Dissection of genotype × environment interaction and assessment of adaptability and grain yield stability of spring bread wheat genotypes

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ABSTRACT

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Additive main effects and multiplicative interactions (AMMI) and genotype (G) main effect plus genotype × environment interaction (GEI) GGE biplot models were used to dissect GEI interaction and to assess adaptability of 26 elite bread wheat lines. A multi environment trial was conducted using 26 elite bread wheat lines along with two check cultivars of Chamran and Chamran-2 in 2014-15 and 2015-16 cropping seasons across six testing sites including; Darab (DAR), Dezful (DEZ), Ahvaz (AHV), Khorramabad (KHR), Zabol (ZAB) and Iranshahr (ISH). The sites are representative of the major irrigated wheat production agro-ecologies in southern warm and dry zone of Iran. In each year, the trials at DAR, DEZ and KHR were grown under normally irrigated conditions while trials at AHV, ZAB and ISH were grown under terminal drought stress conditions. Mixed model analysis using Restricted Maximum Likelihood (REML) method showed significant differences among spring bread wheat genotypes for grain yield in all environments. The highest and lowest BLUE means was observed at KHR15 and ZAB15, respectively. Compared to irrigated environments, genotypes showed 35.4% losses, in average, of grain yield under terminal drought stress environments. Combined analysis of variance showed that genotype × environment interaction (GEI) accounted for 9.4% of the total sum of squares. Significant GEI suggests variability in performance of bread wheat genotypes across environments. Partitioning of GEI through AMMI analysis showed that axes IPCA1, IPCA2, and IPCA3 were highly significant (P>0.01) and explained 33%, 22%, and 13% of the GE sum of squares, respectively. The polygon view of the GGE biplot grouped environments into three sectors. AMMI method and GGE biplot showed that G5 had the highest grain yield stability. G5 and G15 were generally better adapted to terminal drought stress environments (AHV14, AHV15, ISH14, ISH15, ZAB14 and ZAB15), while G28 and G8 were more adapted to irrigated environment conditions. AMMI and GGE biplot methods separated the western and southwest regions from the south and southeast test locations for identifying superior adapted spring bread wheat genotypes. Results showed that geographical location had greater impact than the effect of moisture management on the grouping of genotypes. The specific adaptation strategy is suggested for identifying adapted spring bread wheat cultivars with high grain yield and yield stability for these target environments.

Keywords: spring bread wheat, AMMI model, GGE biplot, GE interaction, REML

INTODUCTION

Iran is one of the major wheat producers and consumers in the world. In recent years, climate change and successive droughts have limited the production of this important crop. In southern areas of Iran, drought and heat stresses during anthesis and grain-filling period are the most important wheat production constraints affecting both irrigated and rainfed wheats (Tahmasebi *et al*., 2014). Thus, the average wheat productivity in Iran is low compared to the global average.

In Iran, irrigated wheat breeding programs are led by the Seed and Plant Improvement Institute (SPII). These programs have been mainly focused on breeding high yielding and widely adapted varieties for four agro-ecological zones including; northern warm and humid zone (Zone 1), southern warm and dry zone (Zone 2), temperate zone (Zone 3) and cold zone (Zone 4) (Jalal Kamali *et al.*, 2012). Yield performance of genotypes in these regions is frequently influenced by unpredictable environmental conditions particularly in southern warm and dry areas (comprises more than 27% of wheat production areas of Iran). Under these conditions, breeders are always faced with significant genotype x environment interactions (GEI) that complicate the identification of superior adapted genotypes.

Drought and heat stresses during anthesis and grain-filling period and appearance of new yellow rust aggressive strains are the most important wheat production constraints in these areas (Jalal Kamali and Duveiller, 2006). Conventional breeding, as major method, is used to develop high yielding wheat cultivars in national wheat breeding programs. High grain yield and yield stability has always been an important objective of such breeding programs. Breeding the high yielding and widely adapted variety resistant to abiotic stresses is the main objective of wheat breeding research programs at SPII. In these programs, cultivars are mostly selected under the favorable conditions. However, SPII wheat breeding programs have recently focused on selection under the combination of both favorable and moisture stress conditions by assessment of elite wheat lines in multi-location yield trials to increase yield potential and improving yield stability.

Due to the high GEI, achieving yield stability is a major problem in stress-prone environments (Cattivelli *et al*., 2008). Diversity in the agro-ecology of the regions may have imposed significant GEI which is an obstacle to crop improvement (Tesemma *et al*., 1998; Yan and Kang, 2002). Knowledge of the nature and extent of GEI is useful to determine whether there is need to develop a widely adapted cultivar for all environments, or specifically adapted cultivars for specific target environments (Bridges, 1989). Selection of cultivars with a high degree of performance stability across a wide range of environments and grouping of the heterogeneous target areas into specific environments with more homogeneous conditions are two strategies to reduce the effects of GEI (Tai, 1979). Breeding cultivars adapted to the wide range of areas are more accepted by breeders due to the ease of working methods and cost-effectiveness of variety evaluation and seed multiplication (Matus-Cadiz *et al*., 2003).

The interpretation of GEI can be simplified in several ways using statistical modeling methods (Mohammadi and Amri, 2016). Multiplicative approaches such as additive main effects and multiplicative interaction (AMMI) (Crossa, 1990; Gauch, 1992) and genotype plus GEI (GGE) biplot analysis (Yan *et al*., 2000) are the most known and appealing methods for modelling GEI in multi-environment trials (METs) and to determine phenotypic stability of genotypes (Mohammadi and Amri, 2016). These multivariate models can help breeders to determine whether the target region is homogeneous or should be grouped into different mega-environments (Dardanelli *et al*., 2006). It also helps to evaluate test environments (Thomason and Phillips, 2006) to effectively identify superior genotypes within a mega-environment (Mohammadi *et al*., 2010). As defined by Yan *et al*. (2000), a mega-environment is a group of locations that consistently share the same best genotype(s).

The main objectives of this study were: (i) to analysis GEI and assess the adaptability and grain yield stability of spring bread wheat genotypes tested under optimum irrigation and terminal drought stress conditions at six test locations of the southern warm and dry zone of Iran, (ii) to identify high-yielding with yield

stability spring bread wheat genotypes with specific/broad adaptation to target areas.

MATERIAL AND METHODS
Plant materials and test locations

Multi environment trials were conducted using 26 elite bread wheat lines along with two check cultivars of Chamran and Chamran-2 (Table 1) in 2014-15 and 2015-16 cropping seasons at six testing sites including; Darab (DAR), Dezful (DEZ), Ahvaz (AHV), Khoramabad (KHR), Zabol (ZAB) and Iranshahr (ISH). The sites are representative of the major irrigated wheat production agro-ecologies in southern warm and dry zone of Iran. Description of testing locations is given in Table 2. In each cropping season, trials at DAR, DEZ and KHR were grown under normally irrigated conditions while trials at AHV, ZAB and ISH were grown under terminal drought stress conditions. In normally irrigated condition, genotypes were well irrigated throughout the cropping cycle while in terminal drought stress experiments, irrigation was stopped from late booting stage.

Genotypes in each trial were planted in 2×14 (2 sub-blocks and 14 entries per each sub-block) alpha lattice design (Patterson and Williams, 1976) with four replications. Plots consisted of six rows that were 6 m long with row spacing of 20 cm. Seeding rate was 400 seeds m^{-2} at each trial. Agronomic practices including fertilizer application and weed management were carried out as recommended at each location. Following harvest, grain yield (kg ha^{-1}) was determined for each genotype at each testing environment.

Table 1. Name and pedigree of 28 bread wheat cultivars/genotypes used in the study

Genotypes	Code	Name/Pedigree
S-93-1	G1	Chamran (check)
S-93-2	G2	WHEAR//2*PRL/2*PASTOR
S-93-3	G3	FRET2/KUKUNA//FRET2/3/PASTOR//HXL7573/2*BAU/5/FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ
S-93-4	G4	PBW343*2/KUKUNA//PARUS/3/PBW343*2/KUKUNA
S-93-5	G5	PASTOR/3/URES/JUN//KAUZ/4/WBLL1
S-93-6	G6	TEPOCA+LR34/ATTILA//TILHI/3/ATTILA*2/PBW65
S-93-7	G7	PGO/SERI//BAU/3/DUCULA/4/FRET2/KUKUNA//FRET2
S-93-8	G8	ROLF07/YANAC
S-93-9	G9	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/SAUAL
S-93-10	G10	GK ARON/AG SECO 7846//2180/4/2*MILAN/KAUZ//PRINIA/3/BAV92
S-93-11	G11	SOKOLL/ROLF07
S-93-12	G12	SOKOLL//FRTL/2*PIFED
S-93-13	G13	ATTILA/BAV92//PASTOR/3/ATTILA*2/PBW65
S-93-14	G14	SOKOLL*2/3/PASTOR//MUNIA/ALTAR 84
S-93-15	G15	ROLF07/3/T.DICOCCON PI94625/AE.SQUARROSA (372)//3*PASTOR
S-93-16	G16	ATTILA/BAV92//PASTOR/3/ATTILA*2/PBW65
S-93-17	G17	YAR/AE.SQUARROSA (518)/3/PRL/SARA//TSI/VEE#5/4/ATTILA/5/BERKUT
S-93-18	G18	ATTILA*2/PBW65/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/YR/4/TRAP#1/7/ATTILA/2*PASTOR
S-93-19	G19	WHEAR/SOKOLL
S-93-20	G20	MARCHOUCH*4/SAADA/3/2*FRET2/KUKUNA//FRET2
S-93-21	G21	KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/OTUS/TOBA97
S-93-22	G22	ONIX/ROLF07
S-93-23	G23	BABAX/LR42//BABAX/3/BABAX/LR42//BABAX/4/T.DICOCCON PI94625/AE.SQUARROSA (372)//3*PASTOR/5/T.DICOCCON PI94625/AE.SQUARROSA (372)//3*PASTOR
S-93-24	G24	SOKOLL/ROLF07
S-93-25	G25	CNDO/R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER/5/2*JANZ/6/SOKOLL
S-93-26	G26	ROLF07/3/T.DICOCCON PI94625/AE.SQUARROSA (372)//3*PASTOR
S-93-27	G27	GOUBARA-1/2*SOKOLL
S-93-28	G28	Chamran-2 (check)

Table 2. Description and characterization of testing locations in 2014-15 and 2015-16 cropping seasons

Location	Cropping season	Code	Moisture management	Altitude (m)	Latitude	Longitude	Temperature Min (°C)	Max (°C)	Ave (°C)	Rainfall (mm)
Darab	2014-15	DAR14	Irrigated	1080	28°47´ N	54°17´ E	10.93	26.07	18.50	202.0
	2015-16	DAR15	Irrigated				10.13	25.48	17.83	236.0
Dezful	2014-15	DEZ14	Irrigated	83	32°15´ N	48°25´ E	9.80	22.10	16.00	124.9
	2015-16	DEZ15	Irrigated				9.10	21.70	15.40	215.2
Khorramabad	2014-15	KHR14	Irrigated	1148	33°30' N	48°25' E	0.20	25.50	12.85	339.6
	2015-16	KHR15	Irrigated				-0.04	25.50	12.73	812.6
Ahvaz	2014-15	AHV14	Drought	18	31°24´ N	48°52´ E	14.00	26.90	20.40	127.0
	2015-16	AHV15	Drought				13.70	26.10	20.00	281.0
Zabol	2014-15	ZAB14	Drought	490	31° 18´ N	61° 15´ E	-4.00	47.40	23.80	110.9
	2015-16	ZAB15	Drought				-4.00	48.40	23.62	22.2
Iranshahr	2014-15	ISH14	Drought	591	27°15' N	60°40' E	10.20	45.50	27.85	37.4
	2015-16	ISH15	Drought				10.80	46.40	28.60	34.6

Statistical analysis

Mixed model analysis of data was performed using restricted maximum likelihood (REML) procedure in META-R V.6.01 software (Alvardo *et al.*, 2017). For each location in each cropping season, genotype was considered as fixed factors. Replicates and replicates × sub-block were added to model as random terms. Means of the genotypes were estimated as best linear unbiased estimates (BLUEs) in each of the 12 trials (6 locations × 2 years combination). The BLUEs were subjected to use in the next step in GGE biplot analysis.

Combined analysis of variance was performed with the PROC GLM procedure using SAS software (SAS Institute, 2008). Year was considered as random effects while location and genotype were treated as fixed effects. The RANDOM statement was set to the TEST option based on alpha lattice design.

AMMI analysis (Crossa, 1990) was emloyed to assess GEI and yield stability of genotypes in Genstat software version 15 (Payne *et al.*, 2012) using original data. In this method, principal component analysis (PCA) is used to decompose the GEI into a number of interaction principal component axes (IPCA). The AMMI model equation is as follows:

Equation (1) $Y_{ger} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + \varepsilon_{ger}$

For the additive parameters; Y_{ger} is the orginl data of yield for genotype (g) in environment (e) and replication (r), μ is the grand mean, α_g denotes genotype effect, β_e indicates environment effect, λ_n is the singular value for interaction principal component (IPC)n, γ_{gn} is the eigenvector value for genotype, δ_{en} is the eigenvector value for environment and ρ_{ge} is the residual and ε_{ger} is the error term. For more interpretation, AMMI's stability value (ASV) based on Purchase (1997) was calculated as follows:

Equation (2) $ASV = \sqrt{[(SSIPCA1/SSIPCA2)(IPCA1_{score})]^2 + (IPCA1_{score})^2}$

where SSIPCA1/SSIPCA2 is the weight given to the IPCA1 value by dividing the IPCA1 SS by the IPCA2 SS; and the IPCA1 and IPCA2 are the genotypic scores in the AMMI model.

Adjusted means (BLUEs) values of 28 bread wheat genotypes in each test locations and year were used for GGE biplot analysis using GenStat 15 (Payne *et al.*, 2012). The GGE model is as follows:

Equation (3) $Y_{ij} - Y_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$

where Y_{ij} is the average performance of genotype i in environment j, Y_j is the average performance of all genotypes in environment j, λ_1 and λ_2 are the singular values for PC1 and PC2, respectively, ξ_{i1} and ξ_{i2} arethe PC1 and PC2 scores, respectively, for genotype i, η_{j1} and η_{j2} are the PC1 and PC2 scores, respectively, for environment j, ε_{ij} is the residual of the model associated with the genotype i in environment j. The data were not transformed (Transform = 0), not standardized (Scale = 0), and were environment centered (centering =2).

RESULTS AND DISCUSSION
Grain yield comparison of wheat genotypes across locations

The results of REML mixed model analysis

for identification of differences between spring bread wheat genotypes across 12 trials using Wald test statistic are shown in Table 3.

Table 3. Variance component and basic statistical parameters from REML analysis of grain yield across six stations in 2014-2015 and 2015-2016 cropping seasons

Trial	Genotype variance	Residual variance	Grand Mean (BLUE) (kg ha⁻¹)	LSD	CV (%)
DAR14	102624*	514320	6340	1027	11.4
DAR15	107530**	389795	5544	896	11.3
DEZ14	170794**	158267	6023	567	6.6
DEZ15	119063**	284023	5310	762	10
KHR14	501631**	1152655	7760	1509	13.3
KHR15	616519**	1476775	8856	1709	13.7
AHV14	69476**	136707	4576	530	8.1
AHV15	100894**	272566	4307	747	12.2
ZAB14	75656*	184293	4163	1187	13.5
ZAB15	47615*	155575	4144	861	13.4
ISH14	72043**	292370	4164	774	13.1
ISH15	171288**	288770	4396	758	12.2

* and **: significant at the 5% and 1% probability levels, respectively.
BLUE= best linear unbiased estimators; CV = Coefficient of variation

Data analysis of grain yield showed that the differences between genotypes in all environments were significant. Grand mean of genotypes (BLUEs) across six testing locations in two cropping season ranged from 4984 kg ha⁻¹ (for G9) to 6107 (for G12), while grand mean of the checks was 5227 (for G1) and 5561 kg ha-1 (for G28). The highest and lowest BLUE means of trials were observed at KHR15 and ZAB15, respectively (Table 4). Compared to irrigated trials (DAR14, DAR15, DEZ14, DEZ15, KHR14 and KHR15), genotypes showed 35.4% loss, in average, of grain yield under terminal drought stress trials (AHV14, AHV15, ZAB14, ZAB15, ISH14 and ISH15) (Table 4).

Table 4. Adjusted means (BLUEs) of 28 spring bread wheat genotypes in 12 environments

Genotype	AHV14	AHV15	DAR14	DAR15	DEZ14	DEZ15	ISH14	ISH15	KHR14	KHR15	ZAB14	ZAB15	Genotype Mean
G1 (Check)	4250	4203	5988	5170	5644	5390	3850	4053	8406	7883	3953	3929	5227
G2	5072	4732	6555	5651	5508	5175	4964	4221	9090	9350	4260	3942	5710
G3	4675	4917	6563	5891	6205	5223	4030	4554	6529	9013	4530	3830	5497
G4	4164	4348	5323	4843	5519	5385	4273	3097	7783	8569	3588	3722	5051
G5	4853	4296	6866	5555	6046	5501	4074	4821	8385	10550	4722	4236	5825
G6	4405	4201	6485	5316	6077	4734	4466	4829	7373	8485	4046	4649	5422
G7	4500	4395	6766	5995	5683	4920	4555	5149	6340	9371	5395	4130	5600
G8	4550	3361	7067	6199	6398	5817	4670	4940	7863	6867	5366	4892	5666
G9	4643	3328	5483	5288	6004	4979	3705	3919	6854	7556	4285	3767	4984
G10	4791	4129	6409	5791	6093	4985	4145	4519	7458	9304	3825	3967	5451
G11	4584	4791	6152	5332	5796	4803	4068	4961	7331	7875	3783	4559	5336
G12	4988	4608	6948	6424	6960	5904	4434	4511	8548	10731	4753	4478	6107
G13	4072	4331	5768	4916	5565	4560	4365	4021	6688	8213	3427	4020	4996
G14	3548	3985	5537	5193	6317	5338	4493	4345	8065	9060	3387	4763	5336
G15	4715	4395	6617	5995	6677	5852	3348	4023	8835	8765	4621	4028	5656
G16	4576	4580	6248	6224	5499	4830	4681	3684	7733	8496	4125	3913	5382
G17	4629	4870	6142	5524	5644	5457	4779	4103	6446	8917	3807	3924	5354
G18	4516	4152	6254	5953	6210	5593	3800	4050	8202	7823	4236	3506	5358
G19	4787	4268	6318	5097	5779	5626	4306	4089	8346	9154	4259	4152	5515
G20	4548	4434	5692	5268	5911	4475	3907	4900	6360	7142	3677	4028	5029
G21	4529	4591	6868	5444	6858	5858	3891	4021	8953	10442	3748	4653	5821
G22	4894	4535	6248	4841	5540	5529	3999	3816	7408	8748	3645	4266	5289
G23	4452	4175	6609	5372	5890	5425	4168	4630	9273	8588	4500	4503	5632
G24	4991	4920	6855	6353	6423	5855	4731	5045	8067	8881	3607	4338	5839
G25	4254	3509	6772	4914	5138	4801	3715	4808	6425	8844	4589	4350	5177
G26	4468	4315	6200	5328	6482	5984	3614	4510	8167	9833	4075	4097	5589
G27	4837	4314	5893	5768	6691	5602	4025	4289	7698	10719	3571	4105	5626
G28(Check)	4839	3937	6878	5599	6111	5080	3552	5181	8673	8813	4780	3291	5561
Trial Mean	4576	4308	6339	5544	6024	5310	4165	4396	7761	8857	4163	4144	

The results of the combined ANOVA across environments for the 28 spring bread wheat genotypes showed that all effects, except genotype × year, were significant on grain yield (Table 5). The location had the highest contribution (84.15%) to the total grain yield variation, while year contributed the least variation (Table 5). Genotype, genotype × location and genotype × location × year variations accounted for 2.93%, 4.8% and 3.4% of the total variation, respectively (Table 5).

The greater variation contributed by location than those from genotype and genotype interaction with other sources of variation indicated that the test locations were very different. Genotypic rank differences over test environments showed the existence of crossover GEI (Crossa, 1990) which showed the necessity to assess the response of the genotypes to environmental variation (Mohammadi and Amri, 2016). Significant GEI suggests inconsistency of performance of spring bread wheat genotypes across test locations.

Table 5. Combined analysis of variance for grain yield of 28 spring bread wheat genotype over six locations and two years

S. O. V.	d.f.	Sum of Squares	Contribution to total Sum of Squares (%)	Mean Squares	$P_r > F$
Year (Y)	1	2045698	0.06	2045698	0.0495
Location (L)	5	2805670495	84.15	561134099	<.0001
Rep. (Y × L)	36	197720304		5492231	<.0001
Blk (Rep. × Y × L)	48	42064716		876348	0.0038
Genotype (G)	27	97747648	2.93	3620283	<.0001
G × Y	27	18929576	0.57	701095	0.1246
G × L	135	160147937	4.80	1186281	<.0001
Y × L	5	136220940	4.09	27244188	<.0001
G × Y × L	135	113421982	3.40	840163	<.0001
Error	924	488699194		528895	
Corrected Total	1343	4089225586			
CV (%)	13.3				

Rep.: Replication.

AMMI analysis

AMMI analysis of variance showed highly significant differences (P>0.01) among genotypes, environments and for GEI (Table 6). Genotype effect explained 3.04% of the total (G + E + GEI) variation. GEI interaction accounted for 9.4% of the total sum of squares. Significant GEI suggests instability of the performance of spring bread wheat genotypes across testing locations. A large sum of squares for environments (explained 87.6% of the total variation) indicated that the environments were diverse, with large differences among environmental means causing variation in grain yield of genotypes. Partitioning of GEI through AMMI analysis showed that axes IPCA1, IPCA2, and IPCA3 were highly significant (P>0.01) and explained 33%, 22%, and 13 % of the GEI sum of squares, respectively (Table 6).

Table 6. Combined ANOVA and AMMI analysis for grain yield (kg ha^{-1}) of 28 bread wheat genotypes evaluated across six locations and two cropping seasons

S. O. V.	d.f.	Sum of squares	Mean squares	SS%
Treatments	335	3360741372	10032064**	
Genotypes	27	102135030	3782779**	3.0
Environments	11	2943937132	267630648**	87.6
Block	36	197720304	5492231**	
GE Interactions	297	314669209	1059492**	9.4
IPCA1	37	103916740	2808561**	33.0
IPCA2	35	69025034	1972144**	21.9
IPCA3	33	41370806	1253661**	13.1
Residuals	192	100356629	522691	31.9
Error	972	530763909	546053	

**: significant at the 1% probability level.

AMMI analysis showed differences among genotypes for grain yield and yield stability across environments. The IPCA score of a genotype in AMMI analysis is an indication of genotype's yield stability across environments. The closer IPCA score to zero, the higher is yield stability of a genotype across environments. Based on IPCA1 score and grain yield, G9, G5 and G4 were among the elite genotypes with high

relative yield stability across environments (Table 7). According to ASV ranking, G5 had the lowest value and the most yield stability.

Although G3 and G23 had relatively high yield stability across environments, their grain yield was relatively low (Table 7).

Table 7. Mean grain yield, IPCAs and AMMI stability values (ASV) for 28 spring bread wheat genotypes tested across 12 environments.

Genotype	Grand mean (kg ha⁻¹)	IPCA1	IPCA2	IPCA3	ASV	Genotype	Grand mean (kg ha⁻¹)	IPCA1	IPCA2	IPCA3	ASV
G1	5231	0.01	-17.44	5.72	17.44	G15	5619	16.06	23.15	-17.12	33.47
G2	6137	-16.90	5.93	-8.39	26.12	G16	5674	30.64	-23.97	-9.57	51.97
G3	5294	-2.45	3.48	8.43	5.07	G17	4970	13.30	-5.24	-4.49	20.69
G4	5653	-3.60	-21.36	-2.39	22.04	G18	5437	-2.86	8.50	-2.17	9.53
G5	5842	3.28	1.01	11.25	5.04	G19	5334	14.04	0.23	8.40	21.13
G6	5164	10.47	12.62	-21.26	20.19	G20	5001	7.80	9.74	12.99	15.26
G7	5597	-16.20	0.74	-7.35	24.40	G21	5356	-8.00	-2.70	11.77	12.35
G8	5606	-22.14	16.66	-1.18	37.25	G22	5646	-8.47	-17.58	-8.63	21.72
G9	5560	-1.14	-11.88	-20.77	12.01	G23	5384	4.08	-0.12	10.74	6.15
G10	5684	-10.06	-6.79	8.33	16.59	G24	5341	5.70	19.64	14.44	21.43
G11	5497	8.58	17.85	-3.61	22.03	G25	5353	3.64	-16.20	0.44	17.10
G12	5052	-9.38	-3.32	19.00	14.51	G26	5519	-8.59	-5.54	1.68	14.06
G13	5798	-16.13	6.97	-16.16	25.26	G27	5037	25.49	5.26	8.73	38.73
G14	5417	9.91	2.88	1.04	15.19	G28	5831	-27.10	-2.52	0.12	40.87

The graphical AMMI-2 analysis based on the first two principal components (PCA1 and PCA2) scores summarizes information of GEI. This method identifies genotypes with either broad or specific adaptation (Oladosu *et al*. 2017). Analysis of genotypic responses in AMMI-2 biplot (Fig. 1) indicates that genotypes could be classified into two different groups. The first group included genotypes; G3, G5 and G22 with the lowest IPCA1 and IPCA2 scores and the lowest contribution to GEI variation, so these genotypes tended to have general yield stability. The second group with the highest IPCA1 or/and IPCA2 had the highest contribution to GEI variation, thus they tended to have specific adaptation.
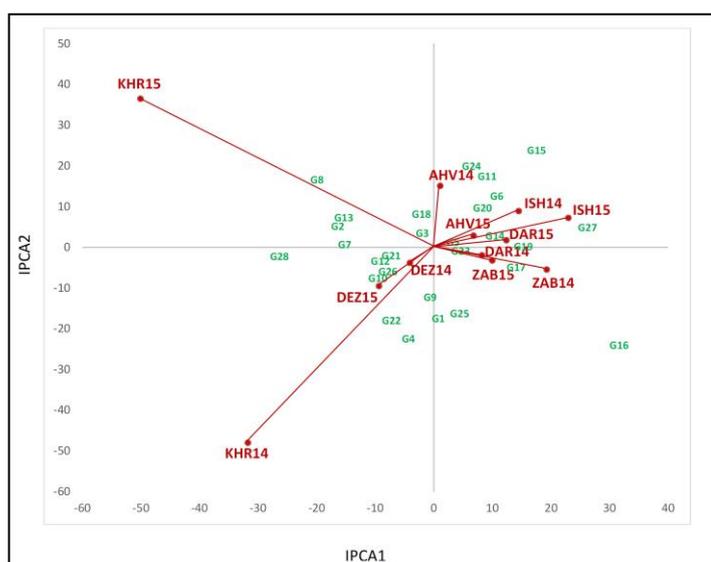
Fig. 1. Biplot based on values of two main components of GEI interaction (AMMI2 model). Environmental codes; DAR, ZAB, DEZ, AHV, KHR and ISH represent the field stations: Darab, Zabol, Dezful, Ahvaz, Khorramabad and Iranshahr, respectively. The numbers 14 and 15 next to the field stations codes represent 2014-15 and 2015-16 cropping seasons, respectively.

Variance, principal components and first four genotypes selected per environment based on AMMI analysis have been presented in Table 8. Among the studied genotypes, G15, G16 and G28 were clearly grouped apart from other genotypes. G28 and G8 were the most adapted genotypes to high yielding environments KHR14 and KHR15, respectively. In both DEZ environments and AHV14, G2 was the most adapted genotype. G16 had high specific adaption to DAR and ZAB environments in both cropping seasons (Table 8). G5 was highly adapted to AHV15 and ISH15 environments. G15 was highly adapted to the ISH15 (Table 8).

Grouping of environments into two groups of terminal drought stress and irrigated shows that G5 and G15 are generally better adapted to terminal drought stress environments (AHV, ISH and ZAB), while G28 and G8 are better adapted genotypes to irrigated conditions of KHR and DEZ. G2 and G16 had an reasonable adaption to both groups of environments (Table 8).

Table 8. Variance, principal components and first four genotypes selection in each environment based on AMMI analysis

| Environment | Variance | Principal component | | | First four genotype selections | | | |
		IPCA1	IPCA2	IPCA3	1	2	3	4
AHV14	225805	6.776	2.848	3.135	G2	G5	G16	G15
AHV15	442408	1.100	15.062	27.876	G5	G24	G2	G10
DAR14	747956	8.210	-1.966	-18.102	G16	G2	G15	G9
DAR15	1251688	12.390	1.715	-0.462	G16	G2	G5	G15
DEZ14	334679	-4.065	-3.857	-0.744	G2	G28	G13	G5
DEZ15	421926	-9.352	-9.565	5.552	G2	G28	G10	G4
ISH14	709684	14.500	8.861	28.115	G5	G24	G19	G23
ISH15	475854	22.983	7.214	-15.658	G15	G16	G2	G11
KHR14	1634279	-31.733	-48.016	3.769	G28	G4	G22	G10
KHR15	2094052	-50.081	36.456	-13.579	G8	G2	G28	G13
ZAB14	1378586	19.274	-5.479	-27.805	G16	G5	G2	G10
ZAB15	600997	9.996	-3.273	7.904	G16	G15	G9	G2

GGE biplot analysis across locations

GGE biplot analysis explained 47.17% (30.29% and 16.88% for PC1 and PC2, respectively) of the total variation caused by (G + GEI) based on grain yield BLUEs of spring bread wheat genotypes across 12 environments (Fig. 2). The GGE biplot is an effective model to identify genotypes with yield stability across environments and to identify the best genotype for mega-environment differentiation (Gauch *et al.*, 2008). The polygon view of the GGE showed spring bread wheat genotypes with relatively higher performance at each location. The perpendicular line drawn to each side of the polygon from the biplot origin divided the biplot into six sectors. Twelve environments were placed into three sectors. The subset of locations in each sector share the best set of genotypes (Yan and Rajcan, 2002). Terminal drought stress environments; ISH14, ISH15, ZAB14 and ZAB15, and irrigated DAR14 made up the first group. Irrigated environments KHR14, KHR15, DEZ14, DEZ15 and DAR15, and drought stress AHV14 were placed in the second sector, while AHV15 formed a single group. The genotype at the vertex in each sector is the best for the locations in that sector. Based on this, G16, G2 and G28 were the best genotypes at these three group, respectively (Fig. 2). The other genotypes within the polygon were less responsive than the genotypes at vertex.

Fig. 3 shows the ranking of the 28 spring bread wheat genotypes based on their mean grain yield and yield stability performance across 12 environments. Yan and Kang (2002) defined a line by the average PC1 and PC2 scores of all environments passing through the biplot origin and called it the average environment coordinate (AEC). The closer to a concentric circle the higher the mean performance. The yield stability of genotypes is showed by a line which passes through the origin and is perpendicular to the AEC. Direction close to

the biplot origin, on this axis, either indicates greater yield stability and reduced GEI. According to Fig, 3, G2 followed by G5, G13 and G22 were identified as genotypes with high grain yield and yield stability performances. Despite high performance and expectation, G16 and G28 (commercial checks) did not show high yield stability.

Fig. 2. Polygon of GGE biplot for determination o the superior spring bread wheat promising lines in different environments. Environmental codes; DAR, ZAB, DEZ, AHV, KHR and ISH represent the field stations; Darab, Zabol, Dezful, Ahvaz, Khorramabad and Iranshahr, respectively. The numbers 14 and 15 next to the field stations codes represent 2014-15 and 2015-16 cropping seasons, respectively.

Fig. 3. Biplot of the average-environment coordination (AEC) for simultaneously selection of grain yield and yield stability of spring bread wheat genotypes (G1-G28) in 12 environments. Environmental codes; DAR, ZAB, DEZ, AHV, KHR and ISH represent the field stations; Darab, Zabol, Dezful, Ahvaz, Khorramabad and Iranshahr, respectively. The numbers 14 and 15 next to the field stations codes represent 2014-15 and 2015-16 cropping seasons, respectively.

Fig. 4 shows the rank of genotypes relative to the ideal genotype. An ideal genotype is defined as the best in all environments with the highest mean performance and absolute yiled stability. The ideal genotype is the hypothetical genotype represented by the small circle with a narrow pointing (Yan 2001). Genotypes that are more desirable are located closer to the ideal genotype point. Ideal genotype visualization (Fig. 4) showed that G2 followed by G5, G13 and G22 located near to the ideal genotype.
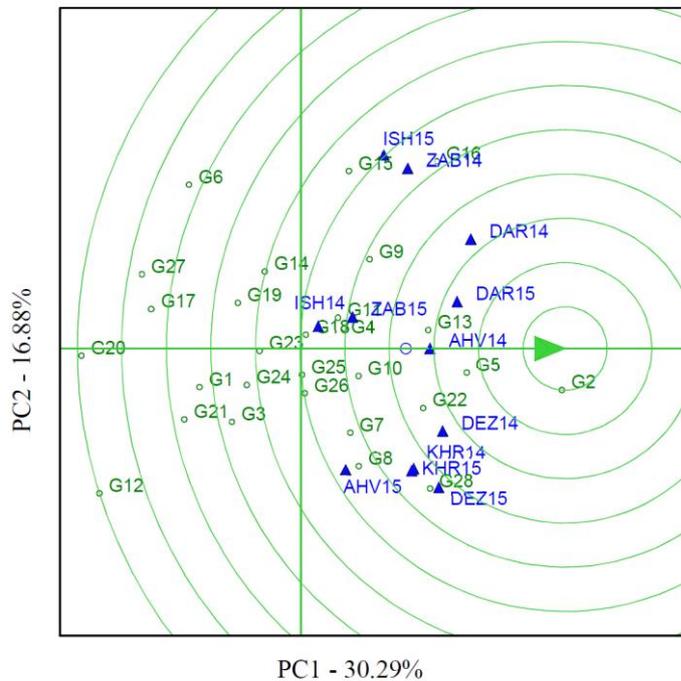
Fig. 4. Biplot of spring bread wheat genotypes (G1-G28) in comparison with ideal genotype based on grain yield and yield stability. Environmental codes; DAR, ZAB, DEZ, AHV, KHR and ISH represent the filed stations; Darab, Zabol, Dezful, Ahvaz, Khorramabad and Iranshahr, respectively. The numbers 14 and 15 next to the field stations codes represent 2014-15 and 2015-16 cropping seasons, respectively.

In GGE biplot, the cosine of the angle between two environment vectors represent an approximate of the correlation coefficient between them. Acute and obtuse angles indicate positive and negative correlation, respectively. Right angles between two environment vectors indicates no correlation (Yan and Kang, 2002). Moreover, environments or locations with longer vectors are more representative and suitable for discrimination of responsive genotypes. Fig. 5 presents the environments' correlation and discriminating ability. The cosine of the angle between two years of all locations vectors are acute and indicate positive correlation. ISH, ZAB and DAR (in both cropping seasons) as well as KHR and DEZ (in both cropping seasons) were positively correlated, because the angles among them were smaller than 90°. Based on Fig. 5, AHV14 and AVZ15 environments (corresponding to Ahvaz location) showed the lowest correlation in two cropping seasons. AHV14 and AHV15 also showed relatively high positive correlation with the KHR (KHR14 and KHR15) and DAR15, respectively. Maximum angle between the environments ISH15 and AHV15, showing a negative correlation between these environments. According to the length of the environments vectors, ISH14 showed the least discrimination for spring bread wheat genotypes' grain yield performance in the studied environments (Fig. 5).
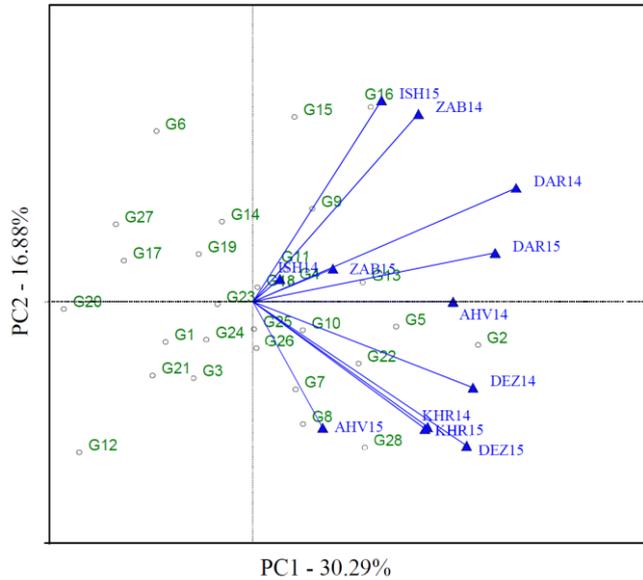
Fig. 5. Biplot of correlation map among environments. Environmental codes; DAR, ZAB, DEZ, AHV, KHR and ISH represent the field stations of Darab, Zabol, Dezful, Ahvaz, Khorramabad and Iranshahr, respectively. The numbers 14 and 15 next to the field stations codes represent 2014-15 and 2015-16 cropping seasons, respectively.

Comparison of environments and location of ideal environment are presented in Fig. 6. The small circle is the location of an ideal environment. In this study, DAR15 followed by AHV14 and DEZ14 were ideal environments in terms of being the most representative of the overall environment.
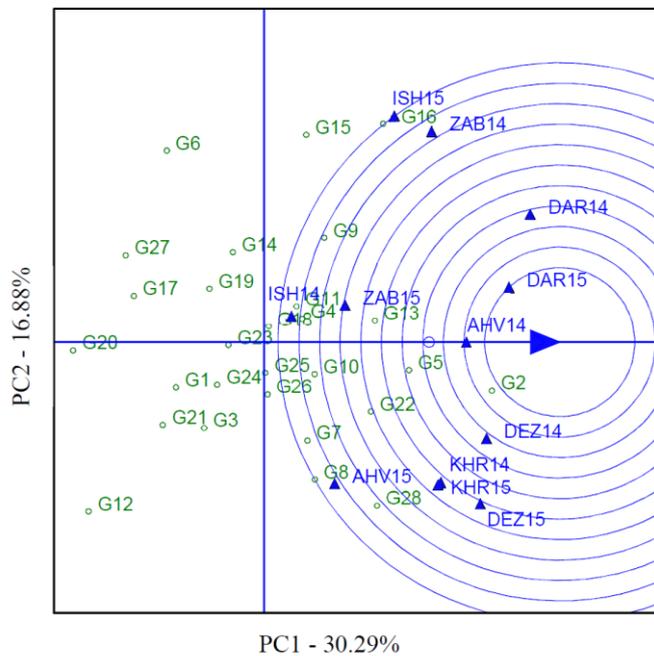
Fig. 6. GGE Biplot showing ranking of environments relative to ideal environment. Environmental codes; DAR, ZAB, DEZ, AHV, KHR and ISH represent the filed stations of Darab, Zabol, Dezful, Ahvaz, Khorramabad and Iranshahr, respectively. The numbers 14 and 15 next to the field station codes represent 2014-15 and 2015-16 cropping seasons, respectively.

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Genotype selection based on GEI dissection

The studied spring bread wheat genotypes showed high variability for yield stability and adaptation to different environments. This can be useful for being used in spring bread wheat improvement programs. The similar environments were grouped by AMMI and GGE biplot methods considering genotypes responses. AMMI and GGE biplot divided test locations into two distinct main groups; the first group included; KHR and DEZ environments and the second group included; ZAB and ISH, while DAR and AHV environments were not in a specific group. AMMI and GGE methods separated the western and southwest regions from the south and southeast test locations. Therefore, it can be suggested that the geographical location had greater impact than the effect of moisture management on grouping of environments. These differences could be attributed to differences in the genetic material tested as well as to differences in the climatic conditions of the test environments (Mohammadi and Amri, 2016). In each group, test environments are relatively similar in terms of genotype response and are relatively uniform because of limitation in genotype × location interaction effects.

AMMI analysis showed differences among genotypes for grain yield and yield stability across environments. According to ASV ranking (Table 5), G5 had the lowest ASV value with high grain yield and yield stability. G5 and G15 are generally better adapted to terminal drought stress environments (AHV, ISH and ZAB locations in both cropping seasons), while G28 and G8 are more adapted genotypes to irrigated conditions of KHR and DEZ field stations. According to GGE biplot analysis, G2 followed by G5, G13 and G22 were identified as genotypes with high yield and yield stability performances. Pedigree dissection of these lines showed that cv. Pastor is common in their pedigree. This spring bread wheat cultivar is high yielding and widely adapted to diverse environments, and was developed and introduced by CIMMYT in 1993 (Martynov *et al.*, 2017). Therefore, using this cultivar as parent of crosses in spring bread wheat breeding programs can lead to the production of breeding lines with high adaptability to different environments.

The results showed that AMMI and GGE biplot models had some differences in terms of specific adaptability and environmental contribution to yield stability of genotypes. In AMMI analysis, yield stability of spring bread wheat genotypes were detected only based on IPCA1 scores which relatively differed from GGE biplot models due to contribution of two IPCAs information in detection of genotypes with yield stability (Oliveira *et al.*, 2009; Miranda *et al.*, 2009; Akter *et al.*, 2014). Despite these differences, the results of AMMI and GGE biplot analyses agreed for some of genotypes. For instance, G5 was detected as genotype with yield stability based on both AMMI and GGE biplot.

The choice between a wide and a specific adaptation strategy may be a key question for national breeding wheat programs (Annicchiarico, 2002). Despite having high performance, G28 (commercial check) did not show high yield stability. On the contrary, other commercial check G1 (Chamran) had grain yield below the grand mean, but had high relative stability across environments. Result of this study suggested that the specific adaptation strategy and grouping the southern warm and dry zone of Iran to sub-zones for identifying adapted spring bread wheat cultivars with high grain yield and yield stability for these target environments.

CONCLUSION

GGE biplot and AMMI analysis showed differences among spring bread wheat genotypes for grain yield and yield stability across different target environments. Based on the results of this study, significant grain yield and yield stability improvement across environments in comparison to check cultivars have been achieved. It is concluded that the geographical location had greater impact than the effect of moisture management on grouping of environments. Both AMMI and GGE biplot methods grouped the southern warm and dry zone to the southwest, and south and southeast regions. Thus, the specific adaptation strategy and grouping the wheat growing areas in southern warm and dry zone of Iran to sub-zones is suggested for identifying the high-yielding and adapted spring bread wheat cultivars for these target

environments.

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