 108/IHL 180 | 1.60* | 15.02** | -2.82** | -3.91** | 10.81** | -2.45** | -19.46** | -19.05** | -3.13* |
| Sakha 108/IHL 185 | -1.27 | 22.53** | -11.88** | 0.33 | 17.12** | 12.68** | -25.16** | 3.03** | 12.55** |
| Sakha 108/IHL 249 | -0.64 | 20.16** | -25.37** | -27.69** | 8.93** | 10.15** | -6.86** | -7.41** | -13.41** |
| Sakha 108/IHL 296 | 1.59* | 13.83** | -15.30** | -11.35** | 12.17** | -4.55** | -2.59 | -12.44** | -9.47** |
| Sakha 109/IHL 180 | 5.69** | 9.13** | 7.59** | 7.78** | -2.73** | 20.48** | 5.40** | -4.83** | 26.27** |
| Sakha 109/IHL 185 | 4.63** | 8.73** | -19.34** | -10.90** | 1.82** | -6.63** | -16.33** | 4.47** | -5.97** |
| Sakha 109/IHL 249 | 0.00 | -5.56** | -1.76 | -1.58* | -4.46** | -6.78** | 1.80 | -0.86 | 8.35** |
| Sakha 109/IHL 296 | 1.07 | 10.32** | 2.74** | -6.79** | -5.22** | 10.69** | 1.91 | 6.33** | 17.08** |
| GZ 10101-5-1-1-1/IHL 180 | 2.08** | 6.30** | 7.33** | 31.71** | -3.67** | 12.01** | 3.79 | -11.50** | 28.49** |
| GZ 10101-5-1-1-1/IHL 185 | -0.35 | 12.94** | -1.17 | 7.95** | 7.48** | 0.86** | 4.91* | 8.08** | 26.88** |
| GZ 10101-5-1-1-1/IHL 249 | -3.46** | -2.22 | -6.59** | -9.23** | -3.57** | 10.43** | 9.05** | 6.15** | 6.63** |
| GZ 10101-5-1-1-1/IHL 296 | -2.77** | 6.67** | -13.81** | -11.42** | -12.17** | 8.46** | 10.07** | 4.98** | 10.29** |
| AR 278-41-1-1-6-3/IHL 180 | 0.98 | 31.51** | 17.78** | 39.92** | 10.09** | -28.95** | -53.70** | 13.95** | 14.92** |
| AR 278-41-1-1-6-3/IHL 185 | 1.97** | 36.08** | 40.87** | 51.55** | 8.26** | -17.89** | -61.76** | 8.80** | 29.19** |
| AR 278-41-1-1-6-3/IHL 249 | -5.90** | 28.89** | -8.10** | -6.59** | 10.71** | -36.87** | -45.37** | 3.20** | 3.85** |
| AR 278-41-1-1-6-3/IHL 296 | 1.97** | 28.78** | 4.81** | 8.66** | 10.43** | -32.47** | -63.61** | 1.14 | 29.47** |
| LSD 0.05 | 1.43 | 3.69 | 1.88 | 1.40 | 1.35 | 0.21 | 3.91 | 1.21 | 2.49 |
| LSD 0.01 | 1.89 | 4.89 | 2.49 | 1.86 | 1.79 | 0.28 | 5.19 | 1.60 | 3.31 |

*** Significant at 0.05 level and ** Significant at 0.01 level**

The maximum highly significant and positive heterobeltiosis for the panicle weight was found in a hybrid combination of Sakha 104/IHL 180, it was also shown that twelve hybrids had a highly significant desirable heterobeltiosis effect for the same trait. Five cross combinations were found to have positive significant and highly significant heterobeltiosis effects for spikelets fertility percentage. Furthermore, the cross combinations Sakha 104/IHL 249 and Sakha 109/IHL 180 recorded highly significant heterobeltiosis effects for panicle weight and spikelets fertility percentage traits. A positive highly significant heterobeltiosis effect was observed in 1000-grain weight in fourteen crosses. The maximum highly significant and positive heterobeltiosis for the grain yield plant$^{-1}$ was found in hybrid Sakha 104/IHL 296 under saline conditions. However, the two cross combinations Giza 178/IHL 180 and Sakha 104/IHL 185 showed high positive heterobeltiosis effects for 1000-grain weight and grain yield plant$^{-1}$ under the same conditions. In this investigation, none of the hybrids exhibited the most serious heterobeltiosis for yield and all yield-related traits but the hybrid combination Sakha 104/IHL 249 exhibited a highly significant heterobeltiosis effect for yield and yield components for all the studied traits except the panicle length trait followed by the cross-combination Sakha 109/IHL 180. In addition, the hybrid combinations Giza 178/IHL 180, Sakha 104/IHL 185, and Sakha 104/IHL 296 were found to have highly significant heterobeltiosis effects for most yield and its related traits under saline field conditions.

The presence of a wide spectrum of heterobeltiosis in either direction with expression of a high degree of desirable heterosis by some crosses for all the traits observed in the present study is consistent with previous reports reporting the presence of high heterosis for such traits in rice (Ghidan and Khedr, 2021; El-Agoury *et al.,* 2023). It was also noted that higher heterosis over better-parent was found in some low-yielding crosses when compared to other crosses that displayed high yield. This suggested that while selecting the best hybrid, besides the heterotic response over the better parent, the mean performance of the crosses should also be given due consideration (Vanave *et al.,* 2018; Singh *et al.,* 2019; Negm *et al.,* 2023).

**Genetic parameters of variance**

The estimates of genetic parameters were computed for the traits studied of 24 crosses and their ten parents in Tables 8A, and 8B. The results above suggested the significance of both additive and non-additive gene effects for agronomic traits. The non-additive ($\sigma^2$D) gene effect due to parental line interactions was found to be highly significant for antioxidative, physiological, morphological yield and yield-related traits, representing the importance of specific combining ability (SCA) and non-additive gene action.

**Table 8A. Genetic parameters estimations for antioxidative activities and physiological traits**

| Genetic parameter | CAT | POX | SOD | Leaf free proline | MDA | Leaf $H_2O_2$ | Stomatal conductance | Transpiration rate | RWC (%) |
|---|---|---|---|---|---|---|---|---|---|
| Additive variance ($\sigma^2$A) | 0.078 | 0.025 | 0.079 | 0.002 | 0.177 | 0.135 | 0.0001 | 0.03 | 1.52 |
| Dominant variance ($\sigma^2$D) | 8.271 | 1.942 | 2.962 | 0.020 | 9.618 | 3.428 | 0.0012 | 2.86 | 133.38 |
| $\sigma^2$A/ $\sigma^2$D | 0.009 | 0.013 | 0.027 | 0.108 | 0.018 | 0.039 | 0.1010 | 0.01 | 0.01 |
| Contribution of Lines | 30.82 | 24.48 | 32.08 | 45.81 | 14.39 | 42.01 | 58.17 | 31.15 | 35.18 |
| Contribution of Testers | 7.60 | 15.07 | 11.76 | 14.00 | 27.27 | 5.32 | 2.21 | 7.00 | 4.16 |
| Contribution of L/T | 61.59 | 60.44 | 56.16 | 40.19 | 58.35 | 52.67 | 39.62 | 61.85 | 60.65 |
| Broad sense heritability ($h^2$b%) | 84.71 | 84.14 | 79.50 | 72.16 | 91.86 | 78.47 | 91.60 | 86.20 | 99.24 |
| Narrow sense heritability ($h^2$n%) | 0.79 | 1.06 | 2.06 | 7.01 | 1.66 | 2.98 | 8.41 | 0.74 | 1.12 |

**CAT: Catalase (mmol min$^{-1}$ g$^{-1}$ protein), POX: Peroxidase (mmol min$^{-1}$ g$^{-1}$ protein), SOD: Superoxide dismutase (mmol min$^{-1}$ g$^{-1}$ protein), Proline (µg g$^{-1}$ FW), MDA: Malondialdehyde (mmol g$^{-1}$ FW), $H_2O_2$: Hydrogen peroxide (mmol g$^{-1}$ FW), Stomatal conductance (mmol m$^{-2}$ s$^{-1}$), Leaf transpiration rate (mmol $H_2O$ m$^{-2}$ s$^{-1}$), RWC: Relative water content**

**Table 8B. Genetic parameters estimations for morphological, yield and yield-related traits of rice genotypes**

| Genetic parameter | Days to flowering (day) | Plant height (cm) | No of tillers | No of panicles | Panicle length (cm) | Panicle weight (g) | Spikelets fertility (%) | 1000-grain weight (g) | Grain yield plant$^{-1}$ (g) |
|---|---|---|---|---|---|---|---|---|---|
| Additive variance ($\sigma^2$A) | 3.013 | 18.50 | 2.32 | 1.99 | 0.25 | 0.01 | 62.63 | 0.19 | 3.87 |
| Dominant variance ($\sigma^2$D) | 4.782 | 22.87 | 5.16 | 4.36 | 1.52 | 0.07 | 69.93 | 2.19 | 12.32 |
| $\sigma^2$A/ $\sigma^2$D | 0.630 | 0.81 | 0.45 | 0.46 | 0.16 | 0.15 | 0.90 | 0.08 | 0.31 |
| Contribution of Lines | 74.61 | 80.68 | 78.86 | 77.52 | 62.95 | 41.02 | 89.32 | 19.94 | 67.68 |
| Contribution of Testers | 12.22 | 8.41 | 3.69 | 5.55 | 3.33 | 25.31 | 1.03 | 37.06 | 10.22 |
| Contribution of L/T | 13.17 | 10.91 | 17.45 | 16.93 | 33.73 | 33.67 | 9.65 | 43.00 | 22.10 |
| Broad sense heritability ($h^2$b%) | 91.09 | 89.03 | 84.94 | 89.65 | 72.20 | 82.46 | 95.85 | 81.29 | 87.41 |
| Narrow sense heritability ($h^2$n%) | 35.21 | 39.81 | 26.35 | 28.07 | 10.09 | 10.97 | 45.29 | 6.35 | 20.88 |

Line × tester interaction contributed to combinations variances were found much more than lines and testers, individually. The contributions of the lines to leaf-free proline, stomatal conductance, days to flowering, plant height, number of tillers plant$^{-1}$, number of panicles plant$^{-1}$, panicle length, panicle weight, spikelets fertility percentage and grain yield plant$^{-1}$ were defined as highest to line × tester interaction. The contributions of testers were found lower than those of line × tester interactions for all traits. Thus, line × tester interactions provide much more variation in the appearance of the traits. It is noteworthy that hybrid combinations had higher values than their parents concerning CAT, POX, SOD, MDA, leaf $H_2O_2$, RWC, and 1000-grain weight traits.

In the current study, under saline field conditions, all the traits under investigation demonstrated high heritability in a broad sense. Therefore, these traits can be used to directly select for future genotype improvements under appropriate environments to increase grain yield and improve tolerance to salt stress. Under the same conditions, low narrow-sense heritability has been found among each trait, suggesting that non-additive gene effects are a major factor regulating the traits.

The reduced narrow-sense heritability was linked to minimal additive gene effects and significant dominance gene influence, as noted by Gholizadeh *et al.* (2014). If these traits are incorporated into a selection strategy aimed at enhancing fixable genetic variance, a widely accepted genotype can be developed. The improvement of characteristics such as high heritability and moderate to low genetic advancement can be achieved by merging superior genotypes from segregating populations that arise from combination breeding, as indicated by Garg *et al.* (2017). The results imply that advancements in these traits can be realized in subsequent generations through the selection of individual plants, followed by hybridization or intermixing of the chosen segregates via recurrent selection. Similar observations have been reported by Abo-Yousef *et al.* (2020) and Ghidan and Khedr (2021).

## CONCLUSION

The current study results indicate significant variability among the genotypes of rice under investigation concerning the traits related to yield, physiological processes, and developmental growth. It could be conducted to use the genotypes Giza 178, Sakha 104, IHL 185, IHL 249, and IHL 296 as a genetic resource for these traits or to combine these physiological traits with some elite high-yielding rice genotypes to enhance salinity tolerance. The appearance of the studied traits could change significantly according to line x tester interactions. Catalase, peroxidase, superoxide dismutase, malondialdehyde, hydrogen peroxide, relative water content, and 1000-grain weight traits were noted to have higher values in hybrid combinations than in their parents. This study demonstrates how the variability and diversity of the identified donors can be used to develop new rice genotypes that can survive in saline environments and could be useful for trait-based breeding. Furthermore, we believe that future research should focus on organizing genes from various genetic resources, such as wild rice relatives, in order to recover salinity tolerance traits lost during domestication.

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## الاختلافات الوراثية للصفات المورفوفسيولوجيه والمحصول وصفاته المرتبطة تحت بيئة الحقل الملحية لسلالات الأرز خلال تحليل السلالة*الكشاف

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### الملخص

يواجه الأرز العديد من عوامل الإجهاد البيئي أثناء النمو بسبب التحديات التي يفرضها تغير المناخ العالمي، والذي يشكل خطرًا كبيرًا على الإنتاجية والتطور الكلي. تعتبر الملوحة من أخطر عوامل الإجهاد البيئي التي تؤثر بشكل كبير على استقرار المحصول. تم تقييم أربعة وعشرين هجينًا تم إنشاؤها من تهجين ستة أمهات مع أربعة آباء قيمت هذه الهجن جنبًا إلى جنب مع آبائهم لمعرفة الاختلافات في الصفات الفسيولوجية والمحصولية في ظل ظروف الحقل الملحية. لوحظ أن التباين بين التراكيب الوراثية كان كبيرا، وكان حجم تباين السيادة أعلى من التباين المضيف لجميع الصفات، مما يكشف عن غلبة عمل الجينات غير المضيفة. تم تحديد السلالة GZ 10101-5-1-1-1 كتركيب وراثى جيد محتمل لمحتوى البيروكسيديز، وفوق أكسيد ديسميوتاز ، والبرولين، والمالونديالدهيد، وبيروكسيد الهيدروجين. وعلاوة على ذلك، وجد أن جيزة 178، وسخا 104، و3-6-1-1-41-278 AR، و185 IHL كانت لديها قدره عامة فعالة لتحسين محصول الحبوب. في برنامج تربية الأرز لتحمل الملوحة، سيتم استخدام أفضل التهجينات الواعدة للحصول على سلالات متفوقة ذات خصائص فسيولوجية وإنتاجية مميزة. أظهرت ثلاث هجن وهي جيزة IHL 180/178، وسخا IHL 296/104، وسخا IHL 185/109 تأثيرات جينات سيادة بالنسبة لنشاط إنزيمات مضادات الأكسدة. تم اعتبار الهجين Sakha 104/IHL 249 ذو قدرة خاصة على الائتلاف للمحصول وبعض الصفات المرتبطة به. لوحظت زيادة كبيرة في نسبة قوه الهجين الإيجابية لنشاط إنزيم مضادات الأكسدة، والمالونديالدهيد، وتركيزات بيروكسيد الهيدروجين بواسطة الهجين AR 278-41-1-1-6-3/IHL 185. بالإضافة إلى ذلك، وجد أن التركيبات الهجينة جيزة IHL 180/178، وسخا IHL 185/104، وسخا IHL 296/104 لها تأثيرات كبيرة في نسبة قوة الهجين متفوقًا على الأب الأفضل للمحصول والصفات المرتبطة به في بيئة حقلية مالحة.

***الكلمات الدالة*** : الأرز، الملوحة، قوه الهجين، المحصول.