Tikrit Journal for Agricultural Sciences (2024) 24 (3): 143-160
DOI: https://doi.org/10.25130/tjas.24.3.13

IRAQI Academic Scientific Journals
المجلات الأكاديمية العلمية العراقية
ISSN:1813-1646 (Print); 2664-0597 (Online)
Tikrit Journal for Agricultural Sciences
Journal Homepage: http://www.tjas.org
E-mail: tjas@tu.edu.iq
TJAS
Tikrit Journal for Agricultural Sciences

Inheritance and Stability of Grain Yield Traits and Its Components under Salt and Normal Conditions of Bread Wheat Genotypes (*Triticum aestivum* L.)

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KEY WORDS:
Salt tolerance, genetic stability, combining ability, bread wheat**.**

Received: 31/01/2024
Revision : 23/06/2024
Proofreading: **25**/08/2024
Accepted: 20/08/2024
Available online: 30/09/2024

ABSTRACT

A field experiment was conducted at an agricultural farm in Baghdad governorate / Iraq (33.05N latitude, 44.32E longitude) by using six parents of bread wheat: Alizz, Ipaa, Saberbeag, Dejla, Furat, and Entesar) and their offspring in a half-diallel according to the Griffing method to evaluate the genetic ability of production in single plants and estimate genetic parameters and stability of related traits under normal and salt stress conditions. Parents and their offspring grew for two winter seasons (2020 and 2021) by using a Randomized Completely Block Design with three replicates in a split-plot arrangement. Main plots included irrigation by saline water (1 and 6 d.m-1) and parents and their F1 were in sub-plots. Results showed that Irrigation with salty water (6) d.m-1 significantly impacted grain yield and its components with important effects of GCA and SCA through high variation of GCA in grain yield. Entesar genotype had significant GCA values in single plant grain yield and inherited its genes. On the other hand, heritability estimates in a narrow sense were high in most yield components. The superior cross (Furat*Entesar) did not show a significant response to saline water. Saberbeag*Entesar cross produced the highest and most stable single plant grain yield (13.37g) in most of the stability parameters estimation methods which could be a promising genotype.

وراثة استقرارية صفات الحاصل ومكوناته تحت ظروف الري الملحي والطبيعي لتراكيب وراثية من حنطةالخبز (*Triticum aestivum* L.)

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الخلاصة

نفذت تجربة حقلية في مزرعة في محافظة بغداد/العراق ضمن خط عرض 33.05 شمالاً وخط طول44.32 شرقاً, باستخدام ستة اباء من حنطة الخبز وهي العز واباء وصابربيك ودجلة وفرات وانتصار وهجنها التبادلية النصفية تبعاً الى طريقة كرفنك الثانية لتقييم القابلية الوراثية الانتاجية للنباتات الفردية وتقدير المعالم الوراثية والثباتية لصفات الحاصل ومكوناته تحت ظروف الشد الملحي والطبيعية. زرعت الاباء وهجنها لسنتين متتاليتين (2020 و2021)م باستخدام تصميم القطاعات العشوائية الكاملة وفق نظام الالواح المنشقة وبثلاث مكررات. تضمنت الالواح الرئيسية مستويات الري الملحي وهما (1 و 6) ديسيسمنز.م-1 وتضمنت الالواح الثانوية الاباء وهجنها. أظهرت النتائج ان صفات الحاصل الحبوبي ومكوناته تأثرت بالمقدرة الاتحادية العامة والخاصة رغم التباين الاكبر للمقدرة الاتحادية العامة لصفة حاصل النبات. تميز الاب انتصار بتأثيرات معنوية موجبة للمقدرة الاتحادية العامة وورث معظم مورثاته الى نسله. من جهة اخرى فان نسبة التوريث بالمعنى الضيق كانت مرتفعة لمعظم الصفات المدروسة. بينما تميز الهجين (صابربيك × انتصار) بأعلى حاصل حبوبي بلغ 13.37 غم فضلا على انه اظهر استقراراية في اغلب طرق تقدير الاستقرارية المستخدمة لصفة حاصل النبات الفردي والذي يمكن ان يعد كتركيب وراثي واعد مقارنة ببقية الهجن الاخرى

الكلمات الافتتاحية: تحمل الملوحة، الاستقرارية الوراثية ، المقدرة الاتحادية ، حنطة الخبز.

INTRODUCTION

Bread wheat is the most important cereal crop in the world and takes part in providing nearly (20%) of food calories (El Shazly *et al.*, 2021). Selecting productive and stable genotypes under salt stress is the most important aim of plant breeders (Zoubeir *et al.*, 2022). Salinity stress caused a reduction of nearly 20% potential yield and affected nearly half of the agricultural land of the world (FAO, 2005). The productivity of Wheat in Iraq is still un insufficient for the full consumption demand due to the increasing population (Hameed and Lateef, 2022), and the shortage of irrigation water resources especially in Salahadin governorate in Iraq (Shareef and Ahmed, 2022). Water and salinity stress are major agriculture problems and cause a reduction in the production of wheat crops' direct and direct effects even leading to the use low low-quality water and supplemental irrigation to diminish water stress effects (Araus, 2005 Zoubeir *et al.*, (2022). Bread Wheat has moderate tolerance salinity, though the expression of genes controlling salt stress can be shifted according to their genome combination in segregating lines (El Shazly *et al.*, 2021). The existence of differences among singular bread Wheat genotypes is regarded as the first step in identifying, utilizing, and selecting promising genotypes in stress tolerance

(Hasan *et al.,* 2022) which is essentially controlled by the interaction among genes and environments in most grain yield components (Noori, and Sokhansanj, 2004). Inheritance of quantitative traits such as grain yield under salt stress conditions is important aim of wheat breeder for Salinity is a complex agricultural problem affected mainly by the gene behavior and gene expression and their interactions with salinity elements therefore, genetic behavior can be predicted with the consideration of selection for the important economic traits. Osmotic pressure is the first disorder of accumulation of salts and toxic ions. Salt-tolerant plants can adjust osmotic pressure avoiding element toxicity and able to preserve **bio synthesis** activities that are necessary for production economic yield (Omrani *et al.,* 2014). Tolerance of salt irrigation can be shifted by the type of gene action which was additive and predominant than dominant for grain yield components under salt stress conditions (Alnaggar *et al.*, 2015). while both types of gene action (additive and dominance) are controlled growth traits under normal conditions (Marzooghian *et al.,* 2014 and Akbarpour, and Dehghani, 2017). Salty irrigation affects the vegetative to the reproductive stage though fewer effects on the last one (Hamam, and Nagim, 2014 and Mansour *et al.*, 2020). Salt irrigation caused a reduction in plant growth other than grain yield components as a result of complex gene behavior under salt conditions which can be determined by the interactions with the environment. Many genotypes exhibited the additive type of gene action for growth traits (plant height, leaf area, and chlorophyll content) under salt irrigation (Omrani *et al.,* 2022).

Also dominance type of gene action was important in grain yield components (Kulshreshtha, and Singh, 2011, Al-jury *et al.,* 2016 and Abdullah and Jassam, 2017). Increasing genetic variation can shift the type of gene action and produce economic yield under seawater and saline conditions that are interpreted by the potential ability to produce and assimilate dry matter to the grain yield (Alnaggar *et al.,* 2015). GCA and SCA are the most common genetic criteria used in predicting of gene behavior of plant traits (such as plant height and grain yield components) that possess significant GCA and SCA effects (El-Hendawy *et al.,* 2005 and Al Sadoon *et al.,* 2018)). Also combining ability analysis refers to the good combiner from the parental lines under investigation (Akbarpour and Dehghani, 2017). The vegetative stage is affected more than the reproductive stage by salt stress which causes additive damage to physiological activities and a reduction in the grain yield of bread wheat (Munns, 2005 and Bai *et al.*, 2011). The variation among genotypes in grain yield components and high heritability, genetic gain from selection, and adaptability under salt stress conditions are the most important genetic parameters that are used as a guide in selection for genetic advance under saline irrigation to improve salt stress of bread Wheat genotypes (Kulshreshtha, and Singh, 2011, Alnaggar *et al.,* 2015 and Yassien *et al.,* 2016).

Middle east suffering from serious problems related to climatic changes that lead to increased salt problems in the poacea family which can be reduced by breeding promising genotypes through proposed efficient selection from segregating lines. Both microclimate factors (as seeding rate) and Macroclimate (as locations) affects significantly performance of bread Wheat genotypes(Jumaa, 2021 and Alqasim and Al-Ghazal, 2024). No method has perfect illustration over all environments therefore different methods are used to investigate the performance, inheritance, and stability of grain yield and its components under normal and stress conditions of bread Wheat genotypes.

MATERIALS AND METHODS

Six parents as shown in Table (1) and their F1s were grown for two winter seasons (2020 and 2021) under salt and non-salt irrigation conditions to estimate genetic behavior for grain yield and its component traits. The experiment was applied by using two levels of salt irrigation (1 and 6) d.m^{-1} in the main plot and the offspring of six parents were in a sub-plot arrangement by using a Randomized Complete Block Design with three replicates. Two sources of water irrigation (1) d.m-1 from river water and 6 d.m-1 prepared by adding sodium chloride to river water according to the formula: ppm=EC*640 (Unknown, 2023). Soil properties analysis in the laboratory of the soil sciences department \ Agriculture College Tikrit University (as shown in table 2). Seeds grown in rows: 20 cm and 10cm between and within distances. Nitrogen was added by 200 Kg.h-1 in two doses: cultivation and tillering stage. Ten plants were taken randomly as a sample to estimate plant height, no. spikes.plant-1, no. grains.plant-1, 1000 grains.plant-1 and individual plant yield. Analysis of variance achieved for data collected and genetic analysis (General and specific combining ability, variance components, heritability, and genetic advance and stability) excluded for significant effects only achieved according to Singh and Chaudhary (1985). Genetic variance components via GCA and SCA were $\sigma^2A=2\sigma^2gca$ and $\sigma^2D=\sigma^2sca$. Significance was tested by using standard error obtained from the square root of additive and dominance variances. Variance of Additive type of gene action($V\sigma^2A$)= $\frac{4}{r2(p+2)}$ [($\frac{2(msgca)2}{K+2}+\frac{2(mse)2}{K+2}$)] and variance of Dominance type of gene action ($V\sigma^2D$)= $\frac{1}{r2}$ [($\frac{2(mssca)2}{K+2}+\frac{2(mse)2}{K+2}$)]. Heritability in narrow sense = σ2A/ σ2D, GA%=i*h2ns*σp, σ2A: Additive gene action, σ2D: dominance gene action, GA: gain from selection divided by grand mean, i: differential selection, h2ns: heritability in narrow sense and σp: phenotypic slandered deviation

Table (1) Pedigree and source of bread Wheat genotypes

No	Name	Pedigree	Source
1	**Al-azz**	Irradiation (Nijah*Maxibak) cross by Gama ray(Iraq)	General Board Agricultural Research \ Ministry of Agriculture \ Iraq
2	**Ibaa99**	Ures/Rows/3/Jup/B/S/ures (Iraq)	The general board of testing and certified seeds \ Ministry of Agriculture \ Iraq
3	**Saber bag**	Australian Cultivar	Field Crops Department \ College of Agriculture \ University of Tikrit
4	**Dijlah**	UK	The general board of agricultural research\ Ministry of Agriculture \ Iraq
5	**Furat**	UK	General Board of Agricultural Research \ Ministry of Agriculture \ Iraq
6	**Entisar**	Irradiation F3-generation of Saber-beag by Australian Wheat (Lagsin) by using Gamma-ray 10 Kilo rad (Iraq)	The general board of agricultural research\ Ministry of Agriculture \ Iraq

Stability parameters in addition to the grand mean were the coefficient of variation (CV), Coefficient of regression (Bi) and square deviation (S2di), Coefficient of determination (R2), Shukula parameters (ri2), Perkins and Jinks Coefficients (Bi), (Dji), Wricks covalence Coefficient(Wi), Superiority measure (Pi), and Non parametric Nassar and Huen (Si(1) and Si(2)) that analyzed by using genotype-environment analysis of replicated values (GEA-R) program of the software analysis of CIMMYT center.OPSTAT and Excel programs were used for statistical analysis.

Table (2) Soil properties

No.	Traits	Value	Unit
1	pH	7.7	
2	Organic matter	15.5	$gram.kilogram^{-1}$
3	N	10	$Milligram.Kilogram^{-1}$
4	P	15.1	$Milligram.Kilogram^{-1}$
5	K	54.5	$Milligram.Kilogram^{-1}$
6	Na	93.3	$Milligram.Kilogram^{-1}$
7	Sand	501	$gram. kilogram^{-1}$
8	Silt	263	$gram. kilogram^{-1}$
9	Clay	224	$gram. kilogram^{-1}$
10	Texture	Sandy Clay Loam	
11	Non salty soil treatments EC	6.3	
12	Overall all Salt Stress treatment EC	9.7	

RESULTS AND DISCUSSION

Analysis of variance showed irrigation by salt water caused significant effects on plant grain yield and its components across years of the wheat genotypes (table 3), which came from negative effects of saline water in plant height and literal branches (Ahmed, 2022). Since genetic analysis should be achieved for each season alone. The differences also were highly significant among genotypes and their interactions which came out from their gene behavior and physiological mechanisms of traits in different environments (Zoubeir *et al.*, 2022).

Table (3) Mean square of pooled analysis for the studied traits

S.O.V.	d.f.	Plant Height (cm)	No.Spikes.Plant-1	No.Grains.Spike-1	1000 grain weight (g)	Single Grain yield (g)
Y	1	1340.77ns	40.13*	928.28ns	854ns	41.09ns
Blocks/L	4	1148.69	3.92	270.19	183.6	43.64
S	1	2088.86**	35.43**	779.18**	23.1*	185.50**
G	20	453.11**	4.95**	282.05**	84.97**	44.70**
Y*S	1	5344.01**	7.64**	6943.02**	43.01**	418.50**
Y*G	20	267.44**	4.50**	195.06**	35.48**	9.79**
S*G	20	311.89**	4.41**	293.91**	89.8**	9.70**
Y*S*G	20	467.36**	3.61**	272.74**	62.39**	9.82**
Pooled Error	164	33.06	0.26	12.52	5.66	1.2

Y: years, S: salt stress, G: genotypes ; *,**: significant at 5% and 1% respectively

Diversity is the raw material of genetic advancement through estimating genetic parameters and using appropriate breeding methods. Additional genetic analysis needs to explain behavior traits under multiple environments. High significant differences for both general and combining ability estimates in plant height and grain yield components which refers to the presence of additive and dominant effects (Table 4).

Additive and dominant effects can be predicted from GCA and SCA respectively and could be illustrated by genetic behavior according to the parent's ability to transmit their genes to their crosses. Variances in GCA more than SCA in plant height and plant yield at salt stress conditions. While SCA variances are higher than GCA in all traits except plant yield(Table 5). Therefore, selection under salt conditions is important in distinguishing good adaptive genotypes (Kulshreshtha and Singh, 2011). Genotypic effects in a diallel mating can be partitioned into two types: additive and dominance variation the ratio of each one could be calculated by dividing one of them to the other. when the ratio of dividing GCA to SCA is close to one refer to the importance of GCA in most traits of yield components. Accordingly, single plant yield exhibited an important additive type of gene action under normal and salt stress conditions. The same results were in plant height, no.grains.spike-1, and 1000 grain weight under salt conditions. Other traits showed preponderance of SCA importance under river water irrigation which means the importance of dominance gene action. Results state selection is recommended for improving grain yield and plant height as the additive gene effects are essential in the selection of superior inbred lines for their persistent performance across generations under ecological stress (salt stress irrigation). Other traits have additive and dominant types of gene action that could be improved by applying bulk selection in early generations followed by single selection in late segregation lines (Noori and Sokhansanj, 2004). Also, recurrent selection is an effective and adequate method for the concentration of favorable genes in early and late segregating lines in grain yield components for increasing potential ability in salt irrigation methods.

Table (4) Single grain yield (g) of genotypes under stress and years effects

Genotypes	**Y1**		**Y2**		**GY**		**GS**		**Mean**
	S0	S1	S0	S1	Y1	Y2	S0	S1	
1*1	9.29	13.06	7.6	7.53	11.18	7.56	8.44	10.3	9.37
2*2	6.42	11.33	8.8	7.46	8.87	8.13	7.61	9.4	8.5
3*3	10.36	10.4	10.03	8.23	10.38	9.13	10.2	9.31	9.75
4*4	11.63	11.1	9.83	8.18	11.36	9	10.73	9.64	10.18
5*5	13.4	11.33	8.76	7.22	12.37	7.99	11.08	9.28	10.18
6*6	11.17	11.43	9.56	8.04	11.3	8.8	10.37	9.74	10.05
1*2	11.78	7.23	11.93	6.37	9.5	9.15	11.85	6.8	9.33
1*3	11	11.1	9.67	6.73	11.05	8.2	10.33	8.91	9.62
1*4	11.63	13.2	10.67	7.81	12.41	9.24	11.15	10.5	10.83
1*5	11.9	11.96	14.68	8.97	11.93	11.83	13.29	10.47	11.88
1*6	12.94	11.93	14.4	11.62	12.43	13.01	13.67	11.78	12.72
2*3	12.37	8.9	14.8	9.48	10.63	12.14	13.58	9.19	11.38
2*4	12.26	15.43	14.33	11.48	13.85	12.9	13.3	13.45	13.37
2*5	10.86	14.2	17.39	8.56	12.53	12.97	14.12	11.38	12.75
2*6	10.7	14.3	17.42	9.85	12.5	13.64	14.06	12.07	13.07
3*4	10.68	10.63	17.06	8.86	10.65	12.96	13.87	9.74	11.81
3*5	13.5	12.66	15.26	9.37	13.08	12.32	14.38	11.02	12.7
3*6	13.49	13.63	16.53	9.82	13.56	13.18	15.01	11.73	13.37
4*5	11.7	15.96	15.4	9.53	13.83	12.46	13.55	12.75	13.15
4*6	13.01	15.93	18.37	12.36	14.47	15.36	15.69	14.14	14.92
5*6	13.72	16.2	18.48	13.33	14.96	15.91	16.1	14.76	15.43

	YS		**Mean**
	Y1	**Y2**	
S0	11.61	13.38	12.49
S1	12.47	9.08	10.78
Means	12.04	11.23	

LSD: Years (1.77), Salt Stress (0.22), Genotypes (0.73), Years*Genotypes (0.73), Years*Salt Stress (0.22), Salt Stress*Genotypes (0.73), Years*Salt Stress*Genotypes (1.47). Y: years, S: salt stress, G: genotypes.

Table (5) Combining ability analysis of stress and non salt stress conditions for single grain yield and its components

SOV	DF	MS traits									
		Plant Height (cm)		**Number Spikes.Plant^{-1}**		**Number Grains.Spike^{-1}**		**1000 Grain Weight (g)**		**Individual Grain Yield (g)**	
		Stress	**Non Stress**	**Stress**	**Non Stress**	**Stress**	**Non Stress**	**Stress**	**Non Stress**	**Stress**	**Non Stress**
Due to GCA	5	310.26**	149.05**	0.86**	1.62**	115.12**	247.78**	28.87**	66.14**	14.85**	17.63**
Due to SCA	15	161.4**	195.49**	1.43**	3.98**	146.13**	116.87**	40.93**	43.9**	9.9**	15.54**
Error	40	9.46	10.49	0.11	0.13	8.67	6.89	4.06	2.8	0.42	0.74
GCA Variance		310.12	148.9	0.85	1.61	114.99	247.68	28.81	66.1	14.84	17.61
SCA Variance		160.34	194.32	1.41	3.96	145.16	116.1	40.47	43.58	9.85	15.45
GCA/SCA		1.93	0.76	0.6	0.4	0.79	2.13	0.71	1.51	1.5	1.13

Significant positive GCA effects under salt and non salt stress conditions were in parent 6 possessed in all studied traits (plant height, no.spikes.plant1, no.grains.spike-1, 1000 grain weight, and individual grain yield). While under salt conditions the significant effects were in individual gain yield for the P4 parent and in plant height, no.grains.spike-1, and 1000 grain weight of the P5 parent. Positive GCA effects in 1000 grain weight, no.spikes.plant-1 and no.grains.spike-1 for P1, P2, and p3 respectively under non-stress conditions (table 6). The results state that possessing P6 parent genes increases plant height and other grain yield components in all environments. The P4 parent has genes affected positively and increasing individual grain yield besides possessed P5 parent genes of grain yield components traits. Consequently, P6 and P5 are good combiners in improving grain yield and its components. Negative GCA effects in P1, P2, and P4 refer to the behavior genes through decreasing genotypic value in most grain yield components.

Specific combining ability is an important metric of the cross's superiority and ability in the genetic advance through inbred and hybrid vigor. While Under salt stress 4*5 and 4*6 have positive significant effects (9.79, 10.14, and 0.89,0.82 in plant height and no.spike.plant-1 respectively). Also significant positive effects in no. grains.spike-1 (8.86) of 2*6 cross and 3*5(5.65) and 5*6(5.48) in 1000 grain weight. 2*4 and 5*6 crosses showed positive significant SCA effects in individual grain yield (2.59 and 2.48 respectively). P5 and P6 are important in producing superior hybrid (5*6) for their gene combination and good performance alone.

Table (6) GCA and SCA effects under stress and non salt stress conditions

Genotypes	Plant Height		Number Spikes.Plant^{-1}		Number Grains.Spike^{-1}		1000 Grain Weight		Grain Yield	
	Stress	Non Stress	Stress	Non Stress	Stress	Non Stress	Stress	Non Stress	Stress	Non Stress
P1	-3.66	-0.38	-0.16	-0.45	-0.95	-2	0.01	0.81	-0.8	-1.28
P2	-4.32	-4.28	0.006	0.25	-2.52	-5.14	0.25	-1.55	-0.47	-0.66
P3	1.6	2.41	-0.01	-0.08	-2.21	1.1	-1.97	0.46	-0.78	0.01
P4	-0.62	-0.85	-0.06	-0.04	1.09	0.72	-0.08	0.16	0.55	0.19
P5	1.94	0.81	-0.13	0.15	2.38	4.26	1.36	-2.22	0.43	0.76
P6	5.07	2.3	0.36	0.18	2.21	1.06	0.42	2.34	1.06	0.97
1*2	4.48	7.27	1.35	-0.02	-15.63	6.41	-1.61	2.65	-2.7	1.31
1*3	8.48	-2.84	-0.8	2.04	1.66	-6.84	-0.29	-2.21	-0.28	-0.88
1*4	3.35	1.07	-0.49	-0.11	2.47	-3.43	1.29	4.39	-0.02	-0.25
1*5	-11.31	-7.36	-0.71	0.03	0.52	-0.14	2.58	0.03	0.05	1.31
1*6	-0.05	-8.15	0.67	-0.11	-6.21	5.71	2.62	-0.91	0.73	1.48
2*3	-0.16	-3.87	0.22	0.53	1.46	3.28	-2.82	2.47	-0.34	1.74
2*4	-0.23	-1.95	-0.15	0.15	6.39	-3.92	1.86	4.27	2.59	1.27
2*5	7.39 -	7.12	0.01	0.33	-1.67	6.25	-1.66	0.03	0.63	1.52
2*6	9.83	-4.76	-0.65	0.16	8.86	-2.54	-1.79	6.24	0.7	1.25
3*4	-6.19	-5.44	-0.76	-0.32	-0.12	0.79	2.11	2.9	-0.8	1.16
3*5	1.33	-7.87	0.32	0.35	-9.25	2.84	5.65	-0.47	0.58	1.1
3*6	2.79	-9.26	-0.3	0.448	4.32	3.25	0.24	0.29	0.66	1.52
4*5	9.79	-1.9	0.89	0.65	6.19	-3.94	-5.89	-2.25	0.98	0.08
4*6	10.14	-1.94	0.82	1.54	-4.21	-0.56	3.38	1.02	1.75	2.02
5*6	5.52	-3.48	-0.21	0.18	5.66	1.47	5.48	0.49	2.48	1.86
SE(gi)	0.57	0.6	0.06	0.06	0.54	0.48	0.37	0.31	0.12	0.16
SE(sij)	1.3	1.36	0.14	0.15	1,24	1.11	0.85	0.7	0.27	0.36

Partitioning genetic variance components to additive and dominant gene action is essential for understanding the relative importance of each type. Significant additive and dominance variances were recorded in all traits under stress and non-stress conditions, which state the acting of both types of gene action (additive and dominance) (Table 7). Heritability estimate in a narrow sense explains the relative portion of additive gene action which were high in plant height (79.45 and 60.1), no.grains.spike-1(61.3 and 81.01), and individual plant yield(75.08 and 69.5) under salt and non salt stress conditions respectively. Other than 1000 grain weight (75.2) in non-stress conditions. Both additive and dominance variances were significant in whole traits except dominance in plant height which means the importance of both additive and dominance type of gene action.

Table (7) Genetic variances components and heritability estimate of studied traits

Parents	MS									
	Plant Height (cm)		**No. Spikes.Plant-1**		**No.Grains.Spike -1**		**1000 Grain Weight (g)**		**Individual Grain Yield (g)**	
	Stress	**Non Stress**	**Stress**	**Non Stress**	**Stress**	**Non Stress**	**Stress**	**Non Stress**	**Stress**	**Non Stress**
VA	620.24 ±38.41	297.8 ±18.81	1.7 ±0.1	3.22 ±0.17	229.98 ±14.47	495.36 ±31.67	57.62 ±3.48	132.2 ±8.29	29.68 ±1.77	35.22 ±2.21
VD	160.34 ±339.66	194.32 ±22.37	1.41 ±0.52	3.96 ±4.44	145.16 ±2.82	116.1 ±13.37	40.47 ±4.7	43.58 ±5.19	9.85 ±1.13	15.45 ±1.77
H2 n.s.	79.45	60.51	54.66	44.84	61.3	81.01	58.74	75.2	75.08	69.5

Evaluation of genotypic performance under different environments in such an important trait (grain Yield) is the first important step in the stability procedure. Interactions of genotypes by environments tested against pooled error and were highly significant in plant yield and other traits as shown in Table 3. Individual plant yield exhibited significant differences among genotypes under salt irrigation. Plant yield in two crosses (4*6 and 5*6) were 14.92 and 15.43g respectively and exceeded their parents and other crosses. Crossing among 4,5 and 6 parents increased the potential ability of production and promoted plant grain yield through enhancing vegetative growth development and net assimilation rate (Omrani *et al.,* 2022). Even though individual grain yield is stable in 5*6 cross under salt and non salt irrigation (table 4). Genotypes production across years were low under salty conditions in most crosses and their parents except 5*6 cross which state homeostasis in plant yield and unaffected by salty environments.

Stability approaches aim to estimate genetic ability in the production of high and stable yields. Phenotypic variations can be shifted and dismissed under multiple environments, therefore, classifying genotypes according to their stability and adaptability is the next contentment step of the breeding program after studying the type of gene action for each trait (Bai *et al.,* 2011, Kulshreshtha and Singh, 2011, Abd El-Shafi *et al.,* 2014, Marzooghian *et al.,* 2014 and Omrani *et al.,* 2022).

Stability input analysis showed highly significant effects of environments, genotypes, and their interactions that tested against pooled deviation (table 3). Different methods were used in the stability estimate ($X\overline{i}$, CV, b, Si, R2, W2, and S2di) of bread wheat genotypes (table 8). Each stability approach has specially considered concepts to determine stable genotypes even though using different methods explains the adequate environmental demands of each approach across environments (Said *et al.,* 2020). Changing stability parameters for each method refer to the differences in stability and adaptability responses among genotypes (Abd El-Shafi *et al.,* 2014). The method of Eberhart and Russell (1966) has two parameters (bi and S2di) which state stable genotype by the value of the coefficient of regression close to one and don't deviate significantly from the regression line in addition to high performance in plant yield which means the adaptation in different environments(Gupta *et al.*, 2022).

Grain yield mean ranged from 8.5 g for 9 genotypes to 15.43 g in genotype 21. plotting yield against coefficient of variation divided genotype into four parts: good productive and stable that have over grand mean and low coefficient of variation include 10, 11, 13, 17, 18, 20, and 21 genotypes. Low productive and high CV were in 1, 2, 5, and 12 genotypes. Low yield and CV were in 3, 4, 8, and 9. High performance and CV revealed the adaptation to the favorable environments in 14, 15, 16, and 19 genotypes (Fig.1). Coefficient of variances can be the inference of homogeneity genotypes under different environments which were 9.82% of genotype 11 to 31.5 % for genotype 7 though low yield. High productivity over grand mean and low coefficient of variation were in the 10, 11,13, 17,18,20, and 21 genotype.

Accordingly, genotypes differ in their production and CV could be illustrated by additional stability methods that correlate negatively or positively with yield and each other (Fasahat *et al.*, 2015).

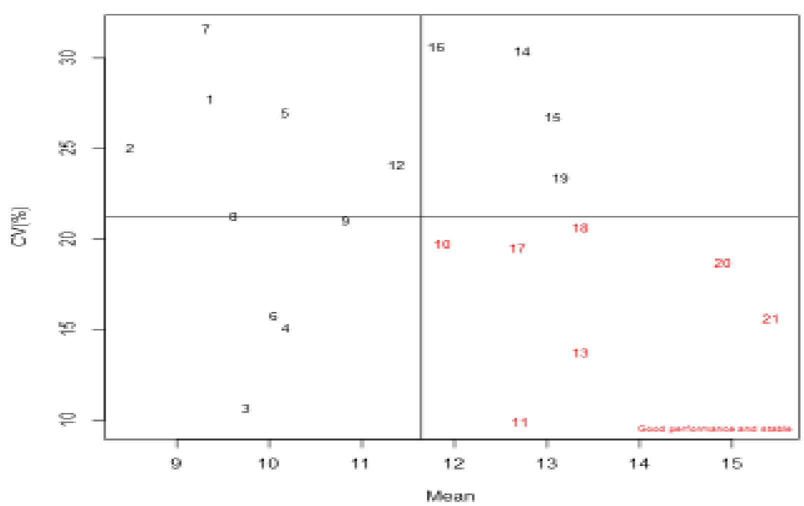

Figure 1. Means of genotypes against coefficient of variation (CV)

Results of stability parameters estimated by using the Eberhart and Russel approach showed no significant differences in coefficient of regression and deviation from regression of plant yield for all genotypes. The symmetrical behavior of genotypes in that environment led to similar responses of genotypes. Stable and adapted genotypes have bi close to one and Si^2 equal to zero. G18 is regarded as the most adapted genotype in all environments (Fig.2). Other genotypes were relevant in favorable environments. although 17, 18, and 10 genotypes have less S2di and B values close to one (table 8). Remarkably genotype 18 has good performance and adapted in favorable environments.

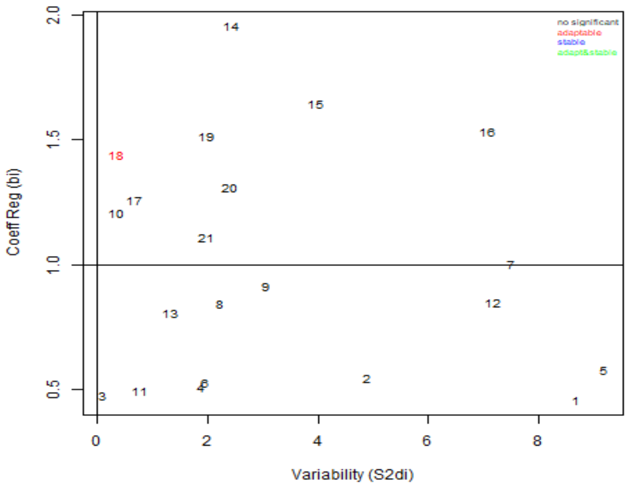

Figure 2. Coefficient regression for the genotypes and their variability

R2 method represents the sum of square contributions of variances which ranged from 0.1 for genotype1 to 0.94 for genotype 18. Shukula procedure of stability aims to calculate the share of each parent to the genotypic environmental interaction. Therefore, the Low Shukla value (ri2) refers to the stable genotype. Low values were in genotypes 10,17 and 18 (0.49, 0.82, and 1.06 respectively). while genotype 1 has a large contribution (7.58) to the total variation (genotypic-environmental variations). Perkins and Jinks's stability procedure regarding stable genotype has adjusted the regression model of Bi near zero. Therefore, in a relation between coefficient of regression and genotype performance 13, 18, 20, and 21 genotypes possessed the lowest value of Bi companied by high performance. Non parametric measures of phenotypic stability of yield give the rank of genotypes in each environment (in a way relative to the average of the environment (Bujak, and Nowosad, 2014)) refer that Hanson's genotype stability procedure used in a small number of genotypes and environments which calculate Di parameter. Di value measures the ratio of sharing each genotype in the variance of GE interaction and the genotypic reaction to changeable environmental conditions with the use of Eberhart and Russel regression. Dji represents mean performance across environments which is calculated through the sum of squares of the differences between the genotypic mean in each environment and the mean of the best genotype divided by twice the number of environments (Lin and Binns, 1988). Consequently, the stable genotype has a small value of Dji in 3, 18, and 10 genotypes (0.42, 0.67, and 0.68 respectively). Wricke's ecovalance defines the share of each genotype in the interaction of GE. According to Wricke's ecovalance method 10,11,13,17,18,20 and 21 genotypes represent stable genotypes as their low values of Wi2 (1.82,4.81,3.71,2.71,3.35,6.48 and 4.74 respectively). High values were in 1 and 5 genotypes (21.04 and 20.81 respectively).

Superiority measure Pi proposed by (Kilic, 2012). Calculating Pi for each genotype which means the differences in performance of genotype in its environments and in all environments which can be used if data aren't irrelevant to linear regression. Small Pi value refers to high performance and fewer differences toward the best genotype. Low values of (pi) refer to the stable genotype according to the superiority production that was low in the 21, 20, and 18 genotypes (0, 0.19, and 2.84 respectively).

Table (8) Stability parameters by using different methods of wheat genotypes

Genotype	Mean	Francis	Eberhart&Russell		Coefficient of determination	Shukla	Perkins &Jinks	Ranking mean	Wricke's Ecovalence	Superiority Measure	Non parametric Nassar&Huehn	
		CV(%)	bi	S2di	R2	ri2	Bi	DJi	Wi	Pi	Si(1)	Si2
1	9.37	27.66	0.45	8.68	0.10	7.58	-0.54	9.01	21.04	22.70	4.5	29.67
2	8.50	24.93	0.54	4.89	0.22	4.46	-0.45	5.22	12.58	25.65	2	7.42
3	9.75	10.55	0.47	0.09	0.73	1.17	-0.52	0.42	3.64	17.79	1	9.33
4	10.18	15.07	0.50	1.87	0.37	2.36	-0.49	2.20	6.88	16.47	1.17	4.42
5	10.18	26.86	0.58	9.17	0.15	7.49	-0.41	9.50	20.81	19.44	2.83	53.75
6	10.05	15.64	0.52	1.96	0.38	2.36	-0.47	2.29	6.87	17.09	1.5	4.67
7	9.33	31.50	1.00	7.48	0.39	5.58	0.002	7.81	15.63	21.94	4.5	31.67
8	9.627	21.16	0.84	2.23	0.58	1.80	-0.15	2.56	5.37	19.33	0.83	4.42
9	10.83	20.92	0.91	3.06	0.55	2.35	-0.08	3.39	6.86	13.11	2.17	11.6
10	11.88	19.63	1.20	0.35	0.91	0.49	0.20	0.68	1.82	6.83	0.5	0.67
11	12.72	9.82	0.49	0.76	0.53	1.60	-0.50	1.09	4.81	4.80	2.5	18
12	11.38	24.01	0.85	7.18	0.33	5.44	-0.14	7.51	15.25	10.44	4.17	36.67
13	13.37	13.62	0.80	1.33	0.66	1.19	-0.19	1.66	3.71	2.92	3.33	14.67
14	12.75	30.27	1.95	2.43	0.87	5.32	0.95	2.76	14.90	4.52	3.33	30.67
15	13.07	26.64	1.64	3.96	0.76	4.57	0.64	4.29	12.88	3.24	2.67	41.33
16	11.81	30.51	1.53	7.08	0.61	6.37	0.53	7.41	17.76	7.78	3.17	39.33
17	12.70	19.42	1.25	0.67	0.88	0.82	0.25	1.01	2.71	4.81	1.83	13
18	13.37	20.54	1.44	0.34	0.94	1.06	0.44	0.67	3.35	2.84	0.83	3.33
19	13.15	23.29	1.51	1.97	0.83	2.53	0.51	2.30	7.34	3.51	2.33	13.67
20	14.92	18.59	1.31	2.41	0.76	2.21	0.31	2.74	6.48	0.19	0.5	2
21	15.43	15.52	1.10	1.98	0.73	1.57	0.10	2.31	4.74	0	0	0

The Non parametric of Nassar and Huhen procedure aims to calculate Si1 and Si2 which means the relative portion of take part rank of each genotype. Non parametric measures give rank for genotypes in each environment in a way relative to the average of the environment. Huhn's stability parameters Si(1): differences in absolute rank mean across environments and Si(2) refers to the rank variances across environments) state that fewer changes in the rank of genotype across environments refer to the stable genotype (Kilic, 2012). Low values indicate high stability of genotypes that were 0, 0, 0.5, 2, 0.5, 0.67, and 0.83, 3.33 were recorded for Si(1) and Si(2)in 21, 10, 20, and 18 genotypes respectively. The caption can also be used to explain any acronyms used in the figure, as well as provide information on scale bar sizes or other information that cannot be included in the figure itself. Plots that show error bars should include in the caption a description of how the error was calculated and the sample size (see Figure 1).

CONCLUSION

The salty environmental stress caused reduction in single grain yield which can be diminished through applied selection technique on the segregating lines as the preponderance additive type of gene action in most studied traits. Crosses more effective than parental lines in tolerance of salty irrigation and exhibited stability of their grain yield in different stability methods simultaneously in the genotypic environmental interactions.

CONFLICT OF INTEREST

The author declares no conflict of interest.

ACKNOWLEDGMENTS

Special thanks for the header of Field Crops department\Agriculture college, Tikrit university.

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