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Original article

Interrelationships between seed yield and related traits in bread wheat genotypes in non-saline and saline environments

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ABSTRACT

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Study of the interrelationships between yield and its components will improve the efficiency of breeding programs especially under saline conditions through appropriate selection criteria. The present research factor analysis was used to obtain more information on the relationship between various characteristics and profound understanding of data structures. Forty one genotypes of bread wheat were grown in two environments (non-saline and saline conditions) based on randomized complete block design with three replications. Electrical conductivity of irrigation water was 2 and 11 dS.m⁻¹ in non-saline and saline environments, respectively. Results indicated that in non-saline environment selection based on the fourth factor including own length and biological yield efficiency have the highest community and high relative contribution in wheat seed yield. On the other hand, the results of factor analysis in the saline environment showed that the selection based on the first factor including biological yield, peduncle length, plant height and chlorophyll content will has the most effectiveness in the seed yield. Therefore, it seems that high yield of wheat plants under saline environments can be obtained by selecting breeding materials with high biological yield, peduncle length, plant height and chlorophyll content.

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1. Introduction

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 production of bread wheat can be enhanced through the development of improved genotypes that are able to production of high yield under different environmental conditions and environmental stresses types, including salinity stress (Colmer et al., 2006). Salt tolerance in bread wheat could be improved by exploiting genetic variation landraces and progenitors using conventional selection methods and breeding techniques. Screening for salt tolerance is an essential part of the breeding programs and several screening and selection schemes have been suggested for salt tolerance improvement in wheat (Houshmand et al., 2005). Salt tolerance of crops may vary with their growth stage (Mass et al., 1994). 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. On the other hand, 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 is as final target of the plant breeders under saline conditions (Dehghani et al., 2012a). Therefore, the evaluation of final seed yield and growth parameters determining seed yield is a critical aspect of breeding programs. But yield is a complex quantitative trait, considerably affected by environmental factors and usually has a low heritability (Sabaghnia et al., 2010). So, the improvement of seed yield through its direct selection and selection of genotypes based on yield is not effective especially under stress conditions in the field. Since the final yield of wheat is determined by yield components. Therefore, the related characters yield and yield components due to easy measurement and having a high heritability can be used as criteria for distinguish salinity tolerant plants and for improvement of seed yield in wheat genotypes especially under stress conditions in the field. The knowledge of genetic association between seed yield and its components under saline conditions would improve the efficiency of breeding programs by identifying appropriate indices for selecting wheat genotypes (Dehghani et al., 2012b). Different statistical techniques have been used to evaluate yield and yield components for breeding programs including correlation, regression, path analysis, factor analysis, principal component and cluster analysis (Leilah and Al-Khateeb, 2005).

Correlation coefficient is an important statistical procedure to evaluate breeding programs for indirect selection of genotypes for higher seed yield (Mohamed, 1999; Hiltbrunner et al., 2007). Simple correlation analysis may not provide a complete understanding about the importance of each component in determining seed yield (Dewey and Lu, 1959). Factor analysis uses to obtain more information on the relationship between various characteristics and profound understanding of data structures. Too, this technique is often used in data reduction to identify a small number of factors that explain most of the variance observed in much larger number manifest variables. Factor analysis attempts to identify underlying variables, or factors, that explain the pattern of correlations within a set of observed variables (Walton, 1972). This technique for the evaluation of different trait relationships was used by (Moghaddam et al., 1998; Mohamed, 1999; Leilah and Al-Khateeb, 2005) in wheat. It has been also used in soybeans (Leilah et al., 1988) and sesame (El-Deeb and Mohamed, 1999).

The main objective of this research was determine the interrelationships between grain yield and related traits in bread wheat by factor analysis and identifying traits which may be useful in breeding higher-yielding genotypes under saline environments in field.

2. Materials and Methods

The experiments were carried out in two non-stress and stress location at the research field of the National Salinity Research Center (NSRC) at Yazd, Iran. The forty one genotypes of bread wheat (*Triticum aestivum* L.) were used in this experiment. All wheat genotypes were selected from the germplasm collection at the Iranian Institute of Seed and Plant Improvement Institute (SPII), Karaj, Iran. Before starting the experiments was conducted

sampling in the different layers of soli (0-30, 30-60, 60-90 cm depth) in both conditions. Relevant soil characteristics of the experimental sites are given in Table 1.

The genotypes cultivated in two non-saline and saline-stressed environments with 3 replications in from of randomized complete block design. The salinity of water used in irrigation in saline and non-saline environments was 10 and 2 dS.m⁻¹ respectively. 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. 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 P₂O₅ ha⁻¹ and 80 kg K₂SO₄ 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 in saline and non-saline environments was 9.5 and 2.7 dS.m⁻¹ respectively. 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 subsample 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 nondestructive 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 (X17) 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. Then Factor analysis was used to obtain more information on the relationship between various characteristics and profound understanding of data structures. Data analysis was performed using SPSS version 19 statistical software.

3. Results and discussion

The analysis of variance results indicated highly significant differences in bread wheat genotypes for all traits under study (data not shown). In order to obtain more information on the interrelationships between various characteristics and profound understanding of data structures was used factor analysis. Results of factor analysis in the non-saline environment indicated that five main factors (groups) were accounted for 77.15% of the total variation in the dependent structure (Table 2). The first factor represents 32.4% of the total variation of the data and this factor includes number of seed per spike, number of spikelet per spike, seed weight per spike and spike weight. The suggested name for this factor is yield components. The second factor included number of fertile tiller, the 100-seed weight, peduncle weight, plant height and peduncle length which accounted for 18.5% of the total variation of the data and it was named the economical yield. The third factor represents 11.2% of the total variation of the data and this factor includes flag leaf length, chlorophyll content, days to heading and days to maturity. The suggested name for this factor is maturity characteristics. The fourth factor included seed yield, own length and biological yield which accounted for 8.4% of the total variation of the data and it was named the seed yield. The fifth factor represents 6.5% of the total variation of the data and this factor includes spike length and harvest index. The suggested name for this factor is harvest index. According to the results of factor analysis, it seems that the selection based on the fourth factor will has the most effectiveness in the seed yield. Therefore, the selection based on the fourth factor included own length and biological yield efficiency have the highest community and high relative contribution in wheat seed yield under non-saline environments (Table 3).

Factor analysis in the saline environment showed that five main factors (groups) were accounted for 75.5% of the total variation in the dependent structure (Table 4). The first factor represents 26.3% of the total variation of the data and this factor includes seed yield, biological yield, peduncle length, plant height and chlorophyll content. The suggested name for this factor is seed yield. The second factor included days to heading, days to maturity, number of spikelet per spike and own length which accounted for 20.0% of the total variation of the data and it was named the maturity characteristics. The third factor represents 13.3% of the total variation of the data and this factor includes spike weight, seed weight per spike, and number of seed per spike. The suggested name for this factor is yield components. The fourth factor included the 100-seed weight, flag leaf length and number of fertile tiller which accounted for 9.6% of the total variation of the data and it was named the economical yield. The fifth factor represents 6.2% of the total variation of the data and this factor includes harvest index, spike length

and peduncle weight. The suggested name for this factor is harvest index. According to the results of factor analysis in the saline environment, it seems that the selection based on the first factor will has the most effectiveness in the seed yield (Table 5). It seems that variables such as biological yield, peduncle length, plant height and chlorophyll content can be used as selection criterion for improving of seed yield in wheat under saline environments in field.

	Depth		1.	Meg.L ⁻¹				Р	к
Location	(cm)	рН	EC (dS.m ⁻) -	K⁺	Na⁺	Mg⁺	Ca⁺	(mg.kg ⁻¹)	(mg.kg⁻¹)
Normal	0-30	7.8	2.9	0.6	37.5	11	10	30.2	114
	30-60	7.5	2.3	0.7	30.8	7.5	9.6	17.45	121
	60-90	7.5	1.8	0.2	26.4	3.3	6.7	3.1	84
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	5.00	177
	60-90	7.3	9.58	0.9	219.7	61.7	48.3	3.7	201

Table 1

Soil properties of the two experimental sites.

Table 2

Rotated (Varimax rotation) factor loadings and communalities for the estimated variables of bread wheat in a non-saline environment

Variables	Factor1	Factor2	Factor3	Factor4	Factor5
Own length (X ₁)	0.01	-0.05	0.40	0.66	-0.02
Number of seed per spike (X ₂)	0.91	-0.23	-0.08	0.15	0.07
Number of fertile tiller (X_3)	-0.00	0.60	0.10	0.46	0.06
Number of spikelet per spike (X ₄)	0.63	-0.04	0.46	0.11	0.33
Flag leaf length (X ₅)	-0.01	0.02	-0.60	0.26	0.33
The 100-seed weight (X_6)	0.05	0.84	-0.22	0.00	-0.29
Seed weight per spike (X ₇)	0.89	0.36	0.14	0.07	-0.09
Peduncle weight (X ₈)	0.29	0.66	0.25	0.16	0.25
Spike weight (X ₉)	0.91	0.32	0.09	0.10	-0.01
Chlorophyll content (X ₁₀)	0.04	-0.06	0.68	0.01	0.11
Plant height (X ₁₁)	0.13	0.67	0.02	0.37	0.44
Days to heading (X_{12})	0.12	-0.10	0.84	-0.06	0.14
Days to maturity (X_{13})	0.18	0.35	0.74	0.24	-0.01
Spike length (X ₁₄)	0.35	0.21	0.03	0.15	0.74
Peduncle length (X ₁₅)	0.06	0.56	-0.34	0.45	0.24
Harvest index (X ₁₆)	0.42	0.08	-0.14	0.22	-0.74
Biological yield (X ₁₇)	0.29	0.32	0.10	0.83	-0.09
Seed yield (SY)	0.20	0.35	0.18	0.81	0.12
Latent roots	5.83	3.33	2.01	1.51	1.18
Factor variance (%)	32.41	18.53	11.21	8.41	6.57

Since, 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. 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. Simple correlation analysis may not provide a complete understanding about the importance of each component in determining seed yield. On the other hand, factor analysis can be used to obtain more information on the relationship between various characteristics and profound understanding of data structures.

Results factor analysis in this study indicated that biological yield, peduncle length, plant height and chlorophyll content were the important variables related to seed yield and can be used as selection criteria for improving seed yield of bread wheat under saline environments. Based on the results, it seems that biological yield, peduncle length, plant height and chlorophyll content 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, peduncle length, plant height and chlorophyll content. Another advantage is that these traits 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.

Table 3

Summary of factors loading for the estimated variables of bread wheat in a non-saline environment.

Variables	Loading	Total communality (%)	Suggested factor name
Factor 1	5.83	32.4%	Yield components
Number of seed per spike (X ₂)	0.91		
Number of spikelet per spike (X ₄)	0.63		
Seed weight per spike (X ₇)	0.89		
Spike weight (X ₉)	0.91		
Factor 2	3.33	18.5%	Economical yield
Number of fertile tiller (X ₃)	0.60		
The 100-seed weight (X_6)	0.84		
Peduncle weight (X ₈)	0.66		
Plant height (X ₁₁)	0.67		
Peduncle length (X ₁₅)	0.56		
Factor 3	2.01	11.2%	Maturity characteristics
Flag leaf length (X_5)	-0.60		
Chlorophyll content (X ₁₀)	0.68		
Days to heading (X_{12})	0.84		
Days to maturity (X_{13})	0.74		
Factor 4	1.51	8.4%	Seed yield
Seed yield(SY)	0.81		
Own length (X ₁)	0.66		
Biological yield (X ₁₇)	0.83		
Factor 5	1.18	6.5%	Harvest index
Spike length (X ₁₄)	0.74		
Harvest index (X ₁₆)	-0.74		
Cumulative variance	13.86	77.15%	

Table 4

Rotated (Varimax rotation) factor loadings and communalities for the estimated variables of bread wheat in a saline environment.

Variables	Factor1	Factor2	Factor3	Factor4	Factor5
Own length (X ₁)	0.21	0.62	-0.24	-0.25	-0.41
Number of seed per spike (X ₂)	-0.13	0.16	0.70	-0.49	0.13
Number of fertile tiller (X ₃)	0.24	0.32	-0.03	0.61	0.31
Number of spikelet per spike (X ₄)	-0.07	0.53	0.47	-0.31	-0.16
Flag leaf length (X₅)	0.25	0.26	0.24	0.72	0.03
The 100-seed weight (X_6)	0.16	-0.22	-0.08	0.82	-0.19
Seed weight per spike (X ₇)	0.19	-0.00	0.80	0.27	-0.14
Peduncle weight (X ₈)	0.47	0.34	0.02	0.01	0.53
Spike weight (X ₉)	0.00	-0.05	0.93	0.05	-0.06
Chlorophyll content (X ₁₀)	0.79	0.21	0.15	-0.10	0.19
Plant height (X ₁₁)	0.91	0.10	0.02	0.23	-0.04
Days to heading (X ₁₂)	-0.01	0.86	-0.00	-0.25	-0.19
Days to maturity (X_{13})	0.28	0.86	0.02	0.02	0.02
Spike length (X ₁₄)	0.14	0.22	-0.05	-0.00	0.65
Peduncle length (X ₁₅)	0.81	-0.22	0.02	0.26	0.05
Harvest index (X ₁₆)	-0.50	-0.22	-0.13	-0.10	0.67
Biological yield (X ₁₇)	0.68	0.36	0.23	0.22	0.00
Seed yield (SY)	0.83	0.26	0.03	0.15	0.17
Latent roots	4.74	3.60	2.40	1.73	1.11
Factor variance (%)	26.34	20.05	13.33	9.62	6.21

4. Conclusion

In summary, we tried to use factor analysis as a predictive tool for analysis of interrelationships between yield-related characters in bread wheat under both the non-saline and saline environments. Generally, factor analysis in this research indicated biological yield, peduncle length, plant height and chlorophyll content can be used as selection criterion for improving of seed yield in wheat breeding programs under saline environments. Therefore, high yield of wheat plants under saline environments can be obtained by selecting breeding materials with high biological yield, peduncle length, plant height and chlorophyll content.

Table 5

Summary of factors loading for the estimated variables of bread wheat in a saline environment.

Variables	Loading	Total communality (%)	Suggested factor name
Factor 1	4.74	26.3%	Seed yield
Seed yield (SY)	0.83		
Chlorophyll content (X ₁₀)	0.79		
Plant height (X ₁₁)	0.91		
Peduncle length (X ₁₅)	0.81		
Biological yield (X ₁₇)	0.68		
Factor 2	3.60	20.0%	Maturity characteristics
Own length (X ₁)	0.62		
Number of spikelet per spike (X ₄)	0.53		
Days to heading (X_{12})	0.86		
Days to maturity (X_{13})	0.86		
Factor 3	2.40	13.3%	Yield components
Number of seed per spike (X ₂)	0.70		
Seed weight per spike (X7)	0.80		
Spike weight (X ₉)	0.93		
Factor 4	1.73	9.6%	Economical yield
Number of fertile tiller (X_3)	0.61		
Flag leaf length (X ₅)	0.72		
The 100-seed weight (X_6)	0.82		
Factor 5	1.11	6.2%	Harvest index
Peduncle weight (X ₈)	0.53		
Spike length (X ₁₄)	0.65		
Harvest index (X ₁₆)	0.67		
Cumulative variance	13.51	75.55%	

References

- 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.
- El-Deeb, A., Mohamed, N., 1999. Factor and cluster analysis for some quantitative characters in sesame (*Sesamum indicum* L.). The Annual Conference ISSR., Cairo University.
- Flowers, T., Yeo, A., 1995. Breeding for salinity resistance in crop plants: where next? Funct. Plant. Biol., 22, 875-884.
- 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.
- Leilah, A., Al-Khateeb, S., 2005. Statistical analysis of wheat yield under drought conditions. J. Arid. Environ., 61, 483-496.
- Leilah, A., Badawi, M., El-Moursi, S., 1988. Yield analysis of soybean. J. Agric. Sci., 13, 2344-2351.

- Maas, E.V., Lesch, S.M., Francois, L.E., Grieve, C.M., 1994. Tiller development in salt-stressed wheat. Crop Sci., 34, 1594-1603.
- 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. Breed., 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.
- Munns, R., James, R.A., 2003. Screening methods for salinity tolerance: a case study with tetraploid wheat. Plant Soil., 253, 201-218.
- 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.
- Sabaghnia, N., Dehghani, H., Alizadeh, B., Mohghaddam, M., 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. Agri. Res., 8, 356-370.
- SPSS, I., 2010. SPSS 19. Users Guied. Chicago, IL., USA.
- Wright, S., 1921. Correlation and causation. J. Agri. Res., 20, 557-585.