

Original Research

Evaluation of adaptability in bread wheat genotypes under dryland conditions in tropical and subtropical locations

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ABSTRACT:

Comparing stability efficiency and range of conformity is becoming significant in bread wheat (*Triticum aestivum* L.). Variable environmental conditions cause to creation of great genotype by environment (G×E) interaction. The yield stability of 18 bread wheat lines and genotypes was surveyed through genotype and genotype × environment interaction using the GGE biplot method. Field experiments were accomplished in 14 rainfed environments in Iran to specify G×E interactions for grain yield of wheat genotypes. The trials were executed as a randomized complete block design with four replications in three years. A combined analysis of variance across environments represented that main and interaction effects (G, E and GE, respectively) were highly significant. Principal component analysis was carry out and PC₁ and PC₂ displayed 31.69% and 26.77% of the total sum of squares, respectively. Therefore, these PCes were used to develop GGE biplot diagrams. Polygon diagram of the biplot displayed two environments, (1)-Gachsaran and Moghan and (2)- Ilam and Khoramabad, for cultivation of wheat in rainfed regions of Iran. The means and stability parameters of the genotypes in the biplot indicated that genotypes G₂, G₉ and G₈ were advisable for Ilam and Khoramabad, Also, G₁₄ and G₁₇ were suitable for Ghachsaran, so these genotypes are adapted to warm rainfed areas of Iran and concluded for release in these locations. The biplot displayed that Khoramabad and Ilam were associated, but had no correlation with Moghan. Furthermore, Ghachsaran and Gonbad were correlated too, but had no association with other locations.

Keywords:

AMMI analysis, Rainfed condition, Stability.

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INTRODUCTION

In crop productions, drought is one of the major environmental challenges and universal climate variation has made this condition more critical (Geravandi *et al.*, 2011; Farshadfar and Hasheminasab, 2013). The reaction of crops to drought pertains on many factors such as growing steps, intensity and time of stress, and cultivar genetics (Beltrano and Marta, 2008); but, the progress in plant's yield under stressed conditions needed genotypes with stress resistance and yield stability. Different procedures have been studied to investigate genotype \times drought stress interaction. Among stability manners for election stable genotypes, the additive main effect and multiplicative interaction model (Gauch and Zobel, 1997) are extensively used for $G \times E$ interaction investigation (Farshadfar and Sadeghi, 2014; Farshadfar and Hatami, 2015; Bavandpori *et al.*, 2015). GGE biplot analysis has devolved into a general analysis system by which most questions that perhaps asked of a genotype by environment stable can be graphically addressed (Yan *et al.*, 2000; Yan, 2001; Yan and Kang, 2003; Yan and Tinker, 2005).

Two sources of variation of the site regression (SREG) model were genotype main effect (G) plus the GE interaction (Farshadfar and Sadeghi, 2014). Genotypes assayed in various years or places mostly have significant changes in yield because of the response of genotypes to environmental effects such as presence of disease pathogens, soil moisture content and soil fertility (Kang *et al.*, 2006). These oscillations are often referred as $G \times E$ interaction (GEI) and are common. $G \times E$ interactions have been studied in wheat, including Crossa *et al.* (1991), Mohammadi *et al.* (2007), Sabaghnia (2014), Kaya *et al.* (2006), Purchase *et al.* (2000) and Kang *et al.* (2006). GEI results from a shift in the relative domain of genotype performance or a shift in the importance of differences between genotype performances from one environment to another. GEI affects breeding improvement because it entangles the presen-

tations of supremacy of any genotype among environments and the election of better genotypes (Magari and Kang, 1993; Ebdon and Gauch, 2002). Another undesirable effect of GEI includes low association between phenotypic and genotypic values, thereby diminishing progress from selection. This results to bias in the calculation of heritability and in the forecasting of genetic advance (Comstock and Moll, 1963). So, the importance and nature of GEI specify the aspects of a selection and testing program.

Plant breeders want to expand broadly regulated genotypes for a wide extend of environments and locations, mostly. But, it is not often feasible to recognize genotypes that are best in yield and yield components in all environments. Moreover, the same genetic system cannot control yield over a different set of environments and locations (Ceccarelli and Grando, 1993). Therefore, plant breeders often expand genotypes for a special environment to gain advantage of special conformities (Annicchiarico *et al.*, 2006). However, breeding for a specific adaptation is more adequate if production areas are dispited into mega-environments, each representing a propose environment for breeding. Mega-environment is a section of the growing area of a plant species having a justly similar environment that causes analogous genotypes to do best there (Gauch and Zobel, 1997). The multivariate models, AMMI and GGE biplot, become evident to be able to extract a large part of the $G \times E$ interaction and were effective in analyzing interaction schemes (Zobel *et al.*, 1988).

Gauch (1992) demonstrated that multivariate models covering a large portion of the $G \times E$ interaction sum of squares clearly separating main and interaction effects, and the model often provided an agronomically punctual interpretation of the data. Differences in genotype stability and adaptability to environment can be qualitatively estimated using the biplot graphical exhibition that distribute the genotypes according to their primary component values (Vita *et al.*, 2010). Lately, Yan

Table 1:Details of wheat genotypes, parentage and environments

Ent.No.	Variety/Line
G ₁	KAUZ/FLORKWA-1 ICW97-0444-0APS-5AP-0APS-050AP-0APS-26AP-0AP
G ₂	SHUHA-7//SERI 82/SHUHA`S` ICW97-0137-7AP-0APS-8AP-0APS-030AP-0AP
G ₃	SW89.2089/KAUZ CMSS93B00870S-2Y-010M-010Y-010M-7Y-0M-6M-0Y
G ₄	SW89.5193/KAUZ CMSS94Y00761S-0300M-0100Y-0100M-18Y-9M-0Y-5M-0Y
G ₅	SERI×3//RL601 0/4×YR/3/P ASTOR/4/BA V92 CMSS96 M05696T-040Y-14M-01 OSY-O1 OM-O1 OSY-4M- OY
G ₆	PBW343 CM85836-4Y-OM-OY-8M-OY-OIND
G ₇	ITAPUA 40-OBLIGADO CM9493-3M-2Y-5M-1Y-0M-0PRY
G ₈	PBW343 CM85836-4Y-0M-0Y-8M-0Y-0IND
G ₉	ATTILA/BABAX//PASTOR CMSS98Y03454T-040M-020Y-030M-040SY-020SY-020M-7Y-0M-0SY
G ₁₀	OTUS CMBW90Y3180-0TOPM-3Y-010M-010Y-10M-015Y-0Y-1KBY-0KBY-0M-0HTY
G ₁₁	ANGRA/2×CAZO CMBW90Y3215-0TOPM-20Y
G ₁₂	NESSER/SERI CMSS93Y02623S-98Y-010Y-010Y-015Y-4Y-05B-0Y-0SY-0AP
G ₁₃	TJN/MV22
G ₁₄	HD2329/SABUF FPSS95B00253S-040Y-020M-040Y-020Y-4M-0Y-0HTY
G ₁₅	YUMAI 13/2×KAUZ
G ₁₆	OPATA/RAYON//KAUZ CMBW90Y2180-0TOPM-3Y-10M
G ₁₇	ZAGROS
G ₁₈	KOUHDASHT

et al. (2000) proposed a GGE biplot that allows visual test of the GE interaction pattern of multi-environment exam (MET) data. The GGE biplot insists two subjects. First, although though the evaluated yield is the combined effect of genotype, environment and genotype by environment interaction, but G and GE are related to, and should be assumed simultaneously, in genotype assessment.

Second, the biplot method developed by Gabriel (1971) was practical to displaying the GGE of a MET, so the term GGE biplot. GGE biplot was made by the first two principal components (PC₁ and PC₂) isolated from exposing environment-centered yield data, i.e., the yield fluctuation due to GGE, to solitary value parsing

(Yan, 1999; Yan *et al.*, 2000). GGE Biplot was display the GE interaction pattern of the data. In addition, the GGE biplot has a usage in choosing better genotypes and test locations for a given environment.

The objective of this study is to understand the adaptation of wheat genotypes using AMMI analysis to evaluate the significance of the GE interaction on seed yield, identify mega environments, determine the best performing genotype for each mega-environment, and discuss the implication of the GE interaction to wheat breeding.

MATERIALS AND METHODS

Eighteen genotypes of wheat (16 genotypes

Table 2. Geographical properties of test locations

S.No.	Location	Rainfall (mm)	Soil type	Altitude (m)	Longitude latitude
1	Ghachsaran	269.5±7.05	Regosols	710	50° 50' E 30° 20' N
2	Gonbad	294.23±6.27	Regosols	45	55° 12' E 37° 16' N
3	Khoramabad	320.96±6.7	Regosols	1148	48° 12' E 33° 29' N
4	Moghan	207.77±5.03	Cammbiosols	32	47° 87' E 39° 39' N
5	Ilam	448.35±11.02	Regosols	975	46° 36' E 33° 47' N

along with, Zagros and Kohdasht as a check) were planted in national regional yield trials (Coded G₁ to G₁₈). Pedigrees of studied genotypes are listed in Table 1. The trails were done across five locations (Ghachsaran, Ilam, Gonbad, khoram abad and Moghan) throughout three years, 2011-2012, 2012-2013 and 2013-2014. The specifications of these locations are presented in Table 2.

The experiment was done in a randomized complete block design with four replications. Because of intense drought conditions in 2011-2012 crop season, Ilams data were not used for analysis and data from 14 environments were exploited. Each experimental unit consisted of a 7.35 m² plot (six rows 7 m long with 0.175 m between rows). To test significant differences among cultivars and locations, combined ANOVA was performed. The AMMI model (Gauch, 1988) was accomplished using blow formula:

where, Y_{ij}: The yield of the ith genotype in the jth environment; μ: General mean; 'g_i' and 'e_j': Genotype and

$$Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^N \lambda_n \gamma_{in} \delta_{jn} + \rho_{ij}$$

environment deviations from the general mean; λ_n: Eigenvalue of the IPC (interaction principal component) analysis axis n; γ_{in} and δ_{jn} - Genotype and environment eigenvectors for axis n; n: The number of IPCs retained in the model; ρ_{ij}: Residual component.

A special F-test (F Ratio), was used to specify of significant numbers of IPCs in AMMI model (Cornelius *et al.*, 1992). The AMMI1 and AMMI2 bip-

lots were drawn and used to assigned the mega-environments and selected genotypes. All statistical analyses were done using RX64 and SAS 6.12 software.

RESULTS AND DISCUSSION

Based on the results of analysis of variance, effects of Genotype (G), Environment (E), and G×E interaction were significant (Table 3). Significant interaction of genotypes and environment, demonstrated that at least some of genotypes showed differently in one of the studied environments; it mentioned genetic mutability and the probability of selecting cultivars with high yield and good performance and yield stability. Interaction of genotypes and environment caused it hard to choose the best performing, most appropriate cultivars with good yield consistency because it diminish the proficiency of selection in wheat breeding programs. The analysis of variance displayed a significant environment effect too. The portion of environment to total changes (G+E+GE) was 87.77%, but in genotypes and genotype × environment interaction this ratio was 1.63 and 9.08% respectively. The low portion of genetic and genetic × environment interaction effects to the environment for grain yield observed in this trial is like to those investigated in other wheat stability studies in drought areas (Mohebodini *et al.*, 2006).

After fitting the GGE model, it was observed that first two PCs explicated 58.46% of the GGE sum of squares for the multi-environment trials (PC₁ = 31.69% and PC₂ = 26.77%, respectively) (Figure 1).

Table 3. Anova analysis of wheat genotypes over locations and years.

S.No	SOV	Df	SS	MS	SS%	(E+G+GE)%
1	Model	293	1884347340	6431220		97.313
2	Environment	13	1640727622	126209817**	87.77	
3	E _(a)	42	50465781	1201566		
4	Genotype	17	21920376	1289434**	1.163	
5	Genotype*Environment	221	171233561	774812**	9.08	
6	E _(b)	714	110074169	154166		
7	CV%	14.7%				

**Significance at 0.01 probability level.

Table 4. Average grain yields of 18 wheat varieties over five place

	Gachsaran	Gonbad	Ilam	Khoram abad	Moghan	Average	Prin1	Prin2
G ₁	1376.667	1942.833	2685.75	<u>3989</u>	<u>3844.333</u>	2773.571 ^{abc}	2.5374	-1.2601
G ₂	1270.833	<u>2825.333</u>	2705	<u>4307.583</u>	3285.833	2891.339 ^a	0.84116	1.2409
G ₃	979.25	2730.333	<u>2890.625</u>	3738.083	3329.833	2722.411 ^{abcd}	0.42276	1.1444
G ₄	1222.25	2720.917	2420.125	3218	3533.417	2637.429 ^{cde}	-0.77847	-1.3934
G ₅	989.8333	<u>2867.917</u>	2590	3434.667	2985.667	2572.446 ^{ef}	-1.4039	0.3826
G ₆	791.6667	2615.417	2703.25	3909.667	3478.917	2699.536 ^{bcd}	0.40713	1.1219
G ₇	850.1667	2693.833	2584.125	<u>4004.75</u>	2844.75	2596.339 ^{def}	-0.80739	1.4048
G ₈	993.4167	2717.75	<u>2978.375</u>	<u>3961.167</u>	3091.833	2732.089 ^{abcd}	0.5717	1.8030
G ₉	1162.917	2541.917	<u>3004</u>	<u>3973.75</u>	3437.417	2811.143 ^{ab}	1.6068	1.0464
G ₁₀	1039.167	2461.5	2807.125	3557.667	3081	2573.732 ^{def}	0.0036	0.2742
G ₁₁	<u>1572.167</u>	<u>2987.5</u>	2697.5	3766.75	2817.167	2773.268 ^{abc}	-0.5451	0.2618
G ₁₂	1353.833	2497.667	<u>2886.75</u>	3570.083	2953.75	2635.679 ^{cde}	0.2773	-0.0386
G ₁₃	1184.417	2674.667	2595.75	3500	2345.917	2450.464 ^f	-1.8783	0.1958
G ₁₄	<u>1724.917</u>	2427.583	2549	3827.167	3465.25	2816.625 ^{ab}	1.1162	-1.5548
G ₁₅	943.0833	2384.833	2449.5	3271.5	2515.667	2303.161 ^g	-2.1172	-0.5654
G ₁₆	1203.833	2518.667	2199.375	3525.75	2909	2490.75 ^{ef}	-1.6463	-1.2743
G ₁₇	<u>1735.25</u>	2638.583	2672.125	3401.333	3548.167	2808.161 ^{ab}	0.71097	-1.7213
G ₁₈	1472.5	<u>2723.833</u>	<u>2852.625</u>	3192.25	<u>3675</u>	2778.286 ^{abc}	0.6816	-1.068
Prin1	0.28842	<u>-30084</u>	<u>-0.4833</u>	0.41477	<u>0.64857</u>			
Prin2	-0.5777	<u>0.35778</u>	<u>0.45893</u>	0.51546	<u>-0.24877</u>			

The lowest mean yield was 791.67 for G₆ in Gachsaran, and the highest mean yield was 4307.58 for G₂ in Khoramabad (Table 4). G₁₇, G₁₄ and G₁₁ genotypes have highest yield in Gachsaran, while the highest yielding genotypes in Khoramabad were G₂, G₇, G₈ and G₉ (Table 5). G₁₁, G₅, G₂ and G₁₇ genotypes in Gonbad and G₉, G₈, G₃ and G₁₂ genotypes in Ilam and G₁₈ in two location are said were the superior (Table 4). At the end, in Moghan G₁, G₁₇ and G₁₈ genotypes showed the highest yield respectively. The highly significant genetic×environment interaction showed that there were both additive and non-additive interaction in multi-environment trials (Table 3). Genetic×environment interaction is achieved when the phenotypic response of genotypes to different environments is not the same (Annicchiarico, 1997). Genotypes are generally ap-

praised based on mean grain yield and plant breeders often must choose best genotypes under various conditions. but this is insufficient, because it does not fully demonstrated permanence of yield efficiency (Crossa *et al.*, 2010). Several statistical methods have been suggested to recognize the appropriate genotypes in the attendance of genetic×environment interaction such as coefficient of regression (b_i), Finlay and Wilkinson (1963), regression coefficient and deviation from linear regression, (S²_d), Eberhart and Russell (1966) and unbiased estimate using stability variance, (S²_i), Shukla (1972). The genetic×environment interaction has been studied by statisticians, quantitative geneticists and plant breeders (Becker and Leon, 1988). Quantitative geneticists are interested in calculate the value of genetic × environment interaction but plant breeders are be

Table 5. Pearson's correlation coefficients among four test locations

S.No.		Ghachsaran	Gonbad	Ilam	Khoramabad	Moghan
1	Ghachsaran	1				
2	Gonbad	-0.079	1			
3	Ilam	-0.034	0.0936	1		
4	Khoramabad	-0.1394	-0.059	0.3362	1	
5	Moghan	0.3389	-0.2717	-0.2776	0.158	1

fond of selecting the suitable genotypes in the attendance of genetic \times environment interaction (Freeman, 1973).

G₁, G₉, G₈, G₇, G₁₃, G₁₅, G₁₆ and G₁₇ genotypes were farthest from the origin of GGE biplot and organized the nook of a polygon when they were joined. Lines that commenced from the biplot center and were perpendicular to the sides of the polygon created seven sectors (Figure 1). These genotypes were better in place situated in their relevant sectors. Hence, G₁ was the best genotype in Moghan, while G₉, G₈ and G₂ were the best genotypes in Ilam and Khoramabad. As the same way, G₁₄, G₁₇ in Gachsaran, and G₇ in Gonbad were the best respectively. According to Figure 1, aforesaid genotypes displayed better conformity to the locations. G₄, G₁₆, G₁₅, G₁₃, G₅, G₁₂, G₁₀ and G₁₁ did not have the highest yield in any of the trail locations. Thus this figure indicated that there are a group of bread wheat among trail locations. These conclusions were investigate based on

the geographical attributes, annual rainfall and other environment template and must be further verified through future multi-environment tests. The Moghan location in northwestern of Iran has different climatic and characteristics of the test locations. However, this geographic characteristics of genotypes G₉ and G₈ were the best genotypes in Ilam and Khoramabad, while genotype G₁ was the best genotype in environment Moghan. In the polygon facade of the GGE biplot, locations in the same segment partake the same winning genotype, and locations in different segments have different winning genotypes. Accordingly, this biplot displayed the attendance or lack of crossover genetic \times environment interaction for the most responder genotypes (Yan and Rajcan, 2002; Dehghani *et al.*, 2010). This investigate recognized rainfed bread wheat locations, a discovery that has results for future wheat breeding programs under these conditions in Iran. Segregating of the target places into different environments and establishment of

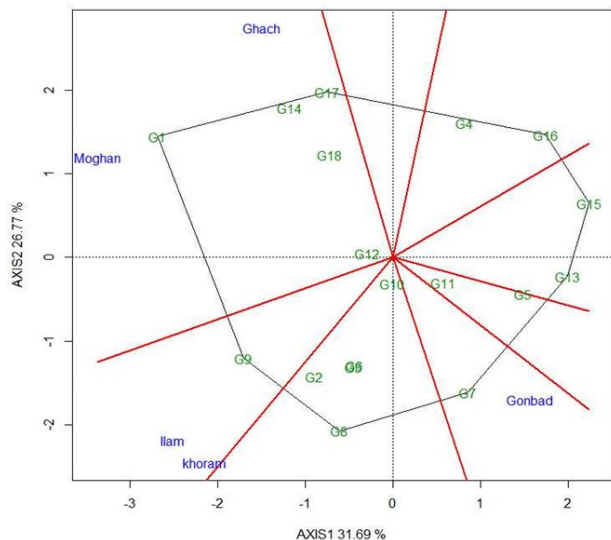


Figure 1. Biplot for identifying winning genotypes and their respective environments.

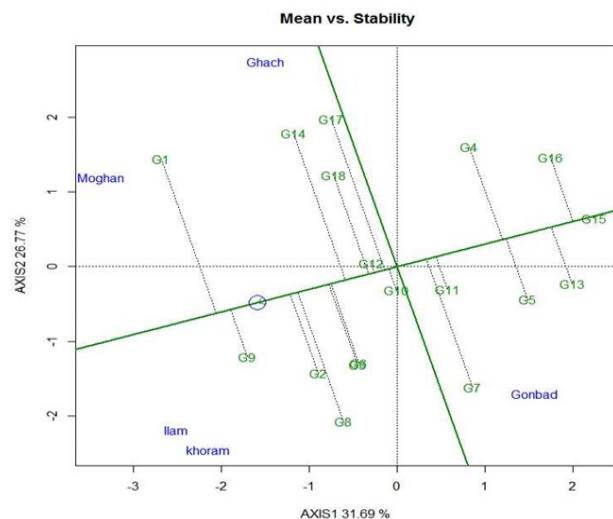


Figure 2. Site regression (SREG) biplot for mean yield and yield stability of 18 bread wheat genotypes for specific genotype \times environment

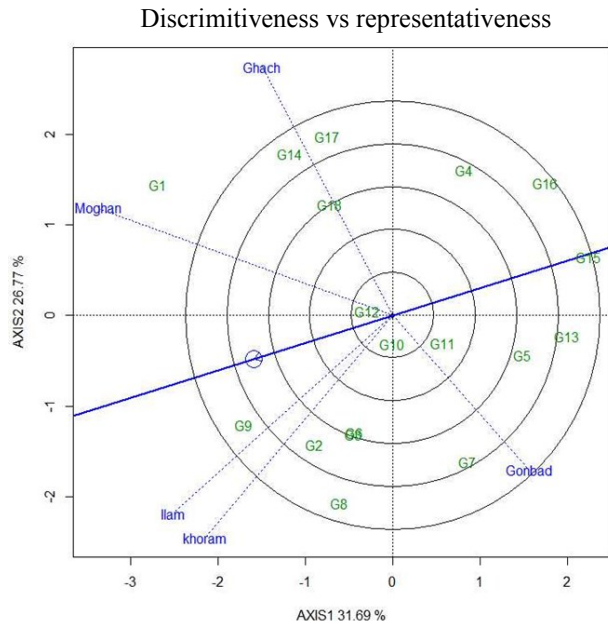


Figure 3. Vector view of the site regression (SREG) biplot of the relationships among test locations

various genotypes in these locations is the best way to apply the genetic \times environment interaction.

Imagination of the yield stability and mean grain yield of the genotypes and check cultivars displayed that the mean yields of the investigated genotypes classified them in the following order: $G_2 > G_9 > G_{14} > \dots > G_{13} > G_{15}$ (Figure 2). Since the two axes of the mean location peculiarities of the GGE biplot are orthogonal, projection of the genotypes on the vertical axis must approximate the genetic \times environment associated with the genotypes (Yan *et al.*, 2000). The longer the projection of a genotype, irrespective of direction, the greater the magnitude of genetic \times environment related with the genotype, which catered an indicator of inconstancy of the genotype across locations. Accordingly, the performance of G_7 , G_8 , G_1 , G_{14} and G_{17} was highly unstable, whereas genotypes G_{12} , G_{10} , G_{11} , G_{15} and G_9 were highly stable (Figure 2).

Due to the mean yield and yield stability of the genotypes, biplot indicated that G_9 is appropriate genotypes. G_9 was the best genotype in Ilam and Khoramabad stations. Also, pursuant to the vector view of the biplot, Khoramabad and Ilam were associated with each

other, but had no correlation with another locations, in addition positive correlation was indicated between Moghan and Ghachsaran. It seems that these finding are suitable for recognizing bread wheat genotypes with high yield and good stability, and for specifying the conjugation among places. Scores gained from SREG analysis for the first two PCs (PC_1 and PC_2) demonstrate mean yield and stability components that are comparable to the main effect and an adaptability indicator such as linear regression coefficient (Goyal *et al.*, 2011). Yan and Kang (2002) reported a significant association between GGE distance (mean against stability application of the biplot) and yield stability statistic (Kang, 1993; Dehghani *et al.*, 2010). As respects of the high efficiency of Kang's (1993) yield stability statistic for concurrent selecting mean yield and stability, recognition of better genotypes based on the best genotype and the ATC axis trait can result in reliable results in genetic \times environment interaction investigations.

A correlation investigation of test locations indicated a relatively powerful positive dependence between Khoramabad and ilam, and as the same way in Moghan and Ghachsaran, as showed by the acute angles among their vectors. Relatively feeble dependence among Gonbadad with cited places were detected, (Figure 3). No linkage was observed among Khoramabad and Ilam with other places (Gachsaran, Gonbad and Moghan), as displayed by the near vertical vectors. Some of these associations could be further proved from the main correlation coefficients, however, some of them are not constant with the original data (Table 5). For example, the biplot anticipate Gonbad has positive or a negative association with the other places, and the correlation coefficients in Table 4 affirm this result. In return, positive correlation coefficients between Gachsaran and Moghan and on the other hand, Khoramabad and Ilam locations were not significant (Table 5). some disagreement are to be anticipated, because the GGE biplot procedure explained just 58% rather than 100%

of the total variation in G+GE templates. Yan *et al.* (2007) expressed that each measured datum includes some error, and as the GGE biplot method makes anticipations based on the ordinary template in the dataset, the anticipations are maybe more trusty than the single data.

Generally, we detect that G₂ (2891.34 kg ha⁻¹) G₉ (2811.14 kg ha⁻¹) and G₈ (2732.09 kg ha⁻¹) genotypes were conformed and appropriate for Khoramabad and Ilam, G₁ (2773.57 kg ha⁻¹) genotype was adapted and appropriate for Moghan and G₁₄ (2816.63 kg ha⁻¹) and G₁₇ (2808 kg ha⁻¹) were conformed for Ghachsaran; consequently, they are introduced for release as new wheat cultivars for these locations.

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