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Assortment of Some Egyptian Bread wheat Genotypes under Salinity Stress Conditions

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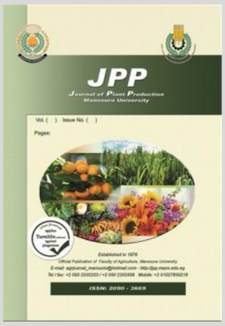

ABSTRACT

This investigation was conducted to examine the influence of salinity stress on agronomic and physiological traits of some bread wheat genotypes at Sakha Agricultural Research Station, Agricultural Research Center, Egypt during 2019/2020 and 2020/2021 seasons under normal and saline affected soil. Salinity treatments, genotypes and its interactions showed significant effects on the most measured traits. Salinity decreased the averages of all agronomic traits. The results presented significant differences between normal and salinity soil conditions for chlorophyll content index, leaf diffusive resistance and leaf transpiration rate traits. However, genotypes appeared significant differences for chlorophyll content index, canopy temperature, carbon dioxide concentration, flag leaf area and chlorophyll fluorescence traits. Meanwhile, the interaction between locations and genotype was significant canopy temperature, flag leaf area and chlorophyll fluorescence only. Canopy temperature in the non-saline soil cleared highest values compared to salinity soil conditions. Grain yield was positively correlated with grain filling rate (GFR), thousand kernel weight (KW), Normalized difference vegetation index (NDVI) and spikes/m^2 (SM^2) however, it was negatively correlated with canopy temperature. This suggests that increasing NDVI, GFR, SM2 and KW in wheat breeding may be an effective strategy for improving productivity in both normal and salinized environments. Genotypes G19 and G20 significantly outperformed all studied genotypes and checked cultivars for grain yield under normal and salinity stress. Salinity tolerance and GGE biplot indices agreed that G19 and G20 had similar trend of the increased stress tolerance of genotypes and it can be source of salinity tolerance in a breeding program.

***Keywords**:* Salt tolerance; GGE biplot; Salinity tolerance indices; Wheat genotypes

INTRODUCTION

Globally, wheat (*Triticum aestivum* L.) is one of the most essential crops, producing over 770 million metric tons per year from 221 million hectares (FAOSTAT, 2023). For millions of people, it is a vital source of nourishment since it supplies about 20% of the calories and protein that people worldwide consume (Kizilgeci *et al.*, 2021; Erenstein *et al.*, 2022). Thus, maintaining the resilience and sustainability of wheat production is essential to supplying the world's expanding population with food (Lopes *et al.*, 2018). Egypt imports over 10 million tons of wheat a year, making it one of the biggest importers (FAOSTAT, 2023). Many nations, like Egypt, rely heavily on wheat flour for human and its straw as a feed for animal. (Milad *et al.*, 2013). It is important to note that the gap between production and consumption is widening because of climate change and increasing population growth. For this reason, the cultivated area should be expanded to include more marginal habitats, characterized by high levels of salinity (Desoky *et al.*, 2021; Gander and Singh, 2023).

However, salinity, drought, extreme temperatures, soil and soil degradation are some of the issues that affect wheat productivity (Raimondo *et al.*, 2020; Saddiq *et al.*, 2021). One of the main abiotic stressors that have a detrimental effect on plant growth and development is soil salinity. (Dimitrijević *et al.*, 2012; Farooq *et al.*, 2022). Salinity is frequently referred to as a "white death," and due to inappropriate anthropogenic activity, approximately 60 million hectares of irrigated land and 32 million hectares of dry land have become salinized globally (Zeehan *et al.*, 2020; Saddiq *et al.*, 2021; Seleiman *et al.*, 2022). An estimated 12 billion US dollars are lost annually by the global economy because of salinity, and this value is continually rising (Lauchli and Luttge, 2004). One of the nations with the most serious salinity issues is Egypt. For instance, irrigation with saline water and little precipitation (<25 mM yearly rainfall) have already salinized 33% of the cultivated area (Ghassemi *et al.*, 1995; Kim and Sultan, 2002). The main impacts of salinity are hyper-osmotic stress and hyper-ionic toxic effects, which restrict seedling germination and growth (Hasegawa *et al.*, 2000). Additionally, by decreasing seed germination, (Sairam *et al.*, 2002), total dry matter accumulation, root/shoot length (Datta *et al.*, 2009), number of spikelet (Tabatabaee *et al.*, 2023), seedling characters (Ehtaiwesh, 2019) and development of shoot and root (Ragaey *et al.*, 2022) salt has a detrimental effect on plant growth.. The balance of primary metabolites, including total soluble sugars, reduced sugars, non-reducing sugars, starch, lipids, and proteins, is also impacted by salt (De Santis *et al.*, 2021; Hussain *et al.*, 2021; Kesh *et al.*, 2022; Masarmi *et al.*, 2023; Sadak and Dawood, 2023). Plant development, growth, and ultimate productivity are all negatively impacted by the damaging effects of salt stress on many physiological processes of plant (Munns 2002; Rady 2011; Zhang *et al.*, 2014; Rios *et al.*, 2017). Salt resistance is an inherent trait of plants to withstand the adverse effects in the leaves or root zone (Odjegba and Chukwunwike, 2012). Through the establishment of national initiatives to reclaim and cultivate additional areas, the Egyptian government is making significant efforts to increase the amount of agricultural land. One of the main issues with farming in the new areas is the salinity of the soil and irrigation water. There are several ways to boost wheat output in salt-affected locations, including planting salt-tolerant cultivars, enhancing the soil's surface,

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subsurface, and vertical drainage systems, and allowing salts to leach directly (Ashraf *et al.*, 2007). The best method to get around the constraints is to use salt-tolerant wheat varieties (Ellis *et al.*,2002). Different wheat cultivars differ in their tolerance to varying levels of salt stress, and their ability to produce grain yields under such conditions varies (Mansour *et al.*, 2020; Banjac *et al.*, 2022). To determine which wheat genotypes are salt-tolerant and which are sensitive, it is essential to evaluate them in situ under actual field salinity conditions. This information can be used to regionalize realized varieties and create more efficient breeding plans for increased wheat productivity in saline environments (El-Hendawy *et al.*, 2017; Mansour *et al.*, 2020; Moustafa *et al.*, 2021; Ahakpaz *et al.*, 2023). Breeding cereal cultivars that can withstand salt is not moving forward very quickly. This is frequently ascribed to the salt tolerance trait's complicated genetic and physiological makeup as well as the absence of a quick and accurate screening method (Almeida *et al.*, 2017; Volkov and Beilby, 2017). As a result, Egyptian wheat breeders ought to assess and describe the bread wheat cultivars' ability to withstand salinity in salt-affected and recently recovered soils. El-Hendawy *et al.* (2009) Numerous researchers used various experimental setups conducted under either controlled or simulated field conditions to demonstrate significant genetic variations in bread wheat's ability to withstand salinity. They evaluated wheat genotypes and reported that grain weight per plant, number of grains per plant, and number of fertile spikes per plant are good screening criteria under field conditions (Muhammad and Hussain 2012; Chahine *et al.*, 2013; Hussain *et al.*, 2015; Jovovic *et al.*, 2018; Guellim *et al.*, 2019; Al-Ashkar *et al.*, 2020). However, It is crucial to check the salt tolerance of field crops until they reach the producing stage and, more crucially, to conduct the evaluation in actual field circumstances, particularly when it occurs in advanced breeding programs (El-Hendawy *et al.*, 2017, Igartua *et al.*, 1995; Allel *et al.*, 2019). To distinguish between tolerant and sensitive genotypes, stress tolerance indices (STIs), which are straightforward mathematical formulas, are frequently employed to quantify and compare grain yields under stressed and non-stressed conditions. Numerous stress tolerance measures exist, including the "SSI" (stress susceptibility index) (Fischer and Maurer, 1978), Smaller SSI values are more desirable since larger SSI values indicate comparatively greater sensitivity to stress. Based on the tested genotypes' performance and contributing characteristics, cluster analysis is a useful biometric tool used to measure the level of genetic divergence. However, it was discovered that the cluster analysis based on the (STI's) parameter is helpful in distinguishing wheat genotypes for salt tolerance (Singh *et al.*, 2015; Darwish *et al.* 2017).

This investigation aimed to: (1) Examine the effects of salinity stress on 32 bread wheat plants produced under actual environmental circumstances, as well as various yield parameters and philological characteristics (2) Detect salt-tolerant genotypes for cultivation in salt affected soils or as source for improving salinity tolerance in the wheat breeding programs (3) determine the appropriate selection indices/criteria for assessing the tolerance of a genotype to salinity.

MATERIALS AND METHODS

Experimental site and plant materials

The investigation was conducted at Sakha Agricultural Research Station, Kafrelsheikh, Agricultural Research Center (ARC), Egypt (latitude 31°5′N and longitude 30°56′E and 7 m above sea level) in two separate field during the two successive wheat growing seasons, 2019/2020 and 2020/2021. Thirty-two bread wheat genotypes (Table 1) which obtained from Wheat Research Department, Field Crops Research Institute, ARC, Egypt were used in this study as plant materials (15 commercial bread wheat cultivars + 17 promising lines).

Table 1. Names and pedigree of the thirty-two studied bread wheat genotypes.

Code#	Name	Pedigree
G1	Sakha 93	SAKHA92/TR8l0328.S.8871-1S-2S-1S-0S
G2	Sakha 94	OPATA/RAYON//KAUZ.CMBW90Y3l80-0TOPM-3Y-010M-010M-010Y-10M-015Y-0Y-0AP-0S.
G3	Sakha 95	PASTOR/SITE/MO/3/CHEN/AEGILOPS SQUARROSA(TAUS)/BCN/4/WBLL1.CMSA01Y00158S-040POY-040M-030ZTM-040SY-26M-0Y-0SY-0S.
G4	Sakha 1001	SIDS1/ATTILA//GOUMRIA17.S. 16498-042S-013S-21S -0S
G5	Misr 1	OASIS/SKAUZ//4*BCN/3/2*PASTOR.CMSS00Y01881T-050M-030Y-030M-030WGY-33M-0Y-0S
G6	Misr 2	SKAUZ/BAV92.CMSS96M03611S-1M-010SY-010M-010SY-8M-0Y-0S
G7	Misr 3	ATTILA*2/PBW65*2/KACHU.CMSS06Y00582T-099TOPM-099Y-099ZTM-099Y-099M-10WGY-0B-0EGY
G8	Giza 168	MRL/BUC//SERI.CM93046-8M-0Y-0M-2Y-0B-0SH
G9	Giza 171	SAKHA93/GEMMEIZA9.S.6-lGZ-4GZ-lGZ-2GZ-0S
G10	Gemmiza 9	ALD “S”/HUAC//CMH74A.630/SX.GM 4583-5GM-lGM-0GM
G11	Gemmiza 11	BOW"S"/KVZ"S"//7C/SER182/3/GIZA168/SAKHA61.GM7892-2GM-lGM-2GM-1GM-0GM
G12	Gemmiza 12	OTUS/3/SARA/THB//VEE.CMSS97Y00227S-5Y-010M-010Y-010M-2Y-1M-0Y-0GM
G13	Shandweel 1	SITE/MO/4/NAC/TH.AC//3*PVN/3/MIRLO/BUC.CMSS93B00567S-72Y-0l0M-010Y-010M-3Y-0M-0HTY-0SH
G14	Sids 14	BOW "S"/VEE"S"//BOW"S"/TSI/3/BANI SEWEF1.SD293-1SD-2SD-4SD-0SD
G15	Line 1	MINO/898.97/5/SW89.5277/BORL95//SKAUZ /3/PRL/2*PASTOR/4/HEILO.S.2011-83-013S-012S-5S-0S
G16	Line 2	PRL/ 2*PASTOR*2// FH6-l-7*2/3/UP2338*2 /KKTS*2// YANAC.CMSSl1B00753T-099TOPY-099M-0SY-30M-0WGY-0S
G17	Line 3	MINO/898.97 // WBLL1*2/KIRITATI.S.2011-81-035S-014S-2S -0S
G18	Line 4	MINO/6/SAKHA 12/5/ KVZ //CNO 67/ PJ 62/3/YD "S" / BLO "S"/4/ K 134 (60)/ VEE.S. 16869 -010S -07S-4S-1S -0S
G19	Line 5	MINO/898.97/3/ WHEAR/TUKURU//WHEAR.S.2011-85-027S-016S-6S-0S
G20	Line 6	HUW234+LR34 /PRINIA*2//SNLG /3/KINGBIRD #1 /4/BAJ 1.CMSS10Y00903T-099TOPM-099Y-099M-099NJ-099NJ-l0WGY-0B-0S
G21	Line 7	PBW343*2/KUKUNA/3/PASTOR//CHIL/PRL/4/PBW343*2/KUKUNA/5/MISR1.S.2011-66-021S-09S-l8S-0S
G22	Line 8	SW89.5277 /BORL95//SKAUZ/3/PRL/2*PASTOR/4/HEILO/5/GIZA168//MAY/NAC.S.2011-121-019S-02S-l4S-0S
G23	Line 9	PBW343*2/ KUKUNA/3/PASTOR//CHlL/PRL/4/PBW343*2/ KUKUNA/5/MISR 1.S.2011-66-021S-09S-l4S-0S
G24	Line 10	SAKHA 94 /4/ WHEAR/VIVlTSl/3/C80.1/3*BATAVIA//2*WBLL1.S.2011-6-017S-09S-6S-0S
G25	Line 11	CHEN/AEGILOPS-SQUARROSA(TAUS)// BCN /3/ 2*KAUZ/4/GEN*2 //BUC/ FLK/3/BUCHIN.S.16280-020S-015S-4S-0S.
G26	Line 12	WBLL1*2/BRAMBLING/3/WHEAR/CHAPIO//WHEAR.S.2011-105-041S-0l0S-5S-0S
G27	Line 13	WBLL1*2/KIRITATI /3/WHEAR/CHAPIO//WHEAR.S.2011-112-019S-017S-1S-0S
G28	Line 14	MUCUY//MUTUS*2/TECUE#1.CMSS11B00372S-099M-099NJ-099NJ-l9WGY-0B-0S
G29	Line 15	UP2338*2/SHAMA/3/MILAN/KAUZ//CHIL/CHUM18/4/UP2338*2/SHAMA/5/COPIO.CMSS10B00326S-099M-0SY-45M-0WGY-0S
G30	Line 16	WHEAR/ SOKOLL/3/ TRCH/SRTU// KACHU.CMSS10Y0020lS-099Y-099M-099NJ-099NJ-2WGY-0B-0S
G31	Sids 12	BUC//7C/ALD/5/MAYA74/ON//1160.l47/3/BB/GLL/4/CHAT"S"/6/MAYA/VUL//CMH74A.630/4*SX. SD7096-4SD-1SD-lSD-0SD
G32	Line 17	MINO/ 898.97//WBLL1*2/ KIRITATI.S. 2011 -81-035S -0l4S-2S -0S

Each treatment (normal and salt) was considered as an independent experiment. Soil description and analyses of the experiment that conducted in saline and non-saline (normal) soil were shown in (Table 2). The 32 bread wheat genotypes were arranged in randomized complete block design (RCBD) with three replications under each treatment in the third week of November. The area of the experimental unit was 4.2 m^2. At the proper time, irrigation, fertilization, weed control, fungicides and others recommended agricultural practices applied.

Table 2. Description and soil analysis of the environments for studied normal and salt-affected soil.

Location	Properties of Soil		Anions (mg/L)				Cations (mg/L)			
	Texture	EC^0	Hco_3^{--}	Co_3^{--}	Cl^-	So_4^{--}	Ca^{++}	Mg^{++}	Na^+	K^+
Normal-soil	Clayey	2.5	2.75	-	6.48	8.15	4.44	3.135	9.525	0.28
Saline-soil	Clayey	7.40	3.5	-	32.64	45.29	18.75	13.9	43.37	0.41

Phenotypic Measurement across two seasons

Agronomic traits were recorded for the following traits: days to heading (DH), days to maturity (DM), grain filling period (GFP), grain filling rate (GFR), plant height (PH), number of spikes per square meter (SM), thousand kernel weight (1000KW) and grain yield (GY) for the thirty-two wheat genotypes evaluated under normal soil and saline affected soil in 2019/20 and 2020/21 seasons. Normalized difference vegetation index (NDVI) was measured by a field portable NDVI sensor (GreenSeeker®handheld crop sensor, Trimble Navigation Limited, Westminster, CO, USA). NDVI was measured between 11:30 am and 2:00 pm (Rouse *et al.*, 1974).

Meanwhile, physiological traits, such as canopy temperature (CEM) were obtained using a near-infrared temperature sensor (CEM DT 8835 infrared and K-type thermometer) at the completed flowering stage of each plot from 1:00pm to 2:00pm on a cloudless day. However, flag leaf area (FLA), carbon dioxide concentration (COCN), cuvette temperature ˚C (CUV), intercellular CO2 concentration (INCO), leaf diffusive resistance (LDI), leaf temperature ˚C (LTM), quantum sensor µmol m^{-2} s^{-1} QUN and leaf transpiration rate µg cm^{-2} s^{-1} (TRN) for studied wheat genotypes evaluated under both environments during only one season.

Salinity tolerance indices (STIs)

Based on grain yield means of the studied genotypes under saline (Ys) and non-saline (Yp) soils over two seasons were obtained to calculate the STSIs. These indices were calculated using the formulas illustrated in Table 3. Where: $\bar{Y}s$ is the mean yields over all genotypes under stress environment, $\bar{Y}p$ is the mean yields over all genotypes under non-stress environment.

Stress tolerance indices (STI) biplot view of grain yield estimated for non-saline (Yp) and saline soil sites (Ys) per seasons and stress tolerance indices *viz* tolerance index (TOL), mean productivity (MP), stress susceptibility index (SSI),stress tolerance index (STI), geometric mean productivity (GMP), harmonic mean (HM), yield index (YI), yield stability index (YSI), and relative stress index (RSI) of the 32 genotypes in both seasons 2019/20 and 2020/21 (averaged seasons).

Table 3. Salinity tolerance parameters with the calculated formulas.

Abbreviation	Stress tolerance indices	Equation	References
TOL	Tolerance Index	$= Yp-Ys.$	Hossain *et al.*, 1990
MP	Mean Productivity	$=(Yp + Ys) / 2.$	Rosielle and Hambline, 1981
GMP	Geometric Mean Productivity	$= \sqrt{Yp * Ys}.$	Fernandez, 1992
HM	Harmonic Mean	$= 2*(Yp*Ys)/(Yp+Ys).$	Chakherchaman *et al.*, 2009
SSI	Salinity susceptibility index	$= [1-(Ys/Yp)]/[1-(\bar{Y}s /\bar{Y}p)].$	Fisher and Mourer, 1978
STI	Stress tolerant index	$= (Yp*Ys)/ \bar{Y}p^2.$	Fernandez, 1992
YI	Yield Index	$= Ys/ \bar{Y}s.$	Gavuzzi *et al.*, 1997
YSI	Yield Stability Index	$= Ys/Yp.$	Bouslama and Schapaugh, 1984
RSI	Relative stress index	$= (Ys-Yp)/ (\bar{Y}s -\bar{Y}p).$	Fischer and Wood, 1979

Statistical analyses

Analysis of variance (ANOVA) for each season and location was performed to collect data. Combined analysis was performed according to Gomez and Gomez (1984) after confirming homogeneity of error across seasons by Levene's (1960) test. The "GENSTAT" statistical package programs used a one-factor model that was integrated across the years with salt treatments to statistically assess the data. LSD was used to evaluate differences at the 0.05 level of probability based on the means of genotypes, years, and salt treatments and their interactions. Spearman correlation heatmap of agronomic traits, Chord chart for the regression coefficients and carve estimation was done to study the relationship between grain yield and other studied characters under salinity treatments using "Origin" statistical computer program. According to Yan and Tinker (2006), the genotype and genotype by environment interaction GGE biplot was performed using GenStat 18 utilizing the means of the genotypes and susceptibility indices under study. The "Origin" statistical computer program was used to estimate the association between grain yield and salinity level (IBM SPSS Corp. 2015).

RESULTS AND DISCUSSION

Agronomic yield traits ANOVA

Results of the Levene (1960) test cleared the homogeneity of the separate error for all the studied yield traits that allow conducting the combined analysis across the two salinity treatments in the two growing seasons (Table 4). Combined analysis of variance cleared significant differences among two seasons for all the tested traits except for DH, GFR, 1000KW and GY; indicating to the large environmental effects on the most studied wheat genotypes traits. These results are in agreement with those reported by (Mahgoub *et al.*, 2022 and 2023) who pointed to climatic conditions vary from year to year at the same location.

Salinity treatments (S) and genotypes (G) showed highly significant effects on all the measured traits.

Variances of year, salinity treatments and genotypes interactions revealed significant for all studied traits, except the GFP, NDVI and 1000KW in years*salinity treatments interaction; 1000KW in years*genotypes interaction; PH in salinity treatments*genotypes interaction and DM, SM and1000KW in years*salinity treatments*genotypes interaction. The significant interactions of genotypes among years and salinity locations suggested that found genetic variability among the genotypes and possibility of selection for promising ones (Hagras *et al.*, 2018 and Mahgoub *et al.*, 2023).

Table 4. Mean squares and its significant of years, salinity treatments, bread wheat genotypes with their interactions for yield traits.

S. O. V.	df	DH	DM	GFP	GFR	PH	NDVI	SM	1000KW	GY
Year (Y)	1	110.51	978.57**	431.38*	0.17	1524.02**	0.068**	2944026.0**	0.002	1.23E+06
Residual	4	28.41	26.98	49.79	106.67	63.22	0.001	7563.0	14.27	4.40E+05
Salinity (S)	1	11288.34**	24464.1**	2516.38**	77779.82**	20053.71**	0.378**	2183916.0**	1032.19**	1.017E+09**
Y.S	1	384.00**	1004.27**	146.27	27166.40**	1368.82*	0.002	4097994.0**	0.001	2.786 E+08**
Residual	4	6.81	22.88	20.4	131.58	74.93	0.017	10654.0	44.78	8.961 E+05
Genotypes (G)	31	366.96**	188.71**	104.98**	1013.12**	582.73**	0.038**	14364.0**	452.63**	8.796E+06**
Y.G	31	27.17**	13.58**	31.34**	313.18**	42.44*	0.011**	17672.0**	0.001	2.745E+06**
S.G	31	14.69**	11.85*	23.49**	311.48**	26.69	0.007**	8891.0*	61.78**	2.304E+06**
Y.S.G	31	9.34**	9.51	16.12**	404.68**	49.06**	0.006**	8327.0	0.001	3.851E+06**
Residual	248	5.17	6.99	7.94	58.31	26.6	0.002	5717.0	18.82	5.09E+05

***, ** and ns refer to P<0.05, P<0.01 and non-significant, respectively.**

The partitioning of sum of squares (years, salinity treatments and genotypes) for the studied grain yield traits was shown in Figure 1. The main portion of total variance due to salinity treatments had the greatest values for DM, GFR, PH and GY traits, recording 69.28, 42.35, 38.70 and 51.44, respectively. These results indicated the large influence of salinity on these performance traits in bread wheat genotypes (Ragab and Taha 2016 and Hagras *et al.*, 2018). However, the variance due to genotypes considered as main portion of total variance for DH, GFP, NDVI and 1000KW, scored 43.47, 30.14, 38.94 and 64.12, respectively. Meanwhile, years* salinity (33.47) and years (24.05) registered the most portion for SM trait, revealing that the salinity effect (location) may be increased on the number of spikes/m^2 under climatic change among years (Grzesiak *et al.,* 2019).

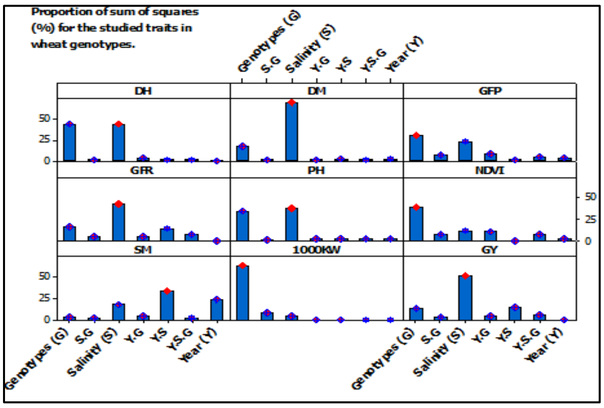


Figure 1. Proportion of sum of squares (years, salinity treatments and genotypes and their interactions) % for the studied traits in wheat genotypes.

DH: days to heading, DM: days to maturity, GFP: grain filling period, GFR: grain filling rate, PH: plant height (cm), NDVI: normalized difference vegetation index, SM: spikes per square meter, 1000KW: 1000 kernel weight (g) GY: grain yield (kg/h).

Mean performance of agronomic traits

Data in Table 5 showed mean performance of 32 bread wheat genotypes under the salinity treatments for the agronomy studied traits. Results presented significant differences between normal and salinity conditions for all studied yield traits. Location with normal soil recorded higher values for all traits compared to salinity (stress) one.

Salinity location decreased total averages of days to heading, days to maturity, GFP grain filling period days, grain filling rate, plant height, normalized difference vegetation index, number of spikes/m^2, thousand kernel weights and grain yield by 10.65%, 10.49%, 10.16%, 44.12%, 13.28%, 11.53%, 32.80%, 8.23% and 48.79% respectively. The significant reduction in grain yield may be due to the lack in agronomic traits performance as grain filling rate, number of spikes/m^2 and thousand kernel weights. Similar results were obtained by Moustafa *et al* (2021) and Abd El-Rady and Koubisy (2023).Salinity may affect photosynthesis and plant development and different traits. Hence, it may be causing shorten days to heading and grain filling period which reduced days to maturity. The plant height reduction was in response to salinity that caused increase protoplasm water pressure with decreasing cell number and size (Mehraban *et al.,* 2019 and Nassar *et al.,* 2020). Then, salinity may be as drought effect and contraction the critical growth stages could minimize number of spikes/m^2 and thousand kernel weights under salinity treatment. Hence, obviously reduction in the yield components such as number of spikes/m^2 and thousand kernel weights caused decreasing wheat grain yield. Similar results were found by Mansour *et al.* (2020) and Khan *et al.* (2022).

Genotypes mean performance of the measured traits across salinity treatments were shown in Table 5. Number of days to heading and maturity values revealed that G18, G4 and G32 were the earliest genotypes, while G10 and G19 were the latest genotypes for both normal and salinity treatments. G18 and G32 recorded the highest values for grain filling period under normal and salinity stress conditions, respectively. However, G19 had the highest grain filling rate values under both treatments conditions. With respect to thousand kernel weights, the highest values were obtained by G30 with 52.14 and 47.50 g under normal and salinity conditions, respectively. Regarding plant height, values ranged from 92.50 cm (G1) to 120.0 cm (G14) and 77.50 cm (G1) to 112.50 cm (G19) under normal and stress treatments, respectively. Meanwhile, normalized difference vegetation index, scored highest values for G8 and G19 under both treatments. The highest values of number of spikes/m^2 were obtained by G5 and G7 under normal and salinity conditions, respectively. Concerning grain yield, G19 and G20 revealed the highest performances under normal conditions, while G9, G19 and G20 were the larger under salinity conditions.

Table 5. Mean performance of 32 bread wheat genotypes under the normal and salinity treatments for the studied traits.

Geno	Days to heading		Days to maturity		Grain filling period		1000 kernel weight		Grain filling rate	
	N	S	N	S	N	S	N	S	N	S
G1	101.01	92.83	156.20	139.70	55.17	46.83	38.53	32.32	49.56	32.74
G2	107.30	96.17	153.20	137.70	45.83	41.50	39.41	40.60	77.41	40.02
G3	103.80	91.17	150.70	132.80	46.83	41.67	45.60	37.31	81.66	44.65
G4	86.80	79.67	141.70	128.00	54.83	48.33	41.81	44.46	61.28	37.27
G5	104.80	93.17	154.20	135.70	49.33	42.50	37.08	30.94	59.55	39.04
G6	106.70	97.00	156.50	138.00	49.83	41.00	28.11	23.93	51.56	28.08
G7	104.30	92.00	153.20	137.70	48.83	45.67	42.46	41.38	79.52	46.44
G8	100.70	92.00	154.80	139.30	54.17	47.33	36.20	32.16	53.77	41.78
G9	105.80	93.83	157.80	139.70	52.00	45.83	46.29	38.45	66.60	48.38
G10	108.20	98.83	157.30	140.80	49.17	42.00	40.24	35.14	54.29	40.44
G11	102.80	90.17	153.70	137.00	50.83	46.83	24.98	26.76	37.87	23.60
G12	102.50	91.50	149.50	133.50	47.00	42.00	33.00	31.38	67.09	33.82
G13	105.80	93.83	155.20	140.20	49.33	46.33	35.94	33.90	63.92	38.84
G14	107.70	95.33	157.20	140.20	49.50	44.83	36.95	34.34	76.17	31.91
G15	104.20	93.50	155.20	137.50	51.00	44.00	39.36	34.74	67.38	36.72
G16	104.30	93.83	152.50	138.70	48.17	44.83	43.73	40.92	80.14	41.62
G17	101.70	88.00	154.80	139.20	53.17	51.17	44.02	37.25	71.56	29.99
G18	84.00	78.17	143.50	126.20	59.50	48.00	44.41	35.09	52.65	27.27
G19	108.20	96.00	156.50	140.70	48.33	44.67	46.91	42.45	82.03	48.60
G20	103.30	91.33	155.00	136.70	51.67	45.33	46.80	47.22	76.75	47.38
G21	94.80	83.67	145.70	129.50	50.83	45.83	47.38	43.74	67.44	27.01
G22	107.20	94.67	150.00	136.80	42.83	42.17	35.50	31.98	66.30	33.08
G23	97.80	87.33	149.00	130.00	51.17	42.67	38.16	35.11	46.62	33.57
G24	104.30	89.67	151.70	134.70	47.33	45.00	41.45	37.09	75.79	37.73
G25	102.30	91.17	148.80	132.80	46.50	41.67	40.36	34.75	63.03	32.28
G26	103.20	92.50	151.80	138.30	48.67	45.83	42.88	35.27	78.39	31.30
G27	106.70	97.50	156.20	140.20	49.50	42.67	40.76	27.34	52.73	26.92
G28	101.80	89.33	152.80	134.80	51.00	45.50	39.37	48.72	66.11	38.90
G29	100.50	90.00	148.00	135.80	47.50	45.83	44.51	40.26	77.79	35.37
G30	103.30	88.83	152.00	138.20	48.67	49.33	52.14	47.50	71.28	40.90
G31	92.70	87.33	152.00	136.00	59.33	48.67	18.53	26.10	33.98	17.93
G32	88.20	79.50	142.50	132.00	54.33	52.50	43.33	42.63	54.18	39.97
Mean	101.77	90.93	152.16	136.20	50.38	45.26	39.88	36.60	64.51	36.05
Reduction %	10.65		10.49		10.16		8.23		44.12	
$LSD_{0.05}$										
Salinity (S)	0.74		1.35		1.28		1.89		3.25	
Genotype (G)	1.83		2.13		2.26		3.49		6.14	
S*G	2.59		3.12		3.28		5.04		8.86	

Con.

Genotype	Grain yield ton		Grain yield kg		Normalized difference vegetation index		Plant height		Spikes per square meter	
	N	S	N	S	N	S	N	S	N	S
1	5.71	3.18	5710	3181	0.56	0.47	92.50	77.50	485.80	326.70
2	7.38	3.49	7378	3489	0.58	0.53	112.50	95.00	465.00	367.90
3	7.98	3.89	7981	3885	0.56	0.52	110.00	95.00	489.00	352.50
4	7.01	3.70	7014	3703	0.55	0.51	95.80	80.83	513.00	288.30
5	6.08	3.46	6080	3461	0.43	0.41	107.50	90.83	556.30	369.20
6	5.32	2.41	5318	2412	0.50	0.41	117.50	98.33	481.20	300.40
7	8.04	4.41	8043	4409	0.59	0.54	104.20	93.33	480.80	385.30
8	6.08	4.13	6080	4134	0.63	0.59	105.00	89.17	493.30	354.20
9	7.19	4.63	7189	4630	0.56	0.57	111.70	103.33	448.30	327.90
10	5.55	3.54	5545	3539	0.57	0.49	114.20	100.83	410.00	341.70
11	3.99	2.32	3991	2324	0.54	0.35	110.80	95.83	361.00	277.10
12	6.52	2.98	6524	2980	0.48	0.34	105.00	89.17	420.00	312.50
13	6.57	3.76	6569	3762	0.57	0.47	112.50	100.83	453.20	277.90
14	7.83	3.04	7825	3039	0.57	0.49	120.00	107.50	510.50	320.00
15	6.99	3.58	6991	3580	0.50	0.48	110.00	98.33	395.70	346.70
16	8.02	3.89	8019	3891	0.58	0.51	109.20	95.00	441.00	294.60
17	7.59	3.49	7590	3493	0.59	0.55	113.30	96.67	492.80	272.50
18	6.57	2.69	6568	2685	0.52	0.39	99.20	86.67	443.80	318.30
19	8.24	4.55	8243	4546	0.65	0.61	119.20	112.50	443.70	325.40
20	8.19	4.49	8187	4494	0.62	0.55	113.30	97.50	523.50	286.20
21	7.09	2.59	7092	2589	0.56	0.45	105.80	93.33	384.50	262.50
22	5.79	2.89	5785	2893	0.57	0.43	112.50	98.33	469.20	328.80
23	4.95	2.97	4951	2974	0.49	0.41	106.70	92.50	535.70	272.90
24	7.36	3.53	7363	3526	0.58	0.46	117.50	99.17	474.00	331.70
25	6.07	2.84	6066	2839	0.55	0.46	101.70	92.50	459.30	338.30
26	7.94	2.98	7943	2978	0.51	0.49	114.20	100.00	454.00	310.40
27	5.41	2.39	5411	2390	0.55	0.45	115.80	98.33	453.30	315.00
28	7.01	3.69	7014	3692	0.50	0.50	105.00	87.50	466.50	239.20
29	7.52	3.44	7519	3437	0.53	0.50	111.70	93.33	426.70	294.20
30	7.24	4.23	7238	4227	0.57	0.60	111.70	95.83	500.30	242.90
31	4.10	1.83	4095	1834	0.39	0.39	100.00	82.50	329.70	240.00
32	6.20	4.34	6198	4337	0.50	0.49	98.30	84.17	454.80	268.30
Mean	6.67	3.42	6672.50	3417.28	0.54	0.48	108.88	94.43	459.87	309.05
Reduction %	48.79		48.79		11.53		13.28		32.80	
$LSD_{0.05}$										
Salinity (S)	0.27		268.2		0.04		2.453		29.25	
Genotype(G)	0.57		573.8		0.04		4.147		60.8	
G*S	0.82		821.4		0.06		NS		87.17	

Physiological traits effect

Data in Table 6 show the mean performance of 32 bread wheat genotypes under the salinity treatments for the physiological measured traits during the 2020/2021 season only. Based on the combined data of saline and non-saline soil locations, results presented significant differences between normal and salinity soil conditions for chlorophyll content index, leaf diffusive resistance and leaf transpiration rate traits. However, genotypes appeared significant differences for chlorophyll content index, canopy temperature, carbon dioxide concentration, flag leaf area and chlorophyll fluorescence traits. Meanwhile, the interaction between locations and genotypes was significant for canopy temperature, flag leaf area and chlorophyll fluorescence only. Similar results were obtained by Hussein *et al.* (2023).

Under the interaction item, canopy temperature in the non-saline soil location cleared highest values compared to salinity soil conditions. Genotypes G18 and G28 recorded the highest values (28.20 and 23.80) under normal and saline soil locations, respectively. Flag leaf area revealed different responses, recording highest values for G29 (81.43) and G17 (84.35) under normal and saline soils, respectively. Genotypes G25 and G29 gave the same highest value (0.73) for chlorophyll fluorescence under normal conditions while, G12 and G25 had the same highest value (0.59) saline soil.

Table 6. Combined mean performance of the physiological studied traits during 2020/21 only under normal and saline soil sites.

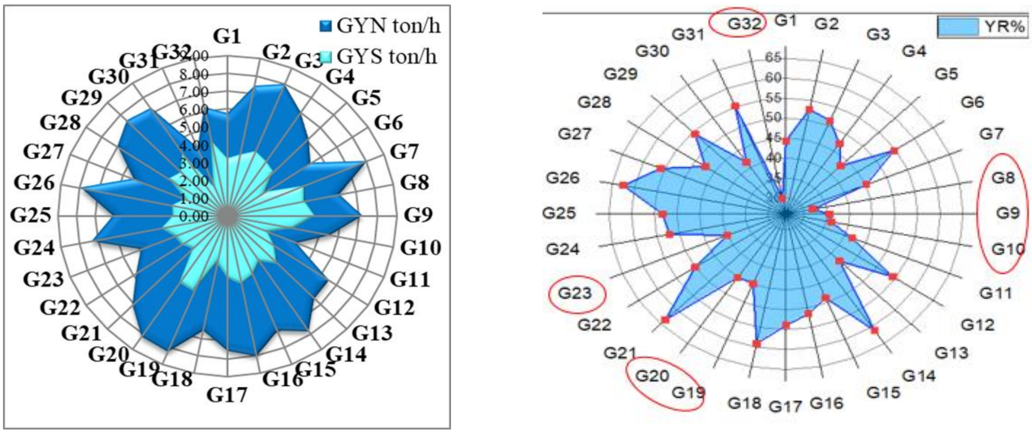
Genotype	CCI	CEM		COCN	CUV	FLA		Fvm		INCO	LDI	LTM	QUN	RWC	TRN	YR
(Geno.)	Comb.	N	S	Comb.	Comb.	N	S	N	S	Comb.	Comb.	Comb.	Comb.	Comb.	Comb.	%
G1	34.40	24.60	23.33	44.52	21.71	42.47	53.70	0.71	0.69	12.81	1.16	18.73	2586	72.56	24.58	44.29
G2	32.69	26.07	21.47	48.74	28.35	59.60	68.20	0.71	0.71	13.91	1.15	20.41	3119	52.77	23.88	52.71
G3	27.22	26.40	21.03	47.43	27.61	52.57	50.85	0.71	0.71	17.34	1.04	19.83	2960	60.33	24.96	51.32
G4	32.96	27.13	22.40	47.71	28.04	45.07	52.50	0.62	0.74	16.95	0.91	21.05	2786	61.56	26.58	47.21
G5	32.11	26.07	21.53	52.61	30.35	54.53	56.15	0.72	0.71	12.21	1.06	23.50	2730	56.81	25.94	43.08
G6	28.54	25.13	22.43	51.82	22.90	55.60	66.30	0.70	0.71	14.59	1.09	20.61	2606	61.22	26.32	54.64
G7	35.75	24.67	21.93	54.96	26.05	63.00	55.60	0.64	0.72	13.67	1.11	22.34	2422	56.48	27.05	45.18
G8	42.07	26.77	21.47	53.58	28.75	55.90	64.90	0.69	0.73	14.09	1.14	21.22	2958	60.49	23.99	32.01
G9	41.19	24.80	21.57	51.68	27.18	61.17	49.85	0.72	0.71	16.92	1.22	20.46	2973	61.42	24.88	35.60
G10	37.93	25.50	22.60	47.37	25.68	60.47	54.05	0.66	0.67	15.23	1.04	21.49	2781	62.03	25.19	36.18
G11	30.11	26.87	22.53	47.60	28.17	58.13	43.90	0.71	0.72	15.34	1.06	22.41	2752	69.86	25.13	41.77
G12	40.17	25.10	23.47	46.18	26.76	54.00	43.20	0.68	0.59	17.84	1.07	23.32	2825	69.84	25.43	54.32
G13	40.24	24.50	21.53	47.82	29.92	49.60	38.65	0.67	0.70	14.70	0.97	23.97	2650	63.32	25.65	42.73
G14	48.40	24.87	21.60	48.30	26.01	68.10	49.00	0.71	0.72	16.16	1.03	25.78	2655	57.28	25.24	61.16
G15	36.67	25.43	19.03	51.81	26.22	46.83	61.30	0.70	0.68	13.45	1.02	24.73	2739	58.09	25.33	48.79
G16	28.44	26.07	21.87	53.32	27.16	54.57	39.50	0.69	0.65	16.22	1.22	23.53	2857	66.32	22.91	51.48
G17	51.32	24.60	22.10	51.59	26.02	61.87	84.35	0.70	0.66	16.54	1.26	21.42	3143	72.79	22.36	53.98
G18	32.96	28.20	24.17	53.66	28.37	65.23	59.25	0.72	0.74	16.78	1.22	21.54	3337	69.66	23.89	59.12
G19	49.45	24.50	22.60	45.90	18.31	69.70	75.80	0.69	0.68	16.45	1.06	22.41	3028	83.36	24.47	44.85
G20	35.41	24.77	22.10	43.63	27.49	58.30	72.40	0.70	0.75	16.82	1.06	23.69	2900	68.68	24.73	45.11
G21	37.99	26.17	23.60	45.04	21.80	63.97	47.80	0.70	0.73	18.88	1.06	21.11	3291	69.51	25.80	63.49
G22	37.93	27.50	22.47	45.85	22.81	60.57	37.95	0.67	0.73	16.12	1.04	21.86	3008	65.17	23.79	49.99
G23	35.27	25.87	22.63	43.39	22.00	70.90	57.10	0.66	0.73	15.86	0.99	21.88	2908	68.37	24.53	39.93
G24	35.72	25.53	21.83	46.61	20.28	51.90	71.75	0.69	0.66	17.71	1.15	20.98	3268	61.80	23.41	52.11
G25	34.87	26.07	21.67	48.43	26.66	58.47	56.00	0.73	0.59	14.55	1.11	22.10	3714	59.44	23.96	53.20
G26	34.93	27.00	20.47	48.73	25.99	64.03	48.55	0.68	0.63	15.62	1.15	22.35	2833	63.46	26.37	62.51
G27	32.38	25.63	22.13	50.42	23.72	64.33	36.10	0.70	0.70	15.12	1.06	25.56	2965	59.24	26.85	55.83
G28	37.65	24.90	23.80	53.26	24.61	64.47	68.10	0.69	0.62	17.16	1.19	21.24	3203	65.11	25.81	47.36
G29	35.07	25.83	22.93	52.02	25.23	81.43	49.95	0.73	0.74	18.26	1.22	20.97	3184	64.58	25.23	54.29
G30	40.54	24.93	20.17	56.03	29.39	67.6	64.45	0.72	0.67	15.88	1.18	24.29	3044	52.75	26.80	41.60
G31	47.45	26.20	21.37	53.68	25.14	51.47	72.80	0.72	0.66	18.41	1.14	21.30	3142	60.89	26.11	55.21
G32	41.94	26.63	21.43	49.12	30.69	68.47	63.65	0.71	0.73	17.11	1.10	24.36	3350	64.88	25.46	30.03
Mean	37.18	23.89	22.04	49.46	25.92	58.09	56.68	0.69	0.69	15.90	1.102	22.20	2960	63.70	25.08	48.47
LSD																
Salinity S	0.68	NS		NS	NS	NS		NS		NS	0.16	NS	NS	NS	4.44	
Genotype G	5.42	1.49		6.396	NS	12.00		0.04		NS	NS	NS	NS	NS	NS	
S*G	NS	2.105		NS	NS	16.97		0.06		NS	NS	NS	NS	NS	NS	

physiological parameters, such as CCI: chlorophyll content index; CEM: canopy temperature; COCN: carbon dioxide concentration; CUV: cuvette temperature ˚C; FLA: flag leaf area; Fv/Fm: chlorophyll fluorescence; INCO: intercellular CO2 concentration; LDI: leaf diffusive resistance; LTM: leaf temperature ˚C; QUN: quantum sensor μmol m^{-2} s^{-1}; RWC: relative water content % and TRN: leaf transpiration rate μg cm^{-2} s^{-1}, of 32 wheat lines evaluated in normal and saline soil sites during 2020/21 only. YR%: yield reduction percent = Normal GY- Salinity GY/ Normal GY *100.

Yield reduction under salinity

The yield reduction percentage (YR%) in Table 6 and Figure 2 showed the grain yield mean performance of 32 genotypes evaluated under salinity compared with yield under normal conditions. In general, yield traits values indicated that all genotypes decreased under salinity soil. YR% values ranged from 30.03% to 63.49% for G32 and G21, respectively. Genotypes G32, G8, G9, G10 and G23 with (30.03, 32.01, 35.60, 36.18 and 39.93) appeared the minimum YR% values, suggesting that these were more obvious salt-tolerant wheat genotypes. Meanwhile, Genotypes G21, G26 and G14 with (63.49, 62.51 and 61.16) cleared the maximum yield reduction, indicating to salt-sensitive genotypes. From obvious results (Tables 5 and

6 and Figure 2), salinity affected physiological and plant growth, decreasing grain yield by deficiencies available water, ion toxicity and nutrients (Ragab and Kheir, 2019 and Al-Ashkar *et al.*, 2019).



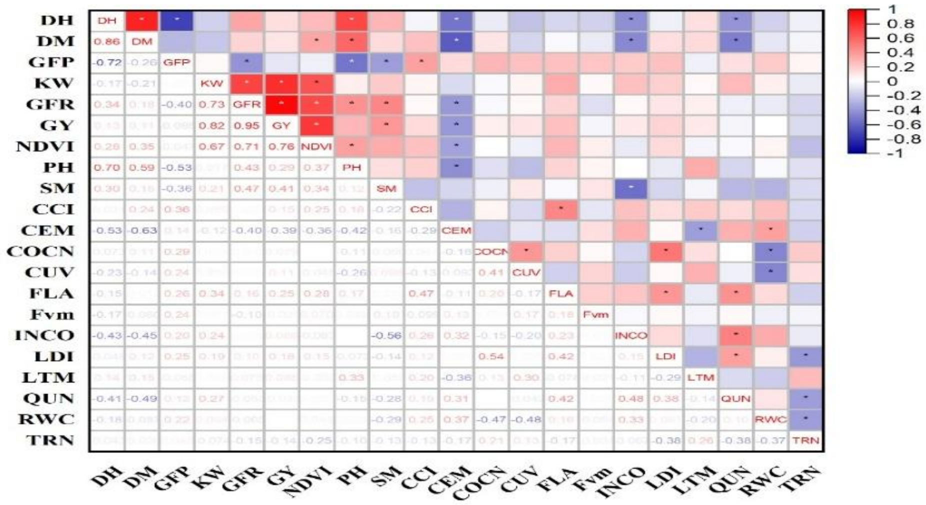
A- Genotypes contribution of yield under normal (GYN) and saline (GYS) soil.

B- Yield reduction (YR %) under salinity conditions.

Figure 2. Graph shows the percentage contribution of each genotype for relative changes in wheat grain yield reduction under salinity conditions.

Correlation coefficients

To determine the most desirable yield traits, the phenotypic correlation coefficients between agronomic traits with grain yield and other physiological parameters were illustrated in Figure 3. From graph, it is observed that a significant positive correlation was found between days to heading (DH) with days to maturity (DM) and plant height (PH). DH and DM were negatively correlated with quantum sensor µmol m^{-2} s^{-1} (QUN), intercellular CO2 concentration (INCO), canopy temperature (CEM) and grain filling period (GFP) while, recorded positive correlated with plant height (PH). Grain filling rate (GFR) was positive correlation with thousand kernel weight (1000KW), grain yield (GY), normalized difference vegetation index (NDVI), PH and spikes/m2 (SM) also revealed negative correlation with GFP and CEM. CEM showed negatively associated with DH, DM, GFR, GY, NDVI, PH and leaf temperature ˚C (LTM) while, scored positive correlation with relative water content % (RWC).



* p<=0.05

Figure 3. Spearman correlation analysis of agronomic and physiological traits

agronomic e.g., DH, days to heading; DM, days to maturity; GFP, grain filling period, KW: thousand kernel weight, GFR, grain filling rate; GY, grain yield kg ha^{-1}; NDVI, Normalized difference vegetation index; PH, plant height cm; SM, spikes per square meter; CCI, chlorophyll content index; physiological parameters, such as CEM, canopy temperature; COCN, carbon dioxide concentration; CUV, cuvette temperature ˚C; FLA, flag leaf area; Fv/Fm: chlorophyll fluorescence; INCO: intercellular CO2 concentration; LDI: leaf diffusive resistance; LTM: leaf temperature ˚C; QUN: quantum sensor µmol m^{-2} s^{-1}; RWC: relative water content % and TRN: leaf transpiration rate µg cm^{-2} s^{-1}, of 32 wheat genotypes evaluated under normal and saline soil sites during 2019/20 and 2020/21 seasons. * Significant level of $p \leq 0.05$.

These results indicated that the days to heading coupled with days to maturity affected the physiological activities as quantum sensor µmol m^{-2} s^{-1}; intercellular CO_2 concentration; canopy temperature which changed grain filling period, thousand kernel and spikes/m^2. Therefore, results revealed the importance of both agronomic and physiological traits on grain yield (Hussein *et al.,* 2023 and Khan *et al.*, 2022).

Generally, grain yield was positively correlated with grain filling rate, thousand kernel weight, normalized difference vegetation index, spikes/m^2, however, was negatively correlated with canopy temperature.

Linear Regression

The regression of grain yield as a dependent variable and other agronomic traits as an independent variable for the 32 bread wheat genotypes to appear the comparison between the saline and non-saline sites (season's average) are illustrated in Figure 4.

The linear regression shapes were the fitted relation describing the regression of grain yield on each trait. The graph showed significant differences between both saline and non-saline sites. The regression line of non-saline site was higher than line under saline soil. For all the eight traits, the linear adjustment between normal and saline soil estimated that high slope (*b*) values ranged between (2.25 to 11333**) for days to heading and normalized difference vegetation index under normal site.

The regression formula of the other bread wheat traits spikes per square meter; showed low slop values (*b* = 3.99 and 7.7) under normal and saline sites, respectively; and days to maturity cleared (*b* = 6.40) in saline site. Meanwhile, both correlation coefficient (r) and coefficient of determination (R^2) showed wide differences values ranged from (r, 0.03 - 0.001) for days to maturity under normal) to (R^2, 0.94** - 0.89**) for grain filling rate in both sites. It is clear that the correlation between yields and other estimated traits were medium or close to zero, indicating to variances between both sites' responses.

Regarding to the slop of the liner regression of the three traits Normalized difference vegetation index (NDVI), grain filling rate (GFR) and thousand kernel weights (1000KW) results revealed significantly and high values (11333**, 84.7** and 127**) (8528**,92.2** and78**) for both normal and saline sites, respectively. These results coupled with highest R^2, recording (0.63-0.50), (0.94-0.94) and (0.73-0.67) for NDVI, GFR and 1000KW in both sites, respectively. Therefore, these traits can be used to distinguish genotypes revealing good level of salinity tolerance. This indicates that improving NDVI, GFR and KW in wheat breeding could be recognized as an effective strategy to enhance production under normal and salinity conditions. Praxedes *et al.* (2010), Bayuelo-Jimenez *et al.* (2012) and Simane *et al.* (1993) also found that the differences in stress-tolerance (salinity or drought) among genotypes were due to both physiological and morphological components of GIs.

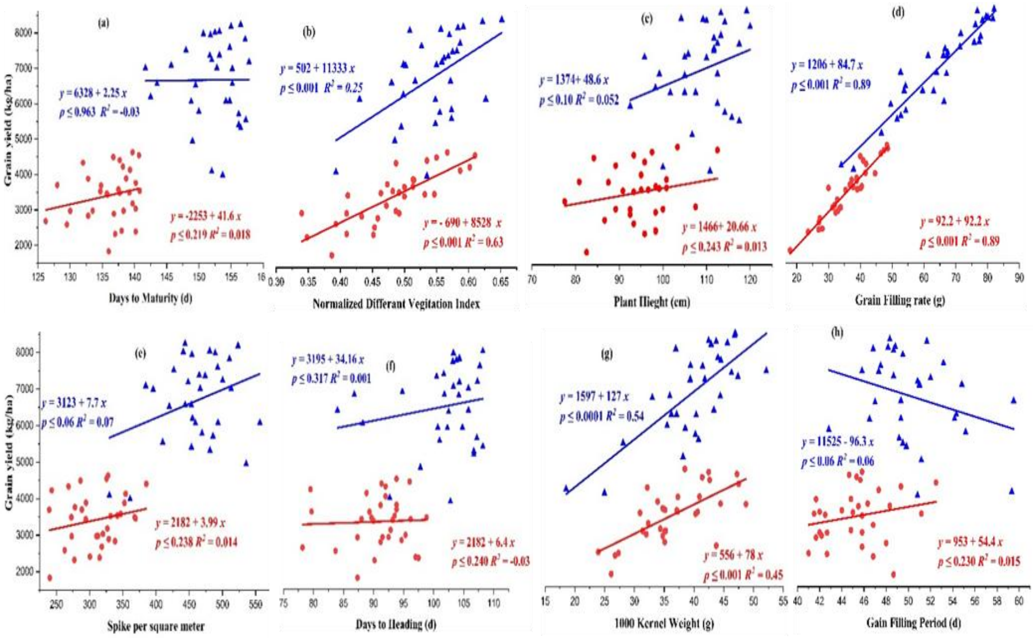


Figure 4. Regression analysis of saline and non-saline sites (season's average) for agronomic traits influenced on grain yield.

In comparison between the saline and non-saline sites, it could be summarized that salinity soil caused significant decrease in grain and biological yield by minimizing number of spikes/m^2, shorten grain filling rate and thousand kernel weights.

Figure 5 represents the linear-relationship between grain yield with different agronomic and physiological traits under normal and salinity conditions. Under normal soil in Figure 5a, traits GFR, GFP, NDVI, Fv/Fm, LDI, CEM and TRN with the huge and strong linear-relationship were more efficient in grain yield as compared to other traits. Meanwhile, parameters FLA, QUN and INCO exhibited lowest relationship. Regarding salinity conditions in Figure 5b, relationships showed different association effects compared to relationships under normal soil. Grain yield of salt-soil presented the most relationship to components GFR, GFP, DM, SM, PH, NDVI and KW. The other showed a moderate to weak relationship with the GY. Results cleared that GFR, GFP and NDVI traits were more efficient related with the GY of both normal and salinity soil. Current findings are in accordance with earlier results of (Khan *et al.*, 2022 and Abd El-Hamid *et al.,* 2020). Wheat crop productivity was more influenced by both agronomic and physiological traits under saline soil in Fig (5 b). As regarding, the excess in salinity increased the effect of GFR, GFP, DM, SM, PH, NDVI, TRN, RWC and QUN. From the present findings, it has been observed that GFR, GFP, DM, SM, PH, NDVI were found to be more effective to improve growth and yield under saline. Then, these traits can be used in screening and understand genotypic differences in growth and yield under either normal or saline conditions.

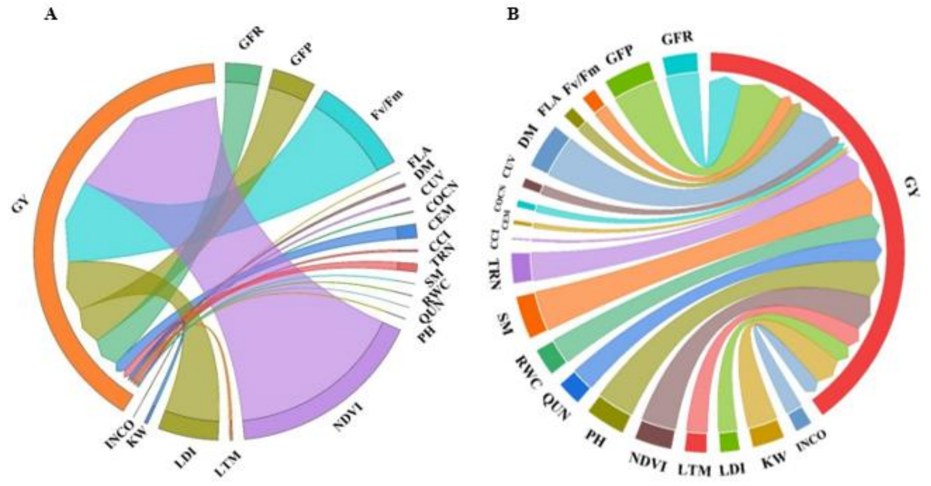


Figure 5. Chord chart for the regression coefficients to show the importance of agronomic and physiological traits for GY.

Grain yield kg ha-^{1}, (traits e.g., DM, days to maturity; GFP, grain filling period, KW: thousand kernel weight, GFR, grain filling rate; NDVI, Normalized difference vegetation index; PH, plant height cm; SM, spikes per square meter; CCI, chlorophyll content index; physiological parameters, such as CEM, canopy temperature; COCN, carbon dioxide concentration; CUV, cuvette temperature ˚C; FLA, flag leaf area; Fv/Fm: chlorophyll fluorescence; INCO: intercellular CO2 concentration; LDI: leaf diffusive resistance; LTM: leaf temperature ˚C; QUN: quantum sensor µmol m–2 s–1; RWC: relative water content % and TRN: leaf transpiration rate µg cm−2 s−1), of thirty-two wheat genotypes evaluated under normal (a) and saline (b) soil per seasons.

Salinity tolerance indices and comparing genotypes

For screening of genotypes under salinity, wheat grain yield under both normal (Yp) and salinity stress (Ys) conditions were estimated for calculating some different sensitivity and tolerance indices. In the present study, mean values of different indices for characterizing salinity tolerance of 32 genotypes to both normal/saline environments conditions were shown in Table 7.

Table 7. Grain yield means (over two years) of normal Y_p and saline soil Y_s sites of 32 genotypes and salinity tolerance/sensitive indices.

Genotype	Y_p	Y_s	RC	TOL	MP	GMP	HM	SSI	STI	YI	YSI	RSI	gy	rank
G1	5710	3181	44.29	2529	4446	4262	4086	0.91	0.41	0.93	0.56	1.09	4446	26
G2	7378	3489	52.71	3889	5434	5074	4738	1.08	0.58	1.02	0.47	0.92	5434	12
G3	7981	3885	51.32	4096	5933	5568	5226	1.05	0.70	1.14	0.49	0.95	5933	5
G4	7014	3703	47.21	3311	5359	5096	4847	0.97	0.58	1.08	0.53	1.03	5359	14
G5	6080	3461	43.08	2619	4771	4587	4411	0.88	0.47	1.01	0.57	1.11	4771	21
G6	5318	2412	54.64	2906	3865	3581	3319	1.12	0.29	0.71	0.45	0.89	3865	30
G7	8043	4409	45.18	3634	6226	5955	5696	0.93	0.80	1.29	0.55	1.07	6226	3
G8	6080	4134	32.01	1946	5107	5013	4922	0.66	0.56	1.21	0.68	1.33	5107	19
G9	7189	4630	35.60	2559	5910	5769	5632	0.73	0.75	1.35	0.64	1.26	5910	6
G10	5545	3539	36.18	2006	4542	4430	4321	0.74	0.44	1.04	0.64	1.25	4542	24
G11	3991	2324	41.77	1667	3158	3046	2937	0.86	0.21	0.68	0.58	1.14	3158	31
G12	6524	2980	54.32	3544	4752	4409	4091	1.11	0.44	0.87	0.46	0.89	4752	22
G13	6569	3762	42.73	2807	5166	4971	4784	0.88	0.56	1.10	0.57	1.12	5166	18
G14	7825	3039	61.16	4786	5432	4876	4378	1.25	0.53	0.89	0.39	0.76	5432	13
G15	6991	3580	48.79	3411	5286	5003	4735	1.00	0.56	1.05	0.51	1.00	5286	16
G16	8019	3891	51.48	4128	5955	5586	5240	1.06	0.70	1.14	0.49	0.95	5955	4
G17	7590	3493	53.98	4097	5542	5149	4784	1.11	0.60	1.02	0.46	0.90	5542	8
G18	6568	2685	59.12	3883	4627	4199	3812	1.21	0.40	0.79	0.41	0.80	4627	23
G19	8243	4546	44.85	3697	6395	6121	5860	0.92	0.84	1.33	0.55	1.08	6395	1
G20	8187	4494	45.11	3693	6341	6066	5803	0.92	0.83	1.32	0.55	1.07	6341	2
G21	7092	2589	63.49	4503	4841	4285	3793	1.30	0.41	0.76	0.37	0.71	4841	20
G22	5785	2893	49.99	2892	4339	4091	3857	1.02	0.38	0.85	0.50	0.98	4339	27
G23	4951	2974	39.93	1977	3963	3837	3716	0.82	0.33	0.87	0.60	1.17	3963	28
G24	7363	3526	52.11	3837	5445	5095	4768	1.07	0.58	1.03	0.48	0.94	5445	11
G25	6066	2839	53.20	3227	4453	4150	3868	1.09	0.39	0.83	0.47	0.91	4453	25
G26	7943	2978	62.51	4965	5461	4864	4332	1.28	0.53	0.87	0.37	0.73	5461	10
G27	5411	2390	55.83	3021	3901	3596	3316	1.14	0.29	0.70	0.44	0.86	3901	29
G28	7014	3692	47.36	3322	5353	5089	4838	0.97	0.58	1.08	0.53	1.03	5353	15
G29	7519	3437	54.29	4082	5478	5084	4718	1.11	0.58	1.01	0.46	0.89	5478	9
G30	7238	4227	41.60	3011	5733	5531	5337	0.85	0.69	1.24	0.58	1.14	5733	7
G31	4095	1834	55.21	2261	2965	2740	2533	1.13	0.17	0.54	0.45	0.87	2965	32
G32	6198	4337	30.03	1861	5268	5185	5103	0.62	0.60	1.27	0.70	1.37	5268	17
Average	6672.50	3417.28	48.47	3255.22	5045.2	4759.63	4493.78	0.99	0.52	1.00	0.52	1.01	5045.2	

Table 7 showed the results among the different genotypes of salinity tolerant parameters obtained by grain yield formulas. Under normal (Yp) and salinity conditions (Ys), the highest grain yield obtained from G19 (8243 kg ha^{-1}) and G9 (4630 kg ha^{-1}) respectively.

Regarding RC index, values ranged from 30.03 to 63.49 for G32 and G21, respectively (Table 7). Then, genotypes G32, G8 and G9 with lower values (30.03, 32.01 and 35.60) of RC were favorable ones. However, G21 and G26 with (63.49 and 62.51) had the highest RC values. The tolerance index (TOL) indicated the yield differences between the normal and stress conditions for genotypes. The lowest TOL was found in G32 (1861) and G8 (1946) however; the highest values were obtained in G26 (4965) and G14 (4786). G32 with the lowest TOL had higher grain yield (4337) than the experimental average for salinity (3417.28) conditions but did not have better grain yield in normal conditions compared to other genotypes. Similar results were obtained by Noreldin and Mahmoud (2017) and Matkovic *et al.* (2022) that could recognize the best genotypes based TOL index. Genotypes G32 and G8 with low SSI values (0.62 and 0.66) were considered as salinity tolerant, showing a lower reduction in grain yield under salinity stress compared to non-stress condition. Meanwhile, genotypes G21 and G26 had the highest SSI (1.30 and 1.28) that act SSI value>1, referring to susceptibility. Noreldin and Mahmoud (2017), Abd El-Hamid *et al.* (2020) and Matkovic *et al.* (2022) indicated to similar results and that SSI appeared to be a suitable selection index to distinguish drought -resistant genotypes.

Indices of MP, GMP, HM, STI, YI, YSI and RSI with the higher value gave more tolerant genotypes to salinity stress. Therefore, genotype G19 had highest values (6395, 6121, 5860 and 0.84) for MP, GMP, HM and STI indices, respectively, showing higher salinity tolerance. Further, the susceptible genotype G31 recorded lowest values (2965, 2740, 2533 and 0.17) for the same indices, respectively (Table 7). However, five genotypes G9, G19, G20, G7 and G32 recorded high value of yield index (YI) being (1.35, 1.33, 1.32, 1.29 and 1.27, respectively). At the same time, four genotypes G32, G8, G9 and G10 showed the highest values (tolerance) of yield stability index (YSI) with (0.70, 0.68, 0.64 and 0.64). Further, these four genotypes G32, G8, G9 and G10 cleared highest tolerance due to the high value of relative stress index (RSI) recording (1.37, 1.33, 1.26 and 1.25). Meanwhile, G21, G26 and G14 revealed high salinity susceptibility for both YSI (0.37, 0.37 and0.39) and RSI (0.71, 0.73 and 0.76). Similarly, Matkovic *et al.* (2022) used stress susceptibility indices for evaluation of salinity tolerance in wheat genotypes. From obvious studies, in RC, TOL and SSI indices, the higher value of these indices referred to more sensitive genotypes to salinity stress. Meanwhile, many researchers reported that high values of MP, GMP, HM, STI, YI, YSI and RSI had similar trend of the increased stress tolerance of genotypes (Hammam and Negim 2014 and Mansour *et al*., 2020).

GT biplot for salt tolerance indices

Biplot analysis can be used to compare different genotypes (G) under different tolerance indices (T) with detecting its relationship. Polygon-view of 32 genotypes by salinity tolerance indices in which-won-where and comparison (GT) biplot Figures (6a&b) showed the status of genotypes in terms of salinity parameters and the relationship between them. GT-graph illustrated that the first two principal components (PC$_1$ and PC$_2$) explained (60.13% and 39.57%) accounting 99.70 % of the total variation. The higher PC$_1$ and indicated the high yields (possibility to detect stable genotypes)

The polygon in Figure (6a) was drawn by connecting the furthest genotypes (G19, G20, G9, G32, G11, G31, G21 and G26) that encompassed all the genotypes. Drawing lines from the original perpendicular to each side of the hull divided the convex hull into sectors. All genotypes fallen at an angular vertex in the same sector of the polygon had a specific index; referred to the best or highest yield capacity of these genotypes in these indices. Polygon showed that the studied indices fell into four sectors with different winning genotypes.

Concerning the best performing genotypes, results cleared that genotypes G19 and G20 were the highest for indices MP, GMP, STI, HM, YI and grain yield in normal conditions. However, genotype G9 was the highest for YI and grain yield in salinity soil; and genotype G32 in YSI and RSI indices. Furthermore, genotype G26 was the best (low) in SSI, RC and TOL indices.

Relations between indices were presented in Figure 6a. Smaller angle between two indices (less than 90^{O}) pointed to positive correlation; large angle (more than 90^{O}) indicated a negative correlation and close to 90^{O} was no correlation (Yan and Kang, 2003). Results revealed that smaller angle between each of Yp, MP, GMP, STI, HM, YI and Ys pointed to positive association between them. Furthermore, YSI and RSI indices had positive correlation and positive correlated with Ys. Meanwhile, Rc was positive correlation with SSI indices and they positively correlated with Ys. TOL close to 90^{O} revealed no correlation with grain yield under salinity (Ys). Then, results mean that increasing MP, GMP, STI, HM, YI, YSI and RSI indices referred to higher grain yield for each of salinity (Ys) and non-stress (Yp) conditions.

Then, Figure 6a results mean revealed that increasing MP, GMP, STI, HM, YI, YSI and RSI indices referred to higher grain yield for each of salinity (Ys) and non-stress (Yp) conditions. Therefore, bread wheat genotypes under both salinity (Ys) and non-stress (Yp) conditions that located in the right side of graph were positively correlated with MP, GMP, STI, HM and YI indices can be considered as salt-tolerant. Similar results according to Mitra (2001) and Karaman (2019) who reported that suitable indices must have a strong correlation with yield under both conditions. Meanwhile, SI and RSI indices in the left side of graph can be considered as salt-susceptibility.

GT (genotype and indices) biplot used to compare salinity tolerance indices for evaluation of genotypes and detect the ideal or best indices Figure 6b. The biplot placed the average environment (indices) coordinates (AEC) method (Yan and Tinker, 2006) to determine the high-yield and similar tolerant indices. The average ordinate environment (AOE) falls on the average environment axis (AEA) line passing through the origin. Then, ranks of the best yielder index were MP followed by GMP, STI, HM and YI showed the same desirable performed score. In contrast SSI and RC were the lowest and seem to be undesirable. Therefore, both GT biplot analyses (polygon and ranking of genotypes) explained that MP, GMP and STI were the desirable tolerant indices as they placed in the centric circle. Then, both GT biplot analyses and ranking of indices (Figures 6a & b and Table 8) confirmed the similarity of the MP, GMP and STI evaluation.

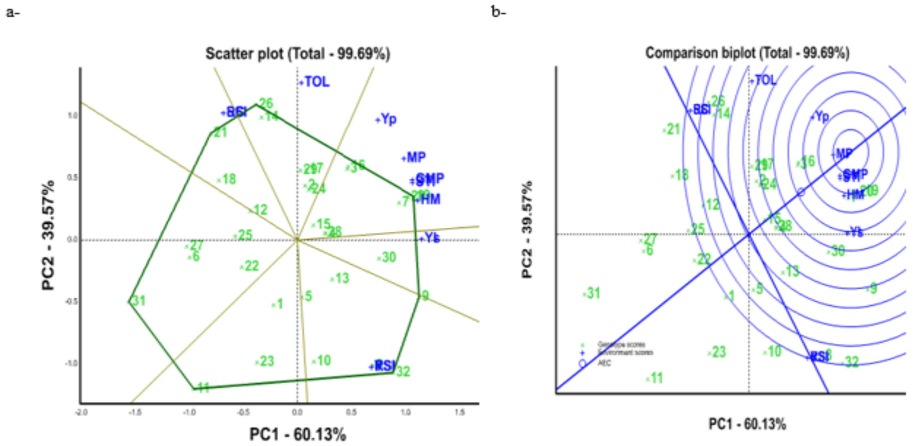


Figure 6. (a) The "which-won-where" of genotype by salinity tolerance indices (GSTI) biplot view and (b) GT (genotype and indices) for comparison of the indices with the ideal ones and showing effects on grain yield estimated for non-saline sites (Yp) and saline soil sites (Ys) (per seasons) and stress tolerance indices.

Table 8. correlation analysis of salinity tolerance/sensitive indices.

	Yp	Ys	RC	TOL	MP	GMP	HM	SSI	STI	YI	YSI
Ys	0.651 0.000										
RC	0.222 0.222	-0.59 0									
TOL	0.782 0.000	0.036 0.846	0.775 0								
MP	0.948 0.000	0.859 0	-0.10 0.596	0.542 0.001							
GMP	0.888 0.000	0.927 0	-0.24 0.178	0.408 0.02	0.988 0						
HM	0.815 0.000	0.969 0	-0.37 0.035	0.278 0.124	0.957 0	0.99 0					
SSI	0.222 0.222	-0.59 0	1 *	0.775 0	-0.1 0.596	-0.24 0.178	-0.37 0.035				
STI	0.871 0.000	0.929 0	-0.26 0.156	0.385 0.03	0.978 0	0.994 0	0.987 0	-0.26 0.156			
YI	0.651 0.000	1 *	-0.59 0	0.036 0.846	0.859 0	0.927 0	0.969 0	-0.59 0	0.929 0		
YSI	-0.222 0.222	0.587 0	-1 *	-0.78 0	0.097 0.596	0.244 0.178	0.373 0.035	-1 *	0.257 0.156	0.587 0.000	
RSI	-0.222 0.222	0.587 0	-1 *	-0.78 0	0.097 0.596	0.244 0.178	0.373 0.035	-1 *	0.257 0.156	0.587 0.000	1 *

Genotype and indices detection

Genotype and indices (GT) biplot for comparison of genotypes under salinity tolerance indices (GSTI) and both normal/saline environments conditions were performed (Figure 7a&b, respectively) to detect the ideal and desirable tolerant genotypes. The biplot used the average environment (indices) coordinates (AEC) method (Yan and Tinker, 2006) to determine the high-yield and stable tolerant genotypes across multiple indices. These indices average (the average values of PC1 and PC2 for all environments) were presented with a circle. The average ordinate environment (AOE) falls on the average environment axis (AEA) line passing through the origin. The genotypes on the right side of the ordinate had a higher yield than the mean yield across environments, while others on the left side had a lower yield.

Then, ranks of the highest yielder genotypes were G19 and G20 followed by G7, G16, G9 and G3 showed more stability. In the contrast, G11, G31, G27 and G6 were the lowest and seem to be undesirable. These findings were similar to the results of other reports for Santana *et al.* (2021) and Sabouri *et al.* (2022).

Genotype by environment (GGE) detection

The GGE biplot of grain yield was performed under four environmental conditions (normal and saline soil in (2019/2020 and 2020/2021 seasons, respectively) for comparison of 32 genotypes to detect the ideal and desirable genotypes (Figure 7b). The biplot graph showed that the two first principal components (PCs) illustrated 54.81% and 23.73%, respectively, explaining 78.54% of the total variation.

Results showed that genotypes G19 and G20 that fall in the centric circle were the desirable genotypes followed by G7, G16, G9 and G3. Meanwhile, genotypes G31 and G11 were the lowest and considered undesirable ones. Similar results were obtained by Sabouri *et al.* (2022) and

Mohammadi *et al*. (2022) whose screened and selected large appropriate genotypes for field saline evaluation.

Therefore, in the present study, both salt tolerance indices GT and environmental GGE biplot analysis explained that G19 and G20 were the desirable salt-tolerant genotypes as they placed above average mean in the centric circle. Then, both graphically biplot analyses confirmed the superiority of the two genotypes G19 and G20. Mohammadi *et al.* (2022) used GGE biplots as a powerful tool to identify and select the bread wheat stable salt tolerance genotypes with high yield.

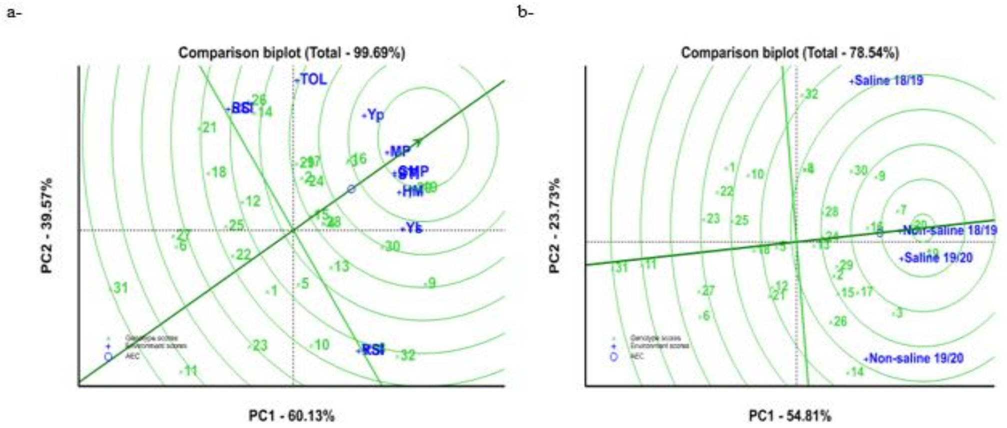


Figure 7. (a) GT (genotype and indices) for comparison of the genotype by salinity tolerance indices (GSTI) biplot view estimated for non-saline sites (Yp) and saline soil sites (Ys) (per seasons) and stress tolerance indices.

CONCLUSION

Saline soil (stress) harmed the agronomic traits of wheat. Genotypes G19 and G20 significantly outperformed all studied genotypes and checked cultivars for grain yield under normal and salinity stress. MP, GMP, HM, STI, YI, YSI and RSI indices agreed that G19 and G20 had similar trend of the increased stress tolerance of genotypes, and it can be used as a source of salinity tolerance in a breeding program. GGE biplot analysis revealed that G19 and G20 were ideal genotypes in terms of yielding ability and stability followed by G7 (Giza 171), G16, G9 (Misr3) and G3 (Sakha 95). This study concluded that G19 and G20 were suitable genotypes to be cultivated under salinity conditions

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تصنيف بعض التراكيب الوراثية من قمح الخبز المصري تحت ظروف الإجهاد الملحي

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الملخص

أجريت هذه الدراسة لاختبار تأثير الإجهاد الملحي على الصفات المحصولية والفسيولوجية لبعض التراكيب الوراثية من قمح الخبز بمحطة بحوث سخا الزراعية، مركز البحوث الزراعية، مصر خلال موسمي ٢٠٢٠/٢٠١٩ و٢٠٢١/٢٠٢٠ تحت ظروف تربة عادية وأخرى متأثرة بالملوحة. أظهرت معاملات الملوحة والتراكيب الوراثية وتفاعلاتها تأثيرات معنوية على معظم الصفات المدروسة. أدت الملوحة إلى انخفاض متوسطات جميع الصفات المحصولية. أظهرت النتائج فروقًا كبيرة بين ظروف التربة العادية والملحية لمحتوى الكلوروفيل ومعدل نتح الأوراق. ومع ذلك، ظهرت اختلافات كبيرة بين الأنماط الجينية لمؤشر محتوى الكلوروفيل ودرجة حرارة النبات وتركيز ثاني أكسيد الكربون ومساحة ورقة العلم وخصائص فلورسنت الكلوروفيل. وفي الوقت نفسه، كان التفاعل بين المواقع والتراكيب الوراثية لدرجة حرارة النبات ومساحة الورقة العلم وفلورسنت الكلوروفيل معنوي فقط. سجلت درجة حرارة النبات في التربة غير المالحة قيم أعلي بوضوح مقارنة بظروف التربة الملحية. ارتبط محصول الحبوب بشكل إيجابي بمعدل امتلاء الحبوب وزن الألف حبة ومؤشر الغطاء النباتي وعدد السنابل بالمتر المربع وارتبط بشكل سلبي بدرجة حرارة النبات. يشير هذا إلى أن تحسين هذه الصفات في تربية القمح يمكن اعتباره استراتيجية فعالة لتعزيز الإنتاج في ظل الظروف العادية والملوحة. أظهرت التراكيب الوراثية G19 و G20 تفوقًا واضحًا على جميع التراكيب المدروسة واختبار الأصناف من حيث إنتاجية الحبوب تحت الإجهاد الطبيعي والملوحة. واتفقت مؤشرات تحمل الملوحة وتحليل GGE biplot على أن التراكيب G19 و G20 لهما اتجاه مماثل لزيادة تحمل التراكيب الوراثية الإجهاد ويمكن استخدامها كمصدر لتحمل الملوحة في برنامج تربية قمح الخبز.