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Graphic analysis of biomass and seed yield of beard wheat in salt stress condition

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ABSTRACT

Salinity is a major restriction to crop production in worldwide and breeding for salinity tolerance maybe result in improving wheat seed yield on saline soils in arid and semi-arid areas agriculture. A population of plants disomic for 4D/4B recombined chromosomes in the genetic background of *T. turgidum* was used to investigate the salinity tolerance of chromosome 4D. Three salt treatments (control, intermediate and high) were applied in and field condition on 23 wheat recombinant lines. The obtained data were analyzed using a genotype $\times$ trait (GT) biplot method based on site regression model. The biplot method facilitates a visual evaluation of superior lines, traits and grouping of lines and traits. The GT biplot explained 81% of the total variation of the standardized data. According to polygon view of biplot there were six vertex lines (3, 18, 165 and 46 and parents Lang. 4D and Capp. 4B). Also among 23 studied genotypes, lines 3 and 46 had good characteristics regarding high seed yield and salt tolerance. The biplot vector view indicate that there were a strong positive association between H-Yield and H-Biom (in high salt treatment), between I-Yield and I-Biom (in intermediate salt treatment), and between C-Yield and C-Biom (in control salt). In other word, seed yield and biomass of intermediate and high salt treatments were correlated positively with each other but they do not have any positive correlation with seed yield and biomass of control salt treatment.

Key word: Biplot, Salinity, Site regression, *Triticum aestivum* L., *Triticum turgidum* L.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is grown in arid and semi-arid areas of the world especially in Middle East and its production increase under environmental stress conditions has become important in recent years, since wheat production in areas with optimum growing conditions does not meet the increasing world demand. The soil salinity problem is present relatively in all irrigated fields of the world and also maybe occurs on non-irrigated field areas [26]. Although, the actual areas of saline soils allover the world is not known, but it is large due to fields' irrigation and of non-irrigated salt affected soils [5]. Therefore, the soils' salinity is important and widespread in crop production throughout the world.

High concentration of salts retards the growth in most of the crops depending on the salts type, the growth stages and the salt tolerance of the crops. Plant breeders to overcome the salinity problem use some properties such as good

germination, seedling growth and biomass accumulation as the criteria for distinguish salinity tolerant plants [28, 35]. Salinity tolerance reflects the ability of a genotype to yield well in a salt stressed condition. Some researchers prefer to use biomass and especially seed yield under salt stress conditions due to ease of measurement and be as the final propose [14]. It is generally declared as the relative seed yield production under salt stressed and non-salt stressed environment [26].

In contrast, an alternative screening procedure has been suggested instead of phenotypic selection for seed yield or yield components [14, 29 and 41]. Although, salt stress tolerance must be regarded from both physiological and genetically aspects [6, 16, and 22], but it has been proposed that improving salt stress tolerance should emphasize on trait-based selection [16 and 41]. It is interesting that physiological traits such as Na^+ , K^+ concentrations and their ratio (Na^+/K^+) in crop leaves are the most important and stable traits in salt tolerance evaluations. Pyramiding of these traits into plant materials via quantitative trait loci mapping and marker assisted selection have a great chance to progress the salt tolerance improving program through the trait-based procedure [16, (Collard et al., 2005).

For different species of wheat, it has been shown that Na^+ toxicity is the major problem in the salt stress [4, 38 and 42]. Therefore, salt resistance of wheat may be improved by performing methods to avoid Na^+ toxicity and to overcome osmotic problems [29]. It has been proved that chloroplast function is impaired when K^+ is displaced by Na^+ [39]. The Na^+ toxicity avoidance can be reached by Na^+ inclusion in vacuoles because of the tonoplast activity [37 and 39]. Breeding of the Na^+ toxicity avoidance has to assemble the different mechanisms which influence to low Na^+ concentration in cytoplasm [45]. Reduction of seed yield due to reduction of growth spread but osmotic adjustment and turgor properties are not limiting [8 and 46]. In contrast, using of Na^+ toxicity avoidance as the physiological trait in salinity tolerance may results in some problems. Salt tolerate genotypes which are selected by such trait in field conditions will not necessarily show their potential under other conditions. Also, selection according to the seed yield under salt stress condition does not necessarily sponsorship that a selected genotype will have the optimal genetic 'makeup' to increase its tolerance [7]. Therefore selection processes must be done in a single experiment and physiological trait which directly related to salinity tolerance.

Usually, genotype by environment (GE) interaction was seen in agriculture experiments and numerous procedures have been used in the exploring of the causes of interactions [12 and 31]). The GGE biplot procedure was proposed firstly for analyzing multi-environment trial data [50] but it could be used for all types of two-way data that assume an entry $\times$ tester structure. The GE interaction refers to yield variation that cannot be explained by the genotype effect (G), or the environment effect (E) [12]. Yan and Rajcan [49] used a genotype by trait (GT) biplot, which the genotypes are assumed as entries and the traits as testers. A GT biplot, effective tool, graphically displays the genotype by trait dataset, permits the visualization of the associations among traits across the genotypes and indicates the trait profile of the genotypes [10, 30 and 48]. The objective of present investigation was to evaluate bread wheat genotypes by traits interaction in field conditions and to study the interrelationships among traits using GT biplot procedure.

MATERIALS AND METHODS

Plant Material

Disomic substitution line that chromosome 4D of bread wheat was substituted for chromosome 4B of cv Langdon with name forth DS4D (4B), which was developed by Joppa and Williams [19]. Also, Giorgi and Cuozzo [17] developed the *Triticum turgidum* homozygous mutant *ph1c*, the source of chromosome 4B. The development of the families which had 4D/4B recombinant chromosomes was described by Dvorak and Gorham [11]. Disomic plants for the 4D/4B chromosomes were produced by the self-pollination of double monosomic 4D/4B-4D F_1 plants and the selection of 4D/4B disomics by C-banding analysis [11].

Statistical Methods

The GT biplot model [49] based on GGE biplot procedure or site regression (SREG) strategy [50] was used to investigate the genotype $\times$ trait interaction in two-way dataset. The used model was based on this formula:

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

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 among 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 . The used scaling procedure between the genotype scores and the trait scores was symmetric. Also, in the GT biplot, a vector is drawn from the biplot origin to each marker of the traits to facilitate visualization of the association among the traits. Simple correlation coefficients between all possible combinations of traits were done based on Snedecor [44]. 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 81% (59% and 22% by PC1 and PC2, respectively) of the total variation of the standardized data (Table 1). This relatively high explanation indicates the good power of biplot model for the interrelationships among the traits. The biplots present data of 23 lines determined for six traits: seed yield and biomass production in control salt treatment (C-Yield and C-Biom, respectively), seed yield and biomass production in intermediate salt treatment (I-Yield and I-Biom, respectively), and seed yield and biomass production in high salt treatment (H-Yield and H-Biom, respectively). The large variation due to the two first IPCs justifies the use of multivariate procedures such as the GGE biplot model for data interpretation [15 and 33]. Also this explanation percentage reflects the complexity of the relationships among the measured traits [32]. Kroonenberg [23], Yan and Kang [48], Rubio et al. [30] and Dehghani et al. [10] declared that the fundamental patterns among the traits should be captured by the biplots.

Table 1. Lambda, relative and cumulative proportions of latent root for the beard wheat dataset

Conditions	Excluded traits	Latent root	Lambda	Relative proportion	Cumulative proportion
Field	None	1	8.85	59	59
		2	5.44	22	81
	Biomass	1	6.68	68	68
		2	3.91	23	91

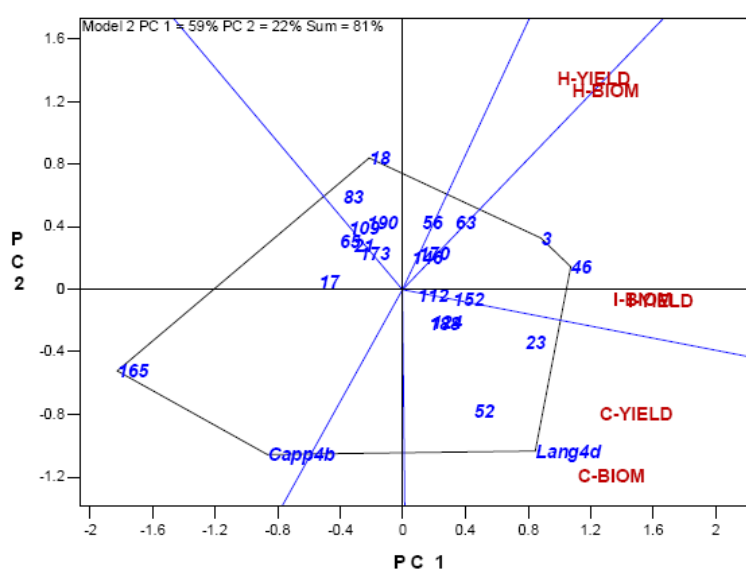


Fig. 1. Bread wheat line by trait biplot polygon view for the whole dataset, showing which line had the highest values for which traits.

Among numerous ways to use a GT biplot, the polygon view helps identify lines with the highest values for one or more traits. It provides the best way for visualizing the interaction patterns between treatments and lines and to effectively interpret a biplot [48]. 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 six vertex lines in this investigation (Fig. 1) which are lines 3, 18, 165 and 46 and parents Lang. 4D and Capp. 4B. These lines are the best or the poorest lines in some or all of the traits. Therefore, it seems that line 3 had the highest values of H-Yield and H-Biom (in high salt treatment) and line 46 had the highest values of H-Yield, H-Biom, I-Yield and I-Biom traits. Parent Lang. 4D had the highest values for C-Yield, C-Biom, I-Yield and I-Biom traits. Also, lines 18, 165 and parent Capp. 4B. were favorable in none of the measured traits (Fig. 1).

A subset of the dataset could be analyzed by removing some of the lines or traits based on special propose. Since yield is important than biomass, we removed all biomass traits, and then grouped the rest by polygon view (Fig. 2). This biplot is generated using a subset of the data and explained 91% (68% and 23% by PC1 and PC2, respectively) of the total variation of the standardized data (Table 1). This relatively high percentage of explanation reflects the good ability of biplot model to data interpretation as well as the importance of seed yield in comparison to biomass. Fig. 2 indicated that there are seven vertex lines including lines 3, 18, 46, 83, 165 and parents Lang. 4D and Capp. 4B. The line 3 had the highest values for H-Yield (high salt treatment), parent Lang. 4D had the highest values for C-Yield (control treatment) and line 46 had the highest values for I-Yield (Fig. 2). So it could be stated that the lines 3 and 46 have very good potential for salt stress tolerance.

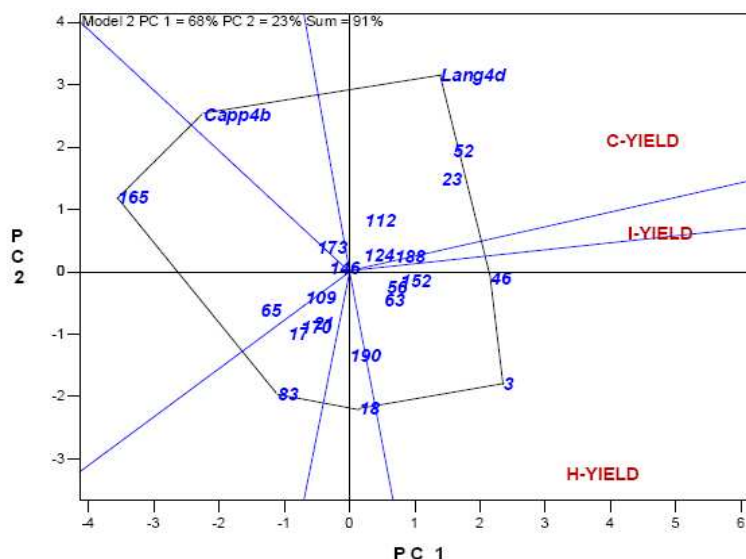


Fig. 2. Bread wheat line by trait biplot polygon view after all biomass traits were removed, showing which line had the highest values for which traits.

In the vector view of the GT biplot, a vector is drawn from the biplot origin to each symbol of the traits to facilitate visualization of the relationships between and among the traits [49]. If the biplot explain a proper amount of the total variation, the correlation coefficient between any two traits can be approximated by the cosine of the angle between their vectors [48]. Two traits are positively correlated if the angle between their vectors is $<90^\circ$, negatively correlated if the angle is $>90^\circ$, independent if the angle is 90° . Most of the correlation predictions can be verified from the original data but some are not consistent with the data. Such mentioned discrepancies are expected because the biplot usually explains less than 100% rather than 100% of the total variation [34]. Traits with longer vectors are more responsive to the treatment combinations; traits with shorter vectors are less responsive to the lines; and those located at the biplot origin are not responsive at all [49].

Table 2. Pearson's correlation coefficients among different traits of 23 bread wheat lines

	Filed condition				
	C-Y	C-B	I-Y	I-B	H-Y
C-B	0.80				
I-Y	0.69	0.57			
I-B	0.51	0.56	0.85		
H-Y	0.32	0.10	0.50	0.36	
H-B	0.30	0.17	0.51	0.55	0.74

* Critical values of correlation $P < 0.05$ and $P < 0.01$ (D.F. 21) are 0.413 and 0.526, respectively.
C-Y, the control condition yield; C-B, the control condition biomass; I-Y, the intermediate salt condition yield; I-B, the intermediate salt condition biomass; H-Y, the high salt condition yield; H-B, the high salt condition biomass.

The vector view represents the correlation coefficient between any two traits in Fig. 3 by the cosine of the angle between the vectors. The most prominent relations in above figure are: a strong positive association between H-Yield and H-Biom (in high salt treatment), between I-Yield and I-Biom (in intermediate salt treatment), and between C-Yield and C-Biom (in control salt) as indicated by the small acute angles between their vectors ($r = \cos 0 = +1$). There was an approximately zero correlations between H-Yield and H-Biom with C-Yield and C-Biom as indicated by the rectangular angles between their vectors ($r = \cos 90 = 0$). Most of the mentioned correlations can be verified from the correlation data (Table 2). For example there was a strong positive association (+0.85) between I-Yield and I-Biom in intermediate salt treatment, between C-Yield and CH-Biom in control condition (+0.74) and between H-Yield and H-Biom in high salt treatment (Table 2). Most of the mentioned predictions for correlations can be

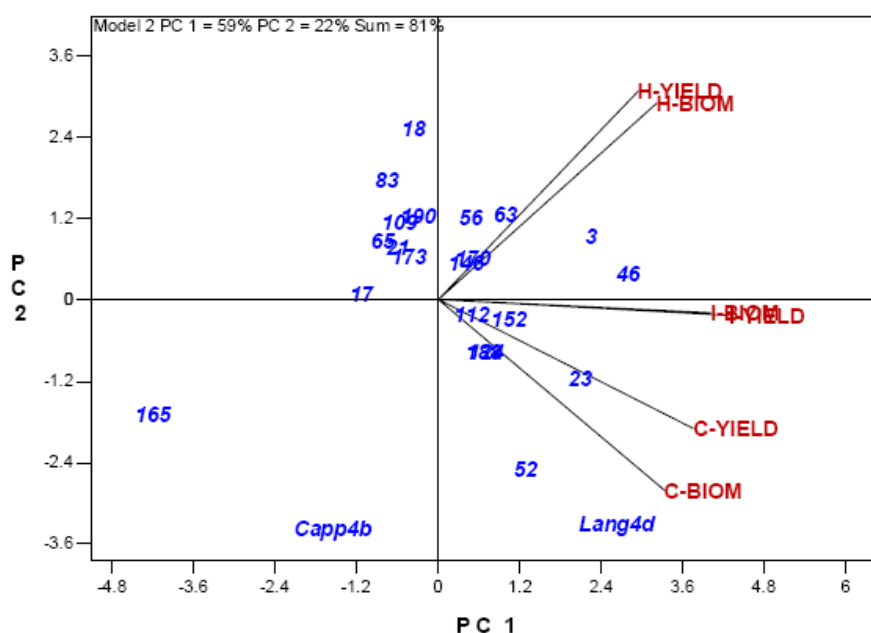


Fig. 3. Bread wheat line by trait biplot vector view for the whole dataset, showing the interrelationship among all measured traits.

verified from the original data but some are not consistent with the data because the biplot explains 81% rather than 100% of the total variation.

Due to importance seed yield and high explanation (91% instead of 81%) of the related subset of the data, the vector view of biplot based on this dataset was drawn (Table 1). According to Fig. 4, there was an approximately zero correlations between ratio of H-Yield (in high salt treatment) with the other measured seed yields (C-Yield, I-Yield). There was a positive association among C-Yield, I-Yield (in control and intermediate salt treatment) as indicated by the small acute angles between their vectors ($r = \cos 0 = +1$). Our results in agreement with seed yield selection in

target environments for development stress tolerant lines [20, 24 and 37]. In other word, this finding in agreement with this idea that selection for stress tolerant lines should be done in target environments [2].

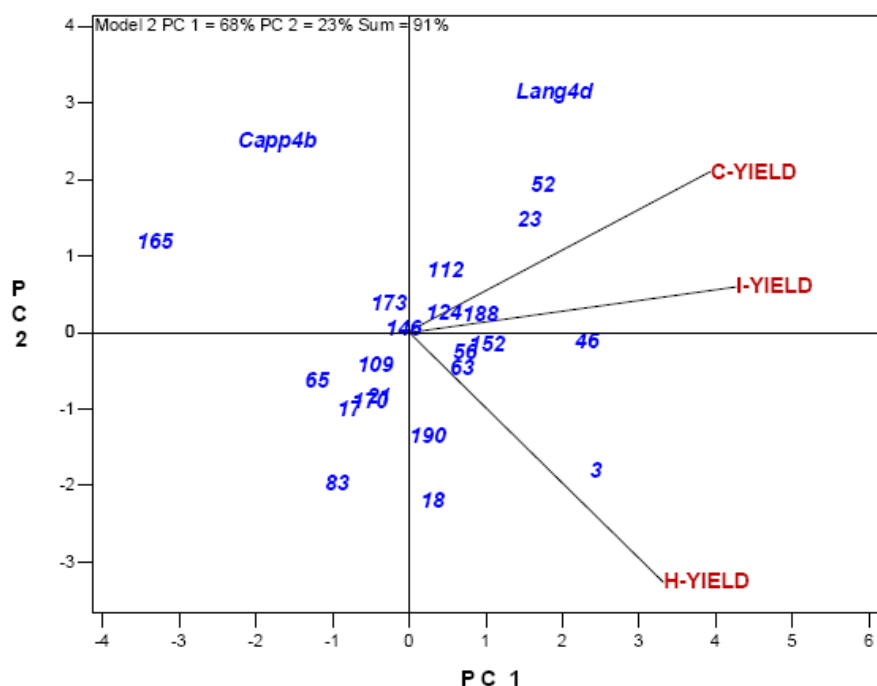


Fig. 4. Bread wheat line by trait biplot vector view after all biomass traits were removed, showing the interrelationship among all measured traits.

DISCUSSION

Salinity is one of the most important abiotic stresses limiting crop production in arid and semiarid areas of world [36]. The salt stress is responsible for considerable crop loss all over world and therefore, crops that are tolerant salinity are called for. Breeding for salt tolerance is a difficult task, and may be indicates progress due to a regarding of various factors. The knowledge of the salt stress effects on crops is not complete and there are not sufficient means for identifying and measuring salinity [13 and 18]. Also salt tolerance changes with crop development stages and there is poor understanding about salinity by crop the interactions [6, 20 and 24]. Fortunately, some of the salt tolerance breeding prerequisites consist on breeding methodology, potential of screening in large numbers of genotypes and suitable genetic variability (in the cultivated species or their wild relatives) are available [43]. Despite wide recognition of the key traits in the salt tolerant genotypes breeding, major gaps exist in knowledge needed to develop salt tolerant genotypes cultivars. However, salt tolerance property is a quantitative character, so large breeding success based on modification of a single gene might not he expected to occur [3].

The biplot model explanation of this investigation varied from 81 to 91 percent for all field dataset and only seed yield traits after biomass traits removal. On the other hand, GT biplot explained most of the variation due to genotype main effects plus genotype by trait interactions. According to Dehghani et al. [10] almost all information contained ANOVA and multiple comparisons of treatment means is graphically displayed in a GT biplot. The biplot model can explore the multi-directionality aspect of data and to extract more information from interaction component [34] and the fundamental patterns among the traits could be captured by this model [23]. Rubio et al. [30] in white lupin, Ma et al. [25] in spring wheat and Dehghani et al. [10] in rapeseed found similar results in the studying of effects of genotype, trait and their interactions.

In this investigation, lines 3 and 46 were the most favorable lines according to seed yield and biomass in both intermediate and high salt treatments. They could be good candidates for the seed yield breeding in salt stress conditions of future programs. Although seed yield and biomass of intermediate and high salt treatments were correlated positively with each other but they do not have any positive correlation with seed yield and biomass of

control salt treatment. Salt tolerate genotypes which are selected in field conditions will not necessarily indicate their potential under other conditions. Also, selection according to the seed yield under salt stress condition does not necessarily sponsorship that a selected genotype will have the optimal genetic 'makeup' to increase its tolerance [7]. It is clear that the biplot methodology is an excellent tool for visual data analysis. Compared with conventional methods of data analysis, the biplot approach has some advantages [33 and 47]. The first advantage of the biplot is its graphical presentation of data, which greatly 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 this method is that it facilitates identification of possible genotypes or traits groups [34].

Therefore selection processes must be done in target environments. Bread wheat is sensitive to salinity during the seedling stage [1 and 9]. Low salinity threshold values of bread wheat seedling growth and survival rate have been reported [16, 21]. The loss of plant stand caused reduction in yield sink capacity by reducing plant density. Therefore, screening of genotypes for salt tolerance based on seedling growth and survival rate is important for the breeding salt tolerant genotypes. Despite wide recognition of the salinity problem for world agriculture, major gaps exist in wisdom required to develop cropping systems for salt affected lands [6, 20]. Such knowledge on the target environment is essential to selection of useful traits and developing screening methods to improvement salt tolerant genotypes [40]. Finally it seems that domestication of halophytic crops to develop high salt tolerant crops is essential [14]. The above mentioned procedures could be used for useful genes identification which could be used for gene transformation when salinity tolerance trait there is not in related species [27]. We conclude that our findings will be useful in selecting material for future breeding programs. Also among 23 studied genotypes, lines 3 and 46 had good characteristics regarding high seed yield and salt tolerance.

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