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Comprehensive Selection Criteria for High-Yielding Bread Wheat (*Triticum aestivum* L.) Hybrids under Salinity Stress

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THE MOST important aspect of this investigation was evaluating a set of wheat genotypes with different responses to salt stress while conducting the selection process on the number of spikes/plant, the number of filled grains/spike, 1000-grain weight, and grain yield/plant traits besides, some physiological attributes and related to salinity tolerance such as Na+, K+ contents, Na^+/K^+ ratio, osmotic adjustment, proline, and glycine betaine contents under control and salinity conditions. The wheat genotypes were divided into two groups according to half diallel analysis. Where, the first one included parents, namely; Sakha 8, Shandweel 1, Masr 1, Giza 171, Sakha 94, Gimeaza 11, and Gimeaza 12, respectively. While the second group was 21 F_1 wheat crosses obtained from half diallel crossing among the seven wheat genotypes. Heterosis over better-parent, general, and specific combining ability effects was the most important measurements for all studied traits for both experiments. Further, the seven wheat genotypes and the highest 5 F1 crosses were evaluated for the salinity tolerance indices test using grain yield/plant trait depending on all data estimated for all studied attributes under salt-stress treatment compared to the control experiment. The final results revealed that; parents 1, 2, and 3 besides, the crosses; P1 X P2, P1 X P3, P2 X P3, P2 X P4, and P3 X P4 exhibited a high trend in salinity tolerance under salinity stress treatment compared to the control experiment. Further, the previous wheat genotypes recorded high levels of salinity tolerance indices. SCoT markers determined the hybrids with the highest salinity tolerance indices. Out of nine primers used, only six generated polymorphic bands with 43 polymorphic bands. Therefore, identifying genetic evidence at the molecular level could be used in the future as a taxonomic tool to tolerate salinity in promising wheat genotypes.

Kewwords: Combining ability, Diallel, Heterosis, Physiological markers, Salt indices PCA, SCoT markers, Wheat.

Introduction

Given the great strategic importance of wheat as a global food crop besides the great damage it inflicts on it due to salt stress, this study was launched to understand the nature of this crisis and come up with clear scientific recommendations in this regard. Salt stress is one of the most serious environmental constraints that destroy agricultural production, significantly reduce crop productivity, and hinder growth and development (Parida & Das, 2005; Nessem & Kasim, 2019). The most serious damage caused by saline stress on plant growth is the severe effect and damage in metabolism processes resulting from decreasing the water level needed to wash salts and direct toxicity, anti-ions, and nutrient disruption (Neumann, 1977). Also, it largely causes physiological dehydration (Munns, 2002). Among the most and greatest damages

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resulting from increased salinity is the excessive impact on photosynthesis (Sudhir & Murthy, 2004) by demolishing the chlorophyll content in the leaves (Rady, 2011). Wheat is considered the most important food crop in the world. Hundreds of millions of people globally depend on food made from the grain of the wheat plant. These grains are ground and made into flour used in making biscuits, bread, cakes, thin biscuits, pasta, spaghetti, and other foods. This crop is the first strategically compared to the rest of the other crops. Wheat covers parts of the Earth's surface more than any other food crop. The major wheat-producing countries are Canada, China, France, India, Russia, Ukraine, and the United States (Shewry, 2009). Global wheat production is about 735 million tons. The wheat acreage cultivated in Egypt is estimated at 3.2 million feddans, according to general statistics 2019 season. However, it is noticeable in the recent period that the wheat area in Egypt declined due to the high level of soil salinity and irrigation water. This, of course, caused a serious decline in wheat productivity in the lands damaged by salinity, especially nearing the seawater in the delta region, besides the destructive effects of salinity stress, which were previously mentioned (El-Mouhamady & Ibrahim, 2020). Note that, the total loss in the final yield due to toxicity of salinity stress may range from 40-50%. (Shavrukov et al., 2011) discussed the salt-stress tolerance and Na+ exemption in wheat, calculating genetic variability, mapping populations, and QTL analysis. They confirmed that genetic analysis of F2 generations among landraces and durum wheat succeeded in clear separation marking on the single, major salinity tolerance gene in the wheat genotypes. Gathering carbohydrate and protein fractions was very important in improving salinity-stress tolerance in wheat genotypes by developing osmotic adjustment under stress conditions compared to the control conditions, especially in the wheat genotype Sakha 93, (Radi et al., 2013). Wheat salinity tolerant species can play an important role when there is no quality water suitable for agriculture. Besides, may be able to develop the ability of salinity tolerance through cultivating it with superior care and excellent management to reduce the devastating effects of salt stress in the soil. In addition, increasing the productivity of marginal lands, (Sahoo et al., 2018). The two wheat genotypes, namely, line 16 and Masr 2, characterized as highly salinity tolerance, exhibited positive results in grain yield and its components traits by estimating salinity tolerance indices for many wheat genotypes. For this reason, it is recommended to use them in the future for improving and developing the Egyptian wheat breeding program for salt-stress endurance (Yassin et al., 2019). Genes related to high Na^+ accumulation in bread wheat were recognized, which may be encompassed in tissue tolerance/osmotic adjustment (Genc et al., 2019). They revealed that reduction in plant Na^+ is unlikely to provide agronomic benefit; in addition, the genotype MW#293, characterized as highly tolerant for Na+ content, supplies an opportunity for improving salinity-stress tolerance in wheat. El-Mouhamady & Ibrahim (2020) discussed salinity tolerance in some wheat entries by using various doses of gamma irradiation. They confirmed that the Egyptian wheat varieties Sakha 8 and its 6 M5 derived mutants recorded high salt-stress tolerance measurements in all studied attributes under salinity conditions compared to the control experiment in the two growing seasons. Bacu et al. (2020) detected the impact of NaCl in different growth stages, pigment content, and GSH content in the seedling stage in bread wheat. The most recent studies on salinity tolerance in wheat genotypes to identify tolerable and/or sensitive varieties to salinity (Al-Ashkar et al., 2020). Genetic differentiation among plant collections offers scenarios for improving plant traits. Molecular genetic markers are one of the effective tools for studying genetic variability between parents and their hybrids. Genetic differences based on the molecular level were reported among barley genotypes (Khatab & Mariey, 2013; Mariey et al., 2016) and wheat (El-Hendawy et al., 2019). Many molecular markers have been established recently, gene-targeted marker arrangements have become an important and useful method in assessing genetic variation (Poczai et al., 2013). SCoT polymorphism method is known as one of the new molecular markers described by Collard & Mackill (2009), who developed SCoT 1 to 36 (Luo et al., 2010) and reported SCoT 37 to SCoT 60, which are reproducible and based on the short conserved region flanking the start codon ATG. Because several advantages of SCoT, such as repeatability, low cost, high polymorphism, and potential in genotyping and revealing polymorphism that might be directly related to gene function. These techniques have been successfully applied in genetic diversity studies of many plant species (Etminan et al., 2016; Etminan et al., 2018;

Qaderi et al., 2019). This method is based on the short conserved region of the translation initiation codon (ATG). CATT box-derived polymorphism is another new promoter-targeted marker, which uses the nucleotide sequence CAAT box. The CAAT box region has a specific nucleotide pattern with aligned sequences and is upstream of the start codon of eukaryotic genes (Singh et al., 2014). Wheat, the development and selection of parental genotypes for crossing requires a careful description and variety identification. Most recently, the morph-physiological and molecular depiction has been frequently used for this process as comprehensive criteria for description. The study aimed to assess promising wheat hybrids superior in tolerating salt stress based on morph-physiological and molecular analysis of these hybrids with their respective parents using SCoT markers. This information can be useful to bridge the gap between wheat production and consumption.

Materials and Methods

Materials

Plant materials

This investigation included seven Egyptian wheat genotypes with various salt-stress tolerance responses: Sakha 8, Shandweel 1, Masr 1, Giza 171, Sakha 94, Gimeaza 11, and Gimeaza 12 in Table 1. These genotypes were obtained from the department of wheat Research, Filed Crop Research Institute, Agricultural Research Center (ARC), Egypt.

Breeding and crossing

The seven wheat genotypes were sown in three planting dates with 7 days intervals to overcome the differences in flowering time among parents for crossing through half diallel technique without reciprocals in the 2018/2019 season. All genotypes (parents and their 21 F1 crosses) were grown under control and salinity-stress conditions in a randomized complete block design with three replicates for each experiment in the 2019/2020 season. The chemical analysis for the two kinds of water was shown in Table 2. The package of all other recommendations of wheat planting is followed in the second season (2019/2020). All calculated data performed from all studied traits under the two experiments were analyzed using half diallel analysis by Griffing (1956) model 1, method 2 (This analysis related to parent and F1hybrids only without reciprocals) for estimating some genetic parameters namely; heterosis over better-parent and general and specific combining ability effects, respectively. The wheat entries were planted on 25th November (optimum sowing date when the temperature is 25°C) for the 2019/2020 season using 15 uniformed seeds in each pot and about four cm sowing depth. After 20 days from sowing, the plants were thinned, and only five seedlings were carefully left in each pot to grow until maturity for each experiment.

Treatment and growth conditions

The plants in the two experiments were grown in 30 X 40cm black plastic bags field with about 15kg of sand washed by tap water to avoid salt accumulation. The control conditions mean controlled irrigation using regular drinking water or tap water until harvesting. While, salinity experiment means irrigating using 20.38% seawater obtained from Alexandria seawater and specifically from Al-Agami resort with EC: (51.50 dsm^{-1}) to be after dilution 10.50 dsm^{-1}, (Table 2) from the first day of sowing at a rate of two liters per each black plastic bags (enough for irrigation and leaching to avoid salt accumulation) until harvesting. The irrigation process for each treatment was done every five days. The harvesting process was done after 155 days from sowing in both experiments. Harvest was done on 29th April in the early morning to avoid overseeding.

TABLE 1. Classification of the 7 wheat genotypes used in a half diallel analysis

Serial No.	Names of genotypes	Origin	Salinity tolerance	Reference
1	Sakha 8	Egypt	Tolerance	(Ragab & Khier, 2019).
2	Shandweel 1	Egypt	Tolerance	(Ragab & Khier, 2019).
3	Masr 1	Egypt	Tolerance	(Ragab & Khier, 2019).
4	Giza 171	Egypt	Moderate	(Ragab & Khier, 2019).
5	Sakha 94	Egypt	Moderate	(Ragab & Khier, 2019).
6	Gimeaza 11	Egypt	Moderate	(Ragab & Khier, 2019).
7	Gimeaza 12	Egypt	Moderate	(Ragab & Khier, 2019).

TABLE 2. Chemical analysis of both types of water irrigation (control water and saline water) using in this study

Characteristics	Control irrigation (Tap or control water)	Saline irrigation using 20% (Seawater)
EC (dsm^{-1})	0.57	10.50
pH (1:2.5)	7.01	8.07
Ca^{++} (mgL^{-1})	1.45	8.74
Mg^{++} (mgL^{-1})	1.41	28.52
Na^{+} (mgL^{-1})	1.69	59.34
K^{+} (mgL^{-1})	0.21	2.19
CO_3^{-} (mgL^{-1})	0.0	0.08
HCO_3^{-} (mgL^{-1})	3.49	3.96
Cl^{-} (mgL^{-1})	0.91	98.15
SO_4^{-} (mgL^{-1})	0.27	0.86

The number of irrigation times from planting to harvest

The control experiment was needed to 28 times for irrigation starting from the sowing day to maturity. Also, the salinity experiment was started to irrigate using salt solution starting the first planting day and the total number of irrigates was 28 irrigate. The addition of irrigation of both water types for both experiment was prohibited before harvest with 15 day. In other words, once the plants reach the stage of physiological maturity, that is, at the age of 125 days from planting. The irrigation process continues for both experiments for two weeks, and irrigation is completely prohibited for the two experiments when the plants are exactly 140 days old, i.e. about two weeks after the end of physiological maturity.

It is noted that, fifteen black plastic bags were allocated to grow each genotype for each replicate in each experiment separately to take the largest number of measurements, especially in the salt stress experiment. Through results of previous papers and studies (Ragab & Khier, 2019) found that 20.38% sea water or sea water diluted by 79.62% with EC 10.50 dsm^{-1} is a dose or salt stress limit that can sort and filter all wheat genotypes under evaluating and determine which of them are tolerant, moderate and sensitive to salt stress**.** Therefore, it was used in this study and was only satisfied with it to prevent wasting time, costs and to preserve the genetic materials, especially hybrids. Further, doses less than that do not give definitive results about the extent of tolerance and a dose higher than 20.38% sea water is often lethal. So, this dose (20.38%) of seawater was the ideal dose in this study according to Ragab & Khier (2019).

Chemical analysis of both water types

All elements evaluated presented in table (2) were obtained from three replicates of each experiment and were analyzed through RCBD (a randomized complete block design for each experiment). pH was conducted in Table 2 by pH Meter (Electrometric method with a glass electrode Hanna USA). Also, EC was determined in mmhos/cm at 25°C according to the method by Piper (1947), Salinity Laboratory Staff (1954). Further, the model of pH and EC Meter is (HI9813-6). All anions and cations elements viewed in Table 2 were determined by the method of Beckman flame spectrophotometer (Gilbert et al., 1950).

Physical analysis of planting soil

The soil used in sowing for both treatments were sandy soil (92.0% sand, 3.5.0% slit, 0.8% organic mater, 8% clay and 3.5% clay) and was physically analyzed using sieving method to remove impurities, homogenize the soil, and stabilize weight according to Gee & Or (2002).

Screening for salinity tolerance (salinity indices)

All salinity tolerance indices were estimated according to Fischer & Maurrer (1978), Bouslama & Schapaugh (1984), Lin et al. (1986), Hossian et al. (1990), Fernandez (1992), Gavuzzi et al. (1997), Golestani & Assad (1998), and the data collected was obtained from three replicates of both experiment for grain yield trait only and was analyzed by RCBD (a randomized complete block design) as follows:-

GYP: Is meaning the grain yield/plant for the control experiment.

GYS: Is meaning the grain yield/plant for the salinity experiment.

YSI: Is meaning yield stability index = YS/YP

where: YS the average of yield under stress and YP= The average of yield under the control experiment.

YI: Is meaning yield index (YS for each

genotype/mean of YS for all genotypes).

MP: Is means (Average yield for both trials): YS + YP/2

STI: Is meaning salinity tolerance index (YP X YS/ (mean of YP) ^{2}

GMP: (YP X YS) $^{0.5}$

YR: Is meaning yield reduction (1-YS/YP)

SSI: Is meaning salinity susceptibility index = DSI = (1-YS/YW)/D where YS = mean yield under salt stress, Yw = mean yield under control condition, and D = environmental stress intensity= 1-(mean yield of all genotypes under stress/mean yield of all genotypes under irrigated conditions).

Plant trial measurement and parameters measured Morphological and physiological:

Fifty plants were taken from each genotype of each replicate for each experiment (The control or saline treatment) to evaluate the following traits as follows:-

1) Number of spikes/plant: It was recorded by counted number of spikes per each individual plant.

2) Number of filled grains/spike: Filled grains of the main panicle with separated and counted.

3) 1000-grain weight: It was recorded as the weight of 1000 random filled grains per plant.

4) Grain yield/plant: was recorded as the weight of grain yield of each individual plant, and adjusted to 14% moisture content.

5, 6 and 7) Determination of Na^+ uptake, K+ uptake and Na/K ratio: Shoots sampling was obtained 45 days from sowing from each experiment because germination/emergence and tillering stages are among the most important and sensitive periods for salt stress in wheat. The salinity treatment by seawater was at 10500 ppm. The samples were weighed and dried for three days at 70^{o}C. Finally, samples were grounded and 1 gram dried powder from each sample for all studied materials under control and salt stress experiments and was taken for Na+ and K+ determination by flame photometer.

8) Osmotic adjustment: It was determined by the formula of Jones & Turner (1978) as follows: Osmotic adjustment=

$$\frac{\text{O.P. x R.W.C.}}{100}(\text{Normal}) - \frac{\text{O.P x R.W.C.}}{100}(\text{drought})^{100}$$

where: O.P= Osmotic pressure, R.W.C.= Relative water content.

9) The proline content: it was determined according to Chinard (1952) and modified method by Bates et al. (1973) for both experiments as follows**:**

1) Approximately 0.5g of plant material "leaf" was homogenized in 10mL 3% aqueous sulfosalicylic acid and the homogenate filtered through what man 2 filter paper.

2) Two mL of filtrate was reacted with 2mL acid-ninhydrin and 2mL of glacial acetic acid in a test tube for 1hr at 100^{o}C, and the reaction terminated in ice bath.

3) The reaction mixture was extracted with 4ml toluene mixed vigorously with a test tube stirrer to 15-20sec.

4) The chromophore containing toluene was aspirated from the aqueous phase, warmed to room emperature and the absorbance read at 520nm using toluene for a blank.

5) The proline concentrations were determined from a standard curve and calculated on a fresh basis is as follows:

[(µg proline)/ 115.5 µg/ µ mole]/ [(g sample/5)]= µ moles proline/ g of fresh weight material.

The results related to proline content are average values at least 3-4 samples for each species.

10) Glycine betaine contents It was carried out for both treatments according to the method of Grieve & Grattan (1983) as follows:

Plant drying method

Half of the freshly harvested plant samples, 12 replicates each containing 24 randomly selected

plants, were immediately submerged into liquid N2 and then dried at ambient temperature under 3.33 Pa pressure in a Virtis* freeze drying apparatus. The other half of the plant samples were placed in paper bags and dried in an oven at 80~ for 4 days. After the tissue was dried, it was ground in a blender and stored at room temperature in glass vials.

Extract preparation: Dried finely-ground plant material (0.500g), was mechanically shaken with 20 ml of deionized H20 for 24 hours at 25~ Time required for this step was determined by extracting the plant samples for 1, 4, 16, 24 and 64 hours. The samples were then filtered and the filtrates were stored in the freezer until analysis.

Total glycine betaine determination: Thawed extracts were diluted I: 1 with 2N H_2SO_4. Aliquots (0.50mL) were measured into heavy walled glass centrifuge tubes and cooled in ice water for 1 h. Cold KI-I_2 reagent (0.20mL), prepared by dissolving 15.7g of iodine and 20.0g of KI in 100mL water 9 was added and the reactants were gently stirred with a vortex mixer. The tubes were stored at 0-4~ for 16hrs and then centrifuged at 10,000 rpm for 15 rain at 0~ The supernatant was carefully aspirated with a fine tipped glass tube. Because the solubility of the complexes in the acid reaction mixture increases markedly with temperature, the tubes must be kept cold until the periodide complex is separated from the acid media. The periodide crystals were dissolved in 9.0mL of 1,2-dichloroethane (reagent grade). Vigorous vortex mixing was frequently required to effect complete solution in the developing solvent. After 2-2.5hrs, the absorbance was measured at 365 nm with a Hitachi Spectrometer model 100-20. Reference standards of GB (50-200 ~tg/mL) were prepared in 1N H_2SO_4. The stability and reproducibility of the absorbance values are dependent on the acid concentration of the periodide reaction medium. We tested this effect using a standard solution of GB (90 lag/mL) at various acid concentrations (0 to 8N $HzSO_4$). Standard curves were prepared with every set of plant samples.

It is noted that both fresh leaves samples for determining the proline and glycine betaine contents were obtained 45 days from sowing.

Molecular biology experiments

DNA isolation and SCoT analysis

Genomic DNA was extracted from fresh leaves of 12 wheat entries (The seven parents which have various responses for salinity tolerant and the best five crosses resulting from these parents using half diallel analysis and recorded highly tolerance of salinity stress according to all results calculated from all studied traits under both conditions.) according to the protocol of Biospin plant genomic DNA extraction Kit (Bio basic). Nine (SCoT) primers SCoT 6, 7, 8, 12, 16, 20, 25, 28 and 32 were selected according to Collard & Mackill (2009). Amplification reactions were carried out in a total volume of 25 µl, containing 40-100ng of isolated genomic DNA, 2.5µL of 10X buffer [100mM Tris-Cl-pH 8.3, 0.5M KCl, 0.1% (w/v) gelatin], 1.5mM MgCl2, 200µM of each dNTPs, 0.5µM primer, 0.5 units Taq DNA polymerase. Amplification conditions was as follow, 95°C for 5min for the initial denaturation step, followed by 35 cycles at 94°C for 1min for denaturation, a primer annealing at 50°C for 1 min, and an extension at 72°C for 2min; finally, the extension was carried out at 72°C for 7min. All PCR amplification products were separated on 1.2% agarose gels in TBA 0.5% then stained with ethidium bromide and visualized under UV light.

The twelve wheat genotypes were 1: (Parent 1), 2: (Parent2) 2, 3: (Parent 3), 4 :(Parent 4), 5: (Parent 5), 6: (Parent 6) and 7: (Parent 7) and the best five hybrids namely; H1: (P1 x P2), H2: (P1 x P3) ,H3: (P2 x P3), H4 : (P2 x P4) and H5: (P3 x P4) according to the protocol of Biospin plant genomic DNA extraction Kit (Bio basic), respectively.

SCoT 6 CAACAATGGCTACCACGC **SCoT 7** CAACAATGGCTACCACGG

SCoT 8 CAACAATGGCTACCACGG **SCoT 12** ACGACATGGCGACCAACG

SCoT 16 ACCATGGCTACCACCGAC **SCoT 20** ACCATGGCTACCACCGCG

SCoT 25 ACCATGGCTACCACCGGG **SCoT 28** CCATGGCTACCACCGCCA

SCoT 32 CCATGGCTACCACCGCAC

PCR-generated SCoT bands were detected on

gels and then scored as absent (0) or present (1), only clear, reproducible bands were scored. The primer name (PN), total number of bands (TNB), polymorphism information content (PIC), polymorphic bands (PB) and polymorphism (%).

Statistical analysis

Analysis of variance (ANOVA test)

The analysis of variance and expected mean squares of the studied characters for hybrids and their parents were computed using the formula of Griffing (1956) model 1, method 2 (This analysis related to parent and their F1 crosses only without reciprocals) using three replicates of each experiment in (RCBD).

Estimation of heterosis

The heterosis of an individual cross was determined for each trait as the increase of the F_1 hybrid mean over its better parent, (i.e. heterobeltiosis), as follows:

$$\text{Heterosis over the better parent \%} = \frac{\overline{F_1} - \overline{B.P.}}{\overline{B.P.}} \times 100$$

where: $\overline{F_1}$ = Mean value of the first generation, $\overline{B.P.}$ = Mean value of the better parent.

L.S.D. values were calculated to test the significance of the heterosis effects, according to the following formula suggested by Wyanne et al. (1970).

$$\text{L.S.D. for better parent heterosis} = t\sqrt{\frac{2MSe}{r}}$$

Estimation of combining ability effects (GCA and SCA)

The analysis of variance for hald diallel analysis including parents and crosses was computed according to Virmani et al. (1997).

$\text{L.S.D.} = T \times \sqrt{2MSe/r}$, *: it means significant at 5%, **: it means significant at 1%

Estimation of combining ability

Griffing (1956) stated that the mathematical model and method 2 in this case was as follows:

$$Xij = U + gi + gj + sij + eijk$$

where: Xij= The value of a cross between parent (i) and parent (j), U= The population mean, gi= The general combining ability (gca) effect of the parental variety, gj= The general combining ability (gca) effect in parental variety, sij= Specific combining ability effect (sca) for the cross, eijk= The mean error effect; (i.e. the environmental effect associated with the individual observations).

The estimates of general combining ability effects (gi^) and specific combining ability effects (sij^) were computed as follows:

$$gi = 1/p+2\ (xi + xij - 2/p\ X\ldots.$$

$$sij = xij-1/p+2\ (xi+xii+xj+xij)+2/(p+1)(p+2)\ x..$$

The variances of both effects and differences between effects were estimated as follows:

$$\text{Var}(gi) = p-1/p(p+2)\ \varrho^2e$$

$$\text{Var}(sij) = 2p+p+2/(p+1)(p+2)\ \varrho^2e\ (i\neq j)$$

$$\text{Var}(sij-sik) = 2(p+1)/(p+2)\ \varrho^2e$$

$(i\neq j,\ k,\ j\neq k1 \text{ and } k\neq 1)$

The principle components analysis

The principal components analysis worked among traits for classifying the first two principal components that were graphically plotted against each other, using biplot graph according to Yan & Rajcan (2002). Hierarchical cluster and bi-plot analysis were performed using software program Minitab v.19 according to Sally et al. (1986).

Unit variance scaling method as follows: The model: $Y_{ijk} = \mu + G_i + E_j + GE_{ij} + B_{ij} + É›_{ijk}$ was applied where μ is the mean, G_i is the effect of the i^{th} genotype, E_j is the effect of the jth environment, GE_{ij} is the interaction of the i^{th} genotype with the jth environment, B_{ij} is the effect of the k^{th} replication in the j^{th} environment, and $É›_{ijk}$ is the random error.

Results

ANOVA and mean performance of the studied traits

Data of ANOVA test obtained in Table 3 detected that mean squares due to genotypes, parents, and F1 crosses were highly significant for all studied traits, namely; the number of spikes/plant, number of filled grains/spike, 1000-grain weight, grain yield/plant and physiological traits related to salinity tolerance namely; Na^+, K^+ uptake, Na^+/K^+ ratio, osmotic adjustment,

proline and glycine betaine contents under control and salinity conditions, indicating wide diversity between parents. Also, mean squares due to parents vs. crosses, which indicate the average heterosis, were highly significant for all studied attributes under the same treatments. In the same track, mean squares due to both general (GCA) and specific (SCA) combining abilities effects were highly significant in all traits under the control and salinity stress experiment. These results confirmed both additive and non-additive types of gene action in inheriting and controlling the previous morphological and physiological traits under control and salinity conditions. The GCA/SCA ratio was less than the unity in all studied attributes under both experiments. This confirms that non-additive gene action is very important in inheriting and controlling these traits under both conditions. Therefore, the selection will be effective using the bulk, and not the pedigree method.

Results of mean values estimated for all morphological and physiological traits under control and salinity stress conditions and presented in Table 4 confirmed that the wheat genotypes; P1, P2, P3, P1 X P2, P1 X P3, P2 X P3, P2 X P4, and P3 X P4 exhibited the highest mean values for all attributes studied in the two experiments. For example, but not limited to grain yield/plant has achieved great superiority under salinity stress conditions compared to the control experiment in the aforementioned superior wheat genotypes where its data was as follows; (55.28 and 38.77gm) for parent 1, (48.94 and 35.14gm) for parent 2, (57.26 and 42.33gm) for parent 3, (77.22 and 63.18gm) for P1 X P2, (82.04 and 68.67gm) for P1 X P3, (77.84 and 59.44gm) for P2 X P3, (69.83 and 54.12gm) for P2 X P4 and (80.03 and 51.19gm) for P3 X P4 under both conditions, respectively. In the same context, the superiority was apparent in other important traits, notably osmotic adjustment and the estimated values of some organic compounds closely related to the endurance of salt stress, such as the content of proline and glycine betaine. The values of osmotic adjustment of the aforementioned superior wheat genotypes were lower than the control osmotic pressure values. In addition, the values of proline and glycine betaine contents were higher under salt stress treatment than the control experiment in the same superior genotypes. These promising wheat genotypes mentioned above also excelled in the rest yield components traits under the salt-stress conditions compared to the control experiment.

TABLE 3. Mean squares of the half diallel analysis for all morphological and physiological traits for the control and salinity conditions

S.O.V	D.F	Number of spikes/ plant		Number of filled grains/ spike		1000-grain weight (gm)		Grain yield/ plant (gm)		Na^+ content (ppm)	
		N	S	N	S	N	S	N	S	N	S
Reps	2	0.75	0.48	1.72	1.49	5.33	8.40	11.79	9.64	0.62	1.07
Genotypes	27	39.56**	42.06**	12.87**	22.08**	115.38**	110.81**	45.90**	63.17**	14.73**	17.39**
Parents	6	271.94**	165.80**	194.27**	386.37**	684.29**	327.10**	16.29**	42.0**	234.97**	128.49**
Parents VS crosses	1	49.56**	123.08**	58.39**	19.07**	175.29**	259.49**	7.19**	18.41**	71.45**	55.12**
Crosses	20	138.97**	255.73**	92.71**	103.15**	405.08**	242.31**	28.93**	35.68**	118.36**	38.23**
GCA	6	234.46**	215.06**	163.77**	182.0**	316.23**	240.0**	60.73**	109.04**	413.88**	296.43**
SCA	21	190.02**	87.55**	55.14**	111.32**	190.64**	158.33**	37.44**	78.22**	276.55**	181.33**
Error	54	1.12	0.67	1.55	1.83	0.37	0.26	0.46	0.87	1.38	1.62
Error term		0.37	0.22	0.51	0.61	0.12	0.08	0.15	0.29	0.46	0.54
GCA/SCA		0.17	0.35	0.42	0.23	0.23	0.21	0.23	0.19	0.21	0.23

N: Normal treatment, S: Salinity treatment

TABLE 3. Cont.

S.O.V	D.F	K^+ content (ppm)		Na/K ratio		Osmotic adjustment	Proline content		Glycine betaine content	
		N	S	N	S		N	S	N	S
Reps	2	7.44	12.05	10.27	8.91	0.93	2.52	4.15	17.43	19.02
Genotypes	27	128.49**	115.68**	27.58**	53.20**	249.23**	10.49**	7.59**	112.39**	77.43**
Parents	6	287.32**	198.17**	79.44**	108.06**	38.09**	574.81**	185.77**	63.52**	111.94**
Parents VS crosses	1	46.22**	201.08**	15.32**	7.21**	4.68**	132.81**	118.69**	3.07**	15.78**
Crosses	20	126.94**	305.02**	298.11**	86.55**	13.56**	403.06**	277.55**	14.09**	12.03**
GCA	6	94.66**	83.57**	271.34**	204.05**	39.88**	72.11**	54.03**	104.35**	110.79**
SCA	21	45.22**	61.45**	67.22**	150.84**	28.07**	40.16**	19.68**	58.39**	69.26**
Error	54	0.94	0.51	0.78	0.23	1.07	1.42	1.05	0.93	0.74
Error term		0.31	0.17	0.26	0.07	0.35	0.47	0.35	0.31	0.24
GCA/SCA		**0.30**	**0.19**	**0.57**	**0.19**	**0.20**	**0.25**	**0.39**	**0.25**	**0.22**

GCA/SCA ratio: MSe of GCA-MS error term /Number of parent + 2/ MSe of SCA-MS error term , N: Normal treatment, S: Salinity treatment.

Genetic parameters

Heterosis

Data on heterosis over better-parent for all studied traits in the two experiments are presented in Table 5. It is noted that the most desirable crosses exhibited significant and highly significant positive values of heterosis over better-parent for the traits; the number of spikes/plant, number of filled grains /spike, 1000-grain weight, grain yield/ plant, K+, proline, and glycine betaine contents under control and salinity conditions were P1 X P2, P1 X P3, P2 X P3, P2 X P4, and P3 X P4, respectively. Further, some crosses recorded the same results in the positive direction for the previous genetic parameter, namely; P4 X P5 and P5 X P7 for both conditions and the cross P4 X P7 under control treatment only for the number of spikes/plant trait, P4 X P6 under control experiment only and P4 X P7 under both conditions for the number of filled grains /spike trait, the crosses; P4 X P5 and P5 X P7 under both conditions for 1000-grain weight trait, P4 X P5 and P4 X P6 for control treatment only, P5 X P6 for salt-stress treatment only and the cross P6 X P7 under both experiment for grain yield/plant trait, P4 X P7 for both conditions and P5 X P7 for control conditions only in K+ content trait and the crosses; P4 X P5 and P4 X P6 for control experiment only besides, P4 X P7, P5 X P6, and P5 X P7 for both treatment in proline content trait, respectively. Conversely, significant and highly significant negatively values of heterosis over better-parent under control and salt-stress conditions were observed in the five promising wheat hybrids mentioned above, namely; P1 X P2, P1 X P3, P2 X P3, P2 X P4, and P3 X P4 for the traits; Na+ content, Na+/K+ ratio, and osmotic adjustment besides, the cross P5 X P6 under salinity treatment only for Na+ content trait.

Combining ability effects

Results shown in Table 6 and associated with GCA effects confirmed that the first three wheat parents, namely; Sakha 8, shandweel 1, and masr 1 exhibited significant and highly significant positively values for the number of spikes/plant, number of filled grains /spike, 1000-grain weight, grain yield/plant, K^+, proline, and glycine betaine contents in this regard under both experiments. While, the same wheat genotypes were recorded the same results but in the negative direction under the same treatments for Na^+, Na^+/K^+ ratio contents, and osmotic adjustment traits, respectively. For SCA effects, five crosses only out of 21 cross exhibited significant and highly significant positive values of this genetic parameter under both conditions for the traits; the number of spikes/plant, number of filled grains /spike, 1000-grain weight, grain yield/ plant, K+, proline, and glycine betaine contents. These superior crosses were P1 X P2, P1 X P3, P2 X P3, P2 X P4, and P3 X P4, respectively. Further, the same five promising wheat crosses recorded significant and highly significant negative values of SCA effects under both conditions for Na+, $Na^{+/}$ K^+ ratio contents, and osmotic adjustment traits in Table 7, respectively.

TABLE 4. Mean performances for all morphological and physiological traits in all wheat genotypes tested under the control and salinity conditions

Entries	Number of spikes/plant		Number of filled grains/ spike		1000-grain weight (gm)		Grain yield/ plant (gm)		Na^+ content (ppm)		K^+ content (ppm)		Na/K ratio		Osmotic adjustment	Proline content		Glycine betaine content	
	N	S	N	S	N	S	N	S	N	S	N	S	N	S		N	S	N	S
P1	**13.76**	**10.33**	**107.22**	**102.31**	**43.15**	**37.86**	**55.28**	**38.77**	**0.22**	**0.28**	**2.94**	**2.77**	**0.074**	**0.101**	**0.96**	**41.19**	**36.45**	**56.34**	**38.17**
P2	**16.56**	**12.05**	**112.08**	**109.23**	**47.88**	**31.15**	**48.94**	**35.14**	**0.27**	**0.32**	**2.63**	**2.51**	**0.102**	**0.127**	**0.73**	**39.18**	**37.02**	**46.12**	**32.07**
P3	**12.84**	**9.14**	**110.37**	**100.02**	**40.27**	**29.46**	**57.26**	**42.33**	**0.31**	**0.38**	**2.88**	**2.42**	**0.107**	**0.157**	**0.87**	**48.76**	**42.15**	**51.13**	**42.08**
P4	8.37	6.26	77.45	38.11	25.13	20.04	34.05	26.14	0.67	0.75	2.13	2.01	0.314	0.37	1.77	23.12	18.56	32.19	25.90
P5	5.69	3.08	96.13	42.19	22.08	17.28	29.07	23.14	0.53	0.78	2.25	1.87	0.235	0.417	1.21	21.05	15.32	28.59	22.07
P6	9.27	7.12	81.03	62.03	30.18	24.09	32.76	21.04	0.39	0.53	2.07	1.93	0.188	0.274	1.45	28.43	19.20	30.86	14.05
P7	8.55	4.26	75.70	55.14	27.39	16.41	37.93	25.78	0.48	0.61	2.31	2.11	0.207	0.289	1.85	25.97	17.44	34.12	27.10
P1 X P2	**22.04**	**19.59**	**125.70**	**113.63**	**48.95**	**46.08**	**77.22**	**63.18**	**0.15**	**0.19**	**3.25**	**2.99**	**0.046**	**0.063**	**0.43**	**73.11**	**77.80**	**65.40**	**67.84**
P1 X P3	**25.31**	**17.45**	**121.08**	**116.27**	**51.23**	**49.55**	**82.04**	**68.67**	**0.17**	**0.24**	**3.73**	**3.45**	**0.058**	**0.088**	**0.58**	**68.55**	**75.14**	**82.04**	**86.93**
P1 X P4	10.48	5.31	81.13	63.49	28.29	24.06	41.07	27.44	0.55	0.96	1.74	1.62	0.316	0.592	2.48	26.18	14.76	29.72	34.65
P1 X P5	7.13	6.02	69.28	55.13	25.30	16.32	35.89	30.81	0.44	0.85	2.01	1.55	0.218	0.548	1.18	30.09	24.05	24.30	16.08
P1 X P6	11.08	7.94	75.04	67.19	24.25	15.80	40.02	34.16	0.83	0.94	1.86	1.42	0.446	0.661	1.56	35.77	31.04	27.15	31.03
P1 X P7	6.38	5.11	61.08	38.24	30.41	24.27	29.38	20.45	0.61	0.78	2.15	1.75	0.283	0.445	2.32	20.03	12.71	32.05	26.17
P2 X P3	**21.03**	**19.01**	**128.97**	**118.56**	**61.08**	**55.42**	**77.84**	**59.44**	**0.24**	**0.25**	**3.54**	**3.26**	**0.067**	**0.07**	**0.39**	**58.32**	**73.15**	**77.33**	**82.64**
P2 X P4	**24.65**	**15.84**	**132.40**	**122.07**	**55.22**	**47.12**	**69.83**	**54.12**	**0.19**	**0.22**	**3.04**	**2.80**	**0.062**	**0.078**	**0.28**	**61.07**	**68.78**	**69.08**	**78.03**
P2 X P5	12.05	4.38	92.81	58.37	35.12	27.05	30.12	24.03	0.56	0.64	2.43	1.69	0.230	0.378	1.17	33.18	28.14	22.04	19.32
P2 X P6	8.38	3.26	70.55	34.88	28.42	22.06	38.09	31.74	0.43	0.51	2.31	1.37	0.186	0.372	1.82	24.19	16.08	27.42	18.05
P2 X P7	10.68	7.29	49.48	28.31	37.59	26.18	36.17	28.41	0.59	0.70	2.50	2.03	0.236	0.344	1.36	31.93	22.92	33.0	15.20
P3 X P4	**22.53**	**16.38**	**130.06**	**124.88**	**52.18**	**47.49**	**80.03**	**51.19**	**0.25**	**0.29**	**3.74**	**3.49**	**0.066**	**0.083**	**0.69**	**59.12**	**63.76**	**58.14**	**65.97**
P3 X P5	10.44	6.12	101.19	74.62	31.27	23.79	42.11	25.76	0.57	0.74	2.69	2.08	0.211	0.355	1.38	23.80	12.44	26.02	11.43
P3 X P6	8.40	6.11	87.66	61.20	28.09	25.21	39.28	19.04	0.46	0.86	2.35	2.17	0.195	0.396	1.96	32.07	27.54	34.18	23.85
P3 X P7	7.15	3.97	54.23	37.52	35.40	29.37	45.64	31.17	0.65	0.94	2.59	1.74	0.250	0.540	2.07	27.13	20.12	37.0	31.15
P4 X P5	11.0	7.98	100.29	65.87	29.81	23.47	36.40	16.88	0.82	0.89	2.20	1.67	0.372	0.532	2.55	26.19	18.04	25.17	20.04
P4 X P6	7.55	4.25	85.06	47.92	23.06	16.92	38.07	14.84	0.51	0.68	1.92	1.38	0.265	0.492	2.15	32.11	14.55	21.73	16.42
P4 X P7	12.11	5.29	91.15	65.31	20.45	14.78	27.60	12.58	0.69	0.88	2.55	2.28	0.270	0.385	2.95	29.01	22.08	24.92	13.86
P5 X P6	6.54	3.77	68.37	49.17	26.68	18.45	33.49	28.56	0.44	0.49	2.27	1.54	0.193	0.318	2.03	34.16	30.10	27.07	20.54
P5 X P7	10.28	6.81	83.09	70.15	30.17	21.07	24.35	15.38	0.79	0.99	2.38	1.93	0.331	0.512	2.28	29.80	23.74	31.65	24.83
P6 X P7	8.32	7.16	79.65	53.04	25.01	17.09	42.06	30.05	0.53	0.72	1.87	1.41	0.283	0.510	1.55	24.02	15.60	28.37	19.61
LSD at 0.05	1.44	1.11	1.69	1.84	0.82	0.69	0.92	1.27	1.60	1.73	1.32	0.97	1.20	0.65	1.41	1.62	1.39	1.31	0.82
LSD at 0.01	2.06	1.59	2.42	2.63	1.18	0.99	1.32	1.82	2.29	2.48	1.89	1.39	1.72	0.93	2.01	2.32	1.99	1.88	1.17

LSD: Least significant differences at 5 and 1%, p: Parent.

TABLE 5. Estimates of heterosis over better-parent for the 21 wheat crosses of all morphological and physiological traits under the control and salinity conditions

Crosses	Number of spikes/ plant		Number of filled grains/Spike		1000-grain weight (gm)		Grain yield/plant (gm)		Na+ content (ppm)		K+ content (ppm)		Na/K ratio		osmotic adjustment	Proline Content		Glycine Betaine Content	
	N	S	N	S	N	S	N	S	N	S	N	S	N	S		N	S	N	S
P1 X P2	**33.09****	**62.57****	**12.15****	**4.02****	**2.23***	**21.71****	**3.68****	**62.96****	**-31.81****	**-40.62****	**10.54****	**7.94****	**-37.83****	**-37.62****	**-41.09****	**77.49****	**110.15****	**16.08****	**76.66****
P1 X P3	**83.93****	**68.92****	**9.70****	**13.64****	**18.72****	**30.87****	**43.27****	**62.22****	**-22.72****	**-14.28****	**26.87****	**24.54****	**-21.62****	**-12.87****	**-33.33****	**40.58****	**78.26****	**45.61****	**106.58****
P1 X P4	-23.83**	-48.59**	-24.33**	-37.94**	-34.43**	-36.45**	-25.70**	-29.22**	150.0**	242.85**	-40.81**	-41.51**	327.02**	486.13**	158.33**	-36.44**	-59.50**	-47.24**	-9.22**
P1 X P5	-48.18**	-41.72**	-35.38**	-46.11**	-41.36**	-56.89**	-35.07**	-20.53**	100.0**	203.57**	-31.63**	-44.04**	194.59**	442.57**	22.91**	-26.94**	-34.01**	-56.86**	-57.87**
P1 X P6	-19.47**	-23.13**	-30.01**	-34.32**	-43.80**	-58.26**	-27.60**	-11.89**	277.27**	235.71**	-36.73**	-48.73**	502.70**	554.45**	62.50**	-13.15**	-14.84**	-51.81**	-18.70**
P1 X P7	-53.63**	-50.53**	-43.03**	-62.62**	-29.52**	-35.89**	-46.85**	-47.25**	177.27**	178.57**	-26.87**	-36.82**	282.43**	340.59**	141.66**	-51.37**	-65.13**	-39.43**	-31.43**
P2 X P3	**26.99****	**57.75****	**15.06****	**8.54****	**27.56****	**77.91****	**35.94****	**40.42****	**-11.11****	**-10.71****	**22.91****	**29.88****	**-34.31****	**-44.88****	**-46.57****	**19.60****	**73.54****	**51.24****	**96.38****
P2 X P4	**48.85****	**31.45****	**18.12****	**11.75****	**15.32****	**51.26****	**42.68****	**54.01****	**-29.62****	**-31.25****	**15.58****	**11.55****	**-39.21****	**-38.58****	**-61.64****	**55.87****	**85.79****	**49.78****	**143.31****
P2 X P5	-27.23**	-63.65**	-17.19**	-46.56**	-26.64**	-13.16**	-38.45**	-31.61**	107.40**	100.0**	-7.60**	-32.66**	125.49**	197.63**	60.27**	-15.31**	-23.98**	-52.21**	-39.75**
P2 X P6	-49.39**	-72.94**	-37.05**	-68.06**	-40.64**	-29.18**	-22.17**	-9.67**	59.25**	59.37**	-12.16**	-45.41**	82.35**	192.91**	149.31**	-38.25**	-56.56**	-40.54**	-43.71**
P2 X P7	-35.50**	-39.50**	-55.85**	-74.08**	-21.49**	-15.95**	-26.09**	-19.15**	118.51**	118.75**	-4.94**	-19.12**	131.37**	170.86**	86.30**	-18.50**	-38.08**	-28.44**	-52.60**
P3 X P4	**75.46****	**79.21****	**17.83****	**24.85****	**29.57****	**61.20****	**39.76****	**20.93****	**-19.35****	**-23.68****	**29.86****	**44.21****	**-38.31****	**-47.13****	**-20.68****	**21.24****	**51.26****	**13.71****	**56.77****
P3 X P5	-18.69**	-33.04**	-8.31**	-25.39**	-22.34**	-19.24**	-26.45**	-39.14**	83.87**	94.73**	-6.59**	-14.04**	97.19**	126.11**	58.62**	-51.18**	-70.48**	-49.11**	-72.83**
P3 X P6	-34.57**	-33.15**	-20.57**	-38.81**	-30.24**	-14.42**	-31.40**	-55.02**	48.38**	126.31**	-18.40**	-10.33**	82.24**	152.22**	125.28**	-34.22**	-34.66**	-33.15**	-43.32**
P3 X P7	-44.31**	-56.56**	-50.86**	-62.48**	-12.09**	-0.30 NS	-20.29**	-26.36**	109.67**	147.36**	-10.06**	-30.67**	133.64**	243.94**	137.93**	-44.36**	-52.26**	-27.63**	-25.97**
P4 X P5	31.42**	27.47**	-9.13**	-34.14**	18.62**	17.11**	6.90**	-35.42**	54.71**	18.66**	-2.22**	-16.91**	58.29**	43.78**	110.74 **	13.27**	-2.80 NS	-21.80**	-22.62**
P4 X P6	-18.55*	-40.30**	4.97**	-22.74**	-23.59**	-29.76**	11.80**	-43.22**	30.76**	28.30**	-9.85**	-31.34**	40.95**	79.56**	48.27**	12.94**	-24.21**	-16.10**	-36.60**
P4 X P7	41.63**	-15.49 NS	17.68**	18.44**	-25.33**	-26.24**	-27.23**	-51.87**	43.75**	44.26**	10.38**	8.05**	30.43**	33.21**	59.45**	11.70**	18.96**	-26.96**	-48.85**
P5 X P6	-29.44**	-47.05**	-28.87**	-20.73**	-11.59**	-23.41**	2.22 NS	23.42**	12.82**	-7.54**	0.88 NS	-28.05**	2.65**	16.05**	67.76 **	20.15**	56.77**	-12.28**	-6.93**
P5 X P7	20.23*	59.85**	-13.56**	27.22**	10.14**	21.93**	-35.80**	-40.34**	64.58**	62.29**	3.03**	-8.53**	59.90**	77.16**	88.42 **	14.74**	36.12**	-7.23**	-8.37**
P6 X P7	-10.24 NS	-0.56 NS	-1.70 NS	-14.49**	-17.13**	-29.05**	10.88**	16.56**	35.89**	35.84**	-19.04**	-33.17**	50.53**	86.13**	6.89 **	-15.51**	-18.75**	-16.85**	-27.63**
LSD at 0.05	1.44	1.11	1.69	1.84	0.82	0.69	0.92	1.27	1.60	1.73	1.32	0.97	1.20	0.65	1.41	1.62	1.39	1.31	0.82
LSD at 0.01	2.06	1.59	2.42	2.63	1.18	0.99	1.32	1.82	2.29	2.48	1.89	1.39	1.72	0.93	2.01	2.32	1.99	1.88	1.17

LSD: Least significant differences at 5 and 1%, p: Parent.

TABLE 6. Estimates of GCA effects for the 7 wheat parents of all morphological and physiological traits under both conditions

Parents	Number of spikes/plant		Number of filled grains/Spike		1000-grain weight (gm)		Grain yield/ plant (gm)		Na^+ content (ppm)		K^+ content (ppm)		Na/K ratio		Osmotic adjustment	Proline content		Glycine betaine content	
	N	S	N	S	N	S	N	S	N	S	N	S	N	S		N	S	N	S
P1	**7.13****	**4.95****	**1.45****	**2.07****	**6.32****	**4.69****	**2.68****	**3.58****	**-0.53****	**-1.48****	**2.46****	**9.72****	**-1.94****	**-3.81****	**-2.88****	**7.28****	**5.23****	**9.60****	**4.12****
P2	**5.18****	**8.05****	**1.97****	**4.38****	**2.34****	**7.02****	**4.07****	**5.29****	**-5.23****	**-2.95****	**9.04****	**4.58****	**-0.87****	**-1.88****	**-1.49****	**11.82****	**6.35****	**6.48****	**1.95****
P3	12.03**	9.34**	6.33**	5.19**	1.90**	3.65**	7.22**	2.29**	-3.14**	-8.11**	1.84**	3.06**	-2.78**	-5.48**	-3.69**	4.07**	3.79**	2.71**	1.69**
P4	-1.97**	-0.78 NS	-0.16 NS	-0.37 NS	0.65 NS-	0.54 NS-	-1.11 NS	-0.42 NS	0.22 NS	-0.18NS	-1.29**	-2.06**	0.66**	0.91**	0.07 NS	0.22 NS	0.72 NS	0.15 NS	0.34 NS
P5	-3.06**	-13.98**	-0.88**	-3.41**	-1.83**	-2.94**	-1.64**	-2.28**	1.75**	0.95**	-2.05**	-5.69**	1.29**	0.73**	0.96**	-2.87**	-1.91**	-4.06**	-1.84**
P6	-4.76**	-3.79**	-3.69**	-1.18**	-1.65**	-2.19**	-5.01**	-3.47**	1.46**	4.39**	-3.40**	-1.86**	0.39**	2.88**	0.73**	-4.27**	-7.18**	-2.55**	-1.57**
P7	**-14.55****	**-3.79****	**-5.02****	**-6.68****	**-6.43****	**-9.69****	**-6.21****	**-4.99****	**5.47****	**7.38****	**-6.60****	**-7.75****	**3.25****	**6.65****	**6.30****	**-16.25****	**-7.0****	**-12.33****	**-4.69****
LSD at 0.05 (gi-gi)	0.74	0.93	0.28	0.41	1.02	1.05	1.39	1.21	0.38	0.05	0.71	0.64	0.05	0.07	0.15	2.15	1.45	1.23	1.09
LSD at 0.01 (gi-gi)	0.82	0.97	0.32	0.53	1.23	1.14	1.58	1.33	0.49	0.21	0.88	0.77	0.12	0.28	0.28	2.36	1.83	1.57	1.24

Salinity tolerance indices

Results viewed in Table 8 and associated with salinity tolerance indices test detected that the wheat genotypes; (Parent 4 and 5 besides the crosses; P1 X P2, P1 X P3, P2 X P3, and P2 X P4) for (YSI) parameter and (P1, P2, P3, P1 X P2, P1 X P3, P2 X P3, P2 X P4, and P3 X P4) for (MP and GMP) parameters exhibited the highest averages for grain yield trait. This fact indicated that these promising wheat genotypes were considered highly tolerant for salinity than the control experiment. In the same context, the five promising wheat hybrids (P1 X P2, P1 X P3, P2 X P3, P2 X P4, and P3 X P4) for the parameters (YI and STI) were recorded mean values higher than one. This confirmed that these superior wheat entries were achieved high salinity tolerance under salt-stress treatment compared to the control treatment, unlike the rest of the other genotypes. While parents number 4 and 5 and the four promising wheat crosses, namely; P1 X P2, P1 X P3, P2 X P3, and P2 X P4 for SSI, recorded mean values lower than one and exhibited the lowest percentages of (YR) parameter affirmed that these superior wheat genotypes were showed high tolerance for salinity stress in this investigation.

Phenotypic diversity among entries

Bi-plot analysis and hierarchical clustering analysis were used to classify wheat parents and their hybrids based on principal component analysis besides the average of all the studied phenotypic characters. All entries were classified into four classes as follow; 1: (1, 2, 3), 2: (8, 9, 14, 15, 19), 3: (4, 13, 17, 18, 22), and class four included the rest entries as shown in (Fig. 1). Also, the hierarchical clustering analysis was to construct a distance matrix using the Euclidean coefficient average linkage method, which is graphically illustrated in the dendrogram and showing similarity among all the 28 entries. In addition, it divided the previous genetic materials into two major groups (Fig. 2). The first group was divided into two subgroups; the first one includes the three tolerant parents; (P1, P2, and P3), and the other groups include their tolerant hybrids; (P1X P2, P1XP3, P2XP3, P2XP4, and P2XP4), which they had the highest GY under both control and salinity stress and showed high performance for almost studied traits and selected for further molecular analysis. The second major group was divided into four groups included all moderately parents and hybrids, as shown in (Fig. 2).

TABLE 7. Estimates of SCA effects for the 21 wheat crosses of all morphological and physiological traits under the control and salinity conditions

Crosses	Number of spikes/ plant		Number of filled grains/ spike		1000-grain weight (gm)		Grain yield/plant (gm)		Na^+ content (ppm)		K^+ content (ppm)		Na/K ratio		Osmotic adjustment	Proline content		Glycine betaine content	
	N	S	N	S	N	S	N	S	N	S	N	S	N	S		N	S	N	S
P1 X P2	**147.98****	**63.12****	**17.45****	**131.04****	**15.68****	**12.07****	**45.19****	**72.08****	**-13.56****	**-7.88****	**7.33****	**11.04****	**-11.05****	**-8.44****	**-12.56****	**37.45****	**16.84****	**27.81****	**31.04****
P1 X P3	**11.08****	**92.05****	**103.11****	**48.22****	**138.11****	**204.47****	**26.12****	**50.38****	**-56.22****	**62.11****	**41.09****	**16.77****	**-33.17****	**-54.21****	**-54.13****	**55.04****	**71.09****	**108.45****	**91.77****
P1 X P4	-20.05**	-12.83**	-14.21**	-39.55**	-3.49**	-10.30**	-2.79**	-6.38**	1.76**	3.81**	-3.45**	-5.60**	13.06**	10.09**	4.55**	-1.64**	-11.24**	-2.59**	-6.31**
P1 X P5	-11.08**	-7.59**	-9.55**	-16.89**	-15.04**	-7.51**	-13.48**	-2.79**	5.23**	7.02**	-1.85**	-0.95**	5.38**	8.13**	3.96**	-19.23**	-3.56**	-13.42**	-4.35**
P1 X P6	-5.92**	-11.49**	-6.11**	-71.18**	-11.46**	-14.03**	-5.16**	-9.47**	8.12**	13.45**	-2.73**	-7.42**	14.76**	9.07**	5.03**	-17.33**	-2.36**	-16.94**	-20.08**
P1 X P7	-13.08**	-40.39**	-18.19**	-41.09**	-7.81**	-22.07**	-6.84**	-1.94**	13.78**	84.97**	-4.08**	-6.09**	25.63**	21.07**	1.56 NS	-1.39**	-38.94**	-24.77**	-28.23**
P2 X P3	**226.39****	**23.17****	**60.08****	**107.24****	**41.33****	**19.84****	**119.23****	**68.77****	**-45.18****	**-32.12****	**18.69****	**21.03****	**-92.55****	**-28.77****	**-18.29****	**18.97****	**136.56****	**88.17****	**29.43****
P2 X P4	**101.24****	**48.69****	**36.13****	**58.92****	**35.02****	**122.75****	**125.31****	**42.39****	**-10.05****	**-29.25****	**15.56****	**12.32****	**-45.23****	**-103.41****	**-24.76****	**127.93****	**15.42****	**118.38****	**105.22****
P2 X P5	-14.55**	-27.38**	-4.19**	-10.48**	-4.16**	-15.49**	-28.09**	-23.04**	18.58**	19.31**	-1.57**	-6.18**	20.03**	17.24**	2.72*	-5.73**	-1.55**	-10.04**	-4.19**
P2 X P6	-6.77**	-13.08**	-32.07**	0.89*	-24.92**	-7.18**	-7.34**	-18.05**	1.99**	2.58**	-5.43**	-2.79**	12.92**	4.12**	6.09**	-16.32**	-7.33**	-54.11**	-1.55**
P2 X P7	-1.99**	-26.33**	-5.06**	-13.27**	-10.14**	-3.74**	-49.83**	-1.71*	6.33**	11.39**	-0.78**	-1.26**	1.68**	1.21*	1.16 NS	-4.82**	-2.49**	-8.76**	-15.49**
P3 X P4	**39.56****	**26.44****	**51.03****	**80.14****	**79.46****	**-14.91****	**94.34****	**78.55****	**-122.98****	**-67.32****	**36.97****	**25.81****	**-72.83****	**-36.09****	**-17.38****	**28.17****	**38.21****	**47.33****	**25.11****
P3 X P5	-4.27**	-16.02**	-13.28**	-9.13**	-8.39**	-2.83**	-15.27**	-6.19**	67.03**	41.30**	-0.22 NS	-0.07 NS	46.35**	35.07**	8.51**	-2.18**	-7.89**	-13.78**	-8.23**
P3 X P6	-12.79**	-5.79**	-8.93**	-5.04**	-27.14**	-10.08**	-12.37**	-36.94**	17.39**	4.01**	-0.12 NS	-0.04 NS	19.06**	10.05**	0.69 NS	-4.06**	-6.37**	-9.44**	-1.85**
P3 X P7	-1.76**	-2.08**	-1.82**	-2.97**	-14.55**	-51.23**	-34.07**	-20.07**	8.03**	14.05**	-4.15**	-2.95**	8.14**	2.79**	1.54 NS	-10.29**	-4.05**	-2.96**	-4.03**
P4 X P5	-8.09**	-12.62**	-16.44**	-18.47**	-12.57**	-8.66**	-2.72**	-4.16**	12.43**	8.72**	-14.98**	-8.33**	1.63**	8.94**	2.85**	-8.03**	-2.16**	-11.14**	-5.21**
P4 X P6	-21.06**	-38.20**	-20.03**	-10.08**	-21.46**	-17.01**	-8.06**	-17.27**	14.69**	0.77**	-10.08**	-4.19**	5.97**	13.60**	3.24**	-11.24**	-21.03**	-5.41**	-8.97**
P4 X P7	-3.69**	-1.58**	-3.78**	-14.03**	-6.31**	-11.03**	-11.69**	-7.23**	7.74**	23.40**	-2.05**	-0.88**	36.21**	29.44**	11.21**	-1.78**	-7.49**	-23.84**	-4.93**
P5 X P6	-7.04**	-18.27**	-1.97**	-4.66**	-38.19**	-21.03**	-14.27**	-9.32**	4.03**	11.03**	-6.13**	-1.49**	19.37**	2.58**	4.96**	-3.62**	-1.86**	-19.63**	-6.23**
P5 X P7	-1.88**	-3.66**	-23.38**	-1.15**	-2.91**	-5.17**	-3.56**	-24.83**	1.96**	14.90**	-11.09**	-9.04**	14.63**	21.07**	7.23**	-5.33**	-2.74**	-1.96**	-1.66**
P6 X P7	-392.23**	-16.16**	-88.79**	-168.46**	-101.06**	-136.86**	-194.65**	-122.78**	58.90**	186.25**	-50.93**	-29.69**	10.01**	36.45**	61.82**	-154.57**	-157.06**	-171.35**	-161.26**
LSD at 0.05 (sij-skl)	0.82	0.77	0.56	0.72	1.36	1.07	1.79	1.49	0.59	0.28	0.49	0.36	1.02	1.15	2.45	1.27	1.19	1.62	1.35
LSD at 0.01 (sij-skl)	0.97	1.02	0.77	1.07	2.78	1.92	2.18	1.81	0.78	0.39	0.65	0.47	1.27	1.28	3.22	1.54	1.33	1.88	1.48

TABLE 8. Estimation of salinity tolerance indices for the 12 wheat genotypes especially for grain yield/plant trait under both treatments

Genotypes	GYP	GYS	YSI	YI	MP	STI	GMP	YR	SSI
Parent 1	55.28	38.77	0.70	0.91	47.02	0.66	46.29	0.30	1.20
Parent 2	48.94	35.14	0.71	0.82	42.04	0.53	41.46	0.29	1.16
Parent 3	57.26	42.33	0.73	0.99	49.79	0.74	49.23	0.27	1.08
Parent 4	34.05	26.14	0.76	0.61	30.09	0.27	29.83	0.24	0.96
Parent 5	29.07	23.14	0.79	0.54	26.10	0.20	25.93	0.21	0.84
Parent 6	32.76	21.04	0.64	0.49	26.90	0.21	26.25	0.36	1.44
Parent 7	37.93	25.78	0.67	0.60	31.85	0.30	31.27	0.33	1.32
P1 X P2	77.22	63.18	0.81	1.48	70.20	1.50	69.84	0.19	0.76
P1 X P3	82.04	68.67	0.82	1.61	75.35	1.74	75.05	0.18	0.72
P2 X P3	77.84	59.44	0.76	1.40	68.64	1.43	68.02	0.24	0.96
P2 X P4	69.83	54.12	0.77	1.27	61.97	1.16	61.47	0.23	0.92
P3 X P4	80.03	51.19	0.63	1.20	65.61	1.26	64.0	0.37	1.48
LSD at 0.05%	11.94	16.87	0.04	0.02	15.43	0.03	11.94	0.07	0.25

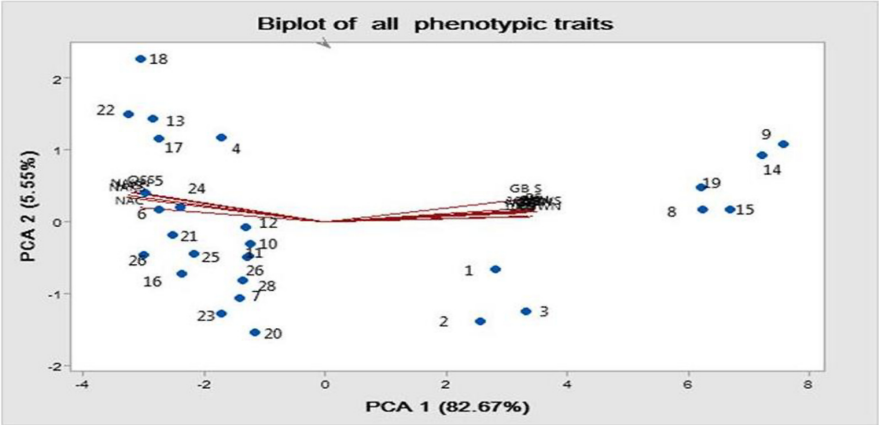

Fig. 1. Bi-plot analysis of morpholoical and physiological traits to classify 28 wheat genotypes their names were 1: P1, 2: P2, 3:P3, 4:P4, 5:P5, 6:P6, 7:P7, 8:P1XP2, 9:P1XP3, 10: P1XP4, 11:P1XP5, 12:P1XP6, 13:P1XP7, 14:P2XP3,15: P2XP4, 16: P2XP5, 17 : P2XP6, 18: P2XP7, 19: P3XP4, 20:P3XP5, 21 : P3XP6, 22: P3XP7, 23:P4XP5, 24: P4XP6, 25: P4XP7, 26 :P5XP6, 27: P5XP7 and 28: P6XP7, respectively

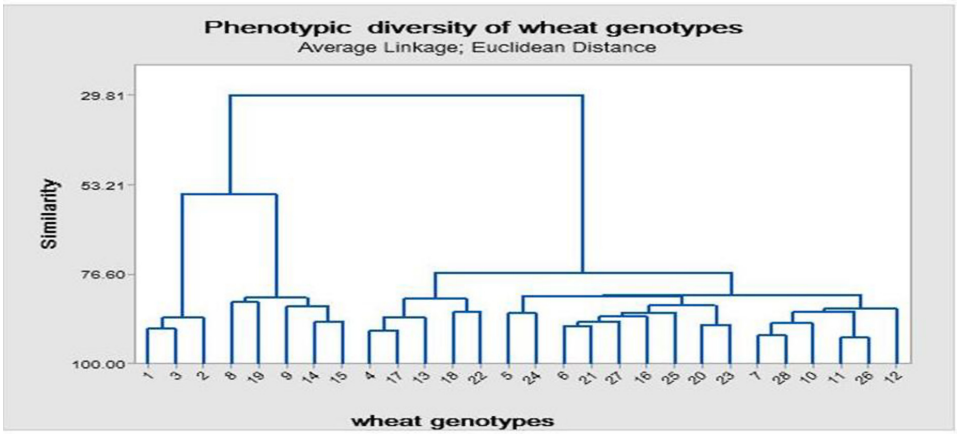

Fig. 2. Cluster analysis based on phenotypic traits to classify 28 wheat genotypes their names were names were 1: P1, 2: P2, 3: P3, 4: P4, 5: P5, 6: P6, 7: P7, 8: P1XP2, 9: P1XP3, 10: P1XP4, 11: P1XP5, 12: P1XP6, 13: P1XP7, 14: P2XP3 ,15: P2XP4, 16: P2XP5, 17: P2XP6, 18: P2XP7, 19: P3XP4, 20 :P3XP5, 21: P3XP6, 22: P3XP7, 23:P4XP5, 24: P4XP6, 25: P4XP7, 26 :P5XP6, 27: P5XP7 and 28: P6XP7, respectively

Molecular markers

SCoT primers were used to fingerprint and find an association among wheat hybrids and their respected parents with 48 bands. Out of nine used primers, only six generated polymorphic bands with a total of 43 polymorphic bands that were scorable and detected on both gels were considered for diversity analysis; two of them were uninformative (SCoT 8 and 28) with 11 bands. Only four primers (SCoT 6, 12, 16, and 25) generate 32 informative 32 bands and show specific bands in parents and respected hybrids, as shown in table 9. Other primers (SCoT 7 and 32) gave only monomorphic bands with two bands and SCoT 20 with one monomorphic band. The highest number of SCoT bands occurred with SCoT 16 with 11 bands, followed by SCoT 12 with eight bands with the highest PIC values 0.48 and 039, respectively. Here, we evaluated nine SCoT primers and studied their ability to discriminate between the salt tolerance of genotypes and their selected hybrids through identifying allele markers. In this study, a total of 48 bands were detected with an average of 5.33 alleles and a PIC value of 0.28 per primer (Table 9). Furthermore, the polymorphism percentage for SCoT primers ranged from 71 to 90% with specific bands with size (Fig 3). Moreover, bands with sizes 1050 and 550 bp were bands using SCoT 6 found on P3 corresponding P2 X P3 and P4 and their hybrid P2 X P4, respectively. Similarly, using SCoT 12, a band was found in P1 and their hybrid P1 X P2 with size 720pb.

TABLE 9. Amplification results generated by SCoT primers in 12 wheat genotypes

Primer number.	Primer sequences (5′→3′)	(Guanin-cytosine content %) GC(%)	Total No. of band	Band size/bp	Number of polymorphic bands (poly %)	PIC (Polymorphic information content)
SCoT 6	CAACAATGGCTACCACGC	56	7	1050-200	5 (71%)	0.36
SCoT 8	CAACAATGGCTACCACGG	56	4	600.250	3 (75%)	0.28
SCoT 12	ACGACATGGCGACCAACG	61	8	1200-350	6 (75%)	0.39
SCoT 16	ACCATGGCTACCACCGAC	56	11	1000-120	10 (90%)	0.48
SCoT 25	ACCATGGCTACCACCGGG	67	6	900-150	5(83%)	0.34
SCoT 28	CCATGGCTACCACCGCCA	67	7	1000-200	6(85%)	0.33

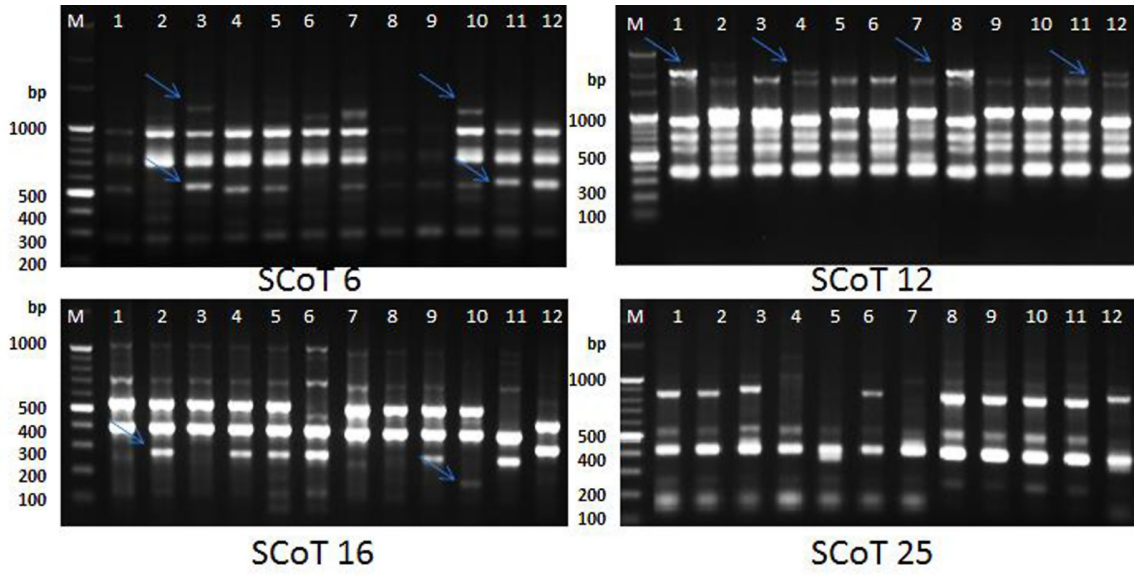

Fig. 3. SCoT profiles produced with different primers, M 100 bp ladder marker; 1: P1 (Sakha 8), 2: P2 (Shandweel 1), 3: P3 (Masr 1), 4: P4 (Giza 171), 5: P5 (Sakha94), 6: P6 (Gimeaza 11), 7: P7 (Gimeaza 12), 8: P1 X P2, 9: P1 XP 3, 10: P2 X P3, 11: P2 X P4 and 12: P3 X P4, respectively

Discussion

Results generated from Table 3 are the largest evidence of the effect of additive and non-additive gene action on selecting important and desired quantitative traits for the breeder, such as high yielding associated with the plant's tolerance to difficult environmental factors challenges like salt stress. In addition, the selection process for these traits will be influential and important in the genetic improvement of wheat to tolerate this dangerous environmental factor if it takes place in the early segregation generations. Therefore, this study succeeded in selecting and using different wheat genotypes in response to salt stress. So that, there is a great opportunity for the breeder to choose the most tolerant genotypes from among the large number of hybrids produced in this context. These results agreed with those reported by El-Mouhamady et al. (2014, 2016), Esmail et al. (2016), El-Mouhamady et al. (2019), El-Mouhamady & Ibrahim (2020), El-Mouhamady & El-Metwally (2020).

By observing all results shown in Table 4, it is clear that the superior genotypes in all studied traits have shown a great tolerance to salt stress under salinity treatment compared to the control, namely; P1, P2, P3, P1 X P2, P1 X P3, P2 X P3, P2 X P4, and P3 X P4 were based in their endurance on a large number of reasons and mechanisms that supported their position in this tolerance. Because they were able to reduce the level losing in the final output and its components to a minimum limit under salinity-stress conditions compared to the control experiment through genetically and physiologically transformation in biological and biochemical processes by the osmotic modification in the cell. This fundamental modification ensures the continuity of plant life under salt-stress conditions by reducing the high osmotic pressure that causes the exit of the water from inside cells to the lowest limits. Besides, converting it to the modified osmotic pressure (osmotic adjustment). Thus, reducing the degree of sodium toxicity in cells and increasing the potassium content is responsible for withstanding salt stress. This, of course, is done through physiological and genetic control of opening and closing the root system (Embryonic adventitious roots) to receive a low rate of sodium element and increase the amount of potassium element. Also, controlling the process of opening and closing of the stomata to prevent the depletion and consumption of a large amount of water during the photosynthesis process besides, preserve it for only vital processes such as germination, growth, leaf and fruiting formation, and high yield production under these critical physiological conditions. Further, the production and excretion of a large level of proline and glycine betaine contents under salt-stress conditions compared to the control experiment in the aforementioned promising wheat genotypes has added a physiological reason to bear not only to the salt stress but also for all environmental stresses that harm plants and destroy the final output (Abdel Sattar & El-Mouhamady, 2012; El-Mouhamady et al., 2016; Sahoo et al., 2018; Selem, 2019; Shaimaa et al., 2019; Yassin et al., 2019; Ebeed et al., 2019; Loutfy et al., 2019; Genc et al., 2019; El-Mouhamady et al., 2019; Abou Alhamd & Loutfy, 2020; Bacu et al., 2020; Al-Ashkar et al., 2020;Gaafar et al., 2020; El-Mouhamady & Ibrahim, 2020). Results shown in Table 5 are related to heterosis over better-parent asserted the fruitful role of dominance and dominance X dominance gene action. Further, this is closely related to the important function of SCA effects for controlling and inheriting salt-stress tolerance in the superior wheat genotypes, namely, P1 X P2, P1 X P3, P2 X P3, P2 X P4, and P3 X P4. This indicates the positive results of wheat tolerance to salt stress obtained from the transgressive segregation in all studied traits, especially the superiority occurring in grain yield/plant and its components under salt-stress conditions, compared to the control experiment. Accordingly, The five promising wheat hybrids superior in all morphological and physiological traits, deservedly to be the actual nucleus for producing wheat lines highly tolerant to salt stress besides the highest output under Egyptian conditions. That is by tracing its cultivation from the first generation to the later segregation generations with the follow-up of selection for salt stress tolerance and high yield in a saline environment besides the control soil. These results agreed with those reported by several investigators (El-Mouhamady et al., 2014; Eldessouky et al., 2016; El-Mouhamady et al., 2016; El-Mouhamady et al., 2019; El-Mouhamady & Ibrahim, 2020). Data of GCA effects obtained in Table 6 detected the important role of additive and additive X additive types of gene action responsible for controlling the previous traits and inheriting the ability of salt-stress tolerance in the recent wheat genotypes. Whatever, the values of SCA effects obtained in Table 7 showed the

impact and the fruitful function of dominance and dominance X dominance types of gene action for increasing and enhancing salinity tolerance in wheat genotypes under salinity treatment compared to the control experiment. In addition, SCA effects were correlated with heterosis over better-parent for screening and testing a large number of hybrids for salinity stress tolerance. This is the desired goal of this investigation (El-Mouhamady et al., 2012a, b, c; Ramadan et al., 2016; Heiba et al., 2016a; Khatab et al., 2019; Tawfik & El-Mouhamady, 2019).

Salinity tolerance indices test succeeded in sorting and sifting 12 wheat genotypes and determining their response to this devastating environmental stress in Table 8. Because this test was based primarily on knowledge of a set of genetic parameters, foremost of which is knowledge of the losing degree in the final output and the degree of sensitivity to salt stress and its linkage with the rest of the basic constants in this test. The most desirable wheat genotypes that exhibited a high rank of YI, MP, and GMP were the first three parents and the five superior crosses namely; P1 X P2, P1 X P3, P2 X P3, P2 X P4, and P3 X P4. Also, these genotypes gave low values in the test parameters YR and SSI, which strongly confirms its high unmatched tolerance under salt stress conditions compared to the control experiment. Because it succeeded well in reducing the loss level in the final yield under salinity conditions, this mechanism was not achieved in the rest of the wheat genotypes under study. This largely reflects the extent of the genetic and physiological changes that enabled these promising genotypes to salt-stress tolerance and maintained a good level in the final output (Esmail et al., 2016; El-Demardash et al., 2017; Yassin et al., 2019).

From the previous results, it could be concluded that the first three wheat parents namely; Sakha 8, shandweel 1, and masr 1 were the most desirable wheat genotypes which exhibited the highest mean values of all morphological and physiological traits under salt-stress treatment compared to the control conditions besides, the crosses; P1 X P2, P1 X P3, P2 X P3, P2 X P4, and P3 X P4, respectively. Also, the five promising wheat hybrids mentioned above were recorded highly significant and positive results of heterosis over better parent, and they were very distinguished concerning the incident superiority for SCA effects which indicates that these genotypes are the actual nucleus for producing salinity tolerance wheat lines in addition, high yielding in this regard. Results of Bi-plot analysis were in good harmony with Dehghani et al. (2012), Saroei et al. (2017), Mariey et al. (2021), who reported that the hierarchical cluster and Bi-plot analysis based on phenotypic traits were aimed to detect homogeneous groups with large heterogeneity among them. Also, they are considered a valuable tool for subdividing the number of genotypes in groups including similarity and dissimilarity genotypes, to help the breeder plan an effective breeding program. Agro-physiological, genotyping, and molecular marker development provide the potential criteria to realize innovative knowledge that could assist the selection and breeding of wheat highly yielded hybrids with increased salt stress tolerance or improved traits under harsh conditions. This, in turn, allows the conception of new genotypes of sustainable wheat. The benefits of genetic differentiation are that the DNA is not affected by the environment and is stable. Moreover, it seems to be a hopeful tool for predicting heterosis in many crops, such as rice (Zhang et al., 1996) and wheat (Martin et al., 1995; Heiba et al., 2016b). The seven parental genotypes used in this study showed large genetic diversity among themselves, indicating an increased potential for strong out-crossing and higher performance of F1 hybrid varieties, which are essential for the occurrence of hybrids (Cox & Murphy, 1990; Zian et al., 2013). Furthermore, combined with DNA marker SCoT 6, 12, and 16, discriminate the parental genotypes under study and their potential hybrids with specific bands shared with parents and represented hybrid, Table 9. These bands presented the same molecular weight in one parent and hybrid. This study reported herein organizes the first analysis of diversity in the wheat genotypes and some respected hybrids for salinity using SCoT markers which are reproducible and reliable markers for hybrids identification and genetic diversity studies on wheat. In this study, the average values of alleles and PIC per primer are comparable with those obtained in wheat genotypes with different levels of salt tolerance using different SCoT primers (Somayeh et al., 2020). These results indicate that the tested primers are highly informative and capable of discriminating between the levels of salt tolerance among studied wheat genotypes and selected promising hybrids.

Conclusion

This study shed light on more points related to reactions associated with exposure of some wheat genotypes to salt stress and discussed the mechanisms of tolerance and the factors associated with this matter. This was done using seven wheat bread varieties; three of them are tolerant to salt stress. The rest of the genotypes were classified as medium endurance. The crossing procedure was done among them using a half diallel system. All genotypes included parents, and their F1 crosses were evaluated under control and salinity conditions by estimating some agro-morphological and physiological traits besides salinity tolerance indices parameters specifically for grain yield/plant trait. Molecular genetics had an effective and significant role in determining the genetic differences at the molecular level between the seven wheat parents and the five best hybrids that were superior in all traits under study in terms of salt stress tolerance. This superiority was under saline stress treatment compared to the natural soil. It also had a vital role in determining the genotypes wheat tolerant to salt stress from sensitive and medium tolerant in this regard. This is the real achievement of improving salinity tolerance of Egyptian wheat varieties and enriching the plant breeding program for wheat tolerance to environmental stresses with these promising genotypes.

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معايير الانتخاب الشاملة لهجن قمح الخبز عالية المحصول تحت الاجهاد الملحي

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كان أهم جانب في هذا البحث هو تقييم مجموعة من الطرز الوراثية للقمح ذات استجابات مختلفة للاجهاد الملحي أثناء إجراء عملية الانتخاب على الصفات عدد السنابل لكل نبات، عدد الحبوب الخصبة لكل سنبلة، وزن الالف حبة ومحصول الحبوب لكل نبات فردي بجانب بعض الصفات الفسيولوجية والمتعلقة بتحمل الاجهاد الملحي مثل محتوي كلا من الصوديوم والبوتاسيوم ونسبة الصوديوم للبوتاسيوم والضغط الاسموزي المعدل وكلا من محتوي البرولين والجليسين بيتايين تحت الظروف الطبيعية وظروف الاجهاد الملحي. تم تقسيم ظرز القمح الوراثية الي مجموعتين بالنسبة لتحليل الهجن النصف تبادلية حيث ضمت المجموعة الأولى الآباء وهم علي الترتيب سخا 8، شندويل 1، مصر 1، جيزة 171، سخا 94، جميزة 11 وجميزه 12 . بينما احتوت المجموعة الثانية على ال21 هجين قمح المتحصل عليهم من تهجين الهجن النصف تبادلية بين طرز القمح السبعة. قوة الهجين بالنسبة لافضل أو احسن اب وتأثيرات القدرتين العامة والخاصة علي التالف كانت من اهم القياسات الوراثية المحسوبة لجميع الصفات المدروسة للتجربتين. علاوة على ذلك، تم تقييم طرز القمح السبعة وأعلى خمسة هجن لاختبار مؤشرات تحمل الملوحة باستخدام صفة محصول الحبوب / النبات اعتمادًا على جميع البيانات المقدرة لجميع الصفات المدروسة تحت معاملة الإجهاد الملحي مقارنة بالتجربة القياسية. اوضحت النتائج النهائية ان اباء القمح رقم (1، 2، 3) بالاضافة الي الهجن الاب الاول X الاب الثاني، الاب الاول X الاب الثالث، الاب الثاني X الاب الثالث، الاب الثاني X الاب الرابع و الاب الثالث X الاب االرابع كانت قد حققت اتجاها عاليا لتحمل الاجهاد الملحي تحت معاملة الاجهاد الملحي مقارنة بالتجربة القياسية. علاوة على ذلك، سجلت طرز القمح السابقة مستويات عالية من مؤشرات تحمل الملوحة. حددت معلمات (SCoT) الهجن ذات اعلي مؤشرات تحمل للاجهاد الملحي. من بين تسعة معلمات وراثية جزيئية مستخدمة، ستة منهم فقط نجحت بالفعل في اعطاء حزم وراثية مختلفة او متعددة الاشكال بمعدل 46 حزمة وراثية مختلفة من نوع (Polymorphic bands). لذلك يمكن استخدام تقنية تحديد الأدلة الوراثية على المستوى الجزيئي في المستقبل كأداة تصنيفية لتحمل الملوحة في التراكيب الوراثية المبشرة للقمح.