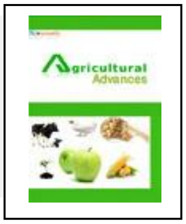
Agricultural Advances (2014) 3(4) 103-110
ISSN 2251-7820
doi: 10.14196/aa.v3i4.1304

Contents lists available at Sjournals

Agricultural Advances

Journal homepage: www.Sjournals.com



Original article

Determination of the most effective traits on wheat yield under saline stress

A. Gholizadeh[a], H. Dehghani[a]*, J. Dvorak[b]
[a]Plant Breeding, Tarbiat Modares University, Tehran, Iran.
[b]Plant Science, University of California, Davis, USA.

*Corresponding author; dehghanr@modares.ac.ir, Plant Breeding Department, Tarbiat Modares University, Tehran, P.O.Box 14115-336 Iran.

ARTICLE INFO

Article history,
Received 03 April 2014
Accepted 23 April 2014
Available online 28 April 2014

Keywords,
Chlorophyll content
Correlation
Stepwise regression
Path analysis

ABSTRACT

Salinity stress is one of the most important abiotic stresses which reduce the crop production in worldwide and breeding for salinity tolerance maybe result in improving wheat seed yield under saline conditions in arid and semi-arid areas agriculture. Identification of effective yield-related traits is the main aim of each breeding program. In this research, the relationship between wheat seed yield and its components under saline condition were investigated by using four statistical procedures including; simple correlation, multiple linear regression, stepwise regression and path analysis. The experiment was conducted under saline field conditions at the research field of the National Salinity Research Center (NSRC) at Yazd, Iran based on randomized complete block design with three replications. Electrical conductivity of irrigation water was 10 ds.m^{-1}. The multiple statistical procedures which have been used in this study indicated that biological yield, harvest index and chlorophyll content were the most effective variables influencing seed yield. Based on the results, it seems that high yield of wheat plants under saline field conditions can be obtained by selecting breeding materials with high biological yield, harvest index and chlorophyll content. This suggests that evaluation for salt tolerance among genotypes can be based on the genetic diversity in biological yield, harvest index and chlorophyll content.

1. Introduction

Salinity is one of the major environmental stresses across agricultural regions of worldwide especially in arid and semi-arid regions can severely limit growth and cereal production (Colmer et al., 2006; Rozema and Flowers, 2008). Bread wheat (*Triticum aestivum* L.) is one of the important crops of the word especially in arid and semi-arid areas and is faced with types of environmental stresses including salt stress (Flower and Yeo, 1995; Rozema and Flowers, 2008). The most efficient way to increase wheat yield is to improve the salt tolerance of wheat genotypes because salinity management through reclamation or improved irrigation techniques is often prohibitively expensive and provides only short-term solutions to overcome salinity (Ashraf and Wu, 1994; Shannon, 1997). Since, most of the experiments are carried out under controlled condition and 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). 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 (Dehghani et al., 2012a). On the other hand, seed yield is a quantitative trait and highly affected by environmental factors and hence has a low heritability, therefore choose based on lower yield in order to improve it may not be very effective hence (Poormohammad Kiani et al., 2009). Yield components and related characters with seed yield due to easy measurement and high heritability can be used as criteria for distinguish salinity tolerant plant and for improvement of seed yield in wheat genotypes especially under saline environments. Therefore, there is the need to examine the interrelationships between various traits, especially between seed yield and other traits (Dehghani et al., 2012b).

Different statistical procedures have been used to evaluate yield and yield components including correlation, regression and path analysis (Mohamed, 1999; Naser and Leilah, 1993; Leilah and Al-Khateeb, 2005; Mohammadi et al., 2011). Correlation coefficient is an important statistical procedure to evaluate breeding programs for high yield, as well as to examine direct and indirect contribution of yield component (Mohamed, 1999; Hiltbrunner et al., 2007). Path coefficient analysis is a statistical technique of partitioning the correlation coefficient into direct and indirect effects; therefore the contribution of each character to yield can be estimated through path coefficient analysis (wright, 1921; Dewey and Lu, 1959). Many researchers have used this technique in rice (Gravois and McNew, 1993), soybean (Board et al., 1997), wheat (Leilah and Al-Khateeb, 2005) and canola (Basalma, 2008). Stepwise multiple linear regression proved to be more effective that the full model regression to determine the predictive equation for yield (Naser and Leilah, 1993; Mohamed, 1999).

This study was carried out to determine the interrelationships between seed yield and related traits in bread wheat by four statistical procedures and identifying traits, which may be useful in breeding higher-yielding genotypes under saline condition in field farm.

2. Materials and methods

The forty one genotypes of bread wheat (*Triticum aestivum* L.) which were used in this experiment were almost all the commercial wheat genotypes cultivated in different parts of Iran. The experiment was carried out in the saline conditions at the research field of the National Salinity Research Center (NSRC) at Yazd, Iran (31°86′N, 53°95′E). Before starting the experiment was conducted sampling in the different layers of soli (0-30, 30-60, 60-90 cm depth) in the experiment location. Relevant soil characteristics of the experimental site are given in Table 1. The genotypes cultivated in saline condition with 3 replications in from of randomized complete block design. The salinity of water used in irrigation was 10dS.m-1. Each plot consisted two rows 20 cm apart and 2 m in length. N, 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}, for the purpose of determining the salinity of soil during growth season, sampling have been done from the depth of 0-30, 30-60, 60-90. The average of salinity rate during growth season was 9.5dS.m^{-1}. Weeds were controlled by hand as needed.

Data were collected on the following 18 characters in all replications on five randomly selected plants from each plot. The traits were own length (X_1), number of seed per spike (X_2), number of fertile tiller (X_3), number of spikelet per spike (X_4), flag leaf length (X_5), 100-seed weight (X_6) (The 100-seed weight was measured on a sub-sample of seed harvested from each plot), seed weight per spike (X_7), peduncle weight (X_8), spike weight (X_9), chlorophyll content (X_{10}) (The chlorophyll content (X_{10}) 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), plant height (X_{11}), days to heading (X_{12}), days to maturity (X_{13}), spike length (X_{14}), peduncle length (X_{15}), harvest index (X_{16}) (The harvest index was calculated as the ratio between grain yield and biological yield), biological yield (X_{17}) and seed yield (SY) were recorded.

The datasets were first tested for normality by the Anderson and Darling normality test using Minitab version 14 statistical software. Simple correlation coefficients were calculated for all possible comparisons using the Pearson correlation coefficient. In order to evaluate the relative contribution and to develop the prediction model for seed yield, multiple linear regression and partial coefficient of determination (R^2) was calculated for each yield component (Snedecor and Cochran, 1981). Stepwise multiple linear regression procedure was used to determine the variable accounting for the majority of total yield variability (Draper and Smith 1966). Correlation coefficients were partitioned into direct and indirect effects using path coefficient analysis (Dewey and Lu, 1959). Data analysis was performed using SAS version 9.1 and SPSS version 19 statistical software.

Table 1

Soil properties of the experimental site.

Location	Depth (cm)	pH	EC ($dS.m^{-1}$)	meqL^{-1}				P ($mg.kg^{-1}$)	K ($mg.kg^{-1}$)
				K^+	Na^+	Mg^+	Ca^+		
Stress	0-30	7.6	9.80	1.7	175.8	52.6	52.3	25.9	209
	30-60	7.6	7.89	0.9	149.8	41.2	38.2	5.0	177
	60-90	7.3	9.58	0.9	219.7	61.7	48.3	3.7	201

3. Results and discussion

The analysis of variance results indicated highly significant difference in bread wheat genotypes for all traits under study (data not shown). The simple correlation coefficients showed there were significant positive correlations between seed yield and all of the measured traits except for number of seed per spike (X_2), number of spikelet per spike (X_4), flag leaf length (X_5), peduncle weight (X_8) and Spike length (X_{14}) (Table 2). Results revealed that was high positive correlations between seed yield with biological yield (X_{17}), harvest index (X_{16}) and plant height (X_{11}). Our observations were consistent with Kumbhar et al. (1983), Mohamed (1999) and Leilah and Al-Khateeb (2005) investigations on wheat plant yield components. However, Moghaddam et al. (1998) showed a negative correlation between plant height and seed yield. Also, the results of correlation coefficient analysis revealed that leaf chlorophyll content (X_{10}) was positively and significantly correlated with the seed yield under saline conditions. Many researchers have reported similar results. A positive correlation between leaf chlorophyll content and yield for wheat and other crops were reported by Araus et al. (1998), Kabanova and Chaika, (2001), Ramesh et al. (2002), Boggs et al. (2003) and Bronson et al. (2003).

The objective of this analysis is to discover individual effects of independent variables on dependent one. Efficiency and precision of model depends on influence and number of components considered on yield. This analysis can be used for prediction of yield components in wheat and other crops (Andales et al., 2007). The multiple linear regression analysis, shown in Table 3, explains the regression coefficients, the p values of the variables on estimation of seed yield. The obtained results showed that the prediction equation for seed yield ($\hat{Y}$) is formulated using the wheat plant variables as follows:

$$\hat{Y}= -1966.6 + 55.4X_1 - 22.2X_2 - 7.1X_3 + 81.7X_4 - 71.5X_5 + 202.0X_6 + 301.6X_7 + 407.2X_8 - 275.7X_9 + 54.5X_{10} - 22.3X_{11} - 47.1X_{12} + 29.5X_{13} - 40.4X_{14} + 6.0X_{15} + 4580.9X_{16} + 0.31X_{17}$$

The formula explains 87% of the total variation within the seed yield components and the remaining 13% maybe due to residual effects. T-test indicated that biological yield (X_{17}), harvest index (X_{16}) and chlorophyll content (X_{10}) seemed to have the greatest effect in wheat seed yield. These results show that they are important variables and could be used in bread wheat breeding programs. Regression analysis is the better way to make crop yield prediction (Xue et al., 2006).

Stepwise multiple linear regression is the more effective that the full model regression to determine the predictive equation for yield (Naser and Leilah, 1993). Table 4 shows the data representing partial and cumulative R^2 as well as the probability for the accepted limiting three wheat variables in seed yield prediction. Stepwise regression for seed yield indicated that 3 variables, including harvest index (61.3%), biological yield (15.1%), and chlorophyll content (3.7%) entered the model (Table 4). According to the results, 80.1% of the total variation in seed yield could be attributed to these three variables. The other variables were not included in the analysis due to their low relative contributions. Regression coefficients for the accepted variables are shown in Table 5. The predicted equation for seed yield ($\hat{Y}$) formula was:

$$\hat{Y} = -466.2 + 4665.6X_{16} + 0.31X_{17} + 34.6X_{10}$$

The correlation coefficients were partitioned direct and indirect effects by using path analysis (Table 6). According to the results of stepwise multiple linear regression analysis, 80.1% of the total variation in seed yield could be attributed to three variables included biological yield (X_{17}), harvest index (X_{16}) and chlorophyll content (X_{10}). Therefore, path analysis was conducted using the results of stepwise regression. The other variables were not included in the analysis, due to their low relative contributions. Results of path analysis indicated biological yield, harvest index and chlorophyll content have positive direct effects on seed yield. The highest direct effects on seed yield were observed with harvest index (1.26) and biological yield (1.19).

Table 3
The regression coefficient (b) of the variables in estimation of seed yield by the multiple linear regression analysis.

Variables	dF	Coefficient of regression (b)
Own length (X_1)	1	55.43 ± 43.76ns
Number of seed per spike (X_2)	1	-22.23 ± 19.69ns
Number of fertile tiller (X_3)	1	-7.10 ± 12.51ns
Number of spikelet per spike (X_4)	1	81.79 ± 60.85ns
Flag leaf length (X_5)	1	-71.52 ± 85.23ns
The 100-seed weight (X_6)	1	202.01 ± 311.1ns
Seed weight per spike (X_7)	1	301.64 ± 172.4ns
Peduncle weight (X_8)	1	407.25 ± 530.5ns
Spike weight (X_9)	1	-275.79 ± 161.7ns
Chlorophyll content (X_{10})	1	54.53 ± 23.12*
Plant height (X_{11})	1	-22.34 ± 32.95ns
Days to heading (X_{12})	1	-47.13 ± 28.02ns
Days to maturity (X_{13})	1	29.53 ± 33.50ns
Spike length (X_{14})	1	-40.40 ± 125.6ns
Peduncle length (X_{15})	1	6.02 ± 45.99 ns
Harvest index (X_{16})	1	4580.94 ± 548.9**
Biological yield (X_{17})	1	0.31 ± 0.040**

* and **: significant at 5% and 1%, ns: not significant, Y-intercept (a): -1966.67, SE:3748.31, R^2: 0.873, Root MSE: 351.793, Adj. R^2: 0.780.

Table 2

Pairwise correlation coefficients between 18 traits of 41 bread wheat genotypes measured in a saline condition.

Trait	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}	X_{15}	X_{16}	X_{17}
X_2	0.11[a]																
X_3	-0.02	-0.17															
X_4	-0.37	0.59	-0.02														
X_5	0.00	-0.26	0.29	-0.27													
X_6	-0.15	-0.55	0.36	-0.33	0.59												
X_7	-0.28	0.31	0.09	0.21	0.41	0.13											
X_8	-0.16	0.30	0.16	0.37	0.11	0.09	0.42										
X_9	-0.20	0.54	-0.03	0.45	0.27	0.01	0.77	0.48									
X_{10}	0.01	-0.19	0.44	0.03	0.30	0.37	0.24	0.47	0.05								
X_{11}	-0.17	0.34	0.25	0.37	-0.09	-0.29	0.05	0.49	0.03	0.18							
X_{12}	-0.34	0.16	-0.02	0.45	-0.39	-0.35	0.02	0.31	-0.01	0.59	0.01						
X_{13}	-0.21	0.09	0.32	0.36	-0.08	-0.11	0.11	0.40	0.02	0.67	0.36	0.77					
X_{14}	0.08	-0.12	0.28	-0.01	0.12	0.03	0.09	0.33	0.06	0.25	0.62	0.18	0.40				
X_{15}	0.14	-0.18	0.33	-0.18	0.44	0.38	0.19	0.34	-0.01	0.01	0.82	-0.30	0.03	0.32			
X_{16}	0.36	0.03	-0.07	-0.16	-0.18	-0.17	-0.35	-0.29	-0.11	-0.24	-0.45	-0.22	-0.28	-0.13	-0.29		
X_{17}	-0.09	0.04	0.38	0.10	0.30	0.11	0.44	0.43	0.16	0.42	0.64	0.21	0.45	0.38	0.46	-0.64	
SY	0.33	0.05	0.35	-0.05	0.08	0.31	0.30	0.19	0.32	0.43	0.40	0.30	0.33	0.20	0.32	0.45	0.48

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

Table 5

Regression coefficient (b) of the accepted variables that can be used to predict wheat seed yield by the stepwise procedure.

Variables	**Coefficient of regression (B)**
Harvest index (X_{16})	4665.66 ± 440.8**
Biological yield (X_{17})	0.31 ± 0.031**
Chlorophyll content (X_{10})	34.64 ± 13.081*

* and **: significant at 5% and 1%, Y-intercept (a): -466.22, SE: 689.34, R^2: 0.801.

Table 6

Path coefficients (direct and indirect) of characters affecting seed yield under saline conditions.

Variables	**Effects via**			**Total correlation**
	(X10)	**(X16)**	**(X17)**	
Chlorophyll content (X_{10})	0.219	-0.305	0.515	0.429
Harvest index (X_{16})	-0.053	1.269	-0.767	0.449
Biological yield (X_{17})	0.094	-0.813	1.198	0.479

Also, the highest indirect effects of positive on seed yield were observed with chlorophyll content (0.51). Generally, the results path analysis showed that biological yield, harvest index and chlorophyll content positively influenced the seed yield and have the greatest importance in relationship to wheat seed yield under saline conditions. Many Researchers have used the path coefficient analysis for partitioning correlation coefficients into direct and indirect effects for improving seed yield via selection for its yield components (Kang et al., 1983; Gravois and McNew, 1993; Board et al., 1997; Kozak and Kang, 2006).

Regarding to the multiple statistical procedures which have been used in this study indicated that biological yield, harvest index and chlorophyll content were the important variables influencing seed yield and can be used as selection criteria for improving seed yield of bread wheat under saline conditions. Based on the results, it seems that biological yield and harvest index 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 based on the genetic diversity in biological yield and harvest index. Another advantage is that the harvest index, together with biological yield, can again be used as a simple and non-destructive measurement to evaluate large number of wheat genotypes in breeding programs. Also, these characters are a yield component and are easier to determine than yield and generally have a high heritability. Donald et al. (1976), Mohammed. (1999) and, Leiah and Al-Khateeb (2005) reported a high, positive, significant, correlation between biological yield and harvest index with seed yield.

Also, the results of different statistical procedures this study indicated that chlorophyll content was one of the most effective traits on seed yield under saline conditions. Salinity stress significantly reduces the total chlorophyll content and the rate of reduction in total chlorophyll depending on salt tolerance of plant species and salt concentrations. In salt-tolerant species, chlorophyll content increased, while in salt-sensitive species it was decreased (Ashraf and McNeilly, 1988). Plant physiologists have found chlorophyll content to be a valuable tool to monitor plant stress response. The chlorophyll content meter is useful for improving nitrogen and fertilizer management and is ideal for crop stress, leaf senescence, plant breeding, health determination and other studies (Peñuelas and Filella 1998; Gitelson et al., 2003). Determination of the relationships of the chlorophyll content, yield and yield components facilitates selection of high yielding varieties from breeding programs (Singh, 2001). The results of different statistical procedures revealed that leaf chlorophyll content was one of the effective traits on seed yield under saline conditions. Similar to these results, Araus et al. (1998), Kabanova and Chaika, (2001), Ramesh et al. (2002), Boggs et al. (2003) and Bronson et al. (2003) were found a positive correlation between leaf chlorophyll content and yield for wheat and other crops. In the present study, the results revealed that leaf chlorophyll content due to rapid and non-destructive measurement can be advised one of the indicators in the improvement of seed yield in bread wheat under saline conditions.

Generally, analysis of four statistical procedures which have been used this study revealed that biological yield, harvest index and chlorophyll content were the most important traits influencing seed yield under saline conditions. This was clear with all used statistical procedures (Table 7). Therefore, high yield of wheat plants under saline conditions can be obtained by selecting breeding materials with high biological yield, harvest index and chlorophyll content.

Table 7
The characteristics effective on seed yield of bread wheat under saline conditions with each one of the used statistical procedures.

Variables	1+	2	3	6
Own length (X_1)	√			
Number of seed per spike (X_2)				
Number of fertile tiller (X_3)	√			
Number of spikelet per spike (X_4)				
Flag leaf length (X_5)				
The 100-seed weight (X_6)	√			
Seed weight per spike (X_7)	√			
Peduncle weight (X_8)				
Spike weight (X_9)	√			
Chlorophyll content (X_{10})	√	√	√	√
Plant height (X_{11})	√			
Days to heading (X_{12})	√			
Days to maturity (X_{13})	√			
Spike length (X_{14})				
Peduncle length (X_{15})	√			
Harvest index (X_{16})	√	√	√	√
Biological yield (X_{17})	√	√	√	√

1+ = Simple correlation, 2 = Multiple linear regression, 3 = Stepwise multiple linear regression and 4 = Path analysis .

References

Andales, A.A., Green, T.R., Ahuja, L.R., Erskine, R.H., Peterson, G.A., 2007. Temporally stable patterns in grain yield and soil water on a dryland catena. Agri. Syst., 94, 119-127.

Ashraf, M., Wu, L., 1994. Breeding for salinity tolerance in plants. Crit. Rev. plant Sci., 13, 17-42.

Basalma, D., 2008. The correlation and path analysis of yield and yield components of different winter rapeseed (*Brassica napus* ssp. *oleifera* L.) cultivars. Res. J. Agri. Biol. Sci., 4, 120-125.

Board, J., Kang, M., Harville, B., 1997. Path analyses identify indirect selection criteria for yield of late-planted soybean. Crop Sci., 37, 879-884.

Boggs, J.L., Tsegaye, T., Coleman, T.L., Reddy, K., Fahsi, A., 2003. Relationship between hyperspectral reflectance, soil nitrate-nitrogen, cotton leaf chlorophyll, and cotton yield: a step toward precision agriculture. J. Sustain. Agri., 22, 5-16.

Bronson, K.F., Chua, T.T., Booker, J., Keeling, J.W., Lascano, R.J., 2003. In-season nitrogen status sensing in irrigated cotton. Soil Sci. Soc. Am. J., 67, 1439-1448.

Colmer, T., Munns, R., Flowers, T., 2006. Improving salt tolerance of wheat and barley: future prospects. Anim. Pro. Sci., 45, 1425-1443.

Dehghani, H., Dvorak, J., Sabaghnia, N., 2012a. Biplot Analysis of Salinity Related Traits in Beard Wheat (*Triticum aestivum* L.). Ann. Biol. Res., 3 (7), 3723-3731.

Dehghani, H., Dvorak, J., Sabaghnia, N., 2012b. Graphic analysis of biomass and seed yield of beard wheat in salt stress condition. Ann. Biol. Res., 3 (9), 4246-4253.

Dewey, D.R., Lu, K., 1959. A correlation and path-coefficient analysis of components of crested wheatgrass seed production. Agron. J., 51, 515-518.

Donald, C., Hamblin, J., 1976. The biological yield and harvest index of cereals as agronomic and plant breeding criteria. Advan. Agron., 28, 361-405.

Draper, N.R., Smith, H., 1966. Applied linear regression, Wiley., New York.

Flowers, T., Yeo, A., 1995. Breeding for salinity resistance in crop plants: where next? Funct. Plant Biol., 22, 875-884.

Gitelson, A.A., Merzlyak, M.N., 2003. Relationships between leaf chlorophyll content and spectral reflectance and algorithms for non-destructive chlorophyll assessment in higher plant leaves. J. plant physiol., 160, 271-282.

Gravois, K.A., McNew, R.W., 1993. Genetic relationships among and selection for rice yield and yield components. Crop Sci., 33, 249-25

Hiltbrunner, J., Streit, B., Liedgens, M., 2007. Are seeding densities an opportunity to increase grain yield of winter wheat in a living mulch of white clover? Field Crops Res., 102, 163-171.

Houshmand, S., Arzani, A., Maibody, S.A.M., Feizi, M., 2005. Evaluation of salt-tolerant genotypes of durum wheat derived from in vitro and field experiments. Field Crops Res., 91, 345-354.

Kabanova, S., Chaika, M., 2001. Correlation analysis of triticale morphology, chlorophyll content and productivity. J. Agron. Crop Sci., 186, 281-285.

Kang, M.S., Miller, J., Tai, P., 1983. Genetic and phenotypic path analyses and heritability in sugarcane. Crop Sci., 23, 643-647.

Kozak, M., Kang, M.S., 2006. Note on modern path analysis in application to crop science. Commun. Biometry Crop Sci., 1, 32-34.

Kumbhar, M.B., Larik, A.S., Hafiz, H.M., Rind, M.J., 1983. Wheat Information Services 57, 42–45.

Leilah, A., Al-Khateeb, S., 2005. Statistical analysis of wheat yield under drought conditions. J. Arid Environ., 61, 483-496.

Milani, P., Malakouti, M., Khademi, Z., Balali, M., Mashayekhi, M., 1998. A fertilizer recommendation model for the wheat field of Iran. Soil and Water Research Institute, Tehran, Iran.

MINITAB INC, 2005. Minitab user's guide, vers. 14. Minitab Inc, Harrisburg, Pennsylvania., USA.

Moghaddam, M., Ehdaie, B., Waines, J., 1998. Genetic variation for and interrelationships among agronomic traits in landraces of bread wheat from southwestern Iran. J. Genet. Breeding., 52, 73-82.

Mohamed, N., 1999. Some statistical procedures for evaluation of the relative contribution for yield components in wheat. Zagazig J. Agri. Res., 26, 281-290.

Mohammadi, M., Karimizadeh, R., Shefazadeh, M.K., Sadeghzadeh, B., 2011. Statistical analysis of durum wheat yield under semi-warm dry land condition. Aust. J. Crop Sci., 5, 1292-1297.

Munns, R., James, R.A., 2003. Screening methods for salinity tolerance: a case study with tetraploid wheat. Plant and Soil., 253, 201-218.

Naser, S., Leilah, A., 1993. Integrated analysis of the relative contribution for some variables in sugar beet using some statstical techniques. Bulletin of the Faculty of Agriculture, University of Cairo., 44, 253-266.

Peñuelas, J., Filella, I., 1998. Visible and near-infrared reflectance techniques for diagnosing plant physiological status. Trends plant sci., 3, 151-156.

Poormohammad Kiani, S., Maury, P., Nouri, L., Ykhlef, N., Grieu, P., Sarrafi, A., 2009. QTL analysis of yield-related traits in sunflower under different water treatments. Plant Breeding., 128, 363-373.

Ramesh, K., Chandrasekaran, B., Balasubramanian, T., Bangarusamy, U., Sivasamy, R., Sankaran, N., 2002. Chlorophyll dynamics in rice (*Oryza sativa* L.) before and after flowering based on SPAD (chlorophyll) meter monitoring and its relation with grain yield. J. Agron. Crop Sci., 188, 102-105.

Richards, R., Dennett, C., Qualset, C., Epstein, E., Norlyn, J., Winslow, M., 1987. Variation in yield of grain and biomass in wheat, barley, and triticale in a salt-affected field. Field Crops Res., 15, 277-287.

Rozema, J., Flowers, T., 2008. Crops for a salinized world. Sci., 322, 1478-1480.

SAS Institute Inc., 2011. SAS/STAT user's guide, second edition. SAS institute Inc., cary, Nc.

Shannon, M.C., 1997. Adaptation of plants to salinity. Advan. Agron., 60, 75-120.

Singh, S.P., 2001. Broadening the genetic base of common bean cultivars. Crop Sci., 41, 1659-1675.

Snedecor G.W., Cochran W.G., 1981 Statistical Methods. 7th ed. Lowa State University Press, Iowa., USA.

Wright, S., 1921. Correlation and causation. J. Agri. Res., 20, 557-585.

Xue, Q., Zhu, Z., Musick, J.T., Stewart, B., Dusek, D.A., 2006. Physiological mechanisms contributing to the increased water-use efficiency in winter wheat under deficit irrigation. J. plant Physiol., 163, 154-164.