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Analysis of Yield Stability and Adaptation of Durum Wheat Promising Genotypes in Temperate Region of Iran

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ABSTRACT
In order to determine stability and adaptation of promising durum wheat genotypes in temperate regions of Iran, eighteen durum genotypes in addition to Dena (durum) and Farsi (bread wheat) as control were studied in three regions of Neyshaboor, Karaj and Kermanshah in a randomized complete blocks design. Since the interaction effects of genotype× year × location was significant, for accurate evaluation of interaction effects and determination of stable genotypes Eberhart, Russel and Ammi methods were used for determine genotypes satiability. The results showed that based on the most used methods genotypes 14 (INTER_16/SNITAN/...), 4 (SNTTAN*2/RBC) and 9 (CBC509CHILE/...) showed good stability and genotypes 14 by producing 7.871 t/ha grain yield showed the best stability and based on Ammi method in five location recognized as superior genotype and genotypes 20 (Farsi), 7 (PNE/2*RASCON_37/3//...) and 8 (PNE/2*RASCON37.3/...) based on the used methods showed weak satiability.
Keywords;Durum wheat, Yield comparison, Satiability analysis, Genotype× environment interaction

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INTRODUCTION
Cereal is the most important world crop and supply 70% of food and ¾ energy and half of protein of world population. The whole world cereal production is 32.3 million tones and wheat has the highest production (500-600 million ton) and the highest harvesting area among cereal crops [1]. About 90% of produced wheat is bread wheat and only 10% is durum while value of durum wheat is higher than bread wheat [2].
Understanding genotype×environment interaction help researcher for better evaluation of genotypes by reducing interaction effect, eliminating unnecessary location and reducing cost and losing resources in unnecessary location. All crop breeder believed the yield satiability but there is no a single agreement on satiability definition and methods of measuring it. There are different methods for evaluating genotype× environment interaction and deterring stable genotypes. Each researcher prefers a method based on the location condition, crop and other factors [3]. Ashraf *et al* [4] by studied in durum and bread wheat respectively, concluded that Eberhart and Russel methods are appropriate methods for demining stable genotypes.
Dogan *et al.* [5] evaluated the adaptation of some soft wheat genotypes in Marmara region of Turkey using 7 wheat genotypes including Momtchill, katea-1، Atilla-12, Kirkpinar-79, Tosun-22, Gemini and Cumhuriyet-75 during 9 years. They used grain yield as a criterion for genotypes satiability also three stability induces including regression coefficient, deviation from regression mean square and coefficient of determination were calculated. Based on the stability parameters Momtchill, katea-1, Gemini and Kirkpinar-79 were stable genotypes which among them Momtchill, katea-1, and Kirkpinar-79 by

producing the higher grain yield than ground mean determined as the best genotypes for all locations. Tosun-22 and Atilla-12 recognized as stable genotypes for unfavorable condition and Cumhuriyet-75 was suitable for favorable environment.

Askarinia *et al*. [6] evaluated the genotype× environment interaction for yield and yield components in 10 wheat genotypes in 8 environments and yield stability based on the Eberhart and Russel methods showed that Pishtaz and Moghan1 by producing higher yield than man of all genotypes and linear regression coefficient near to 1 have good general satiability while, genotypes Khazar and Alvand with favorable environment and Falat, Darab and Roshan with unfavorable environment showed private adaptation.Tarakanovas and Ruzaz [7] evaluated genotype× environment interaction and yield satiability of 13 winter wheat genotypes in four locations in two years in Litovani. The used parameters regression coefficient (b_i), deviation from regression (S_{di}^2) and coefficient of determination (r^2) in this study. Analysis of regression showed that genotypes Zentos, Compliment, LIA3948, Elfas and Marshal are suitable for cultivation in wide range of environment while Vergas and Cubus genotypes were suitable for cultivation in favorable condition and Meunier was suitable for unfavorable environment.

Among multi variation methods AMMI or Additive Main effects and Multiplicative Interaction had been widely used for estimating genotype× environment interaction and stable genotypes [8, 9]. AMMI method is a combination of analysis of variance (ANOVA) and analysis to main parameters which can be used for evaluation of genotypes satiability. In this method first the main additive effects of genotype and environment estimate using ANOVA then multiplicative interaction calculates using analysis to main parameters [10]. It was reported that AMMI model explained the main part of interaction sum of square which had a specific pattern and can increased the accuracy of study [8, 9]. Tarakanovas & Ruzgas [7] also introduced AMMI method as an effective method for study genotype× environment interaction and stated that Biplot results obtained from this can determine appropriate genotypes for cultivation in specific environment. Abamuf and Allaric [11] obtained the main effects of genotype and environment and also genotype× environment interaction using AMMI method in rice genotypes and introduced AMMI method as the most suitable model for evaluation of interaction and determining stable genotypes. Kaya *et al.* [12] evaluated 20 wheat genotypes in 6 locations. They reported that first and second principal components (PCA1 and PCA2) is significant, and explained 78.64% of G×E interaction sum of squares. Biplot componentsshowed that genotypes with high PCA1and small PCA2, had high yield. Yield stability of 19 barley genotypes (*Hordeum vulgare* L.) at eight moderate temperature was studied by Fatahi and Yossefi [13], who reported that the Wrick'scovalence, the variance of a genotype's across environments and the parameter of AMMI1 model were the most suitable parameters and had adequate repeatability. The genotype 5 had high yielding and genotype 16 had low yielding and adapted to low yielding regions. Adaptability and stability of yield of 20hulless barley (*Hordeum vulgar* L.) in moderate areasin six locations (Karaj, Esfahan, Nyshaboor, Yazd, Birjand, Zarghan) fortwo years (2001-2003) was studied by Bahrami et al., 2009. ICNB93-328 and ALELI/4/MOLA/2 genotypes were identified as stable genotypes. GLORIA genotype was recognized specially for the unpropitious weak areas.

Different models have been done to determine the stability of various crops in various places. However, no stability study has been performed for durum wheat in Iran. The objectives of this study were to evaluate the grain yield of promising 18durum wheat genotypes to determine their stabilities using Eberhart and Russell and Ammi analysis.

MATERIAL AND METHOD

In this research eighteen durum genotypes in addition to Dena (durum) and Farsi (bread wheat) as control were studied in three regions of Neyshaboor, Karaj and Kermanshah in a Randomized Complete Blocks design with 3 replications in the 2011-2012 and 2012-2013. The names and genotypes/cultivars code numbers of the durum wheat genotypes are given in Table 1.Technical specifications and agronomic practice was the same in all regions. Genotypes were considered as fixed factors in analysis. Kermanshah station is located in West, Nishapur in Northeast and Karaj stations in northern of Iran. Geographical information for all stations (mean rainfall, annual temperature, latitude and longitude, and height above sea level) is shown in Table 2.

The experimental filed was under fallow in two previous years.In order to prepare the field, it was plowed in spring and then the clods were smashed by the cultivator for two times. The field was further prepared by using vertical disks two times before planting. Seeds were disinfected withBenomyl (2‰) fungicide before planting in order to prevent common bunt. The seeds were sown in plots consisting of 6 rows with a 20 cm row space. The seeding rates were about 400 seeds m^{-2} for all genotypes. The plots were fertilized with 25 kg N ha^{-1} and 50 kg P_2O_5 ha^{-1} at planting and 50 kg N ha^{-1} in spring at stem elongation. Broadleaf and grassy weeds were controlled with a mixture of herbicides Puma Super (1 lit ha^{-1})

andGranstar (20 g a.i) in the tillering stage. The control of the weeds in the treatment was achieved by spraying by using a TEE JET knapsack sprayer with the fixed pressure of 2 atmospheres and the capacity of 400 liters per hectare in the middle of the tillering stage. All of the planting process was carried out based on the particular requirements and custom practices of the region. In growing season date of emergence, days to heading, days to physiological maturing, percentage of lodging, reaction to plant disease and plant height was recorded on 5 selected plants.

Table 1. The code and Pedigree of genotypes

Code	Pedigree
1	PLATA_6/GREEN_17//SNITAN/4/YAZI_1/AKAKI_4//SOMAT_3/3/AUK/GUIL//GREEN
2	RISSA/GAN//POHO_1/3/PLATA_3//CREX/ALLA/4/STOT//ALTAR 84/ALD/5/A...
3	STOT//ALTAR 84/ALD
4	SNITAN*2/RBC
5	BCRIS/BICUM//LLARETA INIA/3/DUKEM_12/2*RASCON_21
6	1A.1D 5+10-6/3*MOJO//RCOL/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1
7	ALTAR 84/CMH82A.1062//ALTAR 84/3/YAZI_10/4/SNITAN/9/USDA595/3/D67...
8	PNE/2*RASCON_37/3/ARTICO/AJAIA_3//HUALITA/4/GUANAY
9	CBC 509 CHILE/5/2*AJAIA_16//HORA/JRO/3/GAN/4/ZAR
10	SORA/2*PLATA_12//SOMAT_3/4/STORLOM/3/RASCON_37/TARRO_2//RASCON...
11	LDN6D(6A)/3*ACONCHI/9/USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV_1...
12	RCOL/POHO_1/3/DIPPER_2/BUSHEN_3//SNITAN
13	GUANAY/4/YAZI_1/AKAKI_4//SOMAT_3/3/AUK/GUIL//GREEN/5/NUS/SULA//5*NU..
14	INTER_16/SNITAN/9/USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV_1/6/ARDEN...
15	RASCON_37/4/MAGH72/RUFO//ALG86/RU/3/PLATA_16/5/PORTO_3*2/6/ARMENT..
16	CF4-JS 40/10/PLATA_10/6/MQUE/4/USDA573//QFN/AA_7/3/ALBA-...
17	SABIL/3/AUK/GUIL//GREEN/4/AUK/GUIL//GREEN
18	SOOTY_9/RASCON_37/3/STOT//ALTAR 84/ALD
19	Triticum durum (Dena)
20	*Triticum aestivum* (Parsi)

Table 2. Climate -Geographical characteristics of experimented locations

Latitude	Longitude	Height above sea level(m)	Average temperature(C)	Average rainfall(mm)	location
36˚ /37	58˚ /29	1320	15/5	253	Neyshabour
35˚/48	50˚/57	1300	16	300	Karaj
34˚/23	47˚ /03	1320	14/3	444/7	kermanshah

At the end of the growing season, the yield of the seed was measured after eliminating the margins of 1*1 m areas from the two middle stacks. The yield was determined and expressed in ton per hectare (t ha^{-1}).

In combined analysis of variance genotype was considered as constant effect while year and location were considered as random effect. SAS software was used for variance analysis and Duncan multiple range test used for mean comparison of the data collected. The tables and figures were drawn using Office Word and Excel. The coefficient of determination (R^2) was computed from individual linear regression analyses. Also, the regression line intercept (a) was evaluated as a stability parameter [14], and the significance of the regression coefficient (the yield of a single genotype on the mean environment), and the grand means of dry-matter and seed yields, were tested by employing the t-test [15].

Two stability parameters were calculated based on the regression coefficient. Regression performance of each genotype in different locations calculating means over all the genotypes. In Ammi method, interaction between the first and second components (IPCA1, IPCA2) were used as stability parameters to genotype and environment. In order to better analyze the interaction of stability parameters ASV [16] was used. Also Biplot AMMI model was used to study the reaction of genotypes to environment. Biplot due to the graphical representation of the response of genotypes and environments in the interaction, are useful tool to identify adapted genotypes to specific environments. Excel, SAS, JMP, GENSTATE softwarewere used for statistical analysis.

RESULT AND DISCUSSION

Combined analysis of variance in three location and two years showed that the effects year, location, year×location, rep×year×location, genotype×year and genotype× location was not significant while genotype, genotype year×location were significant (P≤0.05, Table 3). Non-significant effect of year and location Indicated that there was no significant difference between year and location for yield. In other words, the physical and chemical properties of soil, climatic factors and management are little fluctuation in different years in different places. Based in accordance with the Classification Research Institute, Nishapur, Karaj and Kermanshah research stations, consider as moderate category. country and the great similarity with each other meteorological variables and the meteorological variables are very similar to each other.

Table 3: variance analysis of grain yield of durum wheat genotypes at three places and two years (2011-2013)

Change resources	Free degree (df)	Squares sum (SS)	Average sum (MS)
year	1	35.124	35.124 ns
place	2	107.549	53.774 ns
place× year	2	145.430	72.715 ns
Year ×repeat ×place	12	15.665	1.305 ns
genotype	19	7.309	0.385*
year× genotype	19	5.454	0.287 ns
place× genotype	38	8.851	0.233 ns
Year× genotype× place	38	13.680	0.360*
error	228	55.870	0.245
total	359	394.932	

CV=10.89; *,ns representing significance difference at probability level 5% and non-significance respectively.

Significant genotype effects are indicated genetic differences between cultivars. In combined analysis of variance due to the significant interaction between genotype and in places can be introduced genotypes in different places and years have changed and genotypes yield from year to year and from place to place has been different. Shah Mohammadi [17] also indicated that the interaction of genotype×location×year was significant for barley genotypes. Means comparison showed that the highest grain yield was obtained in genotype No. 14 by 7.87 t. ha^{-1} and the lowest average yield was achieved in genotype No. 8 by 7.87 t.ha^{-1} .

Table4: comparison average yield of studied durum wheat genotypes at different environments.

Genotype number	Average yield (ton/hectare)	genotype rate according to yield	Average yield (ton/hectare)
1	7.441 abcd	14	7.871 a
2	7.801ab	16	7.863 a
3	7.728abcd	2	7.801 ab
4	7.646abcd	6	7.793 ab
5	7.365abcd	17	7.77 abc
6	7.793ab	12	7.755 abcd
7	7.346abcd	3	7.728 abcd
8	7.096d	13	7.696 abcd
9	7.156bcd	20	7.65 abcd
10	7.618abcd	4	7.646 abcd
11	7.61abcd	18	7.636 abcd
12	7.755abcd	10	7.618 abcd
13	7.696abcd	11	7.61 abcd
14	7./871a	19	7.575 abcd
15	7.113cd	1	7.441 abcd
16	7.863a	5	7.365 abcd
17	7.77abc	7	7.346 abcd
18	7.636abcd	9	7.156 bcd
19	7.575abcd	15	7.113cd
20	7.65abcd	8	7.096 d

Average yield of genotypes (ton/hectare): $\bar{M}$=7/576

Mean that had the same letter, according to Duncan test at 5% level not significantly different.

Analysis of variance   of yield based on Eberhart and Russell [14] indicated that genotype and genotype×location was linear and deviation from the regression for genotypes was not significant while the effect of location, genotype×location+location was significant at 5% significant level (Table 5). No significant differences among genotypes indicate that genotypes had not significant genetic differences.

Table 5: Average squares analysis of studied durum wheat genotypes according to Eberhart and Russell method

Average sum	Free degree	Changes resources
0.35530^{ns}	19	genotype
4.3969^{**}	100	environment+(environment×genotype)
416.814^{**}	1	linear environment
0.1518^{ns}	19	Genotype at linear environment
0.2505^{ns}	80	Regression deviation
$^{ns}0.0746$	4	Genotype 1
0.2332^{ns}	4	Genotype 2
0.1380^{ns}	4	Genotype3
0.0236^{ns}	4	Genotype4
0.1764^{ns}	4	Genotype5
0.1389^{ns}	4	Genotype6
0.4377^{ns}	4	Genotype7
0.4341^{ns}	4	Genotype8
0.0723^{ns}	4	Genotype9
0.4594^{ns}	4	Genotype10
0.1782^{ns}	4	Genotype11
0.3286^{ns}	4	Genotype12
0.2580^{ns}	4	Genotype13
0.1706^{ns}	4	Genotype14
0.2958^{ns}	4	Genotype15
0.157^{ns}	4	Genotype16
0.1925^{ns}	4	Genotype17
0.421^{ns}	4	Genotype18
0.3464^{ns}	4	Genotype19
0.4732^{ns}	4	Genotype20
3.7512	19	total
0.245	228	Total deduction (squares)

**,ns representing significance difference at probability level 1% and non-significance respectively .

The difference deviation of regression was not significant, which indicating that the response of genotypes to environmental changes, compliance with the linear model. The difference deviation of regression   with 1 indicated that Genotypes regression coefficients had not significant difference with one that represents a general compatibility consistency of these genotypes (table 6).
Eberhart and Russell [14] used yield mean, regression coefficient and mean-square deviation of the regression of line for determination stable variety over a series of environments. They believed that a stable genotype has near zero estimates of the squared deviations from regression coefficient equivalent to 1. Because deviation from the regression line related to the unpredictable variability of each genotype, and regression coefficient also shows genotype-specific response to environment effects.
Using the results obtained, (Table 4), genotypes 14, 16, 2, 6.17, 12, 3, 13, 20, 4, 18, 10 and 11, had mean yield above the average, respectively and all cultivar had no significant regression coefficient and deviation from the regression line, and so had desirable compatibility. Among this cultivar, genotype No. 4 had the least deviation from the regression line and the highest coefficient of determination (0.99) so this cultivar was the most stable yield with higher yield than average. According to the results of the coefficient of determination genotypes 4, 9 6 and 1 had the highest coefficient of determination and were introduced as stable genotypes. our result in line with finding Petiios who suggested that instead of the mean squared deviation from the regression line, is better used the coefficient determination because this coefficient heavily dependent on the regression line and based on high stable genotype had the highest coefficient of determination.

Table 6: stability parameters for Eberhart regression method and Adaptability coefficient for durum wheat genotypes

Genotype	Average yield (t/ha)	Average sums regression deviation(S^2_{di})	Adaptability coefficient (R_i)^2	Regression coefficient(b_i)
1	7.441	0.0746^{ns}	0.98	0.98^{ns}
2	7.81	0.2332^{ns}	0.955	0.977^{ns}
3	7.728	0.1380^{ns}	0.977	1.062^{ns}
4	7.646	$\underline{0.0236}^{ns}$	0.996	1.142^{ns}
5	7.365	0.1764^{ns}	0.965	0.978^{ns}
6	7.793	0.1389^{ns}	0.981	$\underline{1.1874}^{ns}$
7	7.346	0.4377^{ns}	0.907	0.9056^{ns}
8	7.096	0.4341^{ns}	0.909	0.91^{ns}
9	7.156	0.0723^{ns}	0.983	0.921^{ns}
10	7.618	0.4594^{ns}	0.920	1.008^{ns}
11	7/61	0.1782^{ns}	0.961	0.925^{ns}
12	7.755	0.3286^{ns}	0.9369	0.967^{ns}
13	7.696	0.2580^{ns}	0.9484	0.9549^{ns}
14	7.871	0.1706^{ns}	0.963	0.924^{ns}
15	7.113	0.2958^{ns}	0.942	0.962^{ns}
16	7.863	0.157^{ns}	0.976	1.125^{ns}
17	7.77	0.1925^{ns}	0.967	1.048^{ns}
18	7.636	0.421^{ns}	0.913	0.924^{ns}
19	7.575	0.3464^{ns}	0.947	1.094^{ns}
20	7.65	$\underline{0.4732}^{ns}$	0.916	$\underline{0.997}^{ns}$

Ns non-significance respectively.

STABILITY ACCORDING AMMI METHOD

The result of analysis of variance according to AMMI method was shown in table 7. The effect of cultivar was significant at 5% that indicated significant difference among cultivar. The effect of environment was not significant but the heights of sum of square belong to environments that show effect of environment on gene expression for seed yield.

Interaction of genotype*environment was significant (P≤0.05). The significant interactions of genotypes × environments suggest that grain yield of genotypes varied across different location. The genotype* environment effects were accounted for 9.7% of total sum of squares which is almost four times the effect of genotype 2.23%) and a ninth effect Environment (87.99%). This represents a great variety of environments and the importance of environmental factors in the interaction of genotype and environment in the development of a quantitative trait such as grain yield.

the share of environment in the total variance greater than the proportion of genotype × environment interaction effects and the share of genotype × environment interaction also higher than the proportion of genotype. It was reported that 86.7% of the total sum of squares was attributable to environmental effects, 1.8% to genotypic effects, and 11.5% to G×E interaction effects [18].

Table 7: Variance analysis of AMMI method for grain yield of durum wheat genotypes at different places at 2011-2013

Average sum(MS)	SS%	Square sum(SS)	Free rate	changes
1.100		394.9	359	total
2.751		327.4	119	treatment
0.385^*	2.23	7.3	19	genotype
57.620^{ns}	87.99	288.1	5	environment
1.305^{ns}	4.79	15.7	12	block
0.336^*	9.78	32	95	genotype× environment effect
0.424^*	30.63	9.8	23	IPCA$_1$
0.380^*	25	8	21	IPCA$_2$
0.278^{ns}	44.37	14.2	51	Remaining
0.245		55.9	228	Incorporated error

*،ns representing significance difference at probability level 5% and non-significance respectively .

In order to analyze the interaction × environment using AMMI model, principal component analysis was done on the matrix remaining. Two principal components were significant (P≤0.05). First principal

component 30.63% and second principal component 25%, contributed of the total sum of squares of G×E interaction, respectively, so, the two components justified 55.63% of the total of the sum of squares of interaction. Remain component was declared 44.37% of G×E interaction sum of square. The AMMI model with two principal components (AMMI 2) seem appropriate. Kaya *et al.* [12] in illustrate of performances of 20 bread wheat genotypes across six environments showed that the first two principal component axes (PCA 1 and 2) were significant (p < 0.01) and cumulatively contributed to 78.64% of the total genotype by environment interaction. According to IPCA1 values genotypes No. 5, 9, 14 and 4, with the lowest IPCA1 are the most stable genotype, respectively and genotypes No. 12, 7, 20, and 2, respectively, with the greatest amount of the IPCA1 was the most unstable genotypes. According to IPCA2 values genotypes 7, 2, 4 and 17, respectively, with the lowest IPCA2 were the highest stability and genotypes 20, 8, 14 and 18 with the highIPCA2 values were most of the least stable genotype (Table 8). Based on IPCA2 and IPCA1 values genotype 4 with above-average performance (7.46 t. ha) was the most stable and genotypes 20 was the most unstable genotype. With the least value of ASV (AMMI Stability Value), Genotypes 5, 4, 1 and 9 were stable genotype whereas genotypes 20, 12,7 and 8 respectively with maximum ASV was unstable genotypes. According to this method genotype No. 4 with value and ASV (0.131) had second sustainability ranks among genotypes (Table 8). It is worth noting that by all three methods the unstable genotypes were genotypes No. 20 Persian bread wheat cultivars in this research.

Table 8: grain yield and first and second main components quantities of durum wheat genotypes

ASV	IPCA$_2$	IPCA$_1$	Average yield t/ha	genotype
0.2079	-0.14495	0.12168	7.441	1
0.5106	-0.01650	-0.41662	7.801	2
0.3990	-0.30174	-0.21115	7.728	3
0.1318	-0.04103	-0.10226	7.646	4
0.1132	0.11320	-0.00353	7.365	5
0.4747	-0.35188	-0.26017	7.793	6
0.6658	0.00025	0.54355	7.346	7
0.5672	0.55083	-0.11048	7.096	8
0.2236	0.22323	0.01142	7.156	9
0.3282	0.20165	0.21140	7.618	10
0.3400	0.28787	0.14775	7.61	11
0.7367	-0.07572	-0.59825	7.755	12
0.4456	-0.18957	0.32920	7.696	13
0.3915	0.38426	0.06139	7.871	14
0.4570	-0.25329	0.31054	7.113	15
0.3927	-0.34699	-0.15013	7.863	16
0.5095	-0.06450	-0.41260	7.77	17
0.5526	0.37722	0.32967	7.636	18
0.3683	0.22465	-0.23831	7.575	19
0.7886	-0.57699	0.43891	7.65	20

Average= 7/576

AMMI method was suggested for determination of yield stability in barley genotypes in temperate regions of Iran. The stability analysis based on The Wrick`s covalence, the variance of a genotypes across environments and the parameter of AMMI1 model and also pattern analysis showed that the genotype 5 was high yielding, stable and recommendable for all the regions. Genotype 16 was low yielding and adapted to low yielding regions [13]. In durum wheat, the main component coefficients were sustainable for the stable genotypes selection [19].

According AMMI model, among 5 environments Genotype No. 14 was superior genotype in 4 environments and in Kermanshah (2014-2015) was the dominant (best) genotype. Genotypes 13, 18 and 20 from 6 environments in 3 environment and Genotypes 2 and 12 from 6 environments in two environments were top genotype. Genotypes 16 (dominant), 6 and 3 had good compatibility in the Nyshabvr environment and demonstrated as the four superior genotype emerged in this environment. Genotype 20 (Persian wheat bread) was identified as superior genotypes in Karaj. Genotype No. 12 in Karaj and Kermanshah, Genotype No. 14 in Kermanshah and Genotype No. 18 in Nyshabvr environment were dominant genotype, respectively (Table 11). Based on AMMI model, genotypes No. 12, 2, 17 and 14 were four superior genotype in Kermanshah and Karaj, which reflects similar climatic conditions in these two environments in two different years (Table 9).

Table 9: grain yield and first and second components quantities for places

Superior genotypes respectively from right to left	ASV	IPCA$_2$	IPCA$_1$	Average ton at every hectare	Place code	Cropping year	place
18,13,14,20	0.4498	0.00631	0.36718	6.235	E1	1390-91	Karaj
14,13,20,18	1.0473	0.09857	0.66349	5.203	E2	1390-91	Neyshabour
14,17,2,12	0.5127	0.19645	0.37955	9.73	E3	1390-91	Kermanshah
14,17,2,12	1.5111	0.54601	0.85294	7.676	E4	1391-92	Karaj
3,20,6,16	0.4052	1.10157	0.30937	8.616	E5	1391-92	Neyshabour
10,13,18,14	0.7388	0.26685	0.51119	7.576	E6	1391-92	Kermanshah

($\overline{\mathbf{Y}}$)=7.506 t/$_{ha}$ =average yield

PATTERN ANALYSIS AND ENVIRONMENT STABILITY ANALYSIS
According to IPCA1 values and ASV, environments 5 and 1, with the lowest IPCA1 and ASV respectively, were stable environment and environment 4 and 2, with the highest amounts of IPCA1 and ASV, respectively, were unstable environments. So the environment of 4 and 2, with the highest amounts of IPCA1 and ASV greatest role in shaping the interaction of genotype and environment, respectively. (Figure 1, Table 9).
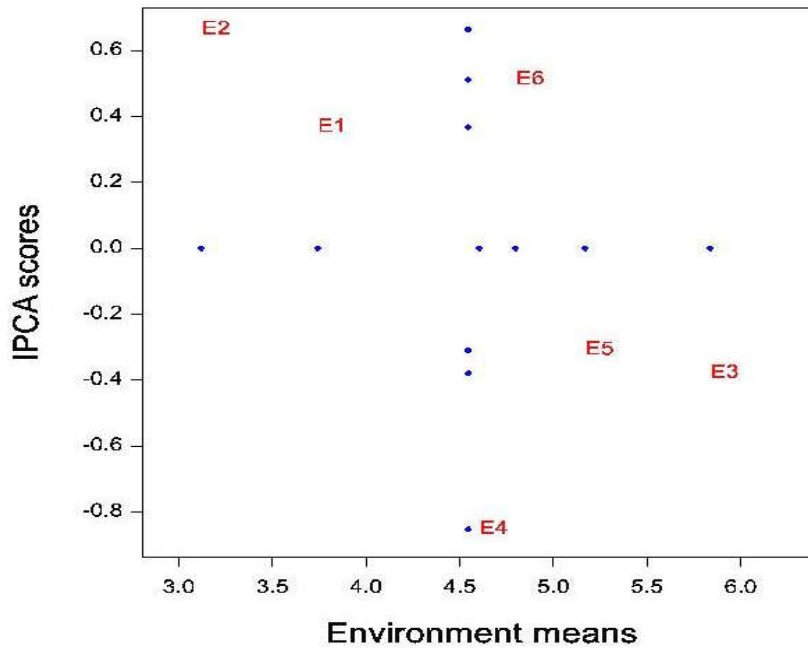

Figure 1 Biplotgraphs of averageenvironment based on IPCA$_1$

Grain quality and resistant to diseases, 18 elite durum wheat genotypes along with two commercial durum (Behrang) and bread wheat (Chamran) cultivars in four locations; Khorramabad, Darab, Dezfoul and Ahwaz, research stations in warm and dry areas of Iran in two growing seasons was studied by Aghaee-Sarbarzeh et al, (2014) who reported that the genotypes; DW-89-3, DW-89-4, DW-89-6, DW-89-8, DW-89-9, DW-89-10, DW-89-11, DW- 89-13 and DW-89-15 had shortest distance to the biplot center, and therefore had higher grain yield stability. Genotypes DW 89-8 and DW-89-11had also higher grain yield and their protein content and semolina extract rate were higher or similar to the cv. Behrang.Yan et al. (1999) revealed that in most years PC1 represents a proportional cultivar response across locations, which leads to no crossover GE interactions, while PC2 represents a disproportional cultivar response across locations, which is responsible for any crossover GE interactions. Consequently, genotypes with large PC1 scores tend to give higher average yield, and locations with large PC1 scores and near-zero PC2 scores facilitates identification of such genotypes [20]. Jahromi *et al*., [21] used Eberhart and Russell, coefficient of determination and AMMI methods for study of Stability analysis for grain yield of promising durum wheat genotypes in southern warm and dry agro-climatic zone of Iran andreported

that Among these genotypes, genotypes 5 (NUS/SULA//5*NUS/4/SULA/ RBCE_2/3/HUI//CIT71/CII) and 14 (CNDO/PRIMADUR//HAIOU_17/3/SN TURK MI83-84 375/ NIGRIS_5/ /TANTLO_1) with the average grain yield of 5926 kg.ha-1 and 5912 kg.ha-1, respectively, based on all methods, had grain yield stability.

According to the Eberhart and Russell, coefficient of determination and AMMI methods, genotype 14 (INTER_16 / SNITAN / ...), 4 (SNTTAN * 2 / RBC) and 9 (CBC509CHILE / ...) showed good stability and genotype 14   with 7.81 t.ha-1 (First rank in yield), were shown excellent stability and based AMMI method on five environmental were superior genotype and genotype 20 (Parsi (control), 7 (PN / 2 * RASCON_37 / 3 // ...) and 8 (PN / 2 * RASCON 37.3 / ...) showed poor stability Based on all methods.

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