Field Screening of Drought and Salinity Tolerant Wheat Genotypes in Hot and Dry Climates

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Abstract

Drought and salinity stresses are among the non-living environmental stresses in arid and semi-arid regions that affect plant growth and yield. The aim of this study was to identify the best wheat genotypes in terms of high yield and tolerance to drought and salinity using bi-plot graphic technique and stress tolerance indices, which was conducted at the research station of the Agricultural and Natural Resources Research Center in 2020. For this purpose, 111 pure bread wheat lines selected from observational experiments that were transformed after 6 generations of autogamy and selection by the bulk breeding method were examined as non-repetitive experiments (augment) in three conditions of normal, dryness, and salinity. During the growing season, Days to the heading: DHE, Days to maturity: DMA, Plant height: PL, Thousand-kernel weight: TKW, Spike length: SL, Seed number per Spike: SNP, Seed weight per spike: SWS, Number of spikelet per spike: NSS, Spike weight: SW, Seed yield: SY, were evaluated and compared with control cultivars. Statistical analysis was performed using SPSS. 16 Excel and Statghraphic software. The experimental results showed great diversity in the genotypes in terms of most of the studied traits and the Seed number per Spike and Thousand-kernel weight were the most important variables affecting seed yield under normal conditions, salinity stress, and drought. Finally, this study showed that the genetic materials in this experiment, with new traits and diversity in yield potential under environmental stress conditions, can provide valuable resources for breeders to improve and produce wheat cultivars tolerant to salt and drought stress.

Keywords Bi-plot analysis · Environmental stresses · Genetic diversity · Bread wheat

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Introduction

Seed yield in wheat is affected by environmental conditions, genetic potential, and their interaction. Although all living and non-living environmental stresses are the main factors in reducing wheat yield, currently salinity and drought stresses are the most important limiting factor for successful wheat production in the world (Shiri et al. 2010a). One of the easiest ways to identify and select tolerant genotypes is to select genotypes under salt stress conditions (Zhu et al. 2016). It seems difficult to identify genotypes that have good yield in all three conditions of normal, salinity, and drought stresses, due to the significant interaction between genotype and environment. In this regard, researchers have proposed different methods, which are: 1. selection based on the potential yield of genotypes, 2. selections based on sustainability criteria, 3. selections based on the composition of yield and yield components and traits that correlate with yield, 4. Using the yield of stress and non-stress conditions. Generally, plant yield is the most important indicator for identifying genotypes adapted to the stressful environ-

ment (Shiri et al. 2010b). Selection based on the yield of genotypes in both stress and non-stress conditions leads to the selection of high-yield genotypes, because the response to selection in non-stress conditions, due to the high heritability of yield in these conditions, is maximum (Gavuzzi et al. 1997). One of the methods for evaluating the genotypes of a species for screening under environmental stress is the use of the bi-plot method, which provides the main effect of genotype and the interaction of genotype in the environment at the same time. This method, unlike the multivariate method of stability analysis; Which considers only the interaction of genotype in the environment, also uses the main effects of genotype. Numerous studies have shown that in most stability analysis experiments, the main effect of the environment is high, while the changes justified by the main effect of genotype and the interaction of genotype in the environment that can be recommended and interpreted are few. In this method, the stability of a genotype's yield is evaluated by the absence of significant changes in the interaction effects of the genotype with the environment when the environmental conditions are not constant, therefore, in the examination of test materials in the programs of the breed, compatible genotypes are evaluated whose variance of the interaction with the environment is small. Since environmental changes are not controllable, the bi-plot method uses the sources of genotype changes and the genotype interaction in the environment to achieve reliable results (Yan et al. 2000; Yan and Tinker 2006). The biplot method helps the breeder to easily evaluate the stability of genotypes and the combination of stability with the yield of genotypes in different environments by graphically showing the interaction of genotypes in the environment. Make it easy to identify target environments in breeding programs. The use of this model to analyze the interaction of genotype in the environment to evaluate genotypes in multidisciplinary experiments in wheat (Yan 2001; Yan and Hunt 2002), corn (Fan et al. 2007; Choukan 2011; Changizi et al. 2014), soybean (Yan and Rajcan 2002), barley (Dehghani et al. 2006; Mortazavian et al. 2014), cotton (Blanche and Myers 2006; Saeid Rahnejat and Farshadfar 2015) and durum wheat (Mohammadi et al. 2010) has been reported.

The use of stress tolerance and stability indices is another reliable method that the simultaneous drawing of performance under stress and non-stress conditions with the stress tolerance index in the biplot diagram gives reliable results. One of the important indicators in this field:

$$STI = \frac{Y_p \times Y_s}{\bar{Y}_p^2}$$

In this regard, Yp, Ys, and are yield under non-stress conditions, yield under stress conditions, and the average yield of genotypes under non-stress conditions, respectively (Fer-

nandez 1992). Based on this index, more stable genotypes have higher STI values. The STI index is more efficient in selecting the top lines due to the use of. In this regard, using the mentioned indicators, an experimental with 111 bread wheat genotypes in the form of augmenting design (without replication) with three cultivars of control wheat in three normal conditions and drought and salinity stresses were investigated to identify superior genotypes in these environments.

Materials and Methods

The aim of this study was to identify the best genotypes of bread wheat in drought and salinity stress environments between 111 lines along with three cultivars Narin, Barzegar, and Sistan as a control. The genetic material of this population was obtained after 6 generations of autogamy and selection through the modified deformed bulk method. The studied lines were planted in 2020 in the research farm of the Agricultural and Natural Resources Research Center (Longitude 15° 53′ to 40° 54′, latitude 46° 31′ to 15° 32′ north, Height 1200 m), in an experiment without repetition in two research farms, one farm in Ardakan (saline conditions) with an electrical conductivity of 10 decisiemens/meter and another in Yazd research station (normal and dry conditions) with an electrical conductivity of 3 decisiemens/meter. Before starting the experiment, composite sampling was performed from the farm soil and different physical and chemical properties of the soil of the planting site were determined. Based on soil test, 100 kg of potassium sulfate, 100 kg of ammonium disulfate before planting, and 250 kg of urea fertilizer were considered as installments in 3 stages of tillering, stalking, and seed filling. Each line was planted in two lines of 2.5 m with a distance of 20 cm between rows. Each line was planted without repetition and to evaluate their production capacity, three cultivars Narin, Barzegar, and Sistan were repeated as controls at intervals of each 20 lines. Irrigation was done by flood method and water salinity was 10 dS/m for salinity treatment. Under saline conditions, sampling was performed from the soil to a depth of 30 cm to determine soil salinity during the growing season. The average salinity of soil saturated extract was obtained during the growing season of 10 dS/m. Using the leaching coefficient during the period, about 25% more water was given to the soil to maintain soil salinity of about 10 dS/m. To create drought stress, irrigation was stopped in the post-flowering stage. Non-saline water was used to irrigate dry and in normal conditions. Seed density was 400 seeds under normal conditions and 500 seeds per square meter under saline conditions so that the number of plants per unit area was the same for all three conditions. Traits measured during the growing

season include Days to the heading: DHE, Days to maturity: DMA, Plant height: PL, Thousand-kernel weight: TKW, Spike length: SL, Seed number per Spike: SNP, Seed weight per spike: SWS, Number of spikelet per spike: NSS, Spike weight: SW, Seed yield: SY. Due to the fact that the experimental materials were non-replicating, statistical analysis of the data was performed based on descriptive statistics including minimum, maximum, range, mean, standard deviation, and coefficient of variation related to all quantitative traits. Seed yield in the studied lines was compared with the mean yield of controls planted on both sides of the genotype as a percentage of production. Relationships between traits were studied by simple correlation calculation. Multivariate analysis by stepwise regression analysis was used to summarize the main aspects of the changes of variables by a fewer number of linear combinations. 1. Factors analysis was calculated to draw the plot using Pearson correlation. Using the first two components, a biplot was drawn for quantitative traits. 2. Using the Selection Index

of Ideal Genotype (SIIG) method, the average yield of genotypes was ranked under three conditions: normal, drought stress, and salinity. Statistical analysis was performed using SPSS. 16 Excel and Statghraphic software.

Results and Discussion

Yield and Yield Components

Under drought and salinity stress, a decrease in mean seed yield, Thousand-kernel weight, spike length, Seed number per spike, Seed weight per spike, number of spikelet per spike, spike weight, and plant height was observed compared to control cultivars (Table 1). The average seed yield of the lines under normal conditions was 5663 kg/ha. This average was obtained in salinity and drought stress conditions of 2100 and 3734 kg/ha, respectively, which is equivalent to 63 and 34% reduction. The intensity of $SI = 1 - \frac{\overline{Y}_s}{\overline{Y}_p}$

Table 1 Mean of studied traits for control varieties and 111 bread wheat genotypes in control, salt and drought stress conditions

Genotype	Condition	SY (kg·ha⁻¹)	TKW (g)	DHE	DMA	SL (mm)	PL (cm)	S.w/spike (g)	No. S/ spike	NO.spikelets/ spike	Spike weight (g)
Narin	N	6571.4	36.7	75	126	100.3	94.3	2.7	51.5	18.8	5.0
	S	3200.0	36.2	77	118	80.1	66.1	2.4	43.4	13.0	4.2
	D	5000	29.9	73	119	100.4	97.3	2.5	44.3	11.4	4.3
Barzegar	N	7285.7	39.5	77	128	100.4	91.0	2.6	48.5	17.7	4.9
	S	3014.3	35	82	121	80.6	57.7	2.3	40.9	13.3	4.3
	D	4428.6	27.9	77	120	100.4	95.7	2.4	44.8	11.0	4.6
Sistan	N	7285.7	39.1	78	128	90.6	92.3	2.7	41.5	17.1	5.0
	S	3100	31.0	82	122	75.6	54.6	2.3	39.8	15.6	4.3
	D	4600	26.8	77	120	100.6	97	2.1	35.9	11.4	4
Mean of Lines	N	5663.1	30.1	78	128	100.5	99.6	2.3	47.1	18.8	4.7
	S	2100.9	32.1	81	122	82.6	65.3	1.6	35.3	14.2	3.6
	D	3734.2	28.4	76	118	100.7	110.7	1.6	35.2	13.4	3.6

N Normal Condition, *S* Salinity Stress, *D* Drought Stress. Other abbreviated letters are on base of abbreviations in materials and methods
DHE Days to heading, *DMA* Days to maturity, *PL* Plant height, *TKW* Thousand-kernel weight, *SL* Spike length, *SNP* seed number per Spike, *SWS* seed weight per spike, *NSS* Number of spikelet per spike, *SW* Spike weight, *SY* seed yield

Table 2 Correlation coefficient of seed yield with the studied traits by experimental conditions and cultivars

Treats	Condition			Cultivar/Lines			
	Normal	Drought	Salinity	Barzegar	Narin	Sistan	Lines
TKW	0.98 **	0.29 ns	0.44 ns	0.55 *	0.03 ns	0.76 *	–0.45 ns
DHE	–0.06 ns	0.23 ns	–0.27 ns	–0.34 ns	–0.41 ns	–0.33 ns	–0.39 ns
DMA	0.11 ns	0.56 *	–0.11 ns	0.90 **	0.90 **	0.82 **	0.63 *
SL	–0.41 ns	–0.45 ns	–0.47 ns	0.75 *	0.88 **	0.46 ns	0.83 **
PL	–0.98 **	–0.85 **	–0.41 ns	0.67 *	0.84 **	0.71 *	0.69 *
SW/Spike	0.82 **	0.89 **	0.99 **	0.99 **	0.97 **	0.77 *	0.89 **
S.no/Spike	–0.31 ns	0.61 *	0.93 **	0.98 **	0.89 **	0.45 ns	0.88 **
Spiklet/Spike	–0.45 ns	–0.43 ns	–0.12 ns	0.78 *	0.72 *	0.41 ns	0.82 **
Spike Weight	0.78 *	0.65 *	0.96 **	0.98 **	0.90 **	0.79 *	0.89 **

DHE Days to heading, *DMA* Days to maturity, *PL* Plant height, *TKW* Thousand-kernel weight, *SL* Spike length, *SNP* seed number per Spike, *SWS* seed weight per spike, *NSS* Number of spikelet per spike, *SW* Spike weight, *SY* seed yield

Table 3 Results of stepwise regression analysis to predict the seed-justifying traits of recombinant inbred lines of bread wheat with parents and controls under normal, salinity and drought conditions

Environment	Traits[a]	Regression coefficients[b]	SE	t	Significant probability
Normal	1000-Seed Weigh	106.247	36.34	2.92	0.004
	DHE	66.68	31.04	2.14	0.03
	SL	323.26	125.58	2.57	0.01
	PL	–48.66	11.78	–4.12	0.0001
	No. S /spike	29.75	12.62	2.35	0.02
Salinity	No. S /spike	13.04	0.202	2.326	0.022
	PL	12.08	–0.358	–3.99	0.000
	SL	131.18	0.226	2.56	0.012
	1000-Seed weigh	37.57	0.24	2.886	0.005
	DHE	32.22	0.185	2.004	0.048
Drought	1000-Seed weigh	52.60	26.35	1.996	0.048
	DHE	56.25	26.62	2.113	0.037
	SL	189.2	68.02	2.782	0.006
	PL	–32.94	8.11	–4.063	0.00
	Spike weight	585.8	153.9	3.805	0.00

DHE Days to heading, *DMA* Days to maturity, *PL* Plant height, *TKW* Thousand-kernel weight, *SL* Spike length, *SNP* seed number per Spike, *SWS* seed weight per spike, *NSS* Number of spikelet per spike, *SW* Spike weight, *SY* seed yield

[a]Dependent Variable: yield per plot (g plot^{-1}). For other abbreviations see materials and methods

[b]The regression coefficient

stress for salinity and drought stress conditions was 0.62 and 0.33, respectively, which is approximately equivalent to the reduction in these conditions.

The correlation coefficient between different traits with seed yield based on different conditions and also based on genotype has been calculated separately in Table 2. When we do not consider the experimental conditions and examine the correlation coefficient based on the cultivar, the correlation coefficients between seed yield and plant height become positive and significant (Table 2). The Seed weight per spike had a positive and significant correlation with seed yield in all three environments: normal, salinity, and drought, which shows the importance of this trait in determining seed yield in three environments.

Stepwise Regression Analysis

In order to identify the important traits that justify the increase in seed yield, multivariate regression analysis was performed. For this purpose, seed yield was studied as a dependent variable and other agronomic traits were studied as independent variables. Regression coefficients and t-test for significance of the studied variables affecting seed yield are given in Table 3. The experimental results showed that un-

Table 4 Results of principal components analysis on the studied traits under normal, salinity and drought conditions

Traits	Salinity Stress				Drought Stress				Normal			
	PC1	PC2	PC3	PC4	PC1	PC2	PC3	PC4	PC1	PC2	PC3	PC4
SY	0.932	0.090	0.016	0.131	0.625	0.405	0.116	–0.318	0.554	0.107	–0.427	0.493
TKW	0.938	0.146	0.127	0.102	0.198	0.473	0.317	0.444	0.189	0.113	0.539	0.764
DHE	0.830	0.076	0.280	–0.120	–0.166	0.814	–0.323	0.065	0.262	0.831	–0.034	–0.035
DMA	0.532	0.303	0.495	–0.124	–0.039	0.838	–0.36	0.021	0.330	0.762	–0.128	0.169
SL	0.521	0.430	–0.400	0.342	0.071	0.203	0.722	–0.43	0.398	0.540	–0.060	–0.121
PLH	–0.453	0.697	0.158	–0.266	–0.497	–0.193	0.178	0.633	–0.117	0.437	0.757	–0.118
S.w/spike	–0.391	0.661	0.304	–0.294	0.909	–0.198	–0.035	0.191	0.745	–0.497	0.135	–0.077
No. S/spike	0.040	0.621	–0.620	0.066	0.847	–0.061	–0.204	0.104	0.824	–0.088	–0.140	–0.220
NO.spikelets/spike	–0.408	0.247	0.081	0.712	0.122	0.434	0.530	0.294	–0.517	0.069	0.388	–0.293
Spike weight	–0.302	0.061	0.566	0.587	0.919	–0.132	–0.031	0.195	0.870	–0.304	0.129	–0.046
Relative variance	35.898	16.857	13.29	11.869	31.43	20.81	12.26	10.61	29.531	21.291	12.712	10.269
Collective variance	35.898	52.754	66.044	77.914	31.47	52.28	64.54	75.15	29.531	50.804	63.516	73.785

DHE Days to Heading, *DMA* Days to Maturity, *PLH* Plant Height, *Seed/Spike* No. of Seeds per Spike, *TKW* 1000-Kernel Weight, *SY* Seed Yield per Plot (g/plot), *NSS* Number of spikelets per spike, *SW* Spike weight

Table 5 Ranking of studied genotypes in terms of yield under three conditions: normal, drought stress and salinity stress using SIIG index

Genotype	Di+	Di−	SIIG	Rank	Genotype	Di+	Di−	SIIG	Rank
1	0.0947152	0.0484518	0.3384284	89	58	0.0789271	0.0630651	0.4441451	55
2	0.0844586	0.059448	0.4131013	65	59	0.0694307	0.0730645	0.5127506	37
3	0.0896494	0.0598872	0.4004853	69	60	0.1037583	0.0388449	0.2723985	101
4	0.1055718	0.039874	0.27415	99	61	0.118394	0.0253002	0.17607	110
5	0.0616515	0.0837788	0.5760754	22	62	0.1049985	0.0394333	0.2730238	100
6	0.0974429	0.0483861	0.3318004	90	63	0.1152671	0.0288219	0.2000287	108
7	0.0866035	0.0602574	0.4103026	68	64	0.1047031	0.0410709	0.2817437	98
8	0.0879141	0.0559378	0.388857	75	65	0.1144095	0.0317584	0.2172736	105
9	0.0593009	0.0920274	0.608131	18	66	0.084308	0.0622667	0.4248122	64
10	0.0817833	0.0658376	0.4459909	51	67	0.1092393	0.0374076	0.2550863	103
11	0.0946732	0.0517335	0.3533548	84	68	0.1025574	0.0417612	0.2893684	97
12	0.0922085	0.0549205	0.3732815	80	69	0.11309	0.0306125	0.2130267	106
13	0.068868	0.0773209	0.5289112	30	70	0.0821225	0.0630651	0.4343699	60
14	0.0735412	0.076214	0.5089238	39	71	0.1121733	0.0320819	0.2223966	104
15	0.0885262	0.0573953	0.3933301	74	72	0.1152395	0.0303257	0.208331	107
16	0.0771564	0.0732057	0.4868626	44	73	0.1267584	0.0184365	0.1269778	112
17	0.0810518	0.0654141	0.4466165	50	74	0.1018347	0.0430903	0.2973284	95
18	0.0975732	0.0505377	0.3412151	88	75	0.0967312	0.0504276	0.3426744	87
19	0.0895253	0.0567833	0.3881061	76	76	0.0809733	0.0608867	0.4292027	62
20	0.08357	0.0670804	0.4452719	52	77	0.0807081	0.0644971	0.4441789	54
21	0.0683935	0.0794186	0.5372942	29	78	0.1167798	0.0273225	0.1896052	109
22	0.0564888	0.0940167	0.6246728	15	79	0.0834178	0.0618059	0.4255908	63
23	0.0390895	0.1110634	0.7396688	3	80	0.1055267	0.0452479	0.3001031	94
24	0.0315074	0.1299327	0.8048355	1	81	0.089906	0.0585868	0.3945431	73
25	0.0473073	0.1059323	0.6912856	8	82	0.0994516	0.0478414	0.3248045	92
26	0.0489572	0.1058873	0.6838297	9	83	0.1241631	0.0229637	0.1560809	111
27	0.0396543	0.1113491	0.7373948	5	84	0.037152	0.1052856	0.73917	4
28	0.0500005	0.0968215	0.6594481	11	85	0.0893744	0.0524652	0.3698912	83
29	0.0443975	0.1016161	0.6959359	7	86	0.0793586	0.0669382	0.4575506	48
30	0.0538841	0.0957658	0.6399325	14	87	0.0963858	0.0505848	0.3441831	86
31	0.0705878	0.0778838	0.5245704	31	88	0.0727595	0.0799568	0.523564	32
32	0.0713599	0.0732274	0.5064581	41	89	0.0616515	0.0861898	0.5829887	20
33	0.0457367	0.1085538	0.7035674	6	90	0.0667005	0.0775363	0.5375628	28
34	0.0501116	0.0975976	0.6607416	10	91	0.0509914	0.0911691	0.6413112	13
35	0.0896228	0.0544558	0.377959	78	92	0.0640894	0.0796283	0.5540604	25
36	0.0920447	0.0545287	0.3720232	82	93	0.0834273	0.0644108	0.4356847	59
37	0.1252584	0.0179122	0.1251107	113	94	0.0597146	0.0822288	0.5793071	21
38	0.1005159	0.0435669	0.3023737	93	95	0.0713932	0.0733466	0.5067477	40
39	0.0878056	0.0579188	0.3974542	72	96	0.0781078	0.0704075	0.4740759	45
40	0.0798375	0.0680676	0.4602114	47	97	0.0650488	0.0767229	0.5411721	26
41	0.1066198	0.039554	0.2705957	102	98	0.0846933	0.0592473	0.4116092	67
42	0.0916989	0.0551946	0.3757456	79	99	0.0901177	0.0558099	0.3824491	77
43	0.136071	0.0098432	0.0674589	114	100	0.0861161	0.0568252	0.3975423	71
44	0.1006423	0.0419699	0.294294	96	101	0.0653655	0.0828926	0.5591101	24
45	0.0856352	0.0601915	0.4127604	66	102	0.0710811	0.0736922	0.5090181	38
46	0.0892766	0.0529024	0.372083	81	103	0.0603496	0.0893566	0.5968799	19
47	0.0880585	0.058519	0.3992358	70	104	0.049937	0.0938052	0.6525936	12
48	0.0628633	0.0802839	0.5608483	23	105	0.0553096	0.0905134	0.6207074	17
49	0.0841383	0.0651098	0.4362523	58	106	0.070125	0.0740256	0.5135296	35
50	0.0741221	0.0710364	0.4893713	43	107	0.0540312	0.0895076	0.6235775	16

Table 5 (Continued)

Genotype	Di+	Di–	SIIG	Rank	Genotype	Di+	Di–	SIIG	Rank
51	0.095367	0.0469196	0.3297541	91	108	0.0781789	0.0650732	0.4542565	49
52	0.0813647	0.0612509	0.4294823	61	109	0.0302996	0.1147768	0.7911476	2
53	0.0814525	0.0651586	0.4444315	53	110	0.0826142	0.0640771	0.4368156	57
54	0.0686948	0.0744001	0.5199356	34	111	0.0942866	0.0506162	0.3493114	85
55	0.0811105	0.0633917	0.4386901	56	Barzegar	0.0708685	0.0834654	0.5232173	33
56	0.0787962	0.0765467	0.4927597	42	Narin	0.0707589	0.0776502	0.5408106	27
57	0.0704301	0.0741863	0.5129869	36	Sistan	0.084308	0.0732816	0.4650154	46

der normal conditions, 1000-seed weight, day to panicle, spike length, plant height, and the number of seeds per spike affect seed yield. Traits affecting seed yield under salinity stress included 1000-seed weight and seed weight per spike and in drought stress conditions 1000-seed weight, number of days to ripening, spike length, plant height, and spike weight. Based on the R2 coefficient, these traits explained 31.83, 30.41, and 39.33% of seed yield changes under normal conditions, salinity stress, and drought stress, respectively.

Experiment with the Main Components

The results of principal components analysis in Table 4 show that the first two components in all three conditions of normal, salinity, and drought had specific values equal to and greater than 0.5, which in total 73.78, 77.91, and 77.15% of the changes. Ali et al. (2021), In the experiment on wheat lines, the estimated variables in wheat were grouped into three main components that explained 86.95% of the changes in total seed yield.

Classification of Genotypes

Based on this, the genotypes studied in this study were classified and genotypes 24, 109, 23, 84, 27, 33, 29, 25, 26, 34, 28, 104, 91, 30, 22, 107, 105, 9, 103 and 89 were ranked as 1–20 as the top twenty genotypes, respectively. Genotype 24 with the lowest distance from the positive ideal genotype (di = 0.0315) and the highest distance from the non-ideal genotype (di = 0.129) was recognized as the highest and closest genotype to the ideal genotype. Narin, Barzegar, and Sistan control genotypes also ranked 27th, 33rd, and 46th, respectively (Table 5). The performance of selected genotypes under drought and normal stress conditions is shown in Fig. 1. Based on this index, genotype 24 with yields of 11,000 and 5400 kg/ha had the highest stress tolerance index (1.86) for normal conditions and drought stress, respectively. Genotypes 23, 25, and 33 also had a high STI index and had good yields under drought stress conditions. Based on this index, genotypes with higher STIs are selected in the screening process, so genotypes with


Fig. 1 Graphic display of biplot based on seed yield of wheat genotypes under drought and normal stress conditions. Hollow circles indicate the yields of genotypes under normal conditions and solid circles indicate yields under drought stress conditions
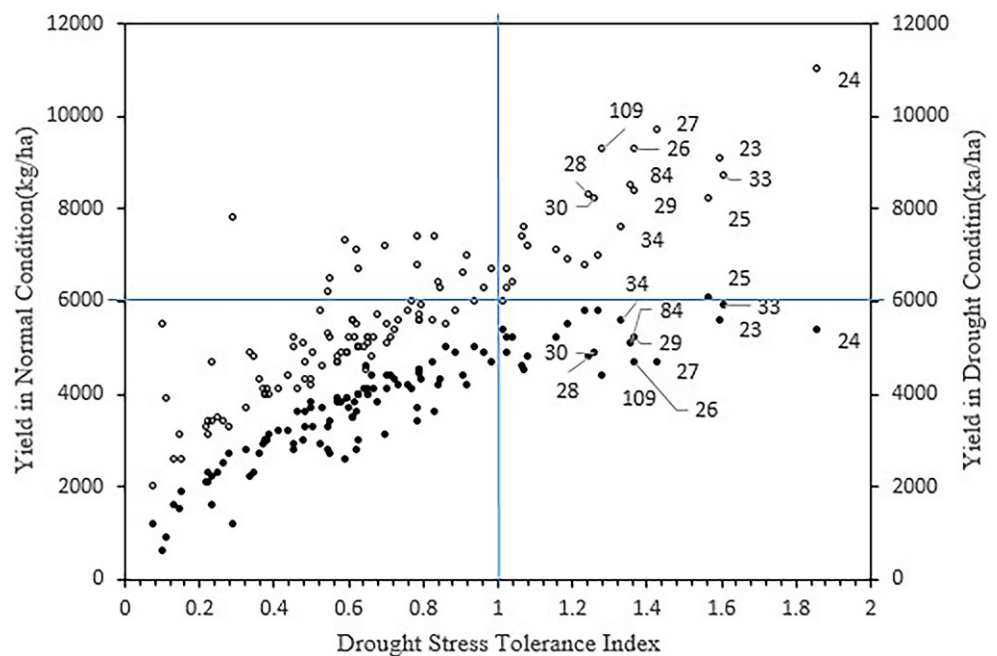
Fig. 2 Graphic display of bi-plot based on seed yield of wheat genotypes under salinity stress and normal conditions. Hollow circles indicate the yields of genotypes under normal conditions and solid circles indicate yields under salinity stress
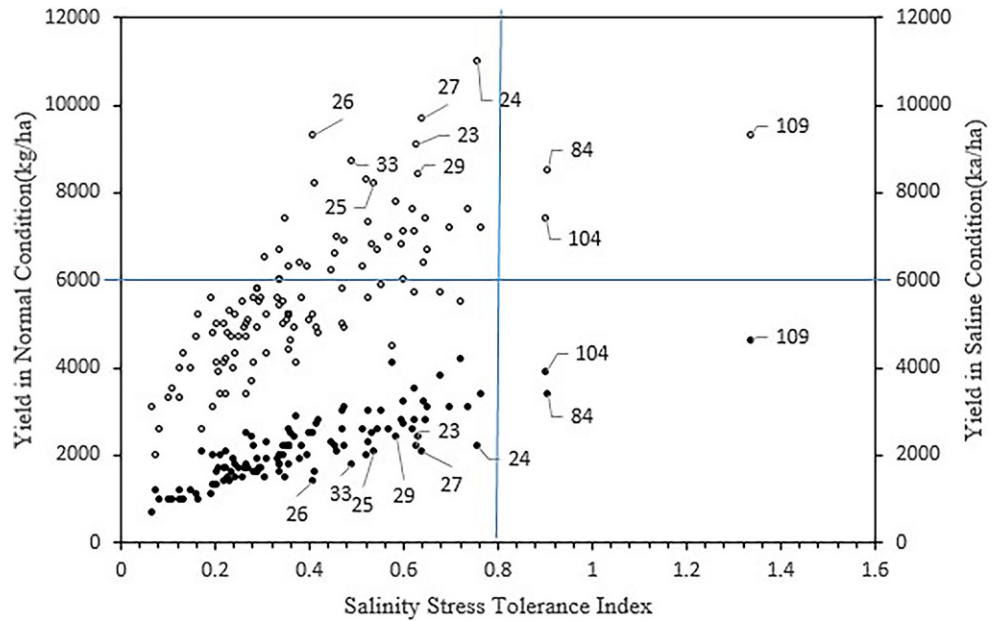
Fig. 3 Graphic display of biplot based on seed yield of wheat genotypes under stress and normal conditions
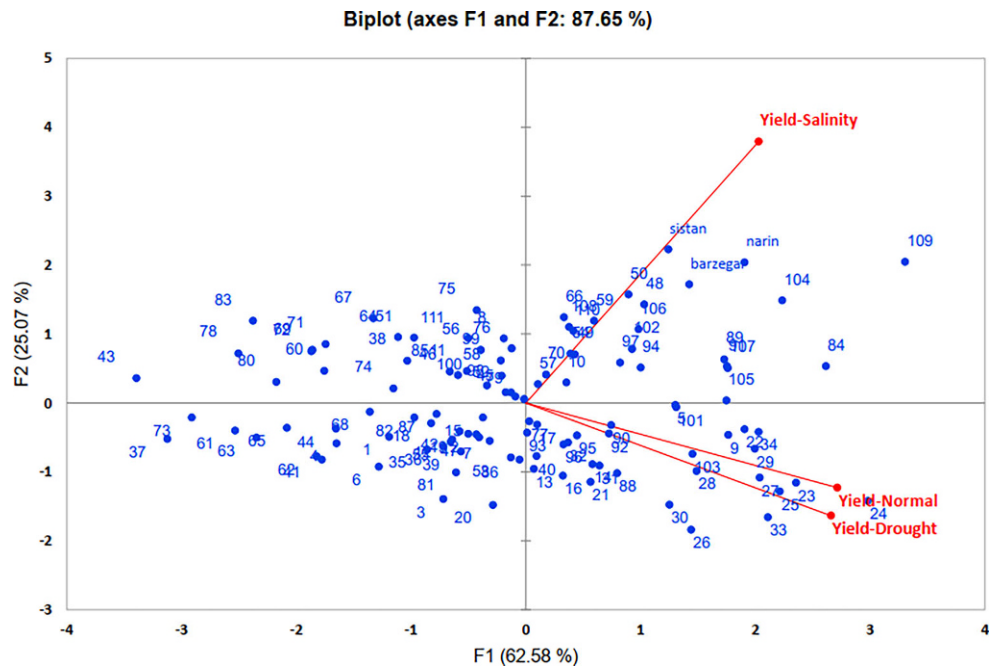
a higher right quadrant in the biplot diagram will be more appropriate (Fig. 1).

STI stress tolerance index was also calculated in the studied genotypes for salinity stress conditions, which is shown in Fig. 2 as a bi-plot diagram. Based on this index, genotype No. 109 with yields of 9300 and 4600 kg/ha had the highest STI index (1.34) under normal conditions and salinity stress, respectively. The position of genotypes No. 104 and 84 in Fig. 2 also indicates the suitability of these cultivars for salinity stress conditions. A comparison of Figs. 1 and 2 shows that the genotypes selected under drought stress conditions are not necessarily suitable for

salinity stress conditions. As shown in Fig. 2, most genotypes that performed well under drought stress conditions had lower yields under salinity stress conditions.

The conformity of Figs. 1 and 2 with the bipolar graphic diagram (Fig. 3) showing the distribution of dots indicates the same results for the selection of drought-tolerant and salinity tolerant genotypes.

Discussion

Arshad et al. (2019), in the sieve of wheat salinity tolerant genotypes, estimated the intensity of SI stress at 0.40 and assessed it as severe stress. Considering that salinity stress was applied from the beginning of cultivation with saline water of 10 dS/m and drought stress was done by stopping irrigation in the post-flowering stage, so calculating the stress intensities of 0.62 and 0.33 for salinity and drought is reasonable. This indicates that the plants have spent most of their growth period under salinity stress and important and effective periods in yield under drought stress. Under these conditions, the plants use the energy produced to maintain the vegetative organs, so the reduction in yield under salinity stress can be attributed to the high accumulation of ions inside the plant and ion toxicity, closure of pores, reduction of leaf area and reduced photosynthetic activity. Also, under salinity and drought stress, a large amount of photosynthetic material in the plant is used to make organic matter for osmotic regulation and a lot of energy is used in this way to deal with the adverse effects of salinity and drought stress by the plant. Decreased energy in the plant reduces the active absorption of various elements and reduces the efficiency of the roots in providing nutrients and water to other organs, followed by reduced growth of shoots and reduced dry matter production (Marschner 2012). Under normal conditions, the correlation between seed yield and 1000-seed weight, seed weight per spike, and spike weight are positive and significant. Under drought stress conditions, the correlation between seed yield and number of days to maturity, seed weight per spike, number of seeds per spike, and spike weight was positive and significant. Under salinity stress, the correlation between seed yield and seed weight per spike, number of seeds per spike, and spike weight were positive and significant. Based on the correlation coefficients in drought and normal stress conditions, there is a significant negative correlation between seed yield and plant height and in salinity stress conditions, this correlation is negative but insignificant. The correlation between seed yield and many other traits was significant. These traits included a number of days to maturity, spike length, seed weight per spike, seed number per spike, number of spikelets per spike, and spike weight. This correlation was almost established in control cultivars, while in Barzegar and Sistan cultivars, the correlation between seed yield and 1000-seed weight was positive and significant. Also, Fouad (2018) in normal irrigation conditions, positive correlation between seed yield with the number of spikes per square meter (0.332), the number of seeds per spike (0.425) and the weight of 100 seeds (0.385) and under drought stress, the phenotypic correlation between seed yield and the number of seeds per spike (0.832) was positive and significant. Arminian and Houshmand (2017), In examin-

ing the role of yield components of wheat genotypes, stated that there was a positive and significant correlation between seed yield and number of seed per spike, harvest index, the number of fertile fives, and flag leaf width and also a high negative correlation between yield and total tiller number, plant height and number There are knots. Therefore, the estimation of correlation and regression analysis between yield and yield components may lead to the effective selection of criteria to improve wheat seed yield. Hosseinpanahi et al. (2011), Experiments showed that in wheat, maintaining more spikes per unit area and producing a higher number of seed per spike is one of the most important factors in the superiority of drought-tolerant cultivars over susceptible cultivars. Nasri et al. (2012), stated that stepwise regression can be used to eliminate the inefficient effects on seed yield in the regression model. Narjesi et al. (2010), In an experiment, showed that under normal conditions, biological yield traits and harvest index played a significant role in seed yield. Traits affecting yield under stress conditions also included biological yield, harvest index, spike length, and 1000-seed weight. The applied principal component analysis (PCA) method allows a complex evaluation of the relationships between features. Therefore, principal component analysis was used to obtain the share of each trait in total diversity, reduce the amount of data and better analyze the relationships between traits. The suitability of the data for component analysis was determined using the KMO test and SPSS software and components with specific values greater than 0.5 were selected. In an experiment conducted by Rymuza et al. (2012), they found the possibility of reducing the seven main traits to three new variables, which included more than 75% of the input data from direct planting and approximately 80% from conventional tillage. Thus, under normal conditions, salinity and drought, seed yield was in the first component and other traits of seed weight per spike, number of seed per spike, number of spikelet per spike, the weight of spike in the first component, day to flowering, day to ripening and Spike length in the second component, plant height in the third component and 1000-seed weight in the fourth component had a good correlation. Under salinity stress, seed yield, 1000-seed weight, day to flowering, day to ripening and spike length in the first component, plant height, number of seed per spike and seed weight per spike in the second component and number of spikelet per spike and Spike weight of the fourth component and in drought stress conditions, seed yield, seed weight per spike, number of seed per spike and spike weight in the first component and rosette flowering, rosette ripening and Thousand-seed weight in the second component and spike length and number of the spikelet in Spike in the third component and plant height trait in the fourth component. Beheshtizadeh et al. (2013), by analyzing the main components in some bread wheat

genotypes under normal conditions, reported the existence of four main components explaining the traits, so that in the first component the number of seeds per spike, the number of spikelet per spike, in the second component the weight of the trait height and in the second component Thousands of seed explained seed yield. The genotypes studied in this study were ranked based on the Ideal Genotype Selection Index (SSIG). The SSIG value varies between zero and one, and the closer the desired genotype is to the ideal genotype, the closer the SIIG value will be to one, and genotypes with an index value close to zero are considered the weakest genotypes (Zali et al. 2015). In this method, the best genotype is the closest genotype to the ideal genotype and the farthest from the non-ideal or weak genotype. The results of genotype classification also confirmed the results of biplot analysis of factor analysis. Thus, most of the known best genotypes were identified as superior genotypes using the SIIG index in the biplot method. in addition to the SIIG index, the STI index was also used as a stress tolerance index under drought and salinity stress conditions. In the screening of salt-tolerant sugar beet genotypes, this method was used to select superior lines (Anagholi et al. 2018). Arshad et al. (2019) also introduced STI, GMP, and MP indices as the most important indicators related to seed yield in the screening of salt-tolerant wheat genotypes.

Conclusion

According to the results of this experiment, the best genotypes for salinity stress are 84, 104, and 109 and the best genotypes for drought stress conditions are 9, 22, 23, 24, 25, 26, 27, 28, 29, 30, 33, 34, 89, 91, 103, 105, 107 and 109. Genotype 109 was selected for both salinity and drought conditions, but other genotypes are not common. Figure 1 does not show the number of some selected genotypes for drought stress to avoid further crowding, which includes numbers 9, 22, 89, 91, 103, 105, and 107, which are located in the upper and right quarters and below genotype 30. These genotypes were selected through modified Balk breeding method and the preliminary tests were also carried out with high precision in different non-stress conditions and drought and salt stress, so we can confidently use the selected genotypes for additional tests and introduction of the line.

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