GRAPHIC ANALYSIS OF TRAIT RELATIONS OF IRANIAN BREAD WHEAT GERMPLASM UNDER NON-SALINE AND SALINE CONDITIONS USING THE BIPLOT METHOD

Amir GHOLIZADEH and Hamid DEHGHANI,*

Plant Breeding and Biotechnology Department, Faculty of Agriculture, Tarbiat Modares University, Tehran, Iran

Gholizadeh A. and H. Dehghani (2016): *Graphic analysis of trait relations of Iranian bread wheat germplasm under non-saline and saline conditions using the biplot method.*- Genetika, Vol 48, No. 2, 473 -486.
Salinity is one of the most important factors that limit crop production in some regions of the world. Knowledge of the interrelationships between yield and its components will improve the efficiency of breeding programs especially under saline conditions through appropriate selection criteria. This study demonstrated that GT biplot was an excellent tool for visual evaluation of superior genotypes, traits and grouping of them with other statistical techniques. The study was conducted under both saline and non-saline conditions in field based on randomized complete block design with three replications. Electrical conductivity of irrigation water were 2 and 10 $dS.m^{-1}$ in non-saline and saline conditions, respectively. The obtained data were analyzed using a genotype $\times$ trait (GT) biplot method based on site regression model. The biplot vector view indicate that there was a strong positive association between PH and BY with seed yield in both non-saline and saline conditions. It seems that PH and BY traits can be used as selection criterion for improving of seed yield in wheat breeding programs, especially under stress conditions in the field. Also among 41 studied genotypes, genotype 32 had good characteristics regarding high seed yield and salt tolerance.
Keywords: Biplot, Salinity, Seed yield, Site regression.

INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is one of the important crops that is faced with types of environmental stresses including salt stress. Increasing production of bread wheat under environmental stress conditions has been become important in recent years (DEHGHANI *et al*., 2012a). Salinity is one of the major environmental stresses across agricultural regions of worldwide which can severely limit growth and cereal production (ROYO and ABIO, 2003; COLMER *et al*., 2006; ROZEMA and FLOWERS, 2008). Iran is one of countries that has suffered from severe salinity problems. For example 44 million hectares of total land area in Iran has become salt

_____

Corresponding author: Hamid Dehghani, Plant Breeding and Biotechnology Department, Faculty of Agriculture, Tarbiat Modares University, Tehran, Iran, Email: dehghanr@modares.ac.ir. Phone: +98 912 5144820. Fax: +98 48292040

affected to varying degrees (HOUSHMAND *et al.*, 2005). Improving the salt tolerance of crop proves the first way to overcome the limitation of crops production in a salinized area. Wheat is a moderately salt-tolerant crop (MASS and HOFFMAN, 1997) and is as a main food in 43 countries (PERVAIZ *et al.*, 2002). Therefore, it is necessary to increase wheat production by raising the wheat seed yield. On other hands, the most efficient way to increasing of wheat yield is improvement for salt tolerance because increasing the salt tolerance of wheat genotypes is very less expensive for farmers in developing countries than using management methods leaching salt from the soil surface and salinity management through reclamation or improved irrigation techniques (ASHRAF and WU, 1994; SHANNON, 1997). Generally, plant breeding is as a complementary and a more stable approach for decreasing the deleterious effects of salinity, with the development of cultivars that can grow and produce appropriate yield under saline conditions (FLOWER and YEO, 1995; SHANNON, 1997). Screening is one of the essential stages of the breeding programs and various screening and selection designs have proposed for salt tolerance improvement in wheat and others crops (KINGSBURY and EPSTEIN, 1984; KELMAN and QUALSET, 1991; PECETTI and GORHAN, 1997). Some factors, such as the lack of effective evaluation methods for salt tolerance to screening the wheat genotypes in breeding programs, low selection efficiency using agronomic parameters, and a complex phenomenon involving morphological, physiological and biochemical parameters between genotypes is inhibited improving salt tolerance of wheat genotypes (ZENG *et al.*, 2002). Improving the seed yield of wheat is always the final and major target in plant breeding. So, the evaluation of growth parameters determining seed yield and final seed yield is a critical aspect of breeding programs. On other hands, Yield is a complex quantitative trait, considerably affected by environment and usually has a low heritability (SABAGHNIA *et al.*, 2010). Therefore, selection of genotypes based on yield is not effective. On the other hand, Morphological traits and related characters with seed yield due to easy measurement and high heritability can be used as criteria for distinguish salinity tolerant plants and for improvement of seed yield in wheat genotypes especially under salt stress conditions. Plant breeders, commonly prefer yield components that indirectly increase seed yield (YASIN and SING, 2010). Therefore, there is necessary to examine the relationships between various traits, especially between seed yield and other traits (DEHGHANI *et al.*, 2012b). Biplot is a graphical tool for breeders and is a plot that simultaneously displays the effects of traits and genotypes. The biplot was originally proposed by GABRIEL (1971) as a graphical tool to present results from principal component analysis (PCA). The GGE biplot is the most commonly used and most useful type of biplot. The GGE biplot methodology was developed by YAN *et al.* (2000) for graphical analysis of genotype by environment data or multi-environment trials (MET) data.

The GGE biplot has been recognized as an innovative methodology in biplot graphic analysis to be applied plant breeding (BALESTRE *et al.*, 2009). Generally, GGE biplot is constructed by plotting the first two principal components (PC_1 and PC_2) derived from singular value decomposition of the environment-centered data. Although GGE biplot procedure was proposed firstly for analyzing multi-environment trial data (YAN *et al.*, 2000) but it can also be equally used for all types of two-way data that genotype × trait (GT) structure. Many researchers have used it to study of the GT data in different crops (YAN and RAJCAN, 2002; RUBIO *et al.*, 2004; DEHGHANI *et al.*, 2008; DEHGHANI *et al.*, 2012a). The GT biplot is one of the applications of the GGE biplot technique to study of the GT data. Also, GGEbiplot as a graphical tool of effective displays the GT dataset, permits the visualization of the associations between traits across the genotypes and shows the trait profile of the genotypes (YAN and KANG, 2003; RUBIO *et al.*, 2004; DEHGHANI *et al.*, 2008).

This study indicated that the GT biplot was an excellent tool for visualizing GT data. This study demonstrated that GT biplot was an excellent tool for visual evaluation of superior genotypes, traits and grouping of genotypes and traits compared with statistical techniques such as linear correlations and other complex methods like path coefficient analysis.

The objectives in research was to evaluate bread wheat genotypes by traits interaction in the non-saline and saline conditions and to study the interrelationships between traits using GT biplot procedure for identifying traits and genotypes which may be useful in breeding programs.

MATERIALS AND METHODS

Plant material

Forty one genotypes of bread wheat (*Triticum aestivum* L.) were used (Table 1) which are commercial wheat genotypes cultivated in different parts of Iran. All wheat genotypes were selected from the germplasm collection at the Iranian Institute of Seed and Plant Improvement Institute (SPII), Karaj, Iran.

Table 1. The codes and name of bread wheat genotypes

Genotype Codes	Genotype names	Genotype Codes	Genotype names
G1	AKBARI-N	G22	MARUN
G2	Alborz	G23	MIHAN
G3	ARUM	G24	MOGHAN1
G4	AZADI	G25	MORVARID
G5	BAM	G26	MV17
G6	BAYAT	G27	NIKNEJAD
G7	BAZ	G28	OMID
G8	BC_RUSHS	G29	PARSI
G9	BC_RUSHW	G30	PISHTAZ
G10	BEZOSTAY	G31	RASUL
G11	FALAT	G32	RUSHAN
G12	GASPARD	G33	SARDARI
G13	HIRMAND	G34	SAYSON
G14	INIA	G35	SEPAHAN
G15	KARACHIA	G36	BUMI YAZD
G16	KARAJ1	G37	SHAHRYAR
G17	KARAJ3	G38	SISTAN
G18	KAVEH	G39	TABASI
G19	KAVIR	G40	VIRINAK
G20	KHAZAR1	G41	ZARIN
G21	KRASSHAH		

Field experiments

The experiments were carried out during 2011-2012 growing seasons at two non-stress and stress location on the research field of the National Salinity Research Center (NSRC) at Yazd, Iran (31°86′N, 53°95′E, 1609 a.m.s.l). Before starting the experiments was conducted sampling in the surface layer of soil (0-30 cm depth) in both conditions. The non-saline field had pH = 7.2-7.6, EC = 2.8-2.9 dS.m^{-1} and the saline field had pH = 4.9-5.2, EC = 8.6-8.8 dS.m^{-1}. The salinity of water used in irrigation in saline and non-saline condition was 10 and 2 dS.m^{-1}, respectively. To determine the salinity of soil during growth season, sampling has been done from the depth of 0-30, 30-60, 60-90. The average of salinity rate during growth season in saline and non-saline condition was 9.5 and 2.7 dS.m^{-1}, respectively. Soil pH was measured in 1:2.5 soil/water suspension with a digital pH meter (Model 671, Metrohm AG Herisau Switzerland) (THOMA, 1996) and the electrical conductivity (EC) was measured in 1:2.5 soil/water suspension with an EC meter (Model Ohm-644, Metrohm AG Herisau Switzerland) (RHOADES, 1996).

A randomized complete block design with three replications was used at both field sites. Each plot consisted two rows 20 cm apart and 2 m in length. Nitrogen, P and K fertilizers were applied based on the soil test and the Iranian Soil and Water Institute (ISWI) recommendation model (MILANI *et al*., 1998). A total of 150 kg N ha^{-1} each time at sowing, top-dressed at tillering stage and at the start of podding. Other fertilizers were applied before plowing at the recommended rates of 115 kg P_2O_5 ha^{-1} and 80 kg K_2SO_4 ha^{-1}. Weeds were controlled by hand as needed. Sixteen traits were measured on 41 genotypes of the two trials. Data were recorded on five randomly selected plants from each plot. The traits were plant height (PH), spike weight (SW), seed weight per spike (SPS), number of seed per spike (NSP), number of spikelet per spike (NSPS), peduncle weight (PW), spike length (SL), peduncle length (PL), days to heading (DH), days to maturity (DM), number of fertile tiller (NFT), grain yield (GY), biological yield (BY) were recorded. The harvest index (HI) was calculated as the ratio between grain yield and biological yield. The 100-seed weight (TSW) was measured on a sub-sample of seed harvested from each plot. The chlorophyll content (CHL) of base, middle and tip (MUNNS and JAMES, 2003) of the third leaves was measured using a SPAD-502 chlorophyll meter (Minolta, Japan) which provides rapid and non-destructive measurements of leaf chlorophyll content.

Statistical Methods

The GT biplot method (YAN and RAJCAN, 2002) based on GGE biplot methodology which base on site regression (SREG) strategy (YAN *et al*., 2000) was used to investigate to GT interaction in two-way dataset. The used statistical model is based on the following formula:

$$\frac{\alpha_{ij} - \beta_j}{\sigma_j} = \sum_{n=1}^{2} \lambda_n \xi_{in} \eta_{jn} + \varepsilon_{ij} = \sum_{n=1}^{2} \xi_{in}^* \eta_{jn}^* + \varepsilon_{ij}$$

where α_{ij} is the mean value of genotype *i* for trait *j*, β_j is the mean value of all genotypes in trait *j*, σ_{ij} is the standard deviation of trait *j* between the genotype means, λ_n is the singular value for principal component n, ξ_{in} and η_{jn} are scores for genotype *i* and trait *j* on principal component n, respectively, and ε_{ij} is the residual associated with genotype *i* in trait *j*. To achieve trait-focused scaling among the genotype scores and the trait scores the singular value λ_n has to be absorbed by

the   singular   vector   for   genotypes ξ_{in} and   that   for   trait λ_{jn}.   That   is,

$$\xi^*_{in} = \lambda_n^{0.5} \xi_{in} \, and \, \eta^*_{jn} = \lambda_n^{0.5} \eta_{jn}.$$

Only PC$_1$ and PC$_2$ are retained in the model and such a model tends to be the best for extracting pattern and rejecting noise from the data. Also, in the GT biplot, a vector is drawn from the biplot origin to each marker of the traits to visualization of the association between the traits. The correlation coefficient between any two traits is approximated by the cosine of the angle between their vectors, the vector view of biplot is the best way for graphical display interrelationships among traits (YAN & RAJCAN 2002). Two traits are positively correlated if the angle between their vectors is < 90°, negatively correlated if the angle is >90°, independent if the angle is 90°. Traits with longer vectors are more responsive to the treatment combinations; traits with shorter vectors are less responsive to the genotypes; and those located at the biplot origin are not responsive at all (YAN and RAJCAN, 2002).

Simple linear correlation coefficients between all possible combinations of traits were worked out according to Snedecor (SNEDECOR, 1957). All biplots were generated using GGEbiplot software and further information on GGE biplot methodology and GGEbiplot package are available at http://www.ggebiplot.com.

RESULTS

The GT biplot for dataset explained 64.3% (41.3% and 23% by PC1 and PC2, respectively) of the total variation of the standardized data in the non-saline conditions (Figure 1). This relatively moderate percentage indicates the complexity of the relationships between the measured traits. FLORES et al. (1998), YAN and KANG (2003), RUBIO et al. (2004), DEHGHANI et al. (2008), DEHGHANI et al. (2012a) represent that the fundamental patterns between the traits should be captured by the biplot. The biplots present data of 41 genotypes determined for sixteen traits under both non-saline and saline conditions in field. The measured traits were including grain yield, PH, SW, SPS, NSP, NSPS, PW, SL, PL, DH, DM, NFT, CHL, TSW, BY and HI. Among different ways to use a GT biplot, the polygon view helps identify genotypes with the highest values for one or more traits (DEHGHANI et al., 2012b). It provides the best way for visualizing the interaction patterns among treatment and genotypes and to effectively interpret a biplot (YAN and KANG, 2003; DEHGHANI et al., 2012a). For this purpose, the lines that are connected with straight lines so that a polygon is formed with all other lines contained within the polygon. According to polygon view of the dataset there are eight vertex genotypes in the non-saline conditions (Figure 1) which are genotypes 26, 17, 41, 32, 40, 7, 31 and 34. Since these genotypes had the longest distance from the origin of biplot are as the best genotypes in some or all of the traits. Therefore, it seems that genotype 32 had the highest values of grain yield (GY) in the non-saline conditions. Also, genotype 32 had the highest values for BY, PH, NFT, PL, TSW and PW traits (Figure 1).

Among 41 studied genotypes in the non-saline conditions, genotypes 17 and 41 were the most favorable genotypes for NSPS, NSP and DM traits (Figure 1). Also, genotypes 26 and 34 have highest values for DH trait. On other hands, the vertex genotypes 40, 7 and 31 were favorable in none of the measured traits (Figure 1). It could be conclude that genotype 32 was the most favorable genotype in non-saline conditions.
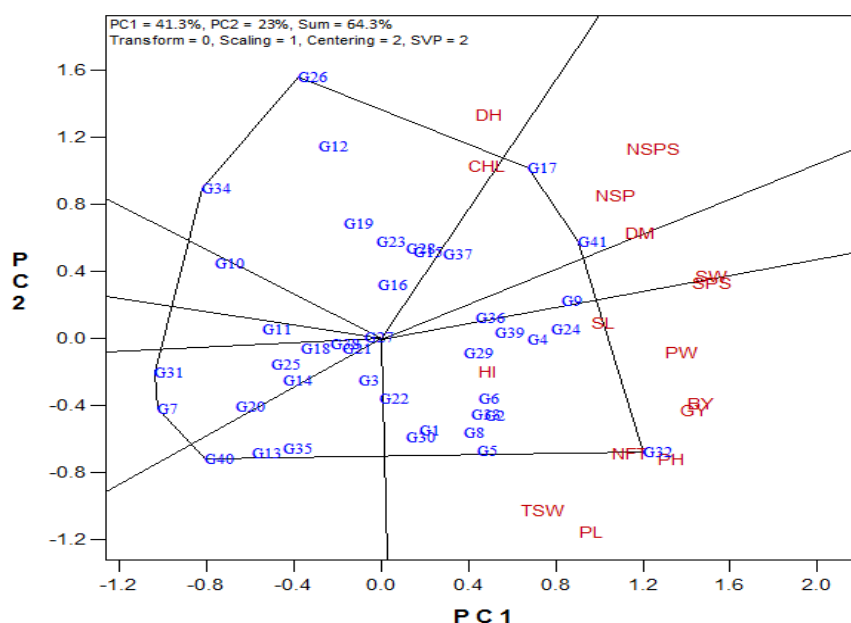
Figure 1. Bread wheat genotype by trait biplot polygon view for the whole dataset in non-sa condition, showing which genotype had the highest values for which traits.

In the saline conditions, the GT biplot for dataset explained 65.6% (38.6% and 27% by PC_1 and PC_2, respectively) of the total variation of the standardized data (Figure 2). This moderate percentage indicates the complexity of the relationships between the measured traits. According to polygon view of the dataset there are seven vertex genotypes in the saline conditions (Figure 2) which are genotypes 17, 32, 33, 13, 7, 25 and 12. These genotypes are the best genotypes in some or all of the traits in the saline conditions.

It seems that genotype 32 had the highest values of grain yield (GY) in the saline conditions. Also, genotypes 32 and 33 were the favorable genotypes for BY, PH, PL and TSW traits (Figure 2). The vertex genotype 17 was the most favorable genotype for NSPS, DH, CHL, DM and PW traits (Figure 2). Also, vertex genotype 13 had the highest values of (HI) in the saline conditions. The vertex genotypes 7, 12 and 25 were favorable in none of the measured traits (Figure 2). Generally, it could be conclude that genotype 32 was the most favorable genotype in saline conditions. So, the genotype 32 can be recommended for cultivation in the saline environments.

In order to determine relationship between traits was used the vector view of GT biplot. The vector view is one of the applications of the GT biplot to study the relationships between and among traits. In the vector view of the GT biplot, a vector is drawn from the biplot origin to each marker of the traits to facilitate visualization of the relationships between and among the traits (YAN and RAJCAN, 2002).
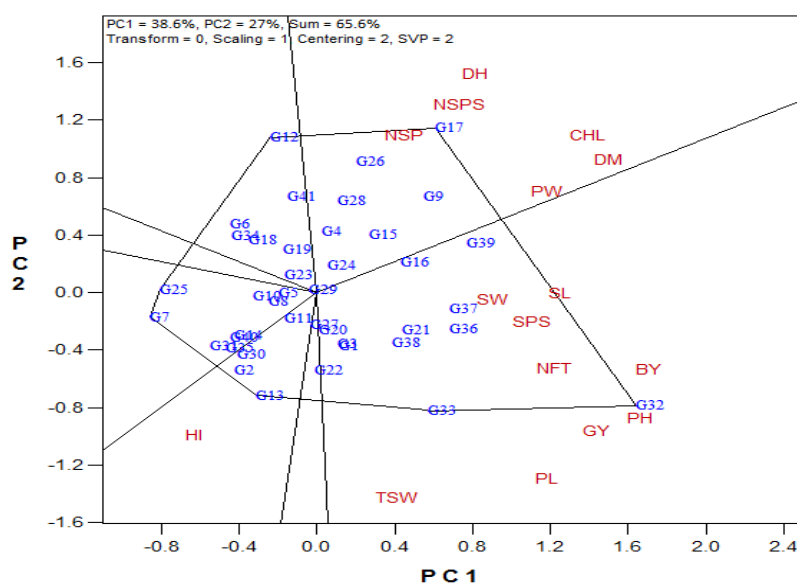
Figure 2. Bread wheat genotype by trait biplot polygon view for the whole dataset in saline condition, showing which genotype had the highest values for which traits.

Table 2. Pearson's correlation coefficients between different traits of 41 bread wheat genotypes in the non-saline conditions.

Trait[a]	NSP	NFT	NSPS	TSW	SPS	PW	SW	CHL	PH	DH	DM	SL	PL	HI	GY
NFT	-0.01[b]														
SNPS	0.65	0.16													
TSW	-0.24	0.40	-0.21												
SPS	0.72	0.29	0.57	0.38											
PW	0.22	0.35	0.32	0.40	0.49										
SW	0.75	0.26	0.59	0.32	0.97	0.54									
PH	0.21	0.12	0.38	-0.22	0.09	0.32	0.12								
CHL	0.08	0.56	0.30	0.38	0.34	0.55	0.33	-0.06							
DH	0.14	-0.10	0.57	-0.25	0.17	0.17	0.15	0.41	0.02						
DM	0.17	0.29	0.50	0.18	0.39	0.53	0.38	0.38	0.32	0.70					
SL	0.28	0.30	0.45	-0.00	0.33	0.35	0.38	0.04	0.52	0.16	0.24				
PL	0.05	0.37	-0.05	0.37	0.16	0.53	0.20	-0.19	0.75	-0.36	0.05	0.31			
HI	0.34	0.11	-0.03	0.25	0.42	-0.03	0.37	-0.13	-0.09	-0.18	0.10	-0.26	0.11		
GY	0.31	0.52	0.29	0.27	0.47	0.40	0.45	0.00	0.56	0.05	0.44	0.25	0.47	0.41	
BY	0.27	0.63	0.37	0.21	0.39	0.48	0.41	0.16	0.63	0.05	0.40	0.33	0.51	0.15	0.90

[a]For trait abbreviations refer to text. [b]Critical values of correlation $P < 0.05$ and $P < 0.01$ (D.F. 39) are 0.39 and 0.30, respectively.

According to Figure 3 in non-saline conditions, there were high positive correlations between grain yield (GY) with BY, PH and NFT. The obtained results can be verified from the correlation data (Table 2). For example there was a strong positive relation (0.90[**]) between grain yield (GY) and BY, between grain yield (GY) and PH (0.56) and between grain yield (GY) and NFT (0.52[**]) in non-saline conditions (Table 2). Also, Figure 3 shows that there were positive correlation

between grain yield (GY) and PW, PL, SPS, SW, TSW, DM and NSP. There was an approximately zero correlations between grain yield (GY) with NSPS, CHL and DM as indicated by the rectangular angles between their vectors (r = Cos 90 = 0).
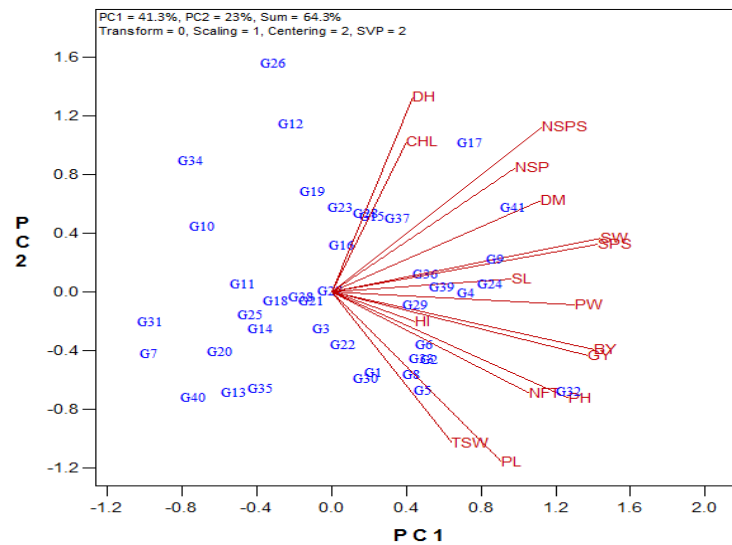

Figure 3. Bread wheat genotype by trait biplot vector view for the whole dataset in non-saline condition, showing the interrelationship among all measured traits.
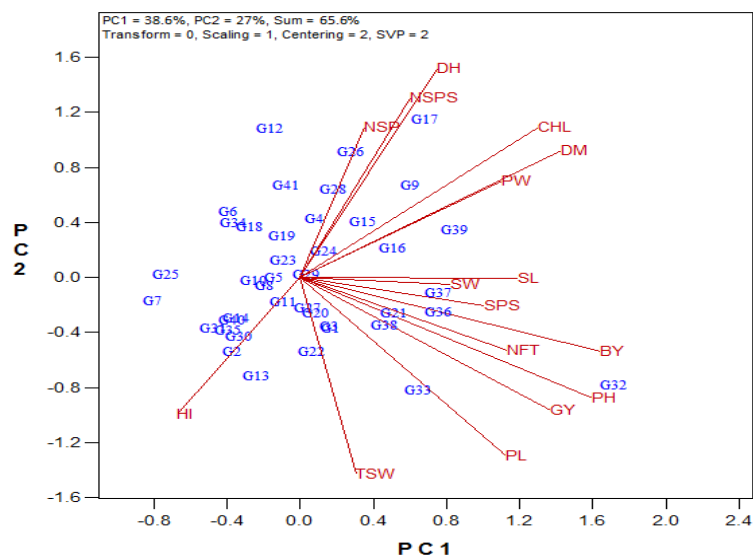

Figure 4. Bread wheat genotype by trait biplot vector view for the whole dataset in saline condition, showing the interrelationship among all measured traits.

The vector view in saline conditions (Figure 4) showed there were high positive correlations between grain yield (GY) with BY, PH and PL. Also, Fig. 4 shows that there were positive correlation between grain yield (GY) and TSW, NFT, SPS, SW and SL. There was an approximately zero correlations between grain yield (GY) with HI, CHL, PW and DM (Figure 4). On other hand, Figure 4 shows negative associations between grain yield (GY) with NSPS, NSP and DH in saline conditions. Most of the mentioned correlations can be verified from the correlation data (Table 3). For example there was a strong positive association (0.88**) between grain yield (GY) and BY and between grain yield (GY) and PH (0.60**) in saline conditions (Table 3). Most of the mentioned predictions for correlations could be verified from the original data but some are not consistent with the data because the biplot explains 64.3 and 65.6% rather than 100% of the total variation in in saline and non-saline conditions, respectively.

Table 3. Pearson's correlation coefficients between different traits of 41 bread wheat genotypes in the saline conditions.

Trait[a]	NSP	NFT	NSPS	TSW	SPS	PW	SW	CHL	PH	DH	DM	SL	PL	HI	GY
NFT	-0.17[a]														
SNPS	0.59	-0.02													
TSW	-0.55	0.36	-0.33												
SPS	0.54	0.19	0.32	0.28											
PW	0.29	0.18	0.31	-0.00	0.26										
SW	0.59	0.11	0.34	0.12	0.86	0.11									
PH	0.34	0.25	0.37	-0.29	0.22	0.44	0.24								
CHL	-0.19	0.44	0.03	0.37	0.26	0.25	0.16	0.18							
DH	0.16	-0.02	0.45	-0.35	-0.03	0.30	-0.05	0.59	0.01						
DM	0.09	0.32	0.36	-0.11	0.10	0.44	-0.01	0.67	0.36	0.77					
SL	-0.12	0.28	-0.01	0.03	-0.00	0.39	-0.07	0.25	0.62	0.18	0.40				
PL	-0.18	0.33	-0.18	0.38	0.27	0.16	0.19	0.01	0.82	-0.30	0.03	0.32			
HI	0.12	-0.13	-0.23	0.22	0.31	-0.37	0.20	-0.39	-0.18	-0.56	-0.45	-0.48	0.15		
GY	-0.00	0.35	-0.12	0.27	0.38	0.03	0.32	0.21	0.60	-0.08	0.23	0.24	0.58	0.15	
BY	-0.01	0.50	-0.00	0.15	0.25	0.17	0.25	0.41	0.64	0.11	0.45	0.36	0.52	-0.14	0.88

[a]Critical values of correlation $P < 0.05$ and $P < 0.01$ (D.F. 39) are 0.39 and 0.30, respectively.

A subset of the dataset can be analyzed by removing some of the genotypes or traits based on special purpose. Since seed yield and related characters with seed yield are important than other traits for selection genotypes, we removed other traits and the biplot was used based on in both traits (BY and PH) (Figure 5 and Figure 6) due to the high correlation in both traits (BY and PH) with seed yield in both non-saline and saline conditions.

According to the high correlation between seed yield with biological yield (BY) and plant height (PH) traits in both non-saline and saline conditions, the biplot was used based on in both traits (BY and PH) (Figure 5 and Figure 6). The mentioned GT biplot explained 83.6% (62.2% and 21.4% by PC_1 and PC_2, respectively) of the total variation of the standardized data. This relatively high percentage indicates the ability of this model and the importance of BY and PH traits compared with other related characters with seed yield. The Figure 5 indicated that there are six

vertex genotypes including genotypes 32, 6, 12, 34, 26 and 37. It seems that genotype 32 had the highest values for BY and PH in saline conditions and for PH in non-saline conditions. Also, the genotype 37 was the favorable genotype for BY and PH in saline conditions (Figure 5). The genotype 6 had the highest values for BY in non-saline conditions. The other vertex lines were not good in any trait (Figure 5). According to the vector view of GT biplot in Figure 6, there was a high positive correlation between BY and PH in saline conditions. Also found a positive correlation between BY and PH under non-saline condition (Figure 6). There was not almost any significant correlation between BY in the non-saline and saline conditions which indicates the selection of genotypes based on BY should be done in target environments.
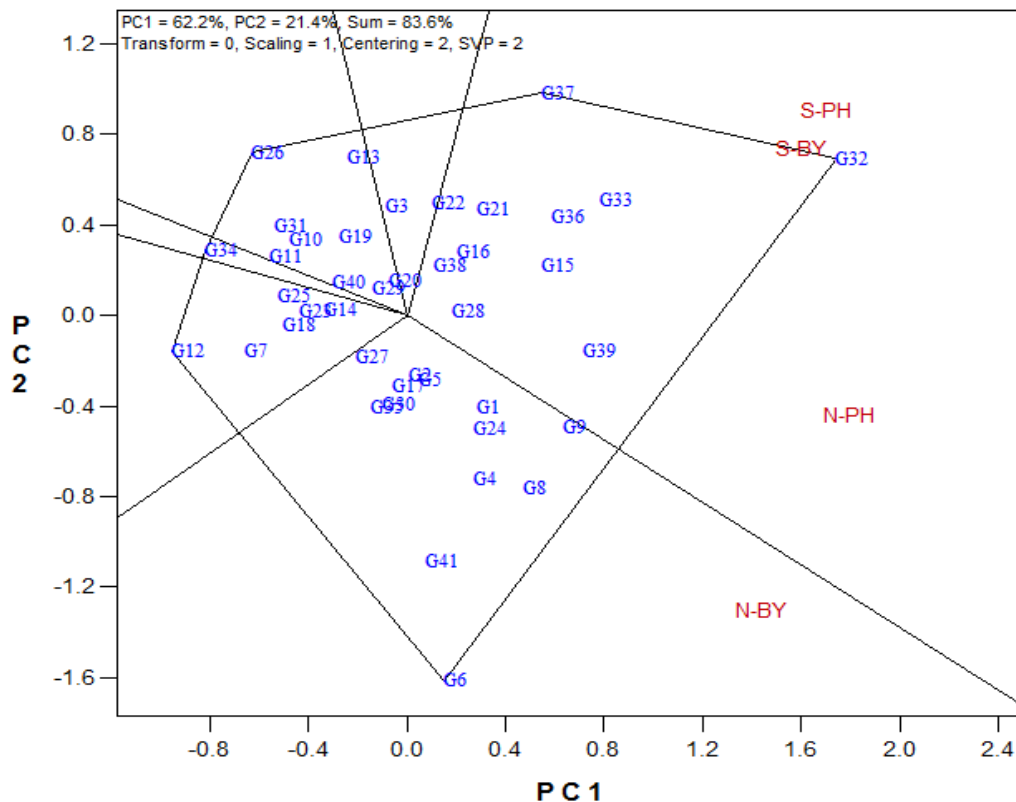

Figure 5. Bread wheat genotype by trait biplot polygon view for BY and PH traits in both non-saline and saline conditions, showing which genotype had the highest values for which traits.
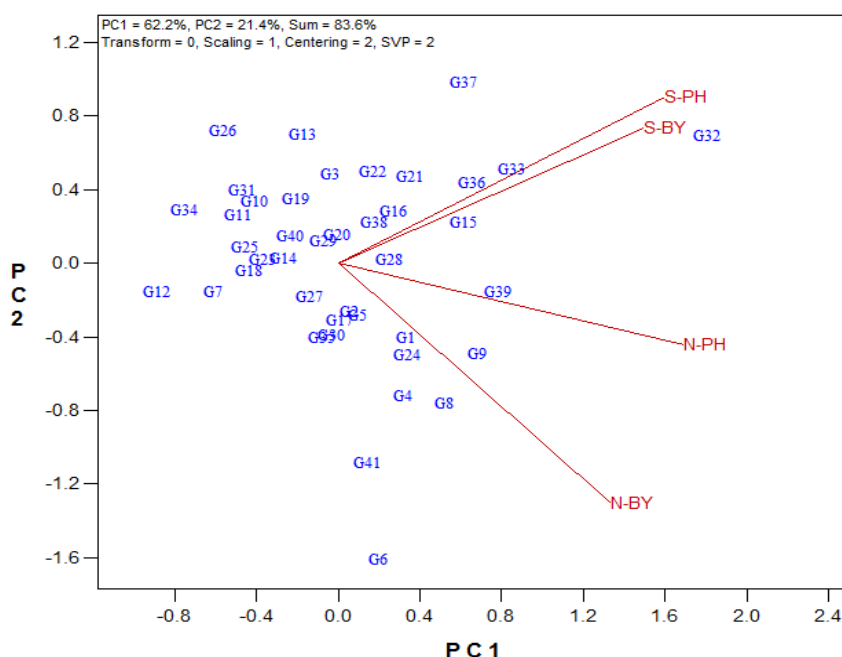
Figure 6. Bread wheat genotype by trait biplot vector view for BY and PH traits in both non-saline and saline conditions, showing the interrelationship among all measured traits.

DISCUSSION

Salt tolerance in bread wheat can be improved by exploiting genetic variation landraces. A degree of tolerance to salinity stress has been found in bread wheat germplasm, especially the landraces that can be used as parents in breeding programs to produce tolerant cultivars of bread wheat (MARTIN et al., 1994). Salt tolerance of crops may vary with their growth stage. However, a difference in the salt tolerance between genotypes may also occur at different growth stages. Therefore, the wheat genotypes must be evaluated at different growth stages regarding to salt tolerance. Most of the experiments are carried out under controlled condition. This is in spite of the fact that genotypic differences observed controlled conditions may not correspond to those observed at the adult stages in the field conditions (HOUSHMAND et al., 2005) because in controlled conditions the plants are not exposed with the conditions such as spatial and temporal heterogeneity of soil chemical and physical properties that prevail in salt affected field conditions (MUNNS and JAMES, 2003). Therefore, in order to evaluate the efficiently of screening methods for improving salt tolerance in crops, reassessment should be carried out under field conditions and at different growth stages (RICHARDS et al., 1987).

The approach used to improvement for salt tolerance for bread wheat should consider the key traits. The evaluation of final seed yield and growth parameters determining seed yield is a critical aspect of breeding programs. On the other hand, seed yield is a quantitative trait, which is largely influenced by the environment and usually has a low heritability. Therefore, selection of genotypes based on yield is not effective. On the other hand, the morphological traits and related characters

with seed yield due to easy measurement and high heritability can be used as criteria for distinguish salinity tolerant plants and for improvement of seed yield in wheat genotypes especially under salt stress conditions.

Knowledge of the interrelationships between yield and its components will improve the efficiency of breeding programs especially under salt stress conditions through appropriate selection criteria. A better understanding of relationships between traits can be obtained by using biplot method. It is clear that the biplot methodology is an excellent tool for visual data analysis. Almost all information contained ANOVA and multiple comparisons of treatment mean is graphically displayed in a GT biplot (DEHGHANI et al., 2008). The biplot approach has some advantages compared with conventional methods of data analysis (YAN and HUNT, 2002; YAN et al., 2007; SABAGHNIA et al., 2011). The first advantage of the biplot is graphical display of data, which largely enhances our ability to understand the patterns of the data. The second is that it is more interpretative and facilitates pair-wise genotype comparisons. The third advantage of the method is an excellent tool for visual evaluation of superior genotypes, traits and grouping of genotypes and traits compared with statistical techniques such as linear correlations and other complex methods like path coefficient analysis (SABAGHNIA et al., 2011; DEHGHANI et al., 2012b). This method for the evaluation of trait relations was used in different crops by YAN and RAJCAN (2002) in soybean, MA et al. (2004) in spring wheat, RUBIO et al. (2004) in white lupin, DEHGHANI et al. (2008) in rapeseed, DARVISHZADEH et al. (2010) in sunflower, DEHGHANI et al. (2012a) in bread wheat.

According to the results of GT biplot in study there was a high correlation between seed yield with biological yield (BY) and plant height (PH) traits in both non-saline and saline conditions. It seems that BY and PH traits are appropriate indices for salinity breeding programs and selection salt stress tolerant genotypes. This suggests that evaluation for salt tolerance among genotypes can be according to the genetic diversity in biological yield and plant height. Another advantage is that the plant height, together with biological yield, can be used again as a simple and non-destructive measurement to evaluate large number of wheat genotypes in breeding programs. In this investigation, genotype 32 was the most favorable genotype according to plant height, biological yield and finally seed yield in the saline condition. It could be good candidate for the seed yield breeding of Iranian wheat genotypes in salt stress conditions. There is remarkable natural genetic variation in processes controlling the salt stress tolerance in bread wheat and the other crop species. This genetic variation could be identified using the key traits related to salt tolerance and exploited through introduction of salt tolerant germplasm into cultivars by breeding methods.

Generally, we conclude that tolerance to high salt conditions in bread wheat genotypes seems to be related to its ability to production of high plant height and biological yield. These findings will be useful in selection material for future breeding programs. Also among 41 studied genotypes, genotype 32 had good characteristics regarding high seed yield and salt tolerance.

REFERENCES

ASHRAF, M., L. WU (1994). Breeding for salinity tolerance in plants. Crit Rev Plant Sci. *13*: 17-42.

BALESTRE, M., R. VON PINHO, J. SOUZA, R. OLIVEIRA (2009). Genotypic stability and adaptability in tropical maize based on AMMI and GGE biplot analysis. Genet Mol Res. *9*: 123-1135.

COLMER, T., R. MUNNS, T. FLOWERS (2006). Improving salt tolerance of wheat and barley: future prospects. Anim Prod Sci. *45*: 1425-1443.

DARVISHZADEH, R., A. PIRZAD, H. HATAMI-MALEKI, S. POORMOHAMMAD-KIANI, A. SARRAFI (2010). Evaluation of the reaction of sunflower inbred lines and their F1 hybrids to drought conditions using various stress tolerance indices. Span J Agric Res. *8*: 1037-1046.

DEHGHANI, H., J. DVORAK, N. SABAGHNIA (2012a). Biplot analysis of salinity related traits in beard wheat (*Triticum aestivum* L.). Ann Biol Res. *3*:3723-3731.

DEHGHANI, H., J. DVORAK, N. SABAGHNIA (2012b). Graphic analysis of biomass and seed yield of beard wheat in salt stress condition. Ann Biol Res. *3*:4246-4253.

DEHGHANI, H., H. OMIDI, N. SABAGHNIA (2008). Graphic analysis of trait relations of rapeseed using the biplot method. Agron J. *100*: 1443-1449.

FLORES, F., M. MORENO, J. CUBERO (1998). A comparison of univariate and multivariate methods to analyze G× E interaction. Field Crop Res. *56*: 271-286.

GABRIEL, K.R. (1971). The biplot graphic display of matrices with application to principal component analysis. Biometrika. *58*: 453-467.

HOUSHMAND, S., A. ARZANI, S.A.M. MAIBODY, M. FEIZI (2005). Evaluation of salt-tolerant genotypes of durum wheat derived from in vitro and field experiments. Field Crop Res. *91*: 345-354.

KELMAN, W.M., CO. QUALSET (1991). Breeding for salinity-stressed environments: recombinant inbred wheat lines under saline irrigation. Crop Sci. *31*: 1436-1442.

KINGSBURY, R., E. EPSTEIN (1984). Selection for salt-resistant spring wheat. Crop Sci. *24*: 310-315.

MA, B., W. YAN, L. DWYER, J. FREGEAU-REID, H. VOLDENG, Y. DION, H. NASS (2004). Graphic analysis of genotype, environment, nitrogen fertilizer, and their interactions on spring wheat yield. Agron J. *96*: 169-180.

MARSCHNER, H. (1996). Mineral nutrition of higher plants, Wiley Online Library.

MARTIN, P., M. AMBROSE, R. KOEBNER (1994). A wheat germplasm survey uncovers salt tolerance in genotypes not exposed to salt stress in the course of their selection. Asp Appl Biol. *39*: 215-222.

MAAS, E., G. HOFFMAN (1977). Crop Salt Tolerance-Current Assessment. J Irr Drain Div-Asce. *103*: 115-134.

MILANI, P., M. MALAKOUTI, Z. KHADEMI, M. BALALI, M. MASJAYEKHI (1998). A fertilizer recommendation model for the wheat field of Iran. Soil and Water Research Institute, Tehran, Iran.

MUNNS, R., R.A. JAMES (2003). Screening methods for salinity tolerance: a case study with tetraploid wheat. Plant Soil. *253*: 201-218.

PECETI, L., J. GORHAM (1997). Screening of durum wheat germplasm for Na-22 uptake under low and moderate salinity. Cereal Res Commun. *25*: 923-930.

PERVAIZ, Z., M. AFZAL, Y. XIAOE, L. ANCHENG (2002). Selection criteria for salt tolerance in wheat cultivars at seedling stage. Asian J Plant Sci. *1*: 85-87.

RHOADES, J.D. (1996). Salinity: electrical conductivity and total dissolved solids. In: Page, A.L. (Ed.), Methods of Soil Analysis. Part 2. Agronomy. ASA, SSSA, Madison, WI, pp: 417–435.

RICHARDS, R., C. DENNETT, C. QUALSET, E. EPSTEIN, J. NORLYN, M. WINSLOW (1987). Variation in yield of grain and biomass in wheat, barley, and triticale in a salt-affected field. Field Crop Res. *15*: 277-287.

ROZEMA, J., T. FLOWERS (2008). Crops for a salinized world. Sci. *322*: 1478-1480.

ROYA, A., D. ABIO (2003). Salt tolerance in durum wheat cultivars. Span J Agric Res. *1*: 27-35.

RUBIO, J., J. CUBERO, L. MARTIN, M. SUSO, F. FLORES (2004). Biplot analysis of trait relations of white lupin in Spain. Euphytica. *135*: 217-224.

SABAGHNIA, N., H. DEHGHANI, B. ALIZADEH, M. MOGHADAM (2010). Interrelationships between seed yield and 20 related traits of 49 canola (*Brassica napus* L.) genotypes in non-stressed and water-stressed environments. Span J Agric Res. *8*: 356-370.

SABAGHNIA, N., H. DEHGHANI, B. ALIZADEH, M. MOGHADAM (2011). Yield analysis of rapeseed (*Brassica napus* L.) under water-stress conditions using GGE biplot methodology. J Crop Improv. *25*: 26-45.

SHANNON, M.C. (1997). Adaptation of plants to salinity. Advan Agron. *60*: 75-120.

SNEDECOR, G.W. (1957). Statistical methods. Iowa State College Press, Ames, Iowa, 534pp.

THOMAS, G.W. (1996). Soil pH and soil acidity. In: Page, A.L. (Ed.), Methods of Soil Analysis (Part 2). Agronomy. ASA, SSSA, Madison,WI, pp: 475–490.

YAN, W., L. HUNT (2002). Biplot analysis of diallel data. Crop Sci. *42*: 21-30.

YAN, W., M. KANG (2003). GGE biplot analysis: A graphical tool for geneticists, breeders, and agronomists, CRC Press, Boca Raton, FL.

YAN, W., M. KANG (2002). GGE biplot analysis: A graphical tool for breeders, geneticists, and agronomists. Ed. Eds, CRC press.

YAN, W., I. RAJCAN (2002). Biplot analysis of test sites and trait relations of soybean in Ontario. Crop Sci. *42*: 11-20.

YAN, W., L. HUNT, Q. SHENG, Z. SZLAVNICS (2000). Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Sci. *40*: 597-605.

YAN, W., M.S. KANG, MA, B.S. WOOD, P.L. CORNELIUS (2007). GGE biplot vs. AMMI analysis of genotype-by-environment data. Crop Sci. *47*: 643-653.

YASIN, A.B., S. SINGH (2010). Correlation and path coefficient analyses in sunflower. J Plant Breeding Crop Sci. *2*: 129-133.

ZENG, L., M. SHANNON, C. GRIEVE (2002). Evaluation of salt tolerance in rice genotypes by multiple agronomic parameters. Euphytica. *127*: 235-245.

GRAFIČKA ANALIZA ODNOSA OSOBINA GERMPLAZME IRANSKE HLEBNE PŠENICE U USLOVIMA NEZASLANJENOSTI I ZASLANJENOSTI KORIŠĆENJEM BIPLOT ANALIZE

Amir GHOLIZADEH[1] and Hamid DEHGHANI[1,*]

[1]Plant Breeding and Biotechnology Department, Faculty of Agriculture, Tarbiat Modares University, Tehran, Iran

Izvod

Poznavanje međuzavisnosti prinosa i njegovih komponenata će poboljšati efikasnost programa oplemenjivanja, posebno u uslovima zaslanjenosti zemljišta preko odgovarajućih kriterijuma. Prikazani su rezultati ispitivanja iranske hlebne pšenice u uslovima zaslanjenosti i nezaslanjenosti zemljišta. Dobijeni rezultati genotipa su analizirani primenom genotip x osobina (GT) biplot metodom zasnovanom na regresionom modelu. Pokazano je da postoji značajna asocijacija visine biljke (PH) i biološkog prinosa (BY) sa prinosom u uslovima zaslanjenosti i nezaslanjenosti zemljišta. Izgleda da visina biljke i biološki prinos mogu da se koriste kao kriterijumi za povećanje prinosa u programima oplemenjivanja pšeenice, posebno u uslovima stresa u poljskim uslovima.