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Screening Some Bread Wheat Genotypes: A Sustainable Approach for Wheat Production Under Salinity Stress Conditions

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ABSTRACT

This study, conducted at Sakha Agricultural Research Station, Kafr El-Sheikh, Egypt, during the 2020/2021 and 2021/2022 growing seasons, investigated the effects of salinity stress on grain yield, its components, physiological and grain quality traits in 21 bread wheat genotypes (*Triticum aestivum* L.), including18 lines and 3 check cultivars to assess the genetic variability and identify salt-tolerant wheat genotypes. To achieve these objectives, the genotypes were evaluated under normal and saline soil conditions. Salinity stress significantly reduced most traits across all genotypes except for some physiological traits (MDA, Proline, and Na/K) and wet dry gluten percentage which exhibited increases under stress. Significant variation was observed among the genotypes for their performance under saline conditions. Based on discriminant scores Lines 5, 8, 12, 13, 18, Misr 4, and Sakha 95 are suitable and demonstrate normal physiological responses to avoid salinity effects. Line 4, Line 2, Line 9, Line 15, Line 3, and Line 7 and Line 6 showed moderate tolerance to salinity. In contrast, Lines 1, 10, 11, 14, 16, 17, and Sakha 96 are classified as sensitive genotypes to salinity stress.

Keywords: bread wheat; salinity; discriminant score.

INTRODUCTION

The world's growing population and climate change are challenging crop production. Salinity is a major stress that limits crop growth, affecting around 20 % of irrigated arable land, and is expected to rise to over 50 % by 2050. Abiotic stresses such as high salt, drought, cold, and heat can decrease staple food crop yield up to 60 % - 70 % especially under climate change conditions (Majeed and Muhammad 2019, Yadav 2020, Mahboob *et al…,* 2023, Kaya and Ashraf 2024, Khan, *et al...,* 2024). Salinity is known as the "white death" and causes an annual economic loss of USD 27.3 billion worldwide (Zeeshan *et al…,* 2020). To improve wheat productivity in salt-affected areas, salt-tolerant wheat cultivars through phyto-melioration rather than using expensive methods like leaching and drainage. Identifying salt-tolerant wheat genotypes is crucial for global food security and sustainability. This low-cost and scalable method offers a sustainable solution for impoverished farmers (Al-Ashkar *et al…,* 2019 and Chaurasia *et al...,* 2022). Improving wheat germplasm by introducing new genes or alleles from landraces and cultivated wheat varieties is necessary to increase tolerance for salt stress, as high salinity reduces agricultural productivity. Efficient screening and multi-trait selection improve yield in breeding programs (Balasubramaniam *et al…,* 2023). It is crucial to consider physiological, biochemical for adapting to salt stress (Afzal *et al...,* 2023).

Correct statistical analysis is necessary for large datasets to identify genotypes. Multivariate analysis identifies variation sources and discriminates salt tolerance. A multivariate analysis of morphological, physiological, and biochemical traits is essential for sustainable crop production in saline environments. Combining adaptive strategies with salt-tolerant wheat genotypes is effective for achieving desirable yields (Aminizadeh *et al…,* 2024 El-Hawary *et al..,.* 2022 and Sallam *et al...,* 2024).

The study aimed to achieve three objectives: 1) evaluate the impact of salinity stress on the grain yield and quality traits of twenty-one wheat genotypes, including their physiological and grain quality traits, using visual aids; 2) identify salinity-tolerant wheat genotypes through multivariate analysis and understand changes in morphological and physiological traits associated with salinity stress, crucial for selecting and developing better salinity-tolerant genotypes; and 3) rank the twenty-one wheat genotypes using discriminant scores as an effective criterion for wheat production, with visual representations. The study's results aim to inform the development of appropriate selection strategies for improving grain yield and salinity tolerance in wheat crops.

MATERIALS AND METHODS

Experiment Description

In the current study two separate field experiments were conducted one in normal soil and the other in saline soil at the experimental farm of Sakha Agricultural Research Station in Kafr El-Sheikh, Egypt, during the 2020/2021 and 2021/2022 growing seasons. The names and pedigrees of the studied genotypes are presented in Table 1. Before planting, soil sampling was randomly collected from depths up to 60 cm to determine the physical and chemical properties of the soil at the experimental site. The analysis of these samples was carried out in the laboratory of the Water and Soil

Research Sec. (Water, Soil and Environment Research Institute, ARC, Egypt) as shown in Table 2.

A randomized complete block design (RCBD) was employed, with four replicates. Each plot covered an area of 3.6 m², comprising six rows, each 3 meters long and spaced 20 cm apart. All agronomic practices were applied following the standard recommendations for wheat crop in the Egyptian fields.

Table 1. The pedigree, of twenty-one tested bread wheat genotypes

No	Genotype	Cross name	selection history
1	Line 1	GALVEZ / WEAVER /3/ VORONA / CNO79 // KAUZ /4/ SAKHA 93 /5/ WAXWING*2/HEILO	S.2013-50-033S-05S-8S -0S
2	Line 2	BABAX / LR42 // BABAX*2 /4/ SNI / TRAP/3/ KAUZ*2 / TRAP // KAUZ /5/ UP2338*2/KKTS*2//YANA	S.2013-69-056S-08S-8S -0S
3	Line 3	BABAX / LR42 // BABAX*2 /4/ SNI / TRAP/3/ KAUZ*2 / TRAP // KAUZ /5/ UP2338*2/KKTS*2//YANA	S.2013-69-056S-08S-12S -0S
4	Line 4	BABAX / LR42 // BABAX*2 /4/ SNI / TRAP/3/ KAUZ*2 / TRAP // KAUZ /5/ UP2338*2/KKTS*2//YANA	S.2013-69-056S-08S-13S -0S
5	Line 5	BABAX / LR42 // BABAX*2 /4/ SNI / TRAP/3/ KAUZ*2 / TRAP // KAUZ /6/ ALTAR 84/AE.SQUARROSA (221) // 3*BORL95 /3/ URES / JUN // KAUZ /4/ WBLL1 /5/ MILAN/S87230//BAV92	S.2013-70-042S-08S-2S -0S
6	Line 6	BABAX / LR42 // BABAX*2 /4/ SNI / TRAP/3/ KAUZ*2 / TRAP // KAUZ /6/ ALTAR 84/AE.SQUARROSA (221) // 3*BORL95 /3/ URES / JUN // KAUZ /4/ WBLL1 /5/ MILAN/S87230//BAV92	S.2013-70-042S-08S-14S -0S
7	Line 7	GALVEZ / WEAVER /3/ VORONA / CNO79 // KAUZ /4/ SAKHA 93 /5/ ATTILA*2 / PBW65*2//KACHU	S.2013-47-045S-09S-13S -0S
8	Line 8	GALVEZ / WEAVER /3/ VORONA / CNO79 // KAUZ /4/ SAKHA 93 /5/ UP2338*2/KKTS*2//YANA	S.2013-48-040S-026S-13S -0S
9	Line 9	BABAX / LR42 // BABAX*2 /4/ SNI / TRAP/3/ KAUZ*2 / TRAP // KAUZ /5/ UP2338*2/KKTS*2//YANA	S.2013-69-056S-08S-7S -0S
10	Line 10	SAKHA 34/4/KAL/BB//CJ 71 S" /3/ HORK"S" /5/ SPARROW / BRONCHITIS /6/ K134 (60) / VEE /7/ ATTILA*2/PBW65*2//KACHU	S.2013-74-039S-05S-3S -0S
11	Line 11	SAKHA 34/4/KAL/BB//CJ 71 S" /3/ HORK"S" /5/ SPARROW / BROCH IS /6/ K134 (60) / VEE /7/ ATTILA*2/PBW65*2//KACHU	S.2013-74-039S-05S-7S -0S
12	Line 12	HUBARA-21 // WAXWING*2/HEILO	S.2013-95-010S-011S-5S -0S
13	Line 13	HUBARA-21 // WAXWING*2/HEILO	S.2013-95-010S-011S-9S -0S
14	Line 14	WBLL1*2/KIRITATI/3/ ATTILA*2/PBW65*2//KACHU	S.2013-124-035S-04S-12S -0S
15	Line 15	FRET2*2/BRAMBLING /6/ ALTAR 84/AE.SQUARROSA (221)//3*BORL95 /3/ URES/JUN//KAUZ/4/WBLL1/5/MILAN /S87230//BAV92	S.2013-174-043S-020S-5S -0S
16	Line 16	BABAX / LR42 // BABAX*2 /4/ SNI / TRAP/3/ KAUZ*2 / TRAP // KAUZ /5/ UP2338*2/KKTS*2//YANA	S.2013-69-056S-08S-17S -0S
17	Line 17	KAMB1*2 / KIRITATI /5/ ATTILA*2 / PBW65 /4/ CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /3/ 2*KAUZ	S.2013-141-014S-014S-6S -0S
18	Sakha 96	MINO /6/ SAKHA 12 /5/ KVZ // CNO 67 / PJ 62 /3/ YD "S" / BLO "S" /4/ K 134 (60) / VEE	S. 16869 -010S -07S-1S-1S -0S
19	Sakha 95	PASTOR // SITE / MO /3/ CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /4/ WBLL1.	CMA01Y00158S-040POY-040M-030ZTM-040SY-26M-0Y-0SY-0S.
20	MISR 4	NS-732/HER/3/PRL/SARA//TSI/VEE # 5/4/FRET2/5/ WHEAR/SOKOLL	CMSA09Y00712S-050Y-050ZTM-0NJ-099NJ-4WGY-0B-0EG
21	Line 18	RET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ*2/5/BOW/URES//2*WEAVER/3/CROC_1/AESQUARROSA (213)//POG	CGSS05B00144T-099TOPY-099M-099NJ-099NJ-7WGY-0B-5Y-0B

Table 2. Chemical analysis of soil at experimental sites during two growing seasons

Season	Soil Texture	EC (ds/m⁻¹)	pH (1:2.5)	SAR	Soluble cations Meq/L				Soluble anions Meq/L			
					Na^+	Ca^{++}	Mg^{++}	K^+	CO_3^-	HCO_3^-	Cl^-	SO_4^{2-}
Non-saline 2020/2021	Clay Loam	1.7	7.32	–	26.9	8.43	4.1	4.5	0.00	3	20.2	20.6
Non-saline 2021/2022	Clay Loam	1.5	7.21	-	25.7	8.32	3.9	4.4	0.00	2.8	20.0	20.4
Saline 2020/2021	Clay Loam	8.26	7.8	14.58	56.2	17.2	12.5	0.8	0.00	6.2	42.3	38.2
Saline 2021/2022	Clay Loam	8.91	7.8	14.38	62.19	19.34	14.09	0.87	0.00	6.93	46.74	42.23

EC: electrical conductivity, (ds/m⁻¹): deciemens per meter pH: potential of hydrogen, SAR: sodium adsorption ratios.

Studied Traits

Agronomic and morphological traits

The morphological and yield component studied characteristics were:

1- Number of days to heading (DH)

2- Number of days to maturity (DM)

3- Plant height (PH, cm)

4- Number of spikes/m2 (NS/m2).

5- Number of kernels per spike (NK/S).

6- 1000-kernel weight (1000KW, gm).

7- Grain yield (GY, ardb/fad.) was determined from each plot and converted to ardb/fed (one ardab=150 kg).

8- Flag Leaf area (FLA cm²).

Physiological traits

During the heading stage, ten flag leaves of the main stem of ten randomly selected plants from each plot were used for physiological study.

1- The Relative Water Content (RWC %) was measured according to the method outlined by Gonzalez and Gonzalez , 2001.

2-Total Chlorophyll content (TCL µg ml^{-1}) using N-N-Dimethylformamide and UV-VIS Spector-photometer according to (Moran, 1982)

3- Malondialdehyde (MDA µmols g^{-1} FW.) was measured according to the methods of (Heath & Packer 1968).

4- The proline content of leaves (mg g^{-1} FW.) was measured using the method described by (Bates, *et al…*, 1973).

5- Sodium content for potassium (Na/K) was determined using flame photometer according to (Chapman and Pratt 1978).

Grain quality traits

1- Crude protein content (protein, %) was measured according to (AOAC 2000).

2- Wet and dry gluten percentage (WG%, DG %) were measured by hand washing 25 g flour, according to the standard method (Anonymous 1983).

Statistical Analysis

Analysis of variance (ANOVA)

Levene test (1960) was run before conducting the combined analysis to test the homogeneity of individual error terms. When the data satisfied the tests; subsequently, a combined analysis of variance (ANOVA) procedure was carried out for the data of the two seasons for each trait to test the impact of control and salinity, genotype, and their interaction on twenty-one bread wheat genotypes (18 lines and three checks). The least significant difference test (LSD) was performed to detect the significant differences among treatment means at the probability level of (0.05).

Hierarchical Cluster (HC), and Discriminant Function Analysis (DFA)

All studied characteristics were used in the hierarchical cluster (HC) analysis to evaluate the genetic similarity and dissimilarity matrix between twenty-one genotypes, characterized into four tolerance groups using Euclidean distance and Ward's method of agglomeration.

Based on average yield under normal and stress conditions over two seasons, among 21 bread wheat genotypes (Table 1), the highest 7 yield genotypes, The moderate seven genotypes and the rest seven low yield genotypes were selected as group one, two and group three. This classification could differentiate groups and then discriminant function analysis (DFA) was performed. Discriminant function analysis (DFA) supplies an equation that gives maximum separation or discrimination between two groups of 21 bread-wheat genotypes. All characters' values were standardized before running discriminant analysis. The discriminant function can be thought of as a multiple regression equation.

Before preceding the analysis, as a part of our data exploration, we test the multicollinearity for all studied traits (independent variables). Discriminant function analysis (DFA) should only include variables that show no multicollinearity. The canonical correlation is the multiple associations between the predictor's independent variables (sixteen measured characters as eight earliness, yield components characters, five physiological traits and three-

grain quality traits) and the discriminant function. It provides an index of overall model fit which is interpreted as being the proportion of variance explained (R^2).

Wilks' lambda is used to test the significance of the discriminant function as a whole. The value of Wilks' lambda ranges between 0 and 1. When Wilks' lambda value closes to 0 and is significant, it means that the DA has the goodness of fit to differentiate the genotypes in two groups and vice versa. Therefore, it tells us the variance of the dependent variable (three groups of 21 bread wheat genotypes) that is not explained by the discriminant function. Finally, we get discriminant scores as a weighted linear combination of the discriminating variables. Discriminant scores were calculated by using coefficients, based on these discriminant scores, we ranked genotypes in our investigation (selection index) at normal and salinity conditions under the Egyptian environment. The data were automated for all kinds of analysis, using the IBM SPSS Statistical Software Package.

RESULTS AND DISCUSION

Climatic and soil properties

The results in Table 2 indicated that the soil texture is clay loam, with electrical conductivity levels of 1.7 and 1.5 (ds/m) for non-saline soil and 8.26 and 8.91 (ds/m) for saline soil for the two growing seasons (2020 /2021 and 2021/2022), respectively. In saline soils, there are higher levels of Na, Ca², Mg², Cl, and SO$_4^{-2}$ compared to non-saline soils. This accumulation leads to osmotic changes that reduce the ability of plant root cells to absorb water from the soil. Majeed and Siyyar 2020, Afzal *et al...,* 2023, and Mostafa 2024 reported that, when electrical conductivity (EC) exceeds 4 ds/m, equivalent to 40 mm NaCl, the soil is considered to saline-affected and crop yield declines when salinity reaches a level of 6-8 ds/m, posing a significant threat to food security.

The pH of all samples (Table 2) is slightly alkaline and the sodium adsorption ratio (SAR) values are higher in saline soils compered to non-saline soils, suggests that higher sodium levels relative to calcium and magnesium, lead to harm soil structure and hinders plant growth by creating a hyper-ionic soil solution (Sparks *et al...,* 2022, Ayars and crown 2024 and Salvato *et al...,* 2024).

Agronomic Traits

Effect of salinity on Growth and development

The effect of salt stress on the growth and yield component is demonstrated in Table 3. The findings show that salinity had significant negative effects on morphological and agronomic traits, leading to reduced earliness by 5.4% and 5.6% for DH and DM, respectively and by 23.7% for PH. Yield and yield components were also affected with reduction in NS/m² by 31.7 %, 1000KW by 41.2 %, NK/S by 40.5 %, and grain yield by 41.5% compared to the control treatment which had significantly higher average values for all the agronomic studied characteristics, over the two growing seasons (Table 3).

Table 3. Mean effects of control and salinity treatments on: days to heading (DH), days to maturity (DM), plant height cm (PH), number of spikes/m²(NS/m²), 1000-kernel weight g (1000KW), number of kernels per spike (NK/S), grain yield ardb/fad (GY), and Flag leaf area cm^2 (FLA) of some wheat genotypes.

Treatment	DH	DM	PH	GY	NS/m²	1000KW	NK/S	FLA
Normal	91.1	147.2	114.9	24.6	398.7	50.3	61.5	45.4
Salinity	86.2	138.9	87.7	14.4	272.2	29.6	36.6	29.2
Reduction %	5.4	5.6	23.7	41.5	31.7	41.2	40.5	35.6
Sig.	**	**	**	**	**	**	**	**

**: highly significant at 0.05 probability levels.

Interaction Effect

The interaction between genotypes and salinity was the most interesting aspect of this study. Salt stress had a detrimental impact on agronomic traits, with significant interaction effects observed between the studied genotypes and salinity conditions for all agronomic traits, except for days to heading (DH) (Tables 4 and 5).

Table 4. Interaction effect for agronomic traits over the two growing seasons of 2020/2021, and 2021/2022 and the reduction percentage (RD%) for days to heading (DH), days to maturity (DM), plant height(PH), number of spike/m² under normal (N) and salinity(S) conditions.

Genotypes	DH			DM			PH			NS/m²		
	N	S	RD%	N	S	RD%	N	S	RD%	N	S	RD%
Line 1	88.5	85.8	3.1	147.4	140.4	4.7	113.8	86.3	24.2	405.5	225.6	44.4
Line 2	90.1	85.8	4.8	146.9	138.6	5.7	117.5	86.3	26.6	398.4	284.9	28.5
Line 3	89.3	83.9	6	147.3	137.9	6.4	107.5	80.6	25	393.5	260.1	33.9
Line 4	90.9	85.4	6.1	147.3	137.9	6.4	116.3	88.1	24.2	400	255.2	36.2
Line 5	95.5	89.5	6.3	147	140.8	4.2	115.6	94.4	18.3	407.8	294.8	27.7
Line 6	95.1	89.1	6.3	148.1	138.8	6.3	116.9	88.1	24.6	370	270	27
Line 7	96.5	93.3	3.3	148.6	141.9	4.5	113.1	90	20.4	380.4	265.1	30.3
Line 8	92.4	88	4.8	148.3	140	5.6	108.8	85.1	21.8	404.3	299.7	25.9
Line 9	86.4	82.5	4.5	145.9	137.4	5.8	115.6	84.4	27	417.5	279.9	33
Line 10	87.4	82.1	6.1	146	136.8	6.3	119.4	88.8	25.6	415	250.2	39.7
Line 11	90.8	87.5	3.6	147.9	137.9	6.8	120.6	87.5	27.4	410.9	230.4	43.9
Line 12	94.9	88.3	7	148.1	137.6	7.1	115.6	88.8	23.2	376.5	314.6	16.4
Line 13	95.6	89.6	6.3	148.1	139.1	6.1	111.9	87.5	21.8	414.3	289.8	30.1
Line 14	93.9	91.1	3	149	139.6	6.3	120.6	90	25.4	407.5	225.5	44.7
Line 15	92	88.4	3.9	148.5	139.5	6.1	116.9	90	23	406	275	32.3
Line 16	90.8	81.9	9.8	147.6	136.4	7.6	115.6	89.4	22.7	386.8	240.3	37.9
Line 17	89.4	83.9	6.2	146.3	137.5	6	117.5	90	23.4	372.5	235.4	36.8
Line 18	93.9	88.8	5.4	147.9	141.1	4.6	118.1	90.6	23.3	398.3	319.5	19.8
MISR 4	94.5	90.4	4.3	149.6	142.4	4.8	113.1	86.3	23.7	417	309.6	25.8
Sakha 95	91.8	86.1	6.2	145.1	140.4	3.2	121.3	90	25.8	420.5	304.7	27.5
Sakha 96	73	68.6	6	139.9	136.3	2.6	96.9	78.8	18.7	360.8	245.3	32
L.S.D		-			1.74			4.72			44.95	

LSD: least significant difference

Table 5. Interaction effect over the two growing seasons of 2020/2021, and 2021/2022 and the reduction percentage (RD %) for 1000 kernels weight(100kw), number of kernels/spikes(NK/S), Flag leaf area cm² (FLA), and grain yield ardb/fad (GY) under normal (N) and salinity (S) conditions.

Genotypes	1000KW			NK/S			FLA			GY		
	N	S	RD%	N	S	RD%	N	S	RD%	N	S	RD%
Line 1	45.9	39.8	13.3	65.1	56.5	13.1	45.24	26.39	41.7	25.5	12.9	49.41
Line 2	46.7	38.7	17.1	63.1	50.3	20.2	43.9	30.42	30.7	25.4	14.7	42.13
Line 3	44.5	41.8	6.1	63.6	62.2	2.5	56.93	28.3	50.3	24.2	14.1	41.74
Line 4	44.8	41.8	6.7	64.4	49.1	23.7	51.42	28.21	45.1	24.1	13.6	43.57
Line 5	47.4	44.6	5.9	63.5	57.2	9.9	41.18	29.4	28.6	26	14.9	42.69
Line 6	43.3	40.1	7.4	58.2	56.4	3.1	44.28	31.21	29.5	22.3	14.1	36.77
Line 7	43.8	41.9	4.3	60.9	56.6	7.1	50.42	27.5	45.5	23.4	14.2	39.32
Line 8	45.5	41.8	8.1	60.1	59.1	1.7	42.37	30.81	27.3	23.8	15.3	35.71
Line 9	48.5	43.6	10.1	67.4	56.2	16.6	40.32	29.91	25.8	26.4	14.5	45.08
Line 10	47.9	41.5	13.4	63.7	57.2	10.5	44.13	23.82	46	25.7	13.6	47.08
Line 11	45.8	40.2	12.2	60.1	59.1	1.7	47.81	27.6	42.3	25.4	13.2	48.03
Line 12	47.5	43.2	9.1	62.1	55.6	10.5	43.66	34.13	21.8	22.7	16.7	26.43
Line 13	46.1	43.3	5.9	64.2	54.1	15.7	43.28	30.4	29.8	25.5	14.9	41.57
Line 14	45.1	38.9	13.7	62.1	56.7	8.7	44.44	25.74	42.1	24.9	12.9	48.19
Line 15	48.5	43.3	10.7	68.3	59.1	13.4	36.27	28.3	22	26.3	14.3	45.63
Line 16	45	40.3	10.4	60.2	55.5	7.8	38.05	22.15	41.8	24.3	13.5	44.44
Line 17	43.5	40.2	7.6	55.9	52.2	6.6	52.22	29.7	43.1	22.6	13.5	40.27
Line 18	48.5	45.5	6.1	64.4	60.7	6.1	44.14	36.72	16.8	25.4	16.8	33.86
MISR 4	46.9	45.8	2.3	64.6	62.8	2.8	54.03	39.7	26.5	25.7	16.1	37.35
Sakha 95	47.7	46.1	3.4	68.5	59.9	12.6	45.1	31.11	31	27.1	15.9	41.33
Sakha 96	41.8	34.2	18.2	52.9	48.1	9.1	44.7	25.3	43.4	21.1	11.6	45.02
L.S.D		3.75			8.43			1.26			0.42	

LSD: least significant difference

The recorded values for the normal treatment were higher than those for the salinity treatment across combined data of the agronomic traits. The research findings showed that genotypes Line 14, Sakha 96, Line 5, and Line 12 experienced the lowest reductions in DM (2.6%), PH (18.4%), and NS/m² (16.4%), respectively. In contrast, genotypes Line 16 displayed the highest reductions in DM at 7.6 %, Line 11 in PH at 27.4 %, and Line 14 in NS/m² at 44.7 %, as shown in Table 4. (Choudhary *et al...,* 2024).

The largest reduction in 1000-kernel weight under salinity stress (Table 5) was observed in Sakha 96 (18.2%)

and Line 2 (17.1%), In contrast, the lowest reduction was observed in Misr 4 (2.3%) and Sakha 95 (3.4). The interaction effect indicates that under salinity stress, the lowest reduction for the number of kernels per spike (NK/S) recorded by Line 8 (1.7%) and Line 3 (2.5%), Meanwhile, the highest reduction for NK/S under the same conditions was recorded by Line 4 (23.7%) and Line 2 (20.2%). This reduction could be attributed to the excessive absorption of salts by the plants, which indirectly affected the plant growth by decreasing the amount of photosynthates, water and other growth factors. Similar findings reported by Aws Kreet and

Samira Hasson (2020), Nadeem *et al…*, (2020) where salt stress resulted in a significant decrease in the average pkant height, number of spikes, and 100-kernel weight.

The Flag leaf area (FLA) ranges from 56.9 cm^2 (line 3) to 36.3 cm^2 (Line 15) under normal soil condition and from 39.7 cm^2 (Misr 4) to 22.1 cm^2 (Line 16) under salinity conditions. This indicates that salinity inhibits leaf area growth. The reduction in flag leaf area of salt-affected plants ranged from 16.8% to 50.3% compared to the control condition. Specifically, Line 18, Line 12, Line 9 Line 15, Misr 4, Line 5, Line 6, and Line 13 exhibited the lowest reduction in FLA (16.8%, 21.8%, 22%, 25.8%, 26.5%, 26.5%, 28.6%, 29.6% and 29.8% respectively). On the other hand, Line 3, Line 10, Line 7, and Line 4 recorded the highest reduction in FLA. This negative effect of salinity on plants may have induced osmotic stress due to the high salt concentration in the culture medium, preventing root cells from obtaining the required water Z. Chamekh *et al…*, 2014).

The grain yield (ardb/fad), (GY) as shown in Table 5 was negatively affected under salt stress compared to the control treatment, while all genotypes displayed a decrease, the extent of grain yield reduction varied among them. Among the genotypes, Line 12, Line 18, Line 8, Line 6, Misr 4, Sakha 95 and Line 7 recorded the lowest reductions in GY, with values 26.4%, 33.9%, 35.7%, 36.8%, 39.32% and 37.35% and 41.3% respectively. (Table 4) The results indicate that Line 1, Line 14, Line 11, Line 10, Line 15, Sakha 96, and Line 9 displayed the highest reduction in GY, with percentages of 49.4 %, 48.2 %, 48.0 %, 47.1 %, 45.6 %, and 45.1 %, respectively (Table 5), this results indicated that at the actual stage of grain production occurs between spike emergence and ripening during the vegetative stage, and shortening this critical period leads to reduced yields (Abbas *et al…*, 2013).

EL Sabagh *et al…*, (2021) stated that influences plant growth and yield attributes primarily due to ion toxicity and osmotic stress. Although, the intrinsic pathways and molecular mechanisms are so far not clear. Salt stress influences cell ion homeostasis by altering ion balance, such as increased Na+ and a simultaneous decreased Ca^{+2} and K+ content. Dadshani *et al...*, (2019) reported that Sodium

toxicity, pollen sterility, decreased assimilate production, and limited allocation of assimilates to grains have been identified as factors contributing to reduced grain yield under salinity stress.

Salinity tolerance is the ability of a plant's genotype to withstand saline conditions and minimize yield losses. This trait is highly complex, governed by multiple genes, and shaped by the interplay between genetic factors, environmental conditions, and their interactions, ultimately affecting the yield that can be economically harvested (Afzal *et al...*, 2023). Reduction in the grain yield has also been observed by Darwish *et al...* 2017, Nadeem *et al…*, 2019, Genedy and Eryan 2022, Afzal *et al...*, 2023 and EL-Seidy *et al…*, 2023.

Physiological Traits

Effect of salinity on some physiological Traits

Salinity has a clear and significant impact on all physiological characteristics of plants. As shown in Table 6, relative water content (RWC%) and total chlorophyll (TCl) exhibited a notable decrease under saline soil conditions compared to normal soil. In contrast, malondialdehyde (MDA), proline content, and the Na/K ratio showed significant increases, reflecting the physiological stress caused by salinity.

Table 6. Mean effects and Reduction Percentage of control and salinity treatments on Relative Water Content (RWC%), Total Chlorophyll (TCL µg ml^{-1}), Malondialdehyde (MDA µmols g^{-1} FW), Proline content (mg g^{-1} FW) and Sodium content for potassium (Na/K) of some wheat genotypes.

Treatment	RWC%	TCL	MDA	Proline	Na/K
Normal	82.90	25.13	205.7	0.142	0.277
Salinity	68.19	16.54	590..8	0.a313	0.670
Reduction %	17.7	34.2	-287.1	-120.4	-141.9
Sig.	**	**	**	**	**

**: highly significant at 0.05 probability levels

Interaction Effect.

The measured physiological characteristics are illustrated in Table 7. The results showed that the studied physiological characteristics are significantly affected by the interaction of salinity and wheat genotypes.

Table 7. Interaction effect over the two growing seasons of 2020/2021, and 2021/2022 and the reduction percentage (RD %) for Relative Water Content (RWC%), Total Chlorophyll (TCL µg ml^{-1}), Malondialdehyde (MDA µmols g^{-1} FW), Proline content (mg g^{-1} FW) and Sodium content for potassium (Na/K) under normal(N) and salinity(S) conditions.

Genotypes	RWC%			TCL			MDA			Proline			Na/K		
	N	S	RD%	N	S	RD%	N	S	RD%	N	S	RD%	N	S	RD%
Line 1	84.59	65.85	22.2	28.3	14.99	47	143.9	699.6	-386.2	0.108	0.268	-148.1	0.244	0.771	-215.9
Line 2	80.38	68.08	15.3	26.72	17.11	36	257.85	607.69	-135.3	0.132	0.317	-140.2	0.296	0.641	-116.6
Line 3	78.84	70.47	10.6	25.87	13.87	46.4	188	513.82	-173.3	0.112	0.304	-171.4	0.269	0.624	-131.9
Line 4	82.74	64.23	22.4	22.34	17.54	21.5	262.11	616.17	-135.1	0.185	0.271	-46.5	0.289	0.734	-153.9
Line 5	81.46	69.79	14.3	25.9	17.13	33.9	187	527.67	-182.2	0.128	0.414	-223.4	0.243	0.786	-223.5
Line 6	85.54	71.29	16.7	20.2	17.26	14.6	270.35	642.96	-137.8	0.169	0.384	-127.2	0.278	0.73	-162.6
Line 7	81.07	70.38	13.2	24.51	13.97	43	217.61	704.91	-223.9	0.149	0.263	-76.5	0.284	0.645	-127.1
Line 8	80.67	68.42	15.2	26.37	16.94	35.8	212.94	548.05	-157.4	0.125	0.238	-90.4	0.292	0.742	-154.1
Line 9	80.62	69.1	14.3	30.37	20.12	33.8	225.15	618.32	-174.7	0.155	0.26	-67.7	0.263	0.628	-138.7
Line 10	81.44	65.14	20	26.27	18.76	28.6	173.58	664.29	-282.7	0.118	0.238	-101.7	0.31	0.679	-119
Line 11	82.87	67.04	19.1	24.48	14.44	41	223.18	708.93	-217.7	0.174	0.366	-110.3	0.307	0.695	-126. 4
Line 12	86.75	69.6	19.8	25.94	16.39	36.8	190.1	418.39	-120.1	0.119	0.436	-266.4	0.259	0.537	-107.6
Line 13	84.52	68.11	19.4	25.52	15.67	38.6	170.62	447.32	-162.2	0.119	0.315	-164.7	0.296	0.687	-132.1
Line 14	83.88	68.75	18	25.69	16.05	37.5	234.88	557.69	-137.4	0.164	0.238	-45.1	0.332	0.692	-108.4
Line 15	86.26	67.83	21.4	24.6	16.21	34.1	240.6	751.74	-212.4	0.149	0.312	-109.4	0.279	0.646	-131.5
Line 16	83.98	70.44	16.1	19.25	14.83	23	226.7	796.89	-251.5	0.154	0.254	-64.9	0.265	0.677	-155.5
Line 17	84.05	68.02	19.1	23.78	15.41	35.2	275.9	719.84	-160.9	0.124	0.278	-124.2	0.339	0.782	-130.7
Line 18	78.98	70.7	10.5	26.7	16.9	36.7	177.14	361.43	-104.3	0.168	0.432	-157.1	0.293	0.598	-104
MISR 4	83.51	74.31	11	26.9	18.1	32.7	171.25	421.85	-146.3	0.167	0.413	-147.3	0.261	0.561	-114.9
Sakha 95	84.87	69.13	18.5	25.2	17.13	32	143.92	428.28	-197.6	0.138	0.346	-150.7	0.225	0.532	-136.4
Sakha 96	84	61.38	26.9	22.7	13.9	38.8	136.62	649.81	-375.6	0.119	0.236	-98.3	0.253	0.685	-170.8
L.S.D	2.93			0.8			40.1			0.013			0.031		

LSD: least significant difference,

Relative water content (RWC) is one of the best growth/biochemical indicators for assessing the stress intensity (Ganji *et al*…, 2012). Table 7 showed that, relative water content (RWC %) of different wheat genotypes was significantly differed under normal and saline soil conditions. The highest RWC was observed in Line 12 (86.75%), Line 15 (86.26%) and Line 1 (84.59%) under normal condition, while Misr 4 recorded the highest RWC (74.31%) under saline soil with low reduction of (11%). This suggests that, Misr 4 undergoes cellular and organ-level changes to thrive in salt stress. The tolerance mechanisms are complex and include changes in stomata conductance, hormonal balance, antioxidant defense mechanisms, osmotic regulation, and ion exclusion. On the other hand, Sakha 96 showed a significant decrease in RWC under saline soils (61.36 %) recording the highest reduction for this trait (26.9%) compared to normal conditions which reflects the sensitivity of this genotype to salinity stress.

Total chlorophyll content (TCL) was highly affected with the interaction between two different soils and genotypes (Table 7). Under normal condition, Line 9 showed the highest content of chlorophyll followed by line 1, Misr 4, Line 2 and Line 18 (30.37, 28.30, 26.9, 26.72 and 26.7 µg ml^{-1} respectively), while Line 6 and Line 16 had the lowest chlorophyll content. Under saline soil, all genotypes exhibited a decrease in chlorophyll content. Line 3, Line 7 and Sakha 96 recorded the lowest TCL (13.87, 13.97 and 13.9 µg ml^{-1} respectively), while Line 9 had the highest TCL (20.1 µg ml^{-1}) followed by Line 10 (18.76 µg ml^{-1}) and Misr 4 (18.1 µg ml^{-1}).

This reduction in total chlorophyll content under salt affected soil is due to increasing oxidation and degradation from the accumulation of reactive oxygen species (ROS), and also through enzyme decomposition and activities such as glutathione reductase. (Afzal *et al*…, 2023, Balasubramaniam *et al*…, 2023 and Norouzi & Akbari, 2024) stated that, such reduction of TCL is likely a result of the plant adopting some physiological and biochemical mechanisms to cope with the stress causing reduction in photosynthetic pigments (chlorophyll). High salinity can reduce chlorophyll levels, damaging chloroplasts and mitochondria. Zang *et al*…, 2010, published that salt stress induced swelling of chloroplast thylakoids and causes destruction of chloroplast envelope leading to chlorophyll reduction under salt stress.

The Malondialdehyde (MDA) is a product of oxidative stress by reactive oxygen species (ROS) that peroxidized the polyunsaturated fatty acids (PUFA) in lipids of cell membranes so quantification of MDA is used as an indicator of cell membrane stability and a tool for determining salt tolerance in plants, Ehtaiwesh *et al*…, 2024. Our findings show that exposures to high salinity resulted in increased the MDA (µmols g^{-1} FW) levels for all tested genotypes (Table 7). The increase in MDA due to salt stress ranged from 104.3 % (Line 18) to 386.2 % (Line1). The genotypes Line 12 and Line 18 exhibited the lowest increase in MDA (120.1 and 104.3 % respectively). In contrast, Line 1 and Sakha 96 showed the greatest increase in MDA content (386.2 and 375.6 % respectively), despite having the lowest MDA concentration under normal conditions with no significant differences (143.9 and 136.62 µmols g^{-1} FW.) respectively , suggesting their potential sensitivity to salinity stress.

Data also indicated that Line 18 produced the littlest amount of MDA (361.43 µmols g^{-1} FW), followed by Line 12, Line 13, Misr 4 and Sakha 95 genotypes which have no significant differences in their MDA contents (418.39, 447.32, 421.85 and 428.28 µmols g^{-1} FW respectively) under saline soil conditions, suggesting their stress resistance capacity. Moreover, a slight increase in MDA concentration suggests high antioxidative ability and stress resistance (Afzal *et al*…, 2023). Many studies suggest that, an increase in MDA is linked to higher stress levels in wheat, and genotypes that accumulate less MDA demonstrate greater tolerance (Balasubramaniam *et al*…, 2023 and Ehtaiwesh *et al*…, 2024).

The proline content showed slight variations among genotypes under normal condition, ranging from 0.108 mg g^{-1} FW. In Line1 to 0.174 mg g^{-1} FW in Line11 as shown in Table 7. Under salinity stress proline content increased significantly, ranging from 46.5 % (Line 4) to 266.4 % (Line 12) compared to normal conditions. The highest accumulation of proline under slat stress was shown in Line 12 and Line 18 with no significant differences followed by Misr 4 (0.436, 0.432 and 0.413 mg g^{-1} FW respectively). In contrast genotypes Line 8, Line 10, Line 14 and Sakha 96, showed a reduced ability to accumulate higher amounts of proline under saline soil. This explains the important strategy of accumulating large amount of proline which acts as a cellular osmotic regulator, helping plants to survive under salt stress compared with sensitive genotypes. (Al-Saadi *et al*…, 2024 and Norouzi and Akbari, 2024)

Significant differences in the average sodium content for potassium (Na/K) content was observed due to the interaction between soil types and different genotypes, under control conditions (Na/K) concentration ranged from 0.225 in Sakha 95 to 0.339 in Line 17. Under saline conditions, a significant increase in the Na/K concentration was observed across all tested wheat genotypes. Line 12, Misr 4 and Sakha 95 showed the least concentrated (Na/K) under salty soil (0.537, 0.561 and 0.532 respectively) with an increase about (107.6, 114.9 and 136.4% respectively) in Na/K concentration. On the other hand, Line 5 and Line 17 recorded the highest Na/K concentration at 0.786 and 0.782 respectively. Ion imbalance happens under salt stress due to contrary relationship between Na$^+$ and K$^+$ ions. Accumulation of Na$^+$ ions in chloroplast, reduce the water potential of the plant and inhibit photosynthesis and exerts toxic effects. High external Na$^+$ concentration is recognized to interfere the uptake of K$^+$ leading to raise Na/K ration in leaves. (Munns and James, 2003) reported the relation between the concentrations of Na/K in plant leaves and its agronomical characters.

Grain Quality Traits
Effect of salinity on quality traits

Data in Table 8 revealed that salinity stress significantly affected the grain quality traits in all tested genotypes. Salt stress caused reduction in protein % by 4.2 % while the reduction increase in wet and dry gluten % by of 25.1% and 19.1% (negative sing), respectively.

Table 8. Mean effects of control and salinity treatments on the protein percentage, Wet gluten (%) and Dry gluten (%)

Treatment	Protein%	Wet gluten%	Dry gluten%
Normal	14.5	13.4	9.3
Salinity	13.9	17.9	11.5
Reduction %	4. 2	-25.1	-19.1
Sig	**	**	**

** **significant at 0.05 probability levels.**

Interaction Effect

Results of grain quality traits as affected by the interaction of salinity and wheat genotypes are depicted in Table 9. The results illustrated that grain quality traits (protein percentage, Wet Gluten percentage, and Dry Gluten percentage) were significantly affected by the interaction between salinity and genotypes. Among the 21 genotypes evaluated, Misr 4, Line 4, Line 6 and Line 7 exhibited the highest grain protein percentages under normal soil condition with values of 14.8, 14.7, 14.6 and 14.6%, respectively. Moreover, Misr 4 genotype maintained its superior in protein content under saline soil condition with value 14.6% protein with the lowest reduction (1.3%) compared with normal soil condition. That's may be due to high external Na^+ concentration interferes with nitrogen uptake leading to reduced protein synthesis in grains. .

Regarding the effects of the treatments in this study on wet gluten%, there were statistically significant increases (negative singe) in the saline conditions compared to normal, ranging from 2.3% in Sakha 95 to 72.2 % in Line 17. The lowest increases in wet gluten percentage were recorded for Line 12, Sakha 95, Line 16, Misr 4, and Line 11 with values of (1.3 %, 2.3 %, 3.7 %, 4.3 %, and 9.7% respectively) all of these genotypes recorded less increase than 10% . In contrast, the highest increase in wet gluten percentage was observed in Line 17 and Line 6 (Table 9).

According to dry gluten percentage, most genotypes exhibited an increase under saline conditions. Line 17 and Line 8 recorded the highest increases, while Line 11 remained unaffected. Notably, Sakha 96 and line 8 increased their dry gluten percentage to 18.3%, and 18.4 respectively achieving the highest percentage of dry gluten under saline soil conditions.

Norouzi and Akbari (2024) observed that the effects of salinity levels on grain quality, wet gluten, and dry gluten in wheat cultivars varied significantly. The results indicated that the wet gluten content tends to increwase with salinity, which could enhance the rising and elasticity properties of wheat flour under saline conditions as also reported by Sezer *et al...*, (2021). Contrary to these findings, some studies have shown that stress conditions can significantly decrease wet gluten content (Norouzi and Akbari 2024).

Table 9.Interaction effect over the two growing seasons of 2020/2021, and 2021/2022 and the reduction percentage (RD %) on the protein percentage, Wet gluten (%) and Dry gluten (%) under normal (N) and salinity(S) conditions.

Genotypes	Protein%			Wet Gluten%			Dry Gluten%		
	N	S	RD%	N	S	RD%	N	S	RD%
Line 1	14.4	14.1	2.1	18.5	25.1	-35.7	9.1	15.2	-67
Line 2	14.3	14.1	2.1	7.7	16.9	-54.4	5.4	10.2	-89
Line 3	14.1	13.4	5.1	8.4	16.9	-50.3	6.6	10.7	-62
Line 4	14.7	13.8	6.1	12.2	22.9	-46.7	10	13.8	-38
Line 5	14.1	13.9	1.4	12.2	13.5	-10.6	8.6	9.7	-13
Line 6	14.6	13.7	6.2	5.1	11.7	-56.4	4.1	7.5	-83
Line 7	14.6	14.3	2.1	15.2	24.9	-39	9.9	15.5	-57
Line 8	14.5	13.9	4.1	12.5	28.3	-55.8	8.9	18.4	-107
Line 9	14.4	13.6	5.6	14.3	21.1	-31.9	11.1	12.5	-13
Line 10	13.4	12.9	3.7	12.7	20.6	-38.3	7.8	13.2	-69
Line 11	13.4	13.3	0.7	19.6	21.7	-9.7	12.6	12.6	0
Line 12	13.1	13.2	0.8	14.9	15.1	-1.3	9.2	10.9	-18
Line 13	13.5	13.3	1.5	11.4	18.6	-38.7	8.1	10.9	-35
Line 14	13.1	12.8	2.3	10.1	16.3	-38	7.6	9.9	-30
Line 15	13.1	12.7	3.1	9.5	12.8	-25.8	7.1	7.2	-1
Line 16	13.6	13.2	2.9	18.2	18.9	-3.7	11.8	12.1	-3
Line 17	13.7	13.1	4.4	3.7	13.3	-72.2	3.4	8.5	-150
Line 18	13.9	13.5	2.9	14.7	17.8	-21.1	7.9	9.1	-15
MISR 4	14.8	14.6	1.3	13.8	14.4	-4.3	14.1	16.2	-15
Sakha 95	13.9	13.6	2.2	13	13.3	-2.3	8.4	9.9	-18
Sakha 96	13.6	12.9	5.1	20.9	29.5	-29.2	12.6	18.3	-45
L.S.D		0.22			0.05			0.27	

LSD: least significant difference

Hierarchical Cluster analysis (HC)

Cluster analysis is an effective method for estimating genetic divergence by classifying closely related genotypes and distinguishing them from diverged genotypes (Khan *et al...*, 2024 and Ehtaiwesh *et al…*, 2024).

Twenty-one genotypes under study were classified into four clusters using Ward's method under both normal and salinity conditions (Fig. 1). The Dendrogram generated from the sixteen traits produced four major clusters.
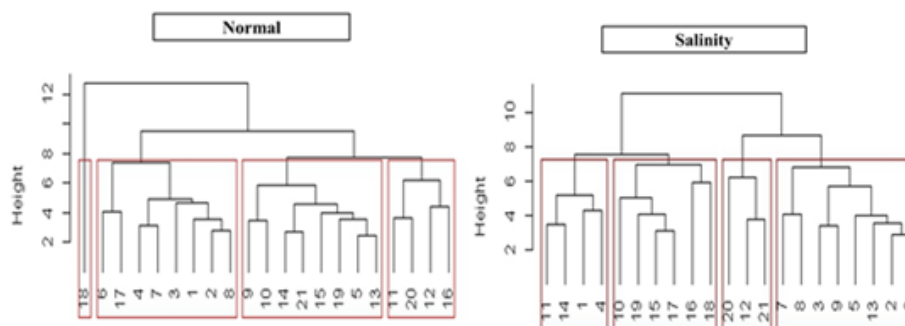

Fig 1. Dendrogram showing clustering of 21 wheat genotypes under normal and salinity conditions based on the Euclidean distance for 16 measured traits.

Under normal conditions, Cluster I comprised one genotype (Sakha 96), and Cluster 2 comprised eight genotypes (Line 6, Line 17, Line 4, Line 7, Line 3, Line 1, Line 2, and Line 8). Cluster 3 included eight genotypes (Line 9, Line 10, Line 14, Line 18, Line 15, Sakha 95, Line 5, and Line 13), while Cluster 4 had four genotypes (Line 11, MISR 4, Line 12, and Line 16), highlighting their distinct separation from the genotypes in the other clusters.

Under salinity conditions, genotypes are divided into two main categories: The first category consisted of two groups firstly, covered four genotypes (Line 11, Line 14, Line 1, and Line 4) The second covered genotypes (Line 10, Sakha 95, Line 15, Line 17, Line 16 and Sakha 96) Figure 1. The second category consisted of two groups firstly, covered three genotypes (MISR 4, Line 12 and Line 18). The second category covered eight genotypes (Line 7, Line 8, Line 3, Line 9, Line 5 Line 13, Line 2, and Line 6) as shown in Figure 1.

Many scientists have used cluster analysis to categorize different wheat genotypes according to salt tolerance status based on various attributes and found similarities between wheat genotypes within a group Darwish *et al...,* 2017, Ehtaiwesh *et al...,* 2024 and Khan *et al...,* 2024.

Linear discriminant analysis (LDA)

Linear Discriminant Analysis (LDA) was used to verify cluster analysis groups and enhance category reliability. The discriminant analysis creates a linear combination of yield-related traits to distinguish between high, moderate, and low-grain-yielding genotypes under salinity conditions as reported by Abu-Ellail *et al...,.* 2020, El-Hawary *et al...,.* 2022 and Aminizadeh *et al...,* 2024. The aime was to determine which characteristics could differentiate among twenty-one genotypes categorized as salt-tolerant (T), moderately tolerant (MT), and salt-sensitive (SG). LDA assigns genotypes based on discriminant function scores, identifies misclassifications, and provides graphical group representations.

Under normal and salinity conditions over two seasons the traits were ranked based on the absolute magnitude of the coefficients in the linear discriminant functions (LDF) as shown in Tables 10 and 11. The two-dimensional discriminant functions with significant Wilks lambda values were strongly associated with the prediction of membership in the genotype group under normal and saline condition. The traits recorded significant coefficients and large Wilks lambda that also, showed in Tables 10 and 11.

The graphical representation (Fig. 2 and 3) illustrates the classification of the twenty-one wheat genotypes into three groups based on the two discriminating functions at two conditions (normal and salinity).

Linear discriminant analysis(LDA) at normal condition

At normal conditions, significant discriminant functions 1 and 2 accounted for 77 % and 20 % of the total variance, with small values of Wilks lambda (0.12 and 0.31 respectively,) as shown in Table 10 which confirmed that two discriminant functions (the number of discriminant functions is equal to groups-1) in all treatments (control and salinity) effectively separated high, moderate, and low-yield genotypes and showed that group means differ.

The variables were loaded into canonical discriminant function one, and it was found that GY (2.22) followed by related yield components NK/S (-1.33), NS/m² (-0.95), and 1000KW (0.61). Additionally, it was observed

that the absolute coefficient for Flag leaf area (FLA) (0.77) was the only discriminatory variable in the canonical discriminant function two.

Table 10. Standardized Discriminant Functions Coefficients at Normal Condition

Variables	Standardized canonical discriminant function coefficient		Wilks' ambda
	Function 1	Function 2	
GYardab	2.22		0.55**
NKS	-1.33		0.45**
NSm²	-0.95		0.40**
W1000Kg	0.61		0.51**
LA		0.71	0.54**
Model sig.	**	**	
Canonical correlation	0.77	0.20	
Wilks' lambda	0.12	0.31	

GY: Grain Yield, NK/S: number of kernels spike, NSm²: number of spike/m², 1000 kernels weight, LA: Leaf area (cm²) and **: significant level.

Table 11. Standardized Discriminant Functions Coefficients at Salinity Condition

Variables	Standardized canonical discriminant function coefficient		Wilks' lambda
	Function 1	Function 2	
GY/ardab	2.52		0.60**
RWC%	1.69		0.51**
1000KW /g	1.33		0.63**
Proline	1.21		0.54**
NK /S	0.98		0.53**
DM	0.92		0.52**
DH	0.90		0.68**
NS/ m²	0.84		0.55**
Protein%	- 0.79		0.70**
TCL	-0.74		0.64**
FLA	- 0.69		0.40**
PH	0.48		0.34**
MDA		-2.01	0.68**
Na/K		0.92	0.66**
Model sig.	**	**	
Canonical correlation	0.83	0.17	
Wilks' lambda	0.025	0.32	

GY: Grain Yield, RWC%: relative water content, W1000K/g:1000 kernels weight, NK/S: Number of kernels spike, DM: days to maturity, DH: days to heading, NSm²: Number of spike/m², TCL: Total Chlorophyll content, LA: Leaf area (cm²), PH: plant height MDA: Malondialdehyde, Na/K: Sodium Content for Potassium and **: significant level.
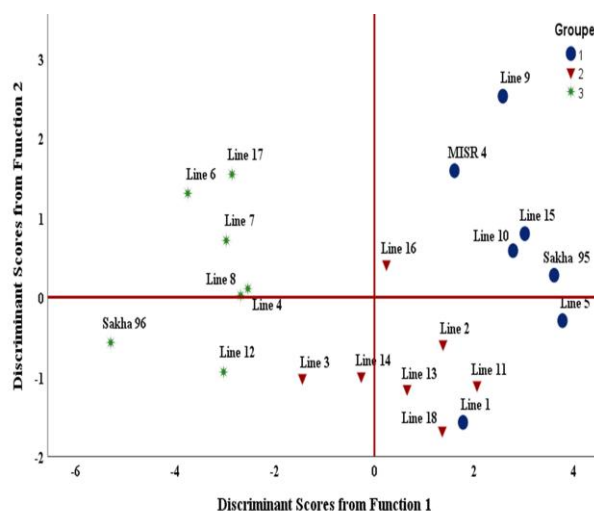

Fig. 2. Graphical representation of discriminant function across normal conditions over two years.
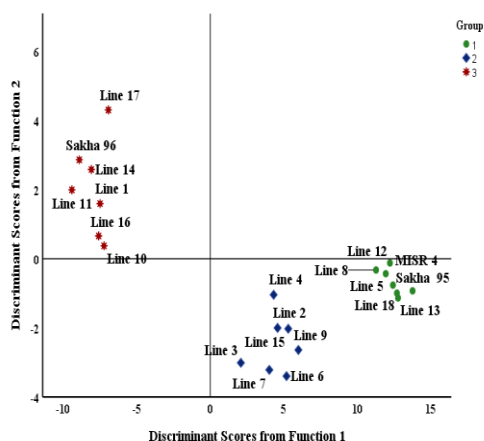Function 1= Grain yield and yield components and Function 2 = FLA: Flag Leaf area (cm²).

Fig. 3. Graphical representation of discriminant function across salinity condition

Function 1= Grain yield, yield components and RWC%: relative water content, TCL: Total Chlorophyll content, F LA: Flag Leaf area (cm²) and Function 2 = MDA: Malondialdehyde, Na/K: Sodium Content for Potassium.

The data in Table 11 indicated that the grain yield (GY) was the most influential variable, followed by NK/S, NS/m², and 1000KW as reflected by the high coefficients and Wilks' lambda. Figure 2 illustrates the classification of the twenty-one wheat genotypes into three groups based on the scores of genotypes by two discriminating functions. Group one (Line 9, MISR 4, Line 15, Line 10, Sakha 95, Line 5, and Line 1) and group two (Line 16, Line 2, Line 11, Line 14, Line 13, Line 18 and Line 3) are positioned on the right side, representing genotypes with the highest grain yield (ardb/fad) and yield components and function two Flag Leaf area (FLA cm²) and indicates high to moderate tolerance to salinity conditions, except for Line 1, which has the smallest LA. In contrast, group three on the left side consisted of genotypes exhibited lower scores for both grain yield (ardb/fad) and yield components under function one and function two. Suggesting these genotypes may be salt-sensitive genotypes (SG), this groups includes Line 17, Line 6, Line 7, Line 8, Line 4, Sakha 96 and Line 12 (Fig. 2). According to (Al-(Ashkar *et al...,* 2019, El-Hawary *et al...,* 2022, Khan *et al...,* 2024 and Sallam *et al...,* 2024) a coefficient greater than ± 0.5, indicates a distinguishing factor. These findings were logical and consistent with the ANOVA results and suggest that selection based on these traits can enhance wheat yield.

Linear Discriminant Analysis (LDA) at salinity condition

Among the 21 genotypes under soil saline conditions over two seasons. Out of 16 agronomic, physiological, and grain quality traits, 14 characteristics have significant coefficients that differentiate between Tolerant (T), Moderate Tolerant (MT) and Sensitive Genotype (SG) under salinity stress conditions. The data in Table 11 indicated that significant discriminant functions one and two accounted for 83 % and 17 % of the total variance, with small values of Wilks lambda (0.025 and 0.32 respectively,) at salinity conditions, suggesting that the discriminant functions model accounts for 83% of the variance in function one and 17% of the variance in function two. Subsequently, the coefficients for each trait are as follows: GY (2.52), RWC % (1.69), 1000 KW/g (1.33), Proline (1.21), NK/S (0.98), DM (0.92), DH (0.90), NS m² (0.84), Protein % (-0.79), TCL (-0.74),

FLA (-0.69), PH (0.48) at function one. In addition, function two contains MDA (-2.01), and Na/K (0.92). Furthermore, the Wilks' lambda for each trait was presented. The scatter plot of discriminant scores of two functions under salinity stress (Fig. 3) displays that group one exhibit the highest grain yield along with yield components as well as physiological traits and consists of Line 5, Line 8, Line 12, Line 13, Line 18, MISR 4 and Sakha 95. Additionally, they demonstrate low values of MDA and Na/K. These traits are recognized for their high breeding value in improving grain yield in wheat, attributed to their favourable coefficients and high Wilks' lambda (Table 11). The importance of these traits has been confirmed by several other studies (El-Hawary *et al...,* 2022, Arazmjoo and Amini 2024, Ehtaiwesh *et al...,* 2024, Khan et al..., 2024 and Sallam *et al...,* 2024. Accordingly, group two exhibit moderate, grain yield and related yield components includes Line 4, Line 2, Line 9, Line 15, Line 3, Line 7 and Line 6. On the other hand, group three exhibite smallest scores for grain yield and the highest scores for MDA and Na/K which were sensitive to saline conditions and includes Line 17, Sakha 96, Line 14, Line 1, Line 11, Line 16, and Line 10 (Fig. 3).

CONCLUSION

Abiotic stresses like heat, drought, salinity, and waterlogging significantly reduce wheat yields in affected regions. In the future, climate instability and water scarcity may turn productive areas into regions with shorter growing seasons and increased salinity. This presents challenges for plant breeders and researchers developing climate-tolerant genotypes.

The observed significant differences in morphological, physiological, and yield traits under salinity highlight genetic variation among the wheat genotypes, suggesting that this diversity can be effectively used in breeding programs. The ANOVA and applied multivariate statistics, including cluster analysis and linear discriminant analysis, helped in selecting elite genotypes with high performance across all traits under study and minimal physiological increases (MDA and Na/K) under salinity for wheat plant-breeding program. Traits such as DM, DH, NK/S, 1000 KW/g, NS/m², FLA, and PH, along with physiological characteristics like RWC %, proline, protein percentage, and total chlorophyll (TCL), are crucial. Also, low Malondialdehyde (MDA) and sodium-to-potassium (Na/K) ratios make these traits valuable for improving wheat grain yield under saline conditions.

In the studied salinity conditions, which also face drought issues, Lines 5, 8, 12, 13, 18, MISR 4, and Sakha 95 are suitable and demonstrate normal physiological responses to avoid salinity effects. Based on discriminant scores Line 4, Line 2, Line 9, Line 15, Line 3, Line 7 and Line 6 exhibit moderate tolerance. Lines 1, 10, 11, 14, 16, 17, and Sakha 96 are the lowest-yielding genotypes, and exhibit high MDA and Na/K, indicating a significant sensitivity to salinity conditions based on their discriminant scores.

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تقييم بعض التراكيب الوراثية لقمح الخبز كمنهج مستدام لإنتاج القمح تحت ظروف الإجهاد الملحي

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الملخص

تم إجراء الدراسة خلال موسمي الزراعة 2020/ 2021 و2022/2021 في المزرعة البحثية بمحطة البحوث الزراعية بسخا بكفر الشيخ، مصر، لتحليل آثار الإجهاد الملحي على محصول الحبوب ومكوناته بالاضافة الي الصفات الفسيولوجية وجودة الحبوب في واحد وعشرين صنفًا وسلاله من قمح الخبز (18 سلالة و3 أصناف) لتقييم التباين الوراثي و اختيار التراكيب الوراثية الاكثر تحملا للملوحة. أظهرت النتائج أن جميع الصفات المدروسة انخفضت بشكل ملحوظ تحت ظروف الملوحة باستثناء بعض الصفات الفسيولوجية (MDA ،نسبة البرولين ونسبة الصوديوم الي البوتاسيوم) بالاضافة الي نسبة الجلوتين الرطب والجاف والتي سجلت قيما مرتفعة كما لوحظ تباين كبير بين التراكيب الوراثية وخاصة في ظل الظروف الملحية. بناءً على درجات التمييز ، فإن السلالات 5 و8 و12 و13 و18 و صنفي مصر 4 و سخا 95 كانت الأكثر تحملا للملوحة وأظهرت استجابات فسيولوجية طبيعية تقلل من تأثير الاجهاد الملحي. في حين أن السلالات 4 و2 و9 و15 و3 و7 و6 أظهرت تحملاً متوسطا للملوحة. وعلى النقيض من ذلك، كانت السلالات 1 و10 و11 و14 و16 والصنف سخا 96 هي أكثر حساسية للملوحة مما يجعلها أقل قدرة على التكيف مع الظروف المالحة.