

Inheritance of some biochemical, morpho-physiological and yield attributes trait of some rice genotypes under salinity condition

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ABSTRACT

Rice is one of the most significant staple crops consumed by the majority of people, but salinity is one of the limiting factors affecting its productivity. The goal of this study was to find genotypes tolerant to salinity and improve the population in salinity breeding programs. Furthermore, the significance of biochemical and physiological traits to an adaptation of growth and yield for nine rice genotypes and their twenty F₁ crosses according to the line tester mating design was investigated during the 2021 and 2022 rice growing seasons at the El-Sirw Agricultural Research Station experimental farm, Damietta governorate, Egypt. These studies revealed the differential behavior of all genotypes. IRRI 147, Sakha 104 and IR 59673-93-2-3-3R were found to be good general combiners for the majority of the studied traits, maintaining a lower Na⁺/K⁺ ratio, less reduction in plant pigments, higher concentrations of reduced ascorbate, and higher proline content. The hybrids of Giza 177/IRRI 147, Sakha 104/Sakha super 300, Sakha 106/IR 59673-93-2-3-3R, and Sakha 107/IR 59673-93-2-3-3R recorded significant positive SCA effects for some physiological traits and grain yield plant⁻¹. The highly significant and positive heterobeltiosis was observed for grain yield plant⁻¹ by hybrid combinations; Sakha 104/Sakha super 300, Sakha 104/IRRI 147, and Giza 177/IRRI 147 recorded the highest values of heterobeltiosis, indicating the superiority of these crosses under salinity conditions and suggesting they may be widely used in rice programs by adopting a breeding approach.

Keywords: Rice, salinity, biochemical, physiological traits, combining ability, heterosis, genetic parameters.

INTRODUCTION

Rice holds a special place in many nations, due to its significance in traditional meals and its status as the primary source of income for numerous people around the world. It is regarded as the second-most significant field crop in Egypt for a staple food after wheat. Furthermore, 50% of the cultivated rice area in Egypt is salt-affected soil in which rice production is dramatically restricted and it needs more improvement (Zayed *et al.*, 2019). Whereas, increasing climate change-related increases in biotic and abiotic stresses, as well as increased competition for precious resources such as land and water, must be overcome in order to achieve this goal. Drought, high salinity, cold, and heat are some of the abiotic stresses that rice plants must contend with as they grow in a constantly changing environment (Zhu, 2016). Rice cultivation is hampered by salt stress, which lowers grain yield and makes the great majority of arable land useless. The challenge of salt stress, which is carried on by natural occurrences and poor irrigation and drainage facilities, is expected to get worse as a result of the many effects of climate change (Wassmann *et al.*, 2009).

In rice production, salt stress is most problematic when it occurs at the early seedling and reproductive growth stages. Salt stress in the early seedling stage is as essential since it determines the final crop stand and grain output, even while salt stress in the reproductive stage directly reduces yield. The evaluation of germplasm is challenging in the field since salt stress manifests itself heterogeneously. In order to breed self-pollinated and cross-pollinated crops, as well as to determine the favorable parents and crosses, besides their general and specific combining abilities, the line x tester analysis method is applied (Aslam *et al.*, 2014; Rahaman, 2016). The success of a plant breeding program greatly depends on the right choice of parents for hybridization and the gene action of

different economic traits. In terms of the expected performance of the hybrids and their offspring, combining ability provides useful information on the choice of parents, according to Patial *et al.*, (2016). Per se Performances do not necessarily reveal which parents are good or poor combiners. Therefore, gathering information on the nature of gene effects and their expression in terms of combining ability is necessary. Combining ability identifies potentially superior parents and hybrids, which helps to describe the pattern of gene effects in the expression of quantitative traits (Zhang *et al.*, 2015). General Combining Ability (GCA) is theoretically fixable and is related to additive gene effects and additive and/or additive epistasis. On the other hand, Specific Combining Ability (SCA) is caused by non-additive gene effects, including dominance, epistasis, or both (Koze, 2017). The presence of non-additive genetic variance is the primary justification for initiating the hybrid program (Pradhan *et al.*, 2006). The preponderance of non-additive gene action in the expression of yield and yield-related traits was reported by Thirumalai *et al.*, (2018) and Ghidan *et al.*, (2019).

Line x tester design is the best analysis for estimating GCA, SCA, and various types of gene actions (Fahmied *et al.*, 2018). Breeding rice varieties to overcome salinity stress is the most promising, least resource-consuming, economically viable, and socially acceptable approach. Salt tolerance is a polygenic trait that allows plants to grow and maintain an economic yield in the presence of non-physiologically high and relatively constant levels of salt. The importance of developing genotypes that are tolerant to salinity with increased yield will be useful. To establish a yield improvement program in rice, performance information, the combining ability effects of parents and hybrids, and the magnitude of gene action involved in the inheritance of quantitative traits are important (Gopikannan and Ganesh, 2013). Salts affect plant growth due to increased soil osmotic pressure, thus interfering with plant nutrition. A high salt concentration in soil solution reduces the ability of plants to acquire water, which is referred to as the osmotic or water deficit effect of salinity. Damage occurs when the concentration is high enough to begin reducing crop growth. A two-phase model was proposed to depict the response of plant growth to salinity (Imolehin and Wada, 2000). The first phase is very rapid, and growth reduction is ascribed to the development of a water deficit. The second phase is due to the accumulation of salts in the shoot at toxic levels and is very slow. Salinity affects photosynthesis by decreasing CO₂ availability as a result of diffusion limitations (FAO, 2000) and a reduction of the contents of photosynthetic pigments (Ghidan and Khedr, 2021). The present research work was carried out with the objectives of assessing combining ability based on mean performance, genetic components for morphological, biochemical, physiological, and yield traits, and their related traits in rice to help in the selection of parents and assist in the choice of breeding strategies for the improvement of salinity tolerance in rice.

MATERIALS AND METHODS

The present investigation was carried out under salinity condition at El-Sirw Agricultural Research Station experimental farm, Damietta governorate during 2022 rice growing season. The nine rice genotypes listed in **Table (1)** were planted during 2021 rice growing season at Rice Research Department at the experimental farm, Sakha Agricultural Research Station, Kafr El-Sheikh, Egypt. Five genotypes; Giza 177, Sakha 104, Sakha 106, Sakha 107, and Sakha 108 were used as lines, while four rice genotypes; Sakha super 300, GZ 6296-12-1-2-1-1, IR 59673-93-2-3-3R and IRRI 147 were used as testers to produce F₁ generations. The parental genotypes were grown in four planting dates with a time difference of up to 15 days to overcome the differences in flowering among parents. Thirty-day-old seedlings of each parent were individually transplanted in the field in five rows. Each row is 5 m long and includes 25 hills. At flowering time, a hybridization process among parents was conducted and the mentioned twenty crosses were produced in the summer season of 2021. In the 2022 season, seeds of parents and their twenty crosses were sown in the nursery, and seedlings were transplanted after 30 days from sowing in a Randomized Complete Block Design (RCBD), with three replicates under salinity conditions at El-Sirw Agricultural Research Station. Each cross consisted of three rows for parent and their F₁, the row was five meters in length with 20cm between rows and hills. All recommended agriculture practices for growing rice production in the salt-affected soil were applied at El-Sirw Agricultural Research Station experimental farm, Damietta governorate. The morphological, physiological, and yield attributes were estimated on these genotypes.

Table 1. The origin, type and salinity tolerance reaction of studied genotypes.

No	Genotypes	Type	Origin	Salinity tolerance
1	Giza 177	Japonica	Egypt	Sensitive
2	Sakha 104	Japonica	Egypt	Moderate
3	Sakha 106	Japonica	Egypt	Sensitive
4	Sakha 107	Japonica	Egypt	Sensitive
5	Sakha 108	Japonica	Egypt	Sensitive
6	Sakha super300	Japonica	Egypt	Tolerant
7	GZ 6296-12-1-2-1-1	Indica/Japonica	Egypt	Moderate
8	IR 59673-93-2-3-3R	Indica	IRRI	Tolerant
9	IRRI 147	Indica/Japonica	IRRI	Tolerant

Soil analysis:

Before land preparation, soil samples were randomly taken at a depth of 0-20 cm from the soil surface, mixed, and then transported to the laboratory, dried, and ground to fine particles. The chemical analysis was carried out using the soil extract 1:5 to estimate the soluble anions and cations. The soil EC and pH were measured in a 1:5 soil-water solution using pH and EC meters. The soil analysis was determined based on the methods of Chapman and Parker (1961). The chemical analysis of the experiment was listed as shown in Table (2).

Table2. Chemical analysis for soil at El Sirw Agricultural Research Station.

pH (1:2.5 soil water suspension)	EC (1:5 soil water extraction)	Soluble cations meq.l ⁻¹ (soil paste):				Soluble anions meq.l ⁻¹ (soil paste):		
		Ca ⁺⁺	Mg ⁺⁺	K ⁺	Na ⁺	HCO ₃ ⁻	Cl ⁻	SO ₄ ⁻⁻
8.25	8.54	8.25	5.34	2.36	53.12	8.53	50.96	9.58

Collected data:

For yield and its attributes, data were recorded prior harvest, twenty plants were taken randomly from the parents and F₁ crosses from each replicate to determine the yield and its components traits. At harvest, each plant was harvested individually. Furthermore, the physiological traits were taken from flag leaf at heading of each genotype in three replications.

Measured traits:

The following traits were measured for parental lines and their F₁ hybrid combinations under salinity conditions.

A- Morphological traits: According to Standard Evaluation System (SES) scores for phenotyping for salinity tolerance at the reproductive Stage (Mondal and Borromeo, 2016), days to heading, Plant height (cm) and Panicle length (cm) were investigated.

B- Physiological traits: these traits measured from flag leaf as follow:

Ascorbic acid (AsA): (mg/g fresh weight): AsA contents were assayed according to the method of Mostofaet *al.*, (2015). The Glutathione contents (GSH) (mg/g fresh weight): were calculated as described by Griffith (1980). Photosynthetic pigments (mg/g fresh weight): Total chlorophyll a and b and carotenoid contents in fresh leaves were estimated according to Lichtenthaler and Buschmann (2001). Trehalose (µg/g fresh weight): Trehalose content was extracted according to Lynch *et al.* (2010). For trehalose quantitation, the anthrone reaction was used based on (Umbreit *et al.*, 1972). Proline determination (mg/g fresh weight): Proline was assayed according to the method described by Bates *et al.* (1973). Sodium (Na⁺) and Potassium (K⁺) content (mg/g fresh weight): Sodium and potassium contents were measured using the method elaborated by Flowers and Yeo (1986). Na⁺/K⁺ ratio: divided sodium content on potassium content.

C- Yield and its components: Number of panicle plant⁻¹, Number of filled grains panicle⁻¹, Number of unfilled grains panicle⁻¹, Panicle weight (g), 1000-grain weight (g), and Grain yield plant⁻¹ (g).

Statistical Analysis:

Line x tester analysis according to Kempthorne (1957) and explained by Singh and Chaudhary (1977) were used to estimate general combining ability (GCA) effects for parents and specific combining ability (SCA) effects for each cross combination under salt-affected soil. 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). The LSD

values were calculated to test the significance of the heterobeltiosis effects according to the formula suggested by Wyanne *et al.* (1970).

RESULTS

Analysis of variance:

The analysis of variance for the biochemical, agro-physiological and grain yield attributes trait are shown in **Table (3)**. The results revealed significant differences among the genotypes, parents, crosses, lines and lines x testers interaction for all the studied traits. The significant and highly significant differences for parents vs. crosses were recorded for all studied traits except the proline content, trehalose content, sodium content and SES score traits. As for testers, the spikelets sterility and proline content were found non-significant.

Mean performance:

The mean performance was found to be significant for all biochemical, physiological, and contributing yield traits under saline soil conditions of parental lines as well as their combinations **Table (4)**. The parental line IRR1 147 followed by the variety Sakha super 300 exhibited the highest photosynthetic pigments of ChIIa and ChIIb, the differences among the crosses were highly significant, and the combination of Sakha 104/IR 59673-93-2-3-3R revealed the highest concentration of ChIIa and this cross have the second content ChIIb after the cross Sakha 108/IR 59673-93-2-3-3R under saline conditions. The results also revealed an increase in photosynthetic pigment carotenoid content in the promising line Sakha super 300 followed by IRR1 147 compared with the parental lines, while the combination Sakha 106/Sakha super 300 among the tested crosses.

The observation of the proline content is significantly presented in **Table (4)**. The parent IR 59673-93-2-3-3R recorded maximum proline than the other parental genotypes while among the crosses, the maximum increase of proline was observed of the combination Sakha 104/Sakha super 300. The results also revealed a significant trehalose increase for all genotypes under saline soil conditions with the maximum content observed in the promising variety Sakha super 300 among the testers. Regarding to the cross combinations, the crosses Sakha 104/IRR1 147 and Sakha 108/IRR1 147 showed the highest mean values in terms of trehalose content among the crosses under saline soil conditions. Regarding to Ascorbic acid content (AsA) and Glutathione content (GSH), the genotypes of IRR1 147 and IR 59673-93-2-3-3R recorded the highest and most desirable mean values under saline soil conditions with mean values, respectively. Among cross combinations, the highest mean values were observed of the two hybrids Giza 177/IR 59673-93-2-3-3R and Sakha 108/IRR1 147 exhibited the desirable mean values of AsA and GSH, respectively.

Among the parental lines, a desirable kind of uptake value was measured in IRR1 147 for Na^+ , K^+ and Na^+/K^+ ratios. The cross combination of Giza 177/IRR1 147 exhibited the lowest and most desirable mean value for Na^+ content. In the meantime, the hybrid combination Sakha 104/IRR1 147 exhibited the highest mean value of potassium under saline conditions.

The salinity tolerance scores according to (SES) calculated for rice varieties and their combinations ranged from 1.67 to 6.33 as shown in **Table (4)**. The rice varieties Sakha super 300 and IRR147 besides the cross combinations Giza 177/IRR1 147 and Sakha 108/IRR1 147 exhibited high degrees of salinity tolerance with salinity tolerance scores of 1.67. The lowest mean values are desirable for days to heading and plant height traits. Two genotypes, Sakha 107 and Sakha 106 recorded the desirable mean values of 90.33 and 90.67 days for heading among lines and testers while the crosses with the lowest mean values were obtained from the combination Sakha 106/GZ 6296-12-1-2-1-1 of 94.67 days under saline conditions. Regarding the plant height, the variety Sakha 108 recorded the lowest and most desirable mean values under saline conditions with mean values of 79.00 cm. The cross combination, Sakha 107/GZ 6296-12-1-2-1-1 exhibited the lowest and desirable mean values of 88.33 cm.

For panicle length under saline soil conditions, the parental line, IRR1 147 exhibited the highest mean value of 24.50 cm. Among cross combinations, the highest mean value was observed of the hybrid Sakha 104/IR 59673-93-2-3-3R (26.81 cm). Regarding, the number of panicle plant⁻¹, the parental genotype IRR1 147 among lines and testers recorded the highest mean value of 24.84. In the meantime, the hybrid combination Sakha 104/IRR1 147 exhibited the highest mean value of 28.67 under saline soil conditions. As regards filled-grain panicle⁻¹ under saline soil conditions, the parental line IRR1 147 showed the maximum mean performance value of 138.65. While, the cross Sakha 108/IR 59673-93-2-3-3R recorded the highest mean value of 154.08 for the same trait.

Additionally, in terms of the spikelets sterility percent, the parental variety, Sakha 104 recorded the lowest desirable mean values of 14.20%. In this concern, the combination Sakha 104/IR 59673-93-2-3-3R recorded the lowest mean values of 21.23%. Concerning the 1000-grain weight under saline soil conditions, the three

parental lines Sakha super 300, Sakha 104, and Giza 177 showed the maximum mean performance values of 25.61, 25.42, and 24.97 g, respectively. While, the two crosses Sakha 104/Sakha super 300 and Sakha 106/Sakha super 300 were recorded the highest mean values of 26.95 and 26.78 g for the same trait, respectively. Regarding the panicle weight, the parental genotype Sakha super 300 among lines and testers recorded the highest mean value of 3.05 g. In the meantime, the hybrid combination Sakha 107/IRRI 147 exhibited the highest mean value of 3.25 g under saline soil conditions. For grain yield plant⁻¹, among lines and testers, the two genotypes IRRI 147 and IR 59673-93-2-3-3R recorded the highest mean values of 34.20 and 31.88 g, respectively. While the highest mean values were observed in the two cross combinations Giza 177/IRRI 147 and Sakha 104/IRRI 147 of 46.52 and 46.24 g, respectively under saline soil conditions.

Estimates of combining ability variances:

General combining ability effects:

The general combining ability effects enable the identification of desirable male and female of nine parents for 20 traits are consolidated in **Table (5)**. The summary of the general combining ability effects of the parents revealed that the parents IRRI 147, Sakha 104, IR 59673-93-2-3-3R and Sakha 108 were found to be good general combiners for many studied traits and could be used in breeding programs under salinity conditions. Among the studied lines and testers under saline soil conditions, the parental line Sakha 104 was observed to have good GCA effects and desirable direction for Chlla, Chllb, proline, trehalose, K⁺ content, Na⁺/K⁺, panicle length, filled grain panicle⁻¹, spikelet sterility, panicle weight, and grain yield plant⁻¹. In the meantime, the tester IRRI 147 was good GCA effects for Chlla, trehalose, AsA, GSH, Na⁺, K⁺, Na⁺/K⁺, SES, panicle length, number of panicle plant⁻¹, and filled grain panicle⁻¹ and grain yield plant⁻¹.

Among the genotypes examined, Sakha 108, Sakha super 300 and Sakha 104 recorded significant positive GCA effects for some photosynthetic pigments, biochemical and physiological traits. The parental genotype Sakha super 300 and Sakha 106 were the best general combiners and exhibited a desirable effect for CAR under saline soil conditions. An overall appraisal of GCA effects revealed that among parental lines, Sakha 108 is a good general combiner for Chlla, Chllb, trehalose, GSH, K⁺, Na⁺/K⁺, SES, plant height and panicle length. The genotypes Sakha 106, Sakha 107 and GZ 6296-12-1-2-1-1 were had the highly desirable significant GCA effects for days to heading and plant height. In the same direction, the genotype IR 59673-93-2-3-3R was identified as a good general combiner among testers for Chllb, Na⁺, K⁺, Na⁺/K⁺, panicle length, the number of panicle plant⁻¹, and filled-grain panicle⁻¹ under saline soil conditions.

Specific combining ability effects:

The estimation of specific combining ability was presented in **Table (6)**. However, the best three hybrids on the basis of significant positive SCA effects for biochemical and physiological traits were Sakha 104/IRRI 147, Sakha 107/GZ 6296-12-1-2-1-1 and Giza 177/IRRI 147. The highest significant SCA effects in desired direction for various characters were exhibited by different hybrids viz., Sakha 106/ Sakha super 300, Sakha 107/IR 59673-93-2-3-3R, and Sakha 108/GZ 6296-12-1-2-1-1 for thousand-grain weight trait. Four crosses viz., Giza 177/IRRI 147, Sakha 104/Sakha super 300, Sakha 106/IR 59673-93-2-3-3R, and Sakha 107/IR 59673-93-2-3-3R were highly significant SCA for grain yield plant⁻¹. As regards the 1000-grain weight under saline soil conditions, the combination Sakha 107/IR 59673-93-2-3-3R gave positive significant heterosis effects. For panicle weight and grain yield plant⁻¹ traits exhibited positive significant SCA effects by the hybrid combination Sakha 104/Sakha super 300 under saline soil conditions.

Genetic parameters of variance:

Genetic parameters, the contribution of parental lines, and their interaction for studying the traits under saline soil conditions in rice genotypes are presented in **Table (7)**. The ratio among additive and dominance were appeared its more than 50% in AsA, K⁺, Na⁺/K⁺ ratio, days to heading, number of panicles plant⁻¹ and grain yield plant⁻¹, indicating the additive and dominance gene action contribute and controlling in these traits. In the present investigation, all the studied traits showed high heritability in a broad sense except for SES and proline content which were moderate heritability in a broad sense which less than 70%. Low narrow-sense heritability has been obtained regarding to Chlla, CAR, proline, GSH, Na⁺, spikelets sterility and 1000-grain weight traits, beside the trait of SES, which was moderate narrow-sense heritability, indicating that non-additive gene effects play an important role in controlling the traits studied. Furthermore, Chllb, trehalose, AsA, K⁺, Na⁺/K⁺, days to heading, plant height, panicle length, number of panicles plant⁻¹, filled grains panicle⁻¹, panicle weight, and grain yield plant⁻¹ were high narrow-sense heritability, indicating that additive gene effects play an important role in controlling these traits it is mentioning here. Where, Broad sense heritability is considered as high if shows value >60%, medium >50–60% and

as low if the value is <50% (Ashok *et al.*, 2013). The narrow-sense heritability was categorized into low (0–10%), medium (10.1–20%) and high (>20.1%) according to (Johnson *et al.*, 1955).

The corresponding contribution of lines, testers, and line × tester interaction for 20 traits were displayed. The maximum contribution of lines was recorded in potassium content (62.35%) followed by proline content (61.16%). While grain yield panicle⁻¹ (76.42%) followed by the number of panicle plant⁻¹ (74.87%) were exhibited the maximum contribution of testers. The proportional contribution on line × tester was found maximum for photosynthetic pigments; spikelets sterility percentage (57.58%) followed by ChIIa (53.26%).

Estimates of heterobeltiosis:

The heterotic responses of hybrids over heterobeltiosis for the presence 20 biochemical and agro-physiological traits under saline soil conditions are presented in **Table (8)**. In this investigation, Sakha 104/IR 59673-93-2-3-3R and Sakha 104/IRRI 147 of the hybrids exhibited the most serious heterobeltiosis for highest number of the traits among studied hybrids. The positive and highly significant heterobeltiosis for the photosynthetic pigments (ChIIa) were found in the cross combinations Sakha 104/IR 59673-93-2-3-3R (1.59%). For ChIIb trait, the highly significant and desirable positive SCA effect heterobeltiosis was recorded for nine crosses combination, the best of them with high heterosis percentage was Sakha 108/IR 59673-93-2-3-3R (8.57%) and Sakha 104/IR 59673-93-2-3-3R (8.33%) under saline soil conditions. In addition, eight hybrid combinations gave positive significant heterosis effects desirable that varied from 2.72 to 14.64% over the respective heterobeltiosis for carotenoids content trait. For proline, the crosses Sakha 104/GZ 6296-12-1-2-1-1 (11.48%), Sakha 104/Sakha super 300 (9.73%) and Sakha 104/IRRI 147 (9.65%) were exhibited highly significant heterobeltiosis effects and for and glutathione contents the cross Sakha 108/GZ 6296-12-1-2-1-1 (16.44%) was the best heterobeltiosis cross under saline soil conditions. With regard to the trehalose content trait, Sakha 104/IRRI 147, Sakha 108/IRRI 147 and Sakha 108/IR 59673-93-2-3-3R were the best crosses combinations which exhibited a desirable combination effect for heterobeltiosis. Negative heterosis was desirable for Na⁺ and Na⁺/K⁺ ratios. The negative and highly significant heterobeltiosis for the Sodium content was found in Sakha 107/IR 59673-93-2-3-3R (-8.84%) and Giza 177/IRRI 147 (-3.55%). In addition, the Na⁺/K⁺ ratios, the hybrid combinations Sakha 104/IR 59673-93-2-3-3R, Sakha 108/IR 59673-93-2-3-3R and Sakha 107/IR 59673-93-2-3-3R exhibited highly significant negative heterobeltiosis.

In most crosses, highly significant and maximum positive heterobeltiosis was observed in grain yield plant⁻¹ as a deviation from the heterobeltiosis under saline soil conditions. Negative heterobeltiosis was desirable for salinity tolerance scores, days to heading, and plant height, but positive heterosis was desirable for the remaining contributed yield traits studied. Two cross combinations; Giza 177/IRRI 147 and Sakha 108/IRRI 147 were the best crosses of salinity tolerance. Non-crosses combinations were having the negative heterobeltiosis for the days of heading, plant height and spikelets sterility percentage under saline soil conditions, indicating the hybrid vigor and based on genetic distance among studied genotypes lead to increasing the tallness, heading date and spikelets sterility as more than the least and better parent for these traits.

The maximum highly significant and positive heterobeltiosis for panicle length and filled grain panicle⁻¹ were found in a hybrid combination Sakha 104/IR 59673-93-2-3-3R and Sakha 108/IR 59673-93-2-3-3R under salinity stress conditions. However, the six crosses showed a highly significant positive heterobeltiosis for the number of panicle⁻¹. The hybrid Sakha 108/IR 59673-93-2-3-3R and Sakha 104/IR 59673-93-2-3-3R recorded the highest significant heterobeltiosis for panicle weight. The crosses, Sakha 107/IRRI 147 and Sakha 104/Sakha super 300 were the best heterobeltiosis for 1000-grain weight. In addition, regards grain yield plant⁻¹, most cross combinations recorded positive, highly significant heterotic effects that varied from 12.38 to 43.48% over the respective heterobeltiosis under saline soil conditions.

Table 3. Analysis of variance for lines/testers design for biochemical and morpho-physiological traits under saline soil condition.

Source of variance	df	Chla (mg/g)	Chlb (mg/g)	CAR (mg/g)	Proline (mg/g)	Trehalose (µg/g)	AsA (mg/g)	GSH (mg/g)	Na ⁺ (mg/g)	K ⁺ (mg/g)	Na ⁺ /K ⁺ ratio
Replications	2	0.001	0.001	0.002	0.010	71.47	0.020	0.23	0.52	0.07	0.001
Genotypes	28	0.161**	0.019**	0.022**	0.105**	12758.52**	1.287**	12.25**	16.49**	10.54**	0.167**
Parents	8	0.153**	0.016**	0.013**	0.125**	9505.59**	1.209**	16.15**	21.20**	12.08**	0.282**
Crosses	19	0.157**	0.017**	0.027**	0.101**	14789.46**	1.129**	9.25**	15.37**	10.07**	0.123**
Parents vs. Crosses	1	0.310**	0.072**	0.009*	0.003	194.18	4.903**	37.99**	0.01	7.00**	0.061**
Lines	4	0.072**	0.023**	0.025**	0.295**	42155.55**	0.458**	8.37**	3.51*	29.84**	0.136**
Testers	3	0.370**	0.055**	0.069**	0.021*	21019.87**	5.398**	25.36**	56.66**	13.72**	0.467**
Lines x testers	12	0.133**	0.005**	0.017**	0.057**	4109.82**	0.286**	5.51**	9.01**	2.58**	0.033**
Error	56	0.002	0.001	0.002	0.008	118.77	0.030	0.58	1.12	0.22	0.004
Mean		2.467	1.476	0.848	1.498	224.38	4.273	20.92	17.97	16.98	1.08

Table 3. Continued

Source of variance	df	SES	Days to heading	Plant height (cm)	Panicle length (cm)	Panicles plant ⁻¹	Filled grain panicle ⁻¹	Spikelet sterility (%)	1000-grain weight (g)	Panicle weight (g)	Grain yield plant ⁻¹ (g)
Replications	2	0.03	3.53	3.46	0.88	1.92	7.85	1.13	0.12	0.012	2.38
Genotypes	28	5.12**	85.79**	198.10**	28.94**	82.06**	1483.22**	66.47**	7.64**	0.477**	204.73**
Parents	8	7.15**	68.65**	264.73**	29.46**	70.19**	1477.22**	52.20**	8.49**	0.592**	104.39**
Crosses	19	4.53**	58.93**	105.28**	28.51**	77.60**	1385.70**	23.01**	7.47**	0.317**	130.73**
Parents vs. Crosses	1	0.01	733.42**	1428.67**	32.88**	261.98**	3384.06**	1006.4**	3.92**	2.597**	2413.50**
Lines	4	2.93**	83.10**	189.50**	33.10**	33.49**	1149.58**	46.30**	1.87**	0.249**	53.69**
Testers	3	16.42**	214.59**	336.38**	118.79*	367.96**	5497.22**	0.07	27.42**	1.281**	634.35**
Lines x testers	12	2.09**	11.96**	19.43**	4.41**	19.71**	436.53**	20.97**	4.35**	0.099**	30.51**
Error	56	0.33	1.81	2.70	0.82	2.00	19.55	1.59	0.44	0.010	1.29
Mean		3.76	100.40	96.11	20.40	19.55	108.86	24.67	24.32	2.57	32.35

Chla and Chlb= Chlorophyll contents type A and B, CAR= Carotenoids, AsA= Ascorbate, GSH= Glutathione, Na⁺= Sodium, K⁺= Potassium, SES= Score of salinity tolerance. Which * Significant at 0.05 level and ** Significant at 0.01 level.

Table 4. Mean performance of lines, testers and crosses with respect to biochemical, physiological and yield studied traits.

Genotype	Chlla (mg/g)	Chllb (mg/g)	CAR (mg/g)	Proline (mg/g)	Trehalose (µg/g)	AsA (mg/g)	GSH (mg/g)	Na ⁺ (mg/g)	K ⁺ (mg/g)	Na ⁺ /K ⁺ ratio
Line										
Giza 177	2.372	1.394	0.762	1.333	127.92	3.301	17.48	20.33	13.99	1.46
Sakha 104	2.683	1.437	0.856	1.576	240.41	3.833	20.64	17.39	18.00	0.97
Sakha 106	2.403	1.344	0.744	1.067	128.70	3.096	18.10	22.63	13.25	1.71
Sakha 107	2.340	1.384	0.867	1.401	231.00	3.588	19.17	19.43	16.19	1.20
Sakha 108	2.327	1.342	0.762	1.471	234.66	3.381	17.22	19.52	16.59	1.18
Tester										
Sakha super 300	2.820	1.527	0.921	1.658	293.20	4.338	21.21	15.74	17.84	0.88
GZ 6296-12-1-2-1-1	2.411	1.439	0.806	1.551	238.32	4.155	19.04	16.65	15.85	1.05
IR 59673-93-2-3-3R	2.784	1.487	0.859	1.756	250.90	4.728	22.77	15.77	17.83	0.88
IRRI 147	2.859	1.542	0.918	1.599	254.29	4.854	23.78	14.38	19.51	0.74
Cross										
Giza 177/Sakha super 300	2.536	1.513	0.959	1.568	215.29	4.198	17.47	18.64	14.81	1.26
Giza 177/GZ 6296-12-1-2-1-1	2.136	1.304	0.636	1.544	128.43	3.962	17.96	20.03	15.66	1.28
Giza 177/IR 59673-93-2-3-3R	2.384	1.453	0.713	1.660	131.83	5.602	20.89	18.10	16.28	1.11
Giza 177/IRRI 147	2.480	1.496	0.837	1.523	227.60	4.923	24.29	13.87	14.84	0.94
Sakha 104/Sakha super 300	2.238	1.555	0.914	1.819	316.16	4.262	21.30	17.75	18.11	0.98
Sakha 104/GZ 6296-12-1-2-1-1	2.200	1.414	0.758	1.757	231.45	3.656	19.26	19.74	17.36	1.14
Sakha 104/IR 59673-93-2-3-3R	2.829	1.609	0.846	1.469	235.03	4.905	22.73	15.44	19.17	0.81
Sakha 104/IRRI 147	2.732	1.493	0.943	1.753	336.80	5.262	22.22	19.33	20.08	0.96
Sakha 106/Sakha super 300	2.690	1.467	0.992	1.085	231.82	3.981	21.65	18.93	14.92	1.27
Sakha 106/GZ 6296-12-1-2-1-1	2.084	1.381	0.868	1.249	139.01	4.044	19.41	22.01	13.81	1.59
Sakha 106/IR 59673-93-2-3-3R	2.123	1.504	0.921	1.331	233.63	4.723	21.51	17.27	18.25	0.95
Sakha 106/IRRI 147	2.384	1.474	0.846	1.426	222.92	5.150	22.09	16.61	16.78	0.99
Sakha 107/Sakha super 300	2.587	1.542	0.953	1.471	159.25	4.119	20.90	20.54	16.46	1.25
Sakha 107/GZ 6296-12-1-2-1-1	2.354	1.495	0.696	1.319	133.11	3.444	21.89	18.46	16.01	1.15
Sakha 107/IR 59673-93-2-3-3R	2.154	1.503	0.824	1.705	234.25	4.531	21.32	14.38	17.00	0.85
Sakha 107/IRRI 147	2.613	1.519	0.881	1.496	146.31	4.521	22.49	15.66	18.35	0.85
Sakha 108/Sakha super 300	2.775	1.554	0.885	1.591	303.67	3.467	21.81	21.40	19.41	1.10
Sakha 108/GZ 6296-12-1-2-1-1	2.379	1.433	0.924	1.372	222.29	4.049	22.17	18.87	17.34	1.09
Sakha 108/IR 59673-93-2-3-3R	2.358	1.614	0.892	1.428	324.61	4.691	21.51	15.87	19.81	0.80
Sakha 108/IRRI 147	2.494	1.577	0.813	1.475	334.22	5.159	24.36	16.30	18.99	0.86
LSD at 0.05	0.080	0.048	0.070	0.150	17.80	0.284	1.24	1.73	0.76	0.11
LSD at 0.01	0.107	0.064	0.093	0.199	23.67	0.377	1.65	2.30	1.01	0.14

Table 4. Continued

Cross	SES	Days to heading	Plant height (cm)	Panicle length(cm)	Panicles plant ⁻¹	Filled grain panicle ⁻¹	Spikelet sterility (%)	1000-grain weight(g)	Panicle weight(g)	Grain yield plant ⁻¹ (g)
Line										
Giza 177	5.67	92.67	87.33	16.92	11.03	86.74	23.74	24.97	2.02	17.14
Sakha 104	3.67	97.33	93.33	18.53	17.08	98.65	14.20	25.42	2.41	25.49
Sakha 106	5.67	90.67	82.00	16.76	10.82	70.39	26.56	24.83	1.79	18.45
Sakha 107	4.33	90.33	81.67	15.76	14.79	78.85	20.64	24.23	1.94	21.73
Sakha 108	4.33	99.67	79.00	18.53	15.12	84.04	20.23	24.11	1.87	20.22
Tester										
Sakha super 300	1.67	105.00	107.33	18.63	17.27	114.40	14.79	25.61	3.05	27.82
GZ 6296-12-1-2-1-1	4.33	93.33	85.33	22.99	18.25	102.45	21.67	21.83	2.38	23.56
IR 59673-93-2-3-3R	2.33	97.00	96.00	22.75	23.45	121.85	18.86	20.61	2.52	31.88
IRRI 147	1.67	98.67	98.67	24.50	24.84	138.65	15.73	24.45	2.85	34.20
Cross										
Giza 177/Sakha super 300	4.33	104.33	106.33	19.49	15.83	108.72	28.05	25.84	2.55	33.82
Giza 177/GZ 6296-12-1-2-1-1	5.00	96.67	92.67	18.83	23.76	90.06	31.67	23.65	2.36	28.07
Giza 177/IR 59673-93-2-3-3R	3.67	103.33	104.33	22.19	27.51	140.30	26.43	24.04	2.68	38.82
Giza 177/IRRI 147	1.67	104.67	102.67	23.12	23.77	131.55	29.48	24.57	2.84	45.86
Sakha 104/Sakha super 300	3.67	107.67	107.67	19.51	15.39	92.29	21.49	26.95	3.01	39.92
Sakha 104/GZ 6296-12-1-2-1-1	4.33	97.33	95.00	17.83	18.99	112.14	27.88	24.02	2.72	32.15
Sakha 104/IR 59673-93-2-3-3R	5.00	102.33	107.33	26.81	22.52	148.63	21.23	23.06	2.89	36.39
Sakha 104/IRRI 147	2.33	101.00	107.33	25.54	28.67	132.08	24.05	24.57	3.11	46.24
Sakha 106/Sakha super 300	4.33	108.33	100.00	17.11	13.34	91.95	29.44	26.78	2.61	25.77
Sakha 106/GZ 6296-12-1-2-1-1	6.33	94.67	90.33	17.50	15.74	91.73	26.69	23.70	2.18	28.33
Sakha 106/IR 59673-93-2-3-3R	3.00	101.67	93.33	21.63	26.95	92.22	28.45	20.43	2.54	39.79
Sakha 106/IRRI 147	3.67	97.67	95.67	21.79	23.86	119.20	26.30	25.37	2.94	40.88
Sakha 107/Sakha super 300	4.33	104.67	101.00	16.54	17.51	86.39	27.22	25.27	2.32	27.52
Sakha 107/GZ 6296-12-1-2-1-1	5.00	97.33	88.33	17.29	18.41	90.74	22.70	23.37	2.36	26.58
Sakha 107/IR 59673-93-2-3-3R	3.00	99.33	98.00	19.95	26.89	128.75	29.79	25.40	2.75	41.14
Sakha 107/IRRI 147	3.67	99.00	102.67	21.39	21.95	122.35	28.68	25.97	3.25	40.06
Sakha 108/Sakha super 300	2.33	111.33	98.33	18.79	13.17	95.12	28.25	25.85	2.32	34.76
Sakha 108/GZ 6296-12-1-2-1-1	5.00	104.67	93.33	20.88	13.54	107.73	26.26	24.60	2.21	28.78
Sakha 108/IR 59673-93-2-3-3R	3.00	106.33	97.00	25.70	22.46	154.08	28.67	22.03	2.98	40.12
Sakha 108/IRRI 147	1.67	104.67	95.33	24.38	23.96	124.80	26.31	23.87	3.10	42.67
LSD at 0.05	0.94	2.20	2.68	1.48	2.31	7.22	2.06	1.09	0.17	1.86
LSD at 0.01	1.25	2.93	3.57	1.96	3.07	9.60	2.74	1.45	0.22	2.47

Chla and Chlb= Chlorophyll contents type A and B, CAR= Carotenoids, AsA= Ascorbate, GSH= Glutathione, Na⁺= Sodium, K⁺= Potassium, SES= Score of salinity tolerance.

Table 5. Estimates of general combining ability (GCA) effects for studied traits of nine parents under salinity condition.

Genotype	Chla (mg/g)	Chlb (mg/g)	CAR (mg/g)	Proline (mg/g)	Trehalose (µg/g)	AsA (mg/g)	GSH (mg/g)	Na ⁺ (mg/g)	K ⁺ (mg/g)	Na ⁺ /K ⁺ ratio
Giza 177	-0.042**	-0.054**	-0.069**	0.072**	-49.59**	0.239**	-1.21**	-0.30	-1.776**	0.084**
Sakha 104	0.073**	0.023**	0.010	0.198**	54.47**	0.089	0.02	0.10	1.508**	-0.089**
Sakha 106	-0.106**	-0.039**	0.052**	-0.230**	-18.54**	0.042	-0.20	0.75*	-1.234**	0.140**
Sakha 107	0.001	0.020*	-0.016	-0.004	-57.16**	-0.279**	0.29	-0.70*	-0.215	-0.036
Sakha 108	0.075**	0.050**	0.024	-0.035	70.81**	-0.091	1.10**	0.15	1.717**	-0.099**
LSD 0.05	0.028	0.017	0.025	0.053	6.29	0.100	0.44	0.61	0.269	0.038
LSD 0.01	0.038	0.022	0.033	0.070	8.37	0.133	0.59	0.81	0.358	0.050
Sakha super 300	0.139**	0.031**	0.086**	0.005	19.86**	-0.427**	-0.74**	1.49**	-0.431**	0.112**
GZ 6296-12-1-2-1-1	-0.196**	-0.090**	-0.079**	-0.054*	-54.53**	-0.601**	-1.22**	1.86**	-1.135**	0.189**
IR59673-93-2-3-3R	-0.057**	0.042**	-0.016	0.017	6.49*	0.458**	0.23	-1.75**	0.930**	-0.159**
IRRI 147	0.114**	0.017*	0.009	0.032	28.19**	0.571**	1.73**	-1.61**	0.637**	-0.142**
LSD 0.05	0.025	0.015	0.022	0.047	5.63	0.090	0.39	0.55	0.241	0.034
LSD 0.01	0.034	0.020	0.029	0.063	7.49	0.119	0.52	0.73	0.320	0.045

Table 5. Continued

Genotype	SES	Days to heading	Plant height (cm)	Panicle length (cm)	Panicles plant ⁻¹	Filled grain panicle ⁻¹	Spikelet sterility (%)	1000-grain weight (g)	Panicle weight (g)	Grain yield plant ⁻¹ (g)
Giza 177	-0.10	-0.10	2.67**	0.10	2.01**	4.62**	1.96**	0.06	-0.076*	0.76*
Sakha 104	0.07	-0.27	5.50**	1.61**	0.68	8.24**	-3.29**	0.18	0.248**	2.79**
Sakha 106	0.57**	-1.77**	-4.00**	-1.31**	-0.74	-14.27**	0.77*	-0.40*	-0.119**	-2.19**
Sakha 107	0.23	-2.27**	-1.33**	-2.02**	0.48	-5.98**	0.15	0.53**	-0.018	-2.06**
Sakha 108	-0.77**	4.40**	-2.83**	1.62**	-2.43**	7.39**	0.42	-0.38*	-0.034	0.70*
LSD 0.05	0.33	0.78	0.95	0.52	0.82	2.55	0.73	0.38	0.058	0.66
LSD 0.01	0.44	1.03	1.26	0.69	1.09	3.40	0.97	0.51	0.078	0.87
Sakha super 300	0.03	4.92**	3.83**	-2.53**	-5.66**	-18.15**	-0.06	1.67**	-0.124**	-3.53**
GZ 6296-12-1-2-1-1	1.37**	-4.22**	-6.90**	-2.35**	-2.62**	-14.56**	0.09	-0.60**	-0.320**	-7.10**
IR59673-93-2-3-3R	-0.23	0.25	1.17**	2.44**	4.55**	19.75**	-0.04	-1.47**	0.082**	3.37**
IRRI 147	-1.17**	-0.95*	1.90**	2.43**	3.73**	12.96**	0.01	0.40*	0.362**	7.26**
LSD 0.05	0.30	0.70	0.85	0.47	0.73	2.28	0.65	0.34	0.052	0.59
LSD 0.01	0.40	0.93	1.13	0.62	0.97	3.04	0.87	0.46	0.069	0.78

Chla and Chlb= Chlorophyll contents type A and B, CAR= Carotenoids, AsA= Ascorbate, GSH= Glutathione, Na⁺= Sodium, K⁺= Potassium, SES= Score of salinity tolerance. Which * Significant at 0.05 level and ** Significant at 0.01 level

Table 6. Estimates of specific combining ability (SCA) effects for studied traits of 20 hybrids under salinity condition.

Cross	Chla (mg/g)	Chlb (mg/g)	CAR (mg/g)	Proline (mg/g)	Trehalose (μg/g)	AsA (mg/g)	GSH (mg/g)	Na ⁺ (mg/g)	K ⁺ (mg/g)	Na ⁺ /K ⁺ Ratio
Giza 177/Sakha super 300	0.013	0.040*	0.087**	-0.011	19.65**	-0.046	-1.95**	-0.51	-0.155	0.000
Giza 177/GZ 6296-12-1-2-1-1	-0.052	-0.048**	-0.071**	0.024	7.17	-0.108	-0.97*	0.50	1.400**	-0.057
Giza 177/IR 59673-93-2-3-3R	0.057*	-0.030	-0.058*	0.070	-50.44**	0.473**	0.51	2.19**	-0.048	0.124**
Giza 177/IRRI 147	-0.018	0.038*	0.042	-0.084	23.63**	-0.319**	2.41**	-2.18**	-1.197**	-0.066
Sakha 104/Sakha super 300	-0.400**	0.006	-0.037	0.115*	16.45*	0.168	0.65	-1.81**	-0.139	-0.101**
Sakha 104/GZ 6296-12-1-2-1-1	-0.104**	-0.014	-0.029	0.112*	6.11	-0.264*	-0.89*	-0.19	-0.186	-0.021
Sakha 104/IR 59673-93-2-3-3R	0.386**	0.049**	-0.003	-0.247**	-51.32**	-0.074	1.12*	-0.88	-0.442	-0.007
Sakha 104/IRRI 147	0.118**	-0.041*	0.069**	0.021	28.75**	0.170	-0.88*	2.87**	0.767**	0.130**
Sakha 106/Sakha super 300	0.231**	-0.021	0.000	-0.193**	5.12	-0.066	1.22**	-1.27*	-0.592*	-0.039
Sakha 106/GZ 6296-12-1-2-1-1	-0.041	0.014	0.040	0.030	-13.31*	0.171	-0.53	1.45*	-0.994**	0.204**
Sakha 106/IR 59673-93-2-3-3R	-0.140**	0.006	0.030	0.042	20.30**	-0.210*	0.11	0.31	1.383**	-0.096*
Sakha 106/IRRI 147	-0.050	0.001	-0.070**	0.121*	-12.11	0.105	-0.81	-0.49	0.203	-0.069
Sakha 107/Sakha super 300	0.021	-0.004	0.029	-0.032	-28.83**	0.392**	-0.02	1.79**	-0.066	0.112**
Sakha 107/GZ 6296-12-1-2-1-1	0.123**	0.070**	-0.064*	-0.125*	19.40**	-0.108	1.47**	-0.66	0.189	-0.061
Sakha 107/IR 59673-93-2-3-3R	-0.216**	-0.053**	0.001	0.191**	59.53**	-0.081	-0.56	-1.13	-0.884**	-0.017
Sakha 107/IRRI 147	0.072*	-0.013	0.033	-0.034	-50.11**	-0.203*	-0.89*	0.01	0.761**	-0.034
Sakha 108/Sakha super 300	0.135**	-0.022	-0.079**	0.120*	-12.38	-0.447**	0.09	1.80**	0.951**	0.029
Sakha 108/GZ 6296-12-1-2-1-1	0.073*	-0.022	0.124**	-0.041	-19.38**	0.309**	0.93*	-1.10	-0.410	-0.065
Sakha 108/IR 59673-93-2-3-3R	-0.087**	0.028	0.030	-0.055	21.93**	-0.109	-1.19**	-0.49	-0.008	-0.004
Sakha 108/IRRI 147	-0.121**	0.016	-0.074**	-0.024	9.84	0.247*	0.17	-0.21	-0.533	0.039
LSD at 0.05	0.057	0.034	0.050	0.106	12.58	0.201	0.88	1.22	0.538	0.076
LSD at 0.01	0.076	0.045	0.066	0.141	16.74	0.267	1.17	1.62	0.715	0.101

Table 6. Continued

Cross	SES	Days to heading	Plant height (cm)	Panicle length (cm)	Panicles plant ⁻¹	Filled grain panicle ⁻¹	Spikelet sterility (%)	1000-grain weight (g)	Panicle weight (g)	Grain yield plant ⁻¹ (g)
Giza 177/Sakha super 300	0.63	-2.83**	1.00	1.11*	-1.22	9.21**	-0.80	-0.35	0.069	0.71
Giza 177/GZ 6296-12-1-2-1-1	-0.03	-1.37	-1.93*	0.27	3.67**	-13.04**	2.68**	-0.28	0.074	-1.47*
Giza 177/IR 59673-93-2-3-3R	0.23	0.83	1.67	-1.16*	0.23	2.89	-2.44**	0.99*	-0.008	-1.19
Giza 177/IRRI 147	-0.83*	3.37**	-0.73	-0.22	-2.68**	0.94	0.56	-0.36	-0.135*	1.96**
Sakha 104/Sakha super 300	-0.20	0.67	-0.50	-0.39	-0.34	-10.85**	-2.11**	0.63	0.201**	4.77**
Sakha 104/GZ 6296-12-1-2-1-1	-0.87*	-0.53	-2.43*	-2.24**	0.22	5.42*	4.13**	-0.03	0.107	0.58
Sakha 104/IR 59673-93-2-3-3R	1.40**	0.00	1.83	1.94**	-3.43**	7.59**	-2.40**	-0.12	-0.126*	-5.65**
Sakha 104/IRRI 147	-0.33	-0.13	1.10	0.69	3.54**	-2.16	0.37	-0.48	-0.182**	0.31
Sakha 106/Sakha super 300	-0.03	2.83**	1.33	0.13	-0.97	11.33**	1.78*	1.04**	0.164**	-4.40**
Sakha 106/GZ 6296-12-1-2-1-1	0.63	-1.70*	2.40*	0.34	-1.61	7.51**	-1.12	0.23	-0.070	1.73*
Sakha 106/IR 59673-93-2-3-3R	-1.10**	0.83	-2.67**	-0.32	2.42**	-26.31**	0.77	-2.16**	-0.106	2.73**
Sakha 106/IRRI 147	0.50	-1.97*	-1.07	-0.15	0.16	7.47**	-1.43	0.90*	0.011	-0.07
Sakha 107/Sakha super 300	0.30	-0.33	-0.33	0.27	1.98*	-2.52	0.18	-1.41**	-0.227**	-2.78**
Sakha 107/GZ 6296-12-1-2-1-1	-0.37	1.47	-2.27*	0.85	-0.16	-1.76	-4.49**	-1.03**	0.010	-0.14
Sakha 107/IR 59673-93-2-3-3R	-0.77*	-1.00	-0.67	-1.28*	1.15	1.94	2.73**	1.87**	-0.003	3.95**
Sakha 107/IRRI 147	0.83*	-0.13	3.27**	0.17	-2.97**	2.34	1.57*	0.57	0.220**	-1.03
Sakha 108/Sakha super 300	-0.70*	-0.33	-1.50	-1.13*	0.55	-7.16**	0.94	0.09	-0.207**	1.70*
Sakha 108/GZ 6296-12-1-2-1-1	0.63	2.13**	4.23**	0.79	-2.12*	1.86	-1.20	1.11**	-0.121*	-0.70
Sakha 108/IR 59673-93-2-3-3R	0.23	-0.67	-0.17	0.82	-0.38	13.89**	1.34	-0.58	0.243**	0.17
Sakha 108/IRRI 147	-0.17	-1.13	-2.57**	-0.48	1.94*	-8.59**	-1.07	-0.62	0.086	-1.17
LSD at 0.05	0.67	1.56	1.90	1.04	1.63	5.11	1.46	0.77	0.117	1.31
LSD at 0.01	0.89	2.07	2.52	1.39	2.17	6.79	1.94	1.02	0.155	1.75

Chla and Chlb= Chlorophyll contents type A and B, CAR= Carotenoids, AsA= Ascorbate, GSH= Glutathione, Na⁺= Sodium, K⁺= Potassium, SES= Score of salinity tolerance. Which * Significant at 0.05 level and ** Significant at 0.01 level

Table 7. Estimates of genetic parameters for the studied traits.

Parameter	Chla (mg/g)	Chlb (mg/g)	CAR (mg/g)	Proline (mg/g)	Trehalose (µg/g)	AsA (mg/g)	GSH (mg/g)	Na ⁺ (mg/g)	K ⁺ (mg/g)	Na ⁺ /K ⁺ ratio
Additive	0.001	0.001	0.001	0.003	623.39	0.049	0.22	0.37	0.438	0.005
Dominance	0.043	0.002	0.005	0.016	1330.35	0.085	1.64	2.63	0.786	0.010
Additive/Dominance	0.03	0.46	0.12	0.16	0.47	0.58	0.13	0.14	0.557	0.553
Contribute line	9.65	28.90	19.76	61.16	60.01	8.53	19.06	4.81	62.35	23.25
Contribute tester	37.09	51.30	41.04	3.32	22.44	75.49	43.31	58.19	21.50	59.87
Contribute L/t	53.26	19.79	39.20	35.52	17.55	15.98	37.63	37.00	16.15	16.88
*H. b=	94.88	71.64	74.86	69.09	94.27	81.67	76.22	72.87	84.94	77.44
*H. n=	3.04	22.48	8.05	9.52	30.08	29.92	8.94	9.02	30.37	27.56

Table 7. Continued

Parameter	SES	Days to heading	Plant height (cm)	Panicle length (cm)	Panicles plant ⁻¹	Filled grain panicle ⁻¹	Spikelet sterility (%)	1000-grain weight (g)	Panicle weight (g)	Grain yield plant ⁻¹ (g)
Additive	0.14	2.74	5.01	1.41	3.38	55.40	0.12	0.18	0.013	5.85
Dominance	0.59	3.38	5.58	1.20	5.90	138.99	6.46	1.30	0.030	9.74
Additive/Dominance	0.24	0.81	0.90	1.18	0.57	0.40	0.02	0.14	0.43	0.60
Contribute line	13.63	29.69	37.89	24.44	9.09	17.47	42.37	5.26	16.50	8.65
Contribute tester	57.24	57.50	50.45	65.79	74.87	62.64	0.05	57.95	63.77	76.62
Contribute L/t	29.12	12.81	11.66	9.77	16.04	19.90	57.58	36.79	19.74	14.74
*H. b=	68.67	77.14	79.70	76.09	82.25	90.86	80.53	76.96	80.55	92.34
*H. n=	13.44	34.55	37.71	41.11	29.95	25.90	1.45	9.44	24.21	34.66

Chla and Chlb= Chlorophyll contents type A and B, CAR= Carotenoids, AsA= Ascorbate, GSH= Glutathione, Na⁺= Sodium, K⁺= Potassium, SES= Score of salinity tolerance.

Table 8. Estimates of heterosis over better parent (HB.P. %) for studied traits of 20 hybrids under salinity condition.

Cross	Chlla (mg/g)	Chllb (mg/g)	CAR (mg/g)	Proline (mg/g)	Trehalose (µg/g)	ASA (mg/g)	GSH (mg/g)	Na ⁺ (mg/g)	K ⁺ (mg/g)	Na ⁺ /K ⁺ ratio
Giza 177/Sakha super 300	-10.08**	-0.92**	4.13**	-5.43**	-26.57**	-3.23**	-17.63**	18.42**	-16.98**	42.80**
Giza 177/GZ 6296-12-1-2-1-1	-11.43**	-9.43**	-21.05**	-0.45**	-46.11**	-4.65**	-5.64**	20.26**	-1.20**	21.59**
Giza 177/IR 59673-93-2-3-3R	-14.37**	-2.26**	-17.07**	-5.43**	-47.46**	18.50**	-8.23**	14.75**	-8.69**	25.66**
Giza 177/IRRI 147	-13.23**	-2.98**	-8.79**	-4.75**	-10.49	1.42**	2.14**	-3.55**	-23.94**	26.58**
Sakha 104/Sakha super 300	-20.64**	1.88**	-0.76**	9.73**	7.83	-1.74**	0.39	12.75**	0.63	11.74**
Sakha 104/GZ 6296-12-1-2-1-1	-18.00**	-1.76**	-11.48**	11.48**	-3.73	-12.01**	-6.66**	18.53**	-3.55**	17.53**
Sakha 104/IR 59673-93-2-3-3R	1.59**	8.23**	-1.59**	-16.35**	-6.33	3.74**	-0.15	-2.11*	6.50**	-8.68**
Sakha 104/IRRI 147	-4.43**	-3.14**	2.72**	9.65**	32.45**	8.41**	-6.55**	34.37**	2.97**	29.73**
Sakha 106/Sakha super 300	-4.61**	-3.93**	7.71**	-34.58**	-20.93*	-8.22**	2.07**	20.22**	-16.39**	44.70**
Sakha 106/GZ 6296-12-1-2-1-1	-13.59**	-4.03**	7.69**	-19.51**	-41.67**	-2.68**	1.98**	32.19**	-12.88**	51.75**
Sakha 106/IR 59673-93-2-3-3R	-23.75**	1.17**	7.18**	-24.21**	-6.88	-0.11	-5.51**	9.49**	2.37**	7.17**
Sakha 106/IRRI 147	-16.59**	-4.41**	-7.85**	-10.82**	-12.33	6.11**	-7.12**	15.48**	-13.99**	33.78**
Sakha 107/Sakha super 300	-8.26**	0.98**	3.51**	-11.28**	-45.68**	-5.05**	-1.48*	30.45**	-7.73**	42.05**
Sakha 107/GZ 6296-12-1-2-1-1	-2.36**	3.89**	-19.68**	-15.00**	-44.15**	-17.11**	14.19**	10.83**	-1.11**	9.84**
Sakha 107/IR 59673-93-2-3-3R	-22.64**	1.12**	-4.96**	-2.89**	-6.64	-4.16**	-6.34**	-8.84**	-4.63**	-3.77**
Sakha 107/IRRI 147	-8.58**	-1.49**	-4.03**	-6.40**	-42.46**	-6.85**	-5.44**	8.88**	-5.90**	14.86**
Sakha 108/Sakha super 300	-1.61**	1.79**	-3.87**	-4.02**	3.57	-20.07**	2.83**	35.93**	8.80**	25.38**
Sakha 108/GZ 6296-12-1-2-1-1	-1.35**	-0.44**	14.64**	-11.58**	-6.73	-2.54**	16.44**	13.31**	4.57**	3.49**
Sakha 108/IR 59673-93-2-3-3R	-15.32**	8.57**	3.84**	-18.64**	29.38**	-0.78**	-5.52**	0.66	11.13**	-9.43**
Sakha 108/IRRI 147	-12.74**	2.29**	-11.41**	-7.74**	31.43**	6.30**	2.45**	13.30**	-2.63**	16.22**

Table 8. Continued

Cross	SES	Days to heading	Plant height (cm)	Panicle length (cm)	Panicles plant ⁻¹	Filled grain panicle ⁻¹	Spikelet sterility (%)	1000-grain weight (g)	Panicle weight (g)	Grain yield plant ⁻¹ (g)
Giza 177/Sakha super 300	160.00**	12.59**	21.76**	4.65**	-8.34**	-4.97	89.68**	0.92	-16.19**	21.57**
Giza 177/GZ 6296-12-1-2-1-1	15.38**	4.32**	8.59**	-18.07**	30.19**	-12.10**	46.18**	-5.27**	-0.56**	19.16**
Giza 177/IR 59673-93-2-3-3R	57.14**	11.51**	19.47**	-2.45**	17.28**	15.14**	40.16**	-3.70**	6.62**	21.76**
Giza 177/IRRI 147	0.00	12.95**	17.56**	-5.65**	-4.31**	-5.12	87.45**	-1.60**	-0.35**	34.07**
Sakha 104/Sakha super 300	120.00**	10.62**	15.36**	4.74**	-10.90**	-19.33**	51.36**	5.25**	-1.20**	43.48**
Sakha 104/GZ 6296-12-1-2-1-1	18.18**	4.29**	11.33**	-22.42**	4.05**	9.46*	96.34**	-5.50**	12.86**	26.12**
Sakha 104/IR 59673-93-2-3-3R	114.29**	5.50**	15.00**	17.83**	-3.98**	21.98**	49.48**	-9.29**	14.83**	14.15**
Sakha 104/IRRI 147	40.00**	3.77**	15.00**	4.24**	15.39**	-4.74	69.37**	-3.34**	9.37**	35.20**
Sakha 106/Sakha super 300	160.00**	19.49**	21.95**	-8.12**	-22.77**	-19.62**	99.08**	4.57**	-14.44**	-7.37**
Sakha 106/GZ 6296-12-1-2-1-1	46.15**	4.41**	10.16**	-23.87**	-13.75**	-10.47**	23.20**	-4.56**	-8.42**	20.23**
Sakha 106/IR 59673-93-2-3-3R	28.57**	12.13**	13.82**	-4.92**	14.91**	-24.32**	50.88**	-17.72**	1.06**	24.81**
Sakha 106/IRRI 147	120.00**	7.72**	16.67**	-11.09**	-3.96**	-14.03**	67.25**	2.15**	3.28**	19.53**
Sakha 107/Sakha super 300	160.00**	15.87**	23.67**	-11.20**	1.35	-24.49**	84.08**	-1.33*	-23.96**	-1.09
Sakha 107/GZ 6296-12-1-2-1-1	15.38**	7.75**	8.16**	-24.78**	0.86	-11.43**	9.95**	-3.58**	-0.84**	12.83**
Sakha 107/IR 59673-93-2-3-3R	28.57**	9.96**	20.00**	-12.31**	14.67**	5.67	58.00**	4.81**	9.14**	29.06**
Sakha 107/IRRI 147	120.00**	9.59**	25.71**	-12.72**	-11.65**	-11.76**	82.39**	6.19**	14.17**	17.11**
Sakha 108/Sakha super 300	40.00**	11.71**	24.47**	0.86	-23.74**	-16.86**	91.05**	0.96	-23.85**	24.93**
Sakha 108/GZ 6296-12-1-2-1-1	15.38**	12.14**	18.14**	-9.18**	-25.80**	5.15	29.81**	2.03**	-7.01**	22.17**
Sakha 108/IR 59673-93-2-3-3R	28.57**	9.62**	22.78**	12.98**	-4.24**	26.45**	52.04**	-8.61**	18.28**	25.85**
Sakha 108/IRRI 147	0.00	6.08**	20.68**	-0.49	-3.57**	-9.99**	67.30**	-2.40**	8.90**	24.74**

Chla and Chlb= Chlorophyll contents type A and B, CAR= Carotenoids, AsA= Ascorbate, GSH= Glutathione, Na⁺= Sodium, K⁺= Potassium, SES= Score of salinity tolerance. Which * Significant at 0.05 level and ** Significant at 0.01 level.

DISCUSSION

Based on the results of the analysis of variance, the genotypes were significantly affected by salt stress. It is an indication that the applied selection was appropriate to select the best genotypes (Al-Naggar *et al.*, 2015; Anshoriet *al.*, 2019). The difference in response could be referred to the tolerant and sensitive genotype responses. The significant differences between lines x testers interaction for these traits suggested that specific combining ability is widely attributed to the expression of these traits and gives significance to dominance or non-additive genetic variances for all these traits (Ghidan, and Khedr, 2021). Several researchers have reported the predominance of dominant gene action for a majority of the yield traits in rice (Abo-Yousef *et al.*, 2020). The significant mean squares of the lines and testers also revealed the prevalence of additive genetic variances for these traits. Previous studies have reported the occurrence of both additive and non-additive gene effects on yield and relevant yield component traits in rice (Rahimi *et al.*, 2010). These findings proved the importance of combining ability studies and showed good prospects for the selection of suitable parents and crosses for the development of suitable hybrids and varieties.

Mean performance:

The mean performance was found to be significant for all biochemical, physiological, and contributing yield traits under saline soil conditions of parental lines as well as their combinations **Table (4)**. The reduction in the synthesis photosynthetic pigments contents chlorophyll a (Chlla), chlorophyll b (Chllb), and carotenoid (CAR) are a common phenomenon that is closely linked to the reduction of plant biomass and yield output (Zayed *et al.*, 2017 and Nasrin *et al.*, 2020). Chlorophyll contents were variably increased or decreased among rice genotypes. Findings were consistent with many earlier reports indicating the salt stress-induced decrease or increase in chlorophyll contents in rice. These studies have also shown that salt-tolerant and moderately tolerant genotypes contained significantly higher chlorophyll contents (Nounjan *et al.*, 2018; Zayed *et al.*, 2018).

There was an increase in proline with increased salinity levels in all rice genotypes (Zayed *et al.*, 2017; Zayed *et al.*, 2018). Ascorbate, polyphenols, glutathione, and carotenoid are examples of non-enzymatic antioxidants (Gupta and Huang, 2014; Talbi *et al.*, 2015) Glutathione is a non-protein thiol present in plants that serves an important role in protecting the plants from stressful conditions. At the optimum level, GSH levels enhanced in response to high salt, especially in leaves compared to roots. This might be due to increased sulfur consumption and metabolism for the formation of antioxidants like GSH (Gill *et al.*, 2013 and Zayed *et al.*, 2017). Generally, the Na^+ and Na^+/K^+ ratio contents, in rice plant were directly enhanced relating to salt concentrations, while potassium (K^+) ion, in salt-stressed plants was significantly reduced (Zayed *et al.*, 2017)

Rice plants with salt tolerant traits generally have high levels of maintenance of ion homeostasis, particularly low Na^+/K^+ or high K^+/Na^+ ratios, through exclusion, compartmentation, and partitioning of Na^+ in shoots or roots (Zayed *et al.*, 2016; Zayed *et al.*, 2017).

One of the problems of salinity is that it makes the plants dwarfed. However, in rice breeding programs, short plants are preferred, so it must be combined that, the plant is short and also has a high yield and tolerant to salinity, so that it can be used under the conditions of saline soils to improve the character of the plant's height. The salinity stress significantly affects the yield traits of rice, such as panicle length, panicle number, and panicle weight, among these contributing traits, causes yield loss under saline soil conditions (Shereenet *al.*, 2005). However, in this study, we found that the panicles number plant⁻¹ is considered the main factor affecting rice yield. This difference is closely related to the differential salt tolerance of rice varieties (Zayed *et al.*, 2016; Zayed *et al.*, 2017).

Estimates of combining ability variances:

General combining ability effects and Specific combining ability effects:

The general combining ability effects enable the identification of desirable male and female of nine parents for 20 traits consolidated. The nature and magnitude of combining ability effects provide guidelines for identifying better parents and their utilization. In the current study, parental lines with high mean and positive GCA are preferred for positive grain yield characteristics, whereas parents with low mean and negative GCA are preferred for negative grain yield characteristics, such as Na^+ , Na^+/K^+ , SES, days to heading, and plant height. Ghidanet *al.*, (2019) suggested that parents with high GCA would produce transgressive segregation at later generations and may be utilized in hybridization programs. Selecting parents is a crucial step in breeding programs to enhance abiotic tolerance. Similar findings were obtained by (Zayed *et al.*, 2016; Zayed *et al.*, 2017). The estimates of specific

combining ability effects revealed that none of the crosses was superior for all the characters. Further, it can be revealed that with high SCA effects, at least one good general combiner was necessary for the hybrids. Combining ability analysis reflects the use of individuals as parents in the hybridization program as well as simultaneously screening the hybrids for coastal saline areas. With the assumptions that differences in general combining ability resulted primarily from differences in the additive gene effects, and that in specific combining ability effects were due to differences in non-additive gene effects, it was conspicuous from the material under the traits like height of the plant, and panicle length, were controlled by additive genes and these characters could easily be manipulated for genetic improvement (Zayed *et al.*, 2017; Ghidan and Khedr, 2021).

Genetic parameters of variance:

All studied traits controlling by non-additive gene action except panicle length indicating the traits didn't fix in the early segregating generation and must be done at the later segregating generation regarding the current set of crosses. Hence, direct selection can be done through these traits for future improvement of genotypes under respective environments for the improvement of salinity stress tolerance and higher grain yield. Earlier workers of Abo-Yousef *et al.* (2020) also reported similar results. The characteristics of high heritability along with moderate or low genetic development can be enhanced by combining superior segregating population genotypes developed from combination breeding (Zayed *et al.*, 2016; Garget *et al.*, 2017; Zayed *et al.*, 2017). Therefore, it appears that hybridization must be an option for the population's use of specific hybrids. The estimated genetic advance for traits also demonstrated the potential to enhance most traits to achieve sufficient high-yield lines. Ahmadikhah (2008) reported low specific heritability for characteristics associated with yield. Gholizadeh *et al.* (2014) also found that low additive gene effects and high dominant gene action caused lower narrow-sense heritability. It shows that a commonly adopted genotype can be produced if these traits are subject to some selection scheme to manipulate fixable genetic variance.

Estimates of heterobeltiosis:

It was observed that the parents of all the hybrids were of one good and one poor combiner indicating the presence of dominance gene action. Therefore, these hybrids are recommended for heterosis breeding, because the usefulness of a particular cross in the exploitation of heterosis is judged by the specific combining ability effect (Zayed *et al.*, 2017; Vanave *et al.*, 2018; Ghidan and Khedr, 2021).

CONCLUSION

In accordance with the findings of the serious investigation, it can be concluded that based on performance and combining ability effects of the genotypes examined, IRRI 147, Sakha super 300 and Sakha 104 recorded significant positive GCA effects for some photosynthetic pigments, biochemical and physiological traits. On the other hand, three hybrids on the basis of significant positive SCA effects for biochemical and physiological traits were Sakha 104/IRRI 147, Sakha 107/GZ 6296-12-1-2-1-1 and Giza 177/IRRI 147. In this investigation, Sakha 104/IR 59673-93-2-3-3R and Sakha 104/IRRI 147 of the hybrids exhibited the most serious heterobeltiosis for highest number of the traits among studied hybrids. The valuable data from this work ought to be utilized to assess rice genetic resources for salinity tolerance in the future.

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وراثة بعض الصفات البيوكيميائية والمورفولوجية والمحصول ومكوناته لبعض التراكيب الوراثية للأرز تحت ظروف الملوحة

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يعتبر الأرز أحد أهم المحاصيل الأساسية التي يستهلكها أغلب سكان العالم، إلا أن الملوحة هي أحد العوامل التي تحد من إنتاجيته. الهدف من هذه الدراسة هو تحديد تراكيب وراثية تتحمل الملوحة ويمكن استخدامها في ظروف التربة المتأثرة بالاملاح وفي العشائر الوراثية في برامج التربية لتحمل الملوحة. تم دراسة أهمية الصفات البيوكيميائية والفسيولوجية فيما يتعلق بالنمو والمحصول لتسعة تراكيب وراثية من الأرز وعشرين هجيناً من هجن الجيل الأول وفقاً لتصميم السلالة × الكشاف خلال موسمي زراعة الأرز 2021 و 2022. وذلك بالمزرعة البحثية بمحطة البحوث الزراعية بالسرو بمحافظة دمياط، جمهورية مصر العربية. وكشفت هذه الدراسات عن الاختلاف في سلوك جميع التراكيب الوراثية تحت الدراسة، وأظهرت النتائج أن سخا 104, IRRI 147 و IR 59673-93-2-3-3R كانت أفضل التراكيب الوراثية بشكل عام لمعظم الصفات مع انخفاض نسبة الصوديوم إلى البوتاسيوم، وايضا مستوى جيد من تركيز الكلوروفيل، وكذلك أعلى تركيزات من الأسكوريات النشط ومحتوى عالي من البرولين. سجلت هجن جيزة 177 / IRRI 147، سخا 104 / سخا سوبر 300، سخا 106 / IR 59673-93-2-3-3R، سخا 107 / IR 59673-93-2-3-3R تأثيرات إيجابية معنوية في قدره الخاصه على الائتلاف لمحصول الحبوب وبعض الصفات الفسيولوجية. لوحظ وجود قوه الهجين معنوى وإيجابي في محصول الحبوب لكل نبات فردى في الهجن التاليه، سخا 104 / سخا سوبر 300، سخا 104 / IRRI 147، جيزة 177 / IRRI 147 سجلت أعلى القيم مما يشير إلى تفوق هذه الهجن تحت ظروف الملوحة ويمكن استخدامها على نطاق واسع في برامج تربيته الأرز لتحمل الملوحة.

الكلمات المفتاحية: الأرز، الملوحة، الصفات البيوكيميائية، الصفات الفسيولوجية، القدرة على الائتلاف، قوه الهجين، المقاييس الوراثية.