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Comprehensive Stability Analysis of Wheat Genotypes through Multi-Environmental Trials

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ABSTRACT

In rainfed areas, due to variable environmental factors, improving the yield stability of the introduced cultivars along with increasing yield should be considered. The main aim of this study is to obtain high-yield wheat genotypes that are stable and adaptable to cold climatic conditions in Iran. For this purpose, 25 wheat genotypes were evaluated in a randomized complete blocks design with three replications during three cropping seasons (2013-2016) under supplementary irrigation and rainfed conditions. PBSTAT-GE software was used for genotype × environment interaction (GEI) analysis and comprehensive sustainability analysis. The results showed that G5, G14, G16 and G18 genotypes had good stability and general adaptation based on parametric and non-parametric stability statistics. Combined analysis of variance based on the Additive Main Effect and Multiplicative Interaction (AMMI) model showed that GEI is significant in the term of grain yield. Also, the ratios between the sum of squares G, GE and IPC1 showed that the AMMI is suitable for data analysis. GGE biplot analysis identified five mega-environments (MEs), in which ME I including E1, E2, E3, E4, E5, E6, and G7, G5, G14, G13, G16, G18, G20 being the superior ME I genotypes. According to AMMI and GGE biplote stability methods, lines G20, G18, G13, G16, G14 and Saein cultivar (G5) can be considered as desirable genetic resources in wheat production programs under variable environments in Iran, due to having the appropriate combination of yield and stability.

Keywords: Adaptability and stability, AMMI, ANOVA, GE interaction, GGE biplot, Wheat

1. Introduction

To analyze genotype × environment interaction (GEI) and determine genotypes adapted to different climatic conditions, the evaluation of genotypes obtained from breeding programs at the national level has an important role in identifying suitable genotypes for target environments (Ayed et al. 2016). Breeders usually evaluate advanced genotypes using their similar responses under different environments to classify environments into similar groups and to determine the best genotype for each environmental group and introduce stable high yield genotype for different environments (Yan et al. 2000). GEI is one of the biggest challenges for researchers, which reduces the efficiency of selection and prediction of genotype yield in target environments (Yan & Fregeau-Reid 2018). One of the methods to reduce GEI and also increase yield is to select and introduce high-yield and stable genotypes in different regions (Kang 1993). Many researchers have used the combined analysis of variance method to estimate GEI, however, combined ANOVA and interaction test lacks the ability to determine the stable genotype (Reynolds et al. 2016). Therefore, various methods have been used to identify stable genotypes, including univariate and multivariate parametric and non-parametric stability methods (Elias et al. 2016). Breeders use parametric stability analysis to reach a series of multivariate experiments. Calculation of stability based on non-parametric rankings does not require statistical assumptions, such as normal distribution of model residuals as well as interaction effects. In addition to being easy to use and interpret, these methods have the least noticeable error in calculations compared to parametric calculations (Huehn 1996). Although parametric and non-parametric univariate statistics are easy to calculate and use, however, these methods cannot well interpret the complex and multidimensional nature of the interaction. Therefore, the use of complementary multivariate methods has been suggested to solve this problem (Naroui Rad et al. 2013). AMMI model as a multivariate parametric method is one of the most widely used and popular methods (Malosetti et al. 2013). The AMMI method distinguishes the main effects (genotype and environment) and interactions and is well used to determine GEI (Lai 2012;

Sadiyah & Hadi 2016). The graphical tools of this method have a special role in the simultaneous evaluation of yield and stability, as well as the selection of MEs and specific adaptability (Ajay et al. 2020). The AMMI model by puncturing genotypes and environments on the biplot, identifies the position of the genotypes relative to each other and the studied environments (Elakhdar et al. 2017). Mohammadi et al. (2015), Ajay et al. (2020), Khan et al. (2020), Lozada & Carter (2020), Mekonnen et al. (2020), Mohammadi et al. (2020) and Verma & Singh (2021) by examining the stability of wheat genotypes reported that the AMMI method with high fitting power, is more suitable than other methods for determining genotypes with general and specific adaptability for different locations. Ahakpaz et al. (2021) by examining 18 rainfed barley genotypes for three cropping years in cold rainfed regions of Iran, reported that the effects of G, E and GEI on grain yield were significant. Also, according to AMMI analysis, there was a significant difference between the first two main components.

Another multivariate method is the Genotype plus GE interaction (GGE) biplot (Yan et al. 2000), which is a powerful graphical model for identifying the best-yield cultivars among different environments. GGE biplot is an analytical method of GEI that simultaneously evaluates the main effect of genotype and GEI. In this method, genotypes are evaluated based on yield in different environments, the combination of stability and yield, the ability of environments to distinguish genotypes, and their representativeness (Yan & Kang 2003). The difference between these two multivariate methods is that GGE biplot is based on environment-centered principal component analysis, while AMMI is based on double-centered PCA (Yan et al. 2007). Ashraful et al. (2017), Bornhofen et al. (2017), Bavandipour et al. (2018) and Singh et al. (2019) reported that the combined application of AMMI and GGE biplot methods provide a powerful tool for identifying high-yielding and adaptable wheat genotypes as well as analyze and interpret multi-environment trials (MET) data in breeding programs.

Phenotypic stability can be divided into two principal types, that is, stability in the biological and agronomic sense. Stability in the biological (static) sense refers to the ability of genotypes to maintain constant production in different environments, with low variation between them, that is, genotypes exhibit "homeostasis". Stability in the agronomic (dynamic) sense indicates that the genotype positively responds to improvements in edaphoclimatic conditions of the environment and can perform above the mean in different locations (Sabaghnia et al. 2015). This behavior is of interest to plant breeders and farmers. It is important for the plant breeder to adopt methods in which genotype stability is associated with high grain yield average. The combination of these two concepts is known as the "ideal genotype" (Yan et al. 2007; Yan 2016).

Today, several statistical packages are used by plant breeders to perform stability analysis, such as CropStat, PBTools, GEA-R and SAS. PBSTAT-GE (Bayuardi-Suwarno et al. 2008) is a web-based software package for comprehensive stability analysis available at http://www.pbstat.com. PBSTAT-GE includes program code development from R packages, including Agricolae and GGE biplot. About twelve univariate parametric and non-parametric stability measures with AMMI and GGE biplot analysis can be performed using this software. PBSTAT-GE also estimates heritability, the correlation between stability parameters, principal components with genotypes biplot, stability statistics and genotypes biplot, G × E heatmap, genotypes and stability parameters heatmap. The simplicity of PBSTAT-GE operation significantly saves researchers time and effort in performing stability analysis and select top genotypes in the breeding programs. The objectives of this study were (i) to evaluate GEI on grain yield of wheat genotypes in the rainfed areas of Iran using univariate and multivariate stability methods (ii) to identify genotypes that have high mean yield and stable performance over test environments, and (iii) to investigate the relationships between the most commonly used stability statistics.

2. Material and Methods

Field trials were conducted in the Miandoab Agricultural Research Station, West Azerbaijan Province, Iran, located at 36°58′ N, 46°06′ E and 1 314 m above sea level. The soil texture of this site was loamy silt with pH 7.9 and the soil field capacity (FC) at a depth of 30 cm was 28.7. Climatic parameters are shown in Figure 1 and Supplementary Table S1. A total of twenty-three wheat genotypes (Table 1) containing 5 cultivars and 18 promising lines along with check varieties Sardari and Azar 2, were included in the stability study. These lines were developed by several breeders at various research stations/institutes of Iran and the International Maize and Wheat Improvement Center (CIMMYT).

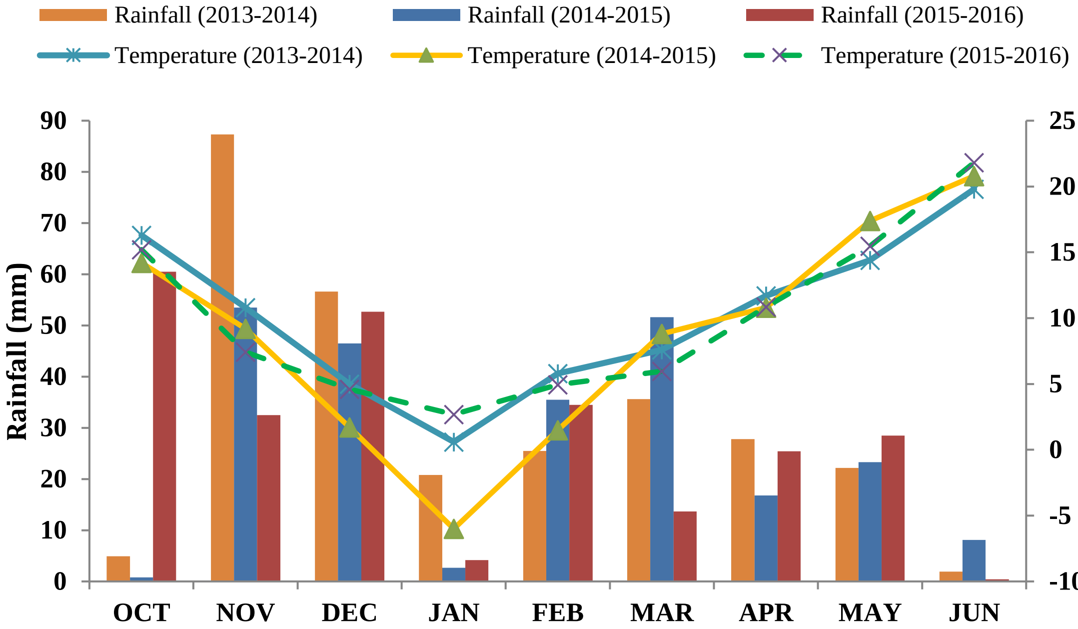

Figure 1- Monthly patterns of temperature of air and rainfall recorded during the course of the experiment

Test materials were phenotyped comprising two trials under drought-stressed (rainfed, RF) and supplementary irrigated (SI) conditions. Each field experiment was arranged based on RCBD with three replications and conducted over three consecutive cropping seasons (2013-2016). A total of 6 environments (combinations of environmental conditions and years) were examined including E1, E3 and E5, representing SI conditions in 2013/2014, 2014/2015 and 2015/2016 seasons, respectively, and E2, E4 and E6 were RF conditions in 2013/2014, 2014/2015 and 2015/2016 seasons, respectively. Under SI conditions, the genotypes were irrigated when the mean soil water content fell to 80% of FC. Fertilizer rates were 90 kg ha^{-1} $CO(NH_2)_2$, 90 kg ha^{-1} $(NH_4)_2HPO4$ and 60 kg ha^{-1} K_2SO_4 used before planting. Each plot consisted of six rows, 4 meter long and 20 cm row spacing (plot size = 4.8 m^2). Grain yield (Y_i, kg ha^{-1}) data were obtained from two middle rows of each plot for each genotype in each test environment.

Table 1- Name, pedigree and origin of tested wheat cultivars and promising lines

Code	*Pedigree / Name*	*Type*	*Origin*
G1	Sardari	Cultivar	IRAN
G2	Azar 2	Cultivar	IRAN
G3	Rasad	Cultivar	IRAN
G4	Ohadi	Cultivar	IRAN
G5	Saein	Cultivar	IRAN
G6	Azar2/87Zhong291-149	Promising line	IRAN
G7	Varan	Cultivar	IRAN
G8	Homa	Cultivar	IRAN
G9	F10S-1//ATAY/GALVEZ87	Promising line	IWWIP
G10	Seafalah/3/Sbn//Trm/K253	Promising line	IRAN
G11	Sardari-101	Promising line	IRAN
G12	Unknown 11	Promising line	IRAN
G13	Sabalan/4/Vrz/3/Or F1.148/Tdl//Blo	Promising line	IRAN
G14	Sabalan//Cno79/Prl"S"/3/Pf82200/4/Ebvd99-1	Promising line	IRAN
G15	SARDARI-HD84//UNKN/HATUSHA	Promising line	IRAN
G16	F130-L-1-12/LAGOS	Promising line	IWWIP
G17	Sara-PBWYT-85-86-22-5	Promising line	IWWIP
G18	PYN/BAU//BONITO	Promising line	IWWIP
G19	Sabalan/84.40023//Seafallah	Promising line	IRAN
G20	SUBEN-7	Promising line	IWWIP
G21	Azar2/78Zhong291-99	Promising line	IRAN
G22	Sardari//Ska/Aurifen	Promising line	IRAN
G23	TIRCHMIR1/LCO//SABALAN	Promising line	IWWIP
G24	TAST/TORIM/3/MLC/4/CWW339.5/SPN/5	Promising line	IWWIP
G25	BJN C 79/4/KVZ/CUT75/3/YMH//61.15	Promising line	IWWIP

IWWIP: International Winter Wheat Improvement Program

After checking the assumption of data normality using SPSS software, comprehensive stability analysis was done for yield data in all environments using PBSTAT-GE software. In this study, the parametric stability measures include CV_i (Coefficient of variability) (Francis & Kannenberg 1978), b_i (Linear regression coefficients) (Finlay & Wilkinson 1963), S^2d_i (Residual MS value) (Eberhart & Russel 1966), W^2_i (Wricke's ecovalence) (Wricke 1962), D_i (Hanson genotypic stability) (Hanson 1970) and σ^2_i (Shukla stability variance) (Shukla 1972) were calculated. Non-parametric stability methods based on yield ranks of genotypes in each environment were Kang yield-stability statistics (YS_i) (Kang 1993), $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$ and $S_i^{(6)}$ methods introduced by Nassar & Huehn (1987), $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ introduced by Thennarasu (1995) and the TOP ranking statistic method (Fox et al. 1990). In addition, PBSTAT-GE performed the ANOVA of the AMMI model for grain yield along with AMMI biplots including $AMMI_1$ biplot (IPC1 vs. yield) and $AMMI_2$ biplot (IPC1 vs. IPC2). GGE biplots were also drawn based on the first two main components obtained from stability analysis by GGE biplot.

3. Results and Discussion

Unpredictable environmental changes produce unpredictable results, therefore, it is necessary to select different types of genotypes that are fully adaptable and able to respond to environmental changes optimally. Climate changes over the years leads to environmental variations and, consequently, the occurrence of significant GEI. The GEI that affects yield is shown in Figure 2. Differences in grain yield between rainfed and supplementary irrigation conditions indicate that there is an interaction between genotypes and environments. Mean yield of genotypes in various environments showed that E1, E3 and E5 had high yield mean than the average of all genotypes (2877.63 kg ha^{-1}) in which maximum grain yield (3593.24 kg ha^{-1}) was related to E1 and the minimum of it (2197.82 kg ha^{-1}) was belonged to E4 environment.

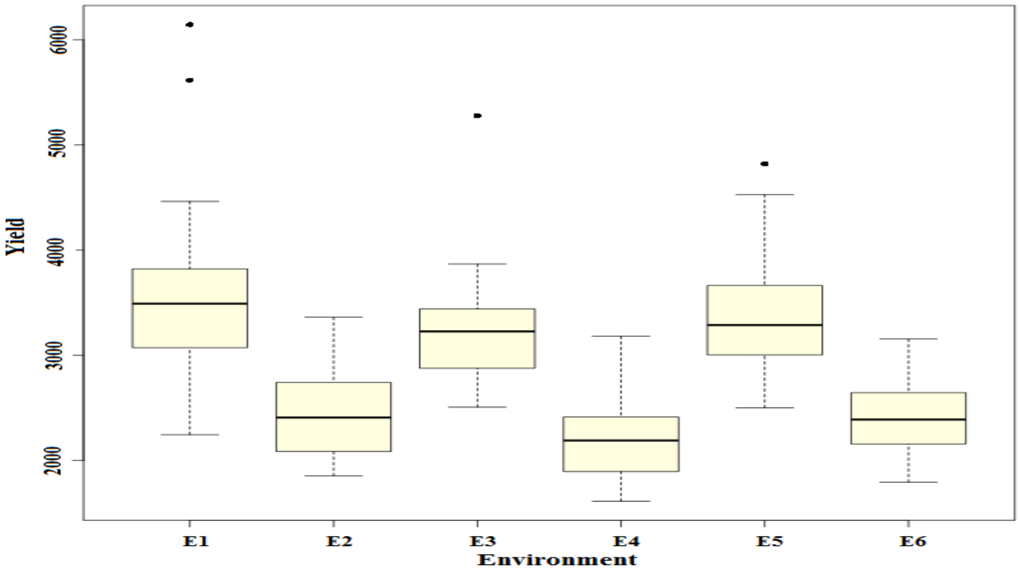

Figure 2- Average grain yield of wheat genotypes across six environments

The grain yield values of the wheat genotypes under supplementary irrigation and rainfed conditions over 3 years are listed in Table 2. In this study, the stress intensity (SI) was calculated according to Fischer's method (Fischer & Maurer 1978) that it was equal to 0.309. Genotype G10 followed by G7 and G5 showed the highest mean yield in both supplementary irrigation and rainfed conditions, while genotypes G12 and G17 had the lowest yield in both experimental conditions. Despite the high mean yield in both environmental conditions, genotypes G10 and G7 showed relatively low stability. Breeders can select genotypes with high mean yield but low stability that have the best response to certain environments (Mohammadi et al. 2012). Saein (G5) was better than the control cultivars Sardari and Azar 2 due to its higher mean yield and general adaptation to the studied environments (Table 2). In this study, genotypes G2, G13, G14 and G16, with high average yield in both supplementary irrigation and rainfed conditions, showed the lowest decrease of relative yield changes during 3 years due to drought stress (Table 2). In a study conducted by Roostaei (2015) on the genotypes of wheat studied in the present study, it was reported that these genotypes performed better under rainfed conditions and traits such as number of kernels per spike and to some extent thousand kernel weight and peduncle length, had a significant role in the yield stability of G2, G13, G14 and G16 genotypes.

According to G × E heatmap (Figure 3), the studied genotypes were divided into two main groups that first group consisting of G10, G6 and G7 genotypes. The second group was divided into 2 subgroups that G23, G25, G22, G17, G4, G15 and G12 genotypes were assigned to the first subgroup and the rest of the genotypes to the second subgroup. The genotypes with equal yield in all environments can be considered as stable genotypes. Accordingly, G22, G23, G25 and G17 genotypes can be considered as stable genotypes. The performance of genotypes in each environment indicates the diversity within that environment, so that the difference in colors related to the genotypes in an environment indicates a variety between genotypes in that environment. Accordingly, under E1, E3 and E5 (SI conditions), genotypic diversity was high (Figure 3).

Visual considering of the distribution of genotypes in the studied environments showed the difference of various genotypes in terms of grain yield in one environment and also the difference between their means from one environment to another, which shows the selection of genotypes based on yield in one place, does not have high validity, thereby, in order to get accurate result, genotypes must be evaluated over years and places to estimate their stability (Eberhart & Russell 1966).

Table 2- The values of grain yield in wheat genotypes under supplementary irrigation and rainfed conditions over three years (2013-16)

	2013/14			*2014/15*			*2015/16*		
Gen.	Y_p	Y_s	*RYC*	Y_p	Y_s	*RYC*	Y_p	Y_s	*RYC*
G1	3034.3	2052.6	0.32	3820.4	1895.2	0.50	3161.4	2158.3	0.32
G2	3491.7	2923	0.16	3227.8	2311.9	0.28	3737.8	2944.3	0.21
G3	3556.5	2469.3	0.31	2954.6	1612.8	0.45	3020.3	2227.4	0.26
G4	2763	2409.1	0.13	2598.1	1960	0.25	2863.1	2265.7	0.21
G5	4297.2	2742.4	0.36	3164.8	2628.5	0.17	3378.3	2518.7	0.25
G6	4463.9	2772.5	0.38	3297.2	1872	0.43	4529.5	3155.7	0.30
G7	5616.7	2793.3	0.50	3868.5	2413.7	0.38	4259.5	2891.2	0.32
G8	3144.4	2659.1	0.15	2672.2	1964.6	0.26	3288.2	2452.8	0.25
G9	3459.3	2015.6	0.42	3473.1	2423	0.30	3835.1	2644.6	0.31
G10	6144.4	3362.8	0.45	5278.7	2520.2	0.52	4821.9	2690.2	0.44
G11	3059.3	1950.7	0.36	3627.8	3182.2	0.12	3134.2	2540.1	0.19
G12	2246.3	1853.5	0.17	2507.4	1807.2	0.28	2721.7	1792.9	0.34
G13	3623.7	2869.1	0.21	3225	2535.1	0.21	3533.1	2356.5	0.33
G14	3760.2	2659.6	0.29	3346.6	2340.5	0.30	3664.1	2869.3	0.22
G15	2871	2370.8	0.17	2555.2	2110	0.17	2501.6	2027.7	0.19
G16	3685.5	2402.2	0.35	3280.1	2375.8	0.28	3542.5	2717.8	0.23
G17	3005.7	2183.4	0.27	2675.1	1965	0.27	3061.4	2022.2	0.34
G18	3868.4	2505.4	0.35	3442.9	2220.5	0.36	3399.9	2390	0.30
G19	3822.7	2218.5	0.42	3405	2190.8	0.36	3812.4	2584	0.32
G20	3899.1	2580.2	0.34	3470.2	2322.2	0.33	3658.1	2379.9	0.35
G21	3083.9	2852.1	0.08	2744.7	2688.3	0.02	2755.2	2286.8	0.17
G22	3184.7	2086	0.34	2987.8	1848.8	0.38	3004.9	2148.7	0.28
G23	3104.1	2036.5	0.34	2933.2	1789.2	0.39	2934.7	1890.3	0.36
G24	3572.4	2339.9	0.35	3311.9	2082.6	0.37	3195.2	2496.5	0.22
G25	3073.6	1901.9	0.38	2877.5	1885.4	0.34	2939	1906.7	0.35
Mean	3593.3	2440.4	0.30	3229.8	2197.8	0.31	3390.1	2414.3	0.28
LSD$_{5\%}$	611.3	536.1	0.12	586.4	470.4	0.18	593.9	463.6	0.15

Y_p: Grain yield under supplementary irrigation conditions (Kg ha^{-1}); Y_s: Grain yield under rainfed conditions (Kg ha^{-1}); RYC: decrease of relative yield changes

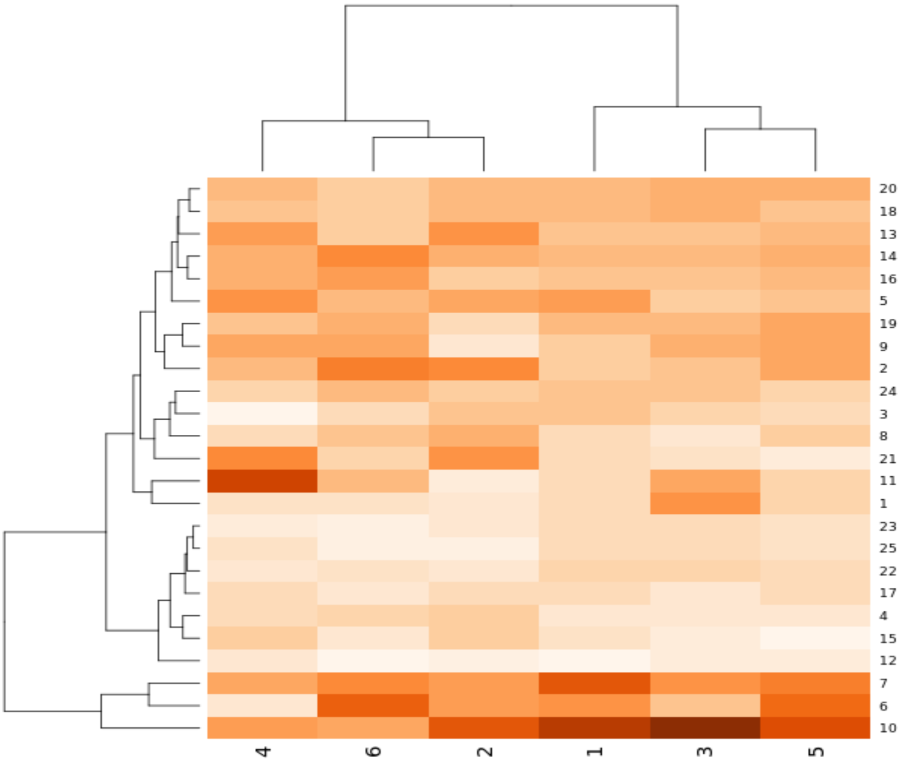

Figure 3- GEI in wheat genotypes under six environments and heatmap for indication of PCs contribution in G+GE

3.1. Univariate indices of parametric stability

According to Francis & Kannenberg (1978), genotype whose yield is higher than the average of all genotypes and its coefficient of variation is lower than the mean of genotypes is introduced as a stable genotype. Therefore, based on the results of Table 3, the genotypes G2, G14, G13, G16 and G5 were considered as stable genotypes compared to other genotypes. Stability of a genotype indicates the genetic potential of a plant that is adapted to growing in the environment (Shahzad et al. 2019). According to the Eberhart & Russel stability method (1966), by assessing the genotypes for general adaptation parameters (dynamic stability), genotypes G5, G24, G23, G22, G25 and G16 had b values close to 1. However, in this method, genotypes with low variance of deviation from regression (S^2d_i), high mean performance and regression coefficient (b_i) close to 1 show better general adaptability across environments (Finlay & Wilkinson 1963; Eberhart & Russel 1966). Accordingly, G5, G14 and G16 with above-average grain yield, were found to be more stable than other genotypes and had higher reliability. Four genotypes G4, G8, G15 and G12, not only were found to be among the lowest yielders but also showed poor adaptation to the test environments. Based on W_i, D_i and σ^2_i parameters, which measure the sums of squares contributed by each genotype to the interaction effect, some high-yielding genotypes, G16 and G18, and low-yielding genotypes, G22, G23, G25, G17 and G24, had the lowest values of these indices and were found to be the most stable across environments (Table 2 and Table 3). This finding offers that selection for genotypic stability based on W_i, D_i and σ^2_i statistics (also called type I stability or static stability) favors below-average-yielding over high yielding wheat genotypes. Similarly, these parameters distinguished stable wheat genotypes in another studies (Farshadfar et al. 2012; Bornhofen et al. 2017; Mohammadi et al. 2020).

The W_i, D_i, CV_i and σ^2_i indices appear to be conservative in introducing stable high-yielding cultivars across environments (Table 2 and Table 3). According to the previous studies, both high yield and type I stability rarely occur in multi-location variety experiments (Karimizadeh et al. 2012; Temesgen et al. 2015). However, these methods can be used to test the reliability of genotypes against yield fluctuations under various environments (Altay 2012). Static stability may be more effective than dynamic stability in a wide range of environments especially in developing countries (Simmonds 1991).

Table 3- Parametric measures of wheat genotypes across six environments

Gen.	CV_i	b_i	P_b_i	S^2d_i	$P\_S^2d_i$	W_i	D_i	σ^2_i
G1	28.53	1.10	0.357	104051	0.077	803074	1597.06	506084
G2	16.12	0.76	0.034*	-31751	0.624	344889	1416.83	207268
G3	25.9	1.09	0.428	-32089	0.627	253512	1416.35	147674
G4	13.54	0.52	0.000**	-72244	0.931	480397	1358.47	295642
G5	21.25	1.00	0.994	15663	0.324	430231	1482.25	262925
G6	30.43	1.55	0.000**	150897	0.034*	1496592	1654.69	958378
G7	32.79	1.90	0.000**	88632	0.100	2164666	1577.64	1394079
G8	17.77	0.70	0.010**	-23237	0.561	430460	1428.8	263075
G9	24.04	1.08	0.473	30766	0.257	502356	1502.49	309964
G10	36.04	2.43	0.000**	71907	0.132	4280565	1556.29	2774013
G11	20.11	0.50	0.000**	228127	0.008**	1724950	1745.54	1107308
G12	18.52	0.57	0.000**	-38765	0.679	531684	1406.89	329091
G13	17.3	0.83	0.140	-55797	0.814	94170	1382.47	108973
G14	18.43	0.94	0.608	-74110	0.942	77096	1355.72	32620
G15	12.87	0.47	0.000**	-68583	0.907	593983	1363.85	369720
G16	19.26	0.95	0.678	-75699	0.951	68683	1353.37	27133
G17	19.83	0.81	0.099	-79418	0.969	112304	1347.86	55582
G18	22.97	1.14	0.223	-81844	0.979	73998	1344.26	30599
G19	25.51	1.26	0.021*	-62178	0.862	241450	1373.21	139808
G20	23.02	1.18	0.122	-86169	0.993	77695	1337.81	33010
G21	9.52	0.26	0.000**	-36007	0.657	1202544	1410.81	766608
G22	22.72	0.97	0.765	-86913	0.995	21945	1336.7	-3347
G23	24.63	1.01	0.963	-83928	0.987	31908	1341.15	3150
G24	21.34	1.00	0.993	-76046	0.952	63390	1352.86	23681
G25	24.15	0.97	0.825	-81068	0.976	44409	1345.41	11303

CV_i: Coefficient of variability; b_i Linear regression coefficient; S^2d_i: Residual MS value; W_i: Wricke's ecovalence; D_i: Hanson genotypic stability; σ^2_i: Shukla's stability variance; * and **: Significant at 5% and 1% probability level, respectively

3.2. Univariate indices of non-parametric stability

Several non-parametric stability methods have been proposed based on the genotype ranking ratio in each environment. Genotypes with the same rank in all environments are considered as stable genotypes (Thennarasu 1995; Huehn 1996). Simultaneously selection based on yield and stability (YS_i) is the combination of mean yields and Shukla stability parameter in a statistical test (Kang 1993). The genotype with the highest yield and the lowest Shukla stability parameter is assigned the rank of one. Genotypes with high YS_i values above the mean of all genotypes were selected as the most stable genotypes, which included G5, G14, G2, G10, G20, G13, G7, G19, G16, G6, G9 and G18 genotypes, respectively (Table 4). In fact, this method of stability analysis introduces high yielding genotypes as stable cultivars. Nassar & Huehn (1987) proposed the values of $S_i^{(1)}$ and $S_i^{(2)}$ to test the stability of genotypes based on the genotype ranking in the environment. Genotypes with minor changes in ranking are the most stable (Kaya & Sahin 2015). For each genotype, $Z_i^{(1)}$ and $Z_i^{(2)}$ measures were computed according with the rank of adjusted data and summed on the genotypes to gain Z-scores. Based on Table 4 results, both of these indices were more than the critical value of $\chi^2_{(0.01,\ 25)} = 44.31$, which showed that the stability rank was significantly different between the studied genotypes. Based on $Z_i^{(1)}$, $Z_i^{(2)}$, G6, G10 and G11 genotypes were the most unstable genotypes in terms of grain yield. Vaezi et al. (2018) pointed out that $S_i^{(1)}$ and $S_i^{(2)}$ display static concept of stability. So, $S_i^{(1)}$ and $S_i^{(2)}$ could be used as an agreement method that select genotypes with moderate yield and yield stability. The other two non-parametric indices $S_i^{(3)}$ and $S_i^{(6)}$, combine stability and yield based on yield ranks of genotypes in each environment. The lowest value for each of these measures indicates the maximum stability for a particular genotype (Huehn 1996; Kaya & Sahin 2015). In this experiment, based on $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$ and $S_i^{(6)}$ indices, G18, G14 and G16 were the most stable genotypes with yields higher than total mean (Table 4). Fox et al. (1990) proposed a non-parametric superiority statistics for evaluating general adaptability. Accordingly, the ranking of genotypes was done separately in each environment and the number of environments in which each genotype was in the top (TOP), middle (MID) and low (BOT) third of the ranks was calculated. A genotype with a higher rank in the upper third is considered a genotype with wide adaptability. In this study, G7, G10, G6, G2 and G5 genotypes had high adaptability and in contrast, G8, G19 and G9 genotypes showed the lowest adaptability. In fact, stable genotypes which are selected by TOP method have high mean yield (Mohammadi et al. 2009). Sabaghnia et al. (2015) and Mohammadi et al. (2020) reported that the TOP and YS_i indices were associated with mean yield and the dynamic concept of stability, so these procedures could be used to recommend cultivars adapted to desirable conditions. Genotypes with lowest values of Thennarasu's (1995) non-parametric stability measures, which were calculated from the ranks of adjusted yield means, are considered more stable. According to the $NP_i^{(1)}$, G22 followed by G14, G16, G25 and G23 were identified as stable in comparison to other genotypes. Based on $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$, genotype G22 followed by G25, G23, G17 and G12 had the lowest values and were the most stable. The more unstable genotypes based on $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ were G10 followed by G7, G6, G11 and G2 (Table 4). The coincidence of the $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ indices was also seen by Mohammadi et al. (2009) and Golkar et al. (2020) in wheat and safflower, respectively. The results showed that Thennarasu and Nassar & Huehn measures are part of the concept of static stability and the selected stable genotypes by these indices may not have high yield (Ahmadi et al. 2015; Vaezi et al. 2018). In present study, genotypes G14, G16 and G18, with the lowest Thennarasu's statistics and high mean yields, were introduced as genotypes with general adaptability (Table 4). According to Farshadfar et al. (2012), Thennarasu's (1995) non-parametric stability parameters do not add important information to statistics obtained by Nassar & Huehn (1987). Therefore, the use of Huehn non-parametric stability measures could be a method of selection as there is a statistical procedure available to examine the significance of $S_i^{(1)}$ and $S_i^{(2)}$. However, Thennarasu's stability indices would be effective alternatives to parametric procedures.

Table 4- Non-parametric measures of wheat genotypes across six environments

Gen.	YS_i	$S_i^{(1)}$	$Z_i^{(1)}$	$S_i^{(2)}$	$Z_i^{(2)}$	$S_i^{(3)}$	$S_i^{(6)}$	*TOP*	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$
G1	8	7.53	0.15	52.17	0.00	14.15	1.77	1	4.17	0.22	0.41	0.47
G2	21	10.20	0.85	77.37	1.19	17.21	3.45	2	7.83	0.92	1.03	1.30
G3	7	8.47	0.01	48.57	0.02	6.82	1.18	0	5.17	0.30	0.37	0.50
G4	3	10.87	1.56	83.37	1.83	4.59	1.08	0	8.17	0.41	0.43	0.56
G5	23	10.27	0.91	75.60	1.03	12.88	2.71	1	7.67	0.90	0.93	1.21
G6	17	13.33	6.04	126.67	10.34	39.45	4.73	3	10.00	2.22	1.40	1.82
G7	19	11.20	1.99	91.47	2.89	5.27	2.55	4	7.67	2.56	2.38	3.05
G8	9	10.27	0.91	69.47	0.57	6.93	1.42	0	7.00	0.48	0.51	0.69
G9	16	10.13	0.79	70.27	0.62	25.38	3.45	0	6.33	0.97	0.79	1.05
G10	20	13.93	7.57	144.17	15.76	11.00	4.80	4	10.83	10.83	4.38	5.57
G11	6	13.07	5.41	121.47	8.95	32.45	3.70	1	9.67	0.77	0.83	1.07
G12	-2	7.87	0.05	51.87	0.00	0.14	0.16	0	4.33	0.17	0.27	0.32
G13	19	8.20	0.00	45.77	0.07	13.21	2.50	1	5.17	0.52	0.66	0.88
G14	22	5.47	1.96	22.00	1.67	2.33	1.07	0	3.00	0.38	0.57	0.73
G15	0	11.00	1.73	81.37	1.60	5.48	1.15	0	7.50	0.34	0.41	0.54
G16	17	5.20	2.34	18.80	2.05	5.21	1.47	0	3.00	0.33	0.42	0.55
G17	4	5.20	2.34	19.87	1.92	1.83	0.72	0	4.00	0.21	0.21	0.27
G18	15	7.07	0.38	34.67	0.56	4.00	1.40	0	4.67	0.42	0.54	0.71
G19	18	9.13	0.16	54.97	0.02	10.28	2.21	0	5.83	0.73	0.70	0.94
G20	20	7.20	0.30	37.07	0.41	5.98	1.70	0	4.67	0.52	0.63	0.82
G21	6	12.60	4.40	112.70	6.84	27.53	3.13	1	8.50	0.50	0.70	0.91
G22	5	3.07	6.63	6.80	3.79	1.81	0.65	0	1.67	0.09	0.13	0.17
G23	2	5.53	1.87	21.77	1.70	2.06	0.64	0	3.17	0.15	0.20	0.27
G24	11	7.07	0.38	34.27	0.58	2.40	1.01	0	5.00	0.40	0.42	0.55
G25	1	4.67	3.21	14.80	2.57	1.10	0.51	0	3.00	0.15	0.17	0.22

Test measures

$Z^{(1)}$-sum = 51.92	E ($S^{(1)}$) = 8.32	E ($S^{(2)}$) = 52	$\chi^2_{(0.01, 25)} = 44.31$
$Z^{(2)}$-sum = 66.96	Var ($S^{(1)}$) = 4.16	Var ($S^{(2)}$) = 539.07	$\chi^2_{(0.01, 1)} = 6.64$

YSi: Rank-sum stability index; $S^{(i)}$, $NP^{(i)}$: Nassar & Huehn's and Thennarasu's non-parametric stability statistics, respectively; Z_1 and Z_2: the standard values of $S^{(1)}$ and $S^{(2)}$, respectively

3.3. Rank correlation between yield, parametric and non-parametric stability indices

Spearman's rank correlation between stability parameters and mean yield are given in Table 5. There was a very significant positive correlation between yield with YS_i and TOP ($P < 0.01$) which showed that these measures allow simultaneous identification of stable and high yielding genotypes. Farshadfar et al. (2012) and Khalili & Pour-Aboughadareh (2016) also reported a strong positive correlation between yield and TOP, indicating that TOP is a suitable statistics for identifying high-yield genotypes. Yield improvement is possible by changing the yield stability by increasing the TOP measure that can be directly related to the development of specific genotypes by improving the growing environmental conditions. However, the $S_i^{(3)}$, $S_i^{(6)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ showed a positive significant correlation with each other and a strong negative correlation with yield. These results are in agreement with the work of Temesgen et al. (2015). Therefore, selection based on these stability statistics will be less effective when yield improvement is the main target of selection. $S_i^{(1)}$ had a significant positive correlation with Thennarasu and Nassar & Huehn statistics which can be considered as an alternative and useful parameter for selection of stable genotypes. Mohammadi et al. (2009) reported that the $S_i^{(1)}$ and $S_i^{(2)}$ are related to the static concept (biological) of stability. However, association among $S_i^{(1)}$ and $S_i^{(2)}$ with yield was not significant (Table 5), which indicating that these measures could be used as a mediating method for the selection of highly stable genotypes (Vaezi et al. 2018).

Table 5- Spearman rank correlation among mean yield and stability parametric and non-parametric measures in wheat genotypes across six environments

	Yield	CV_i	b_i	S^2d_i	W_i	D_i	σ^2_i	YS_i	$Si^{(1)}$	$Si^{(2)}$	$Si^{(3)}$	$Si^{(6)}$	*TOP*	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$
CV_i	-0.30															
b_i	-0.17	-0.07														
S^2d_i	-0.41*	0.20	0.50*													
W_i	-0.27	0.08	0.80**	0.87**												
D_i	-0.41*	0.20	0.50*	1.00**	0.87**											
σ^2_i	-0.27	0.08	0.80**	0.87**	1.00**	0.87**										
YS_i	0.94**	-0.19	0.04	-0.27	-0.08	-0.27	-0.08									
$Si^{(1)}$	-0.37	0.00	0.76**	0.78**	0.89**	0.78**	0.89**	-0.19								
$Si^{(2)}$	-0.38	0.01	0.77**	0.80**	0.92**	0.80**	0.92**	-0.20	0.99**							
$Si^{(3)}$	-0.52**	0.05	0.39	0.75**	0.63**	0.75**	0.63**	-0.43*	0.72**	0.72**						
$Si^{(6)}$	-0.74**	0.19	0.46*	0.74**	0.66**	0.74**	0.66**	-0.61**	0.74**	0.75**	0.92**					
TOP	0.62**	-0.22	-0.48*	-0.72**	-0.67**	-0.72**	-0.67**	0.45*	-0.65**	-0.68**	-0.65**	-0.76**				
$NP_i^{(1)}$	-0.41*	-0.04	0.70**	0.71**	0.80**	0.71**	0.80**	-0.24	0.97**	0.96**	0.73**	0.76**	-0.65**			
$NP_i^{(2)}$	-0.82**	0.17	0.50*	0.63**	0.61**	0.63**	0.61**	-0.69**	0.76**	0.76**	0.73**	0.89**	-0.66**	0.80**		
$NP_i^{(3)}$	-0.86**	0.13	0.49*	0.66**	0.62**	0.66**	0.62**	-0.73**	0.74**	0.76**	0.74**	0.91**	-0.74**	0.77**	0.97**	
$NP_i^{(4)}$	-0.86**	0.14	0.49*	0.65**	0.61**	0.65**	0.61**	-0.73**	0.75**	0.76**	0.72**	0.89**	-0.71**	0.78**	0.98**	1.00**

* and **: Significant at the 5% and 1% probability level, respectively

The strong positive correlation of S^2d_i with W_i and σ^2_i showed that S^2d_i can be used not only to evaluate the predictability of the estimated response obtained from linear regression, but also to assess the relative contribution of genotype to GEI and indirectly its biological stability (Mohammadi et al. 2012). The positive and highly significant correlation of S^2d_i, W_i, σ^2_i and D_i with Thennarasu and Nassar & Huehn non-parametric indices (Table 5) showed that these parameters have a similar role in ranking the stability of genotypes as previously confirmed by Roostaei et al. (2014); Dia et al. (2016), Bornhofen et al. (2017), Vaezi et al. (2018) and Golkar et al. (2020). According to Temesgen et al. (2015), various stability parameters justify genotypic efficiency differently, regardless of yield performance. Therefore, GEI evaluation and yield stability should be based on a combination of sustainability measures.

In order to better understand the relationships between stability statistics, Heatmap of genotypes and stability parameters were drawn (Figure 4). In this figure, genotypes were ranked based on stability statistics. In this way, the parameters were categorized in two main clusters. The first cluster was assigned to mean yield (Y_i), TOP and YS_i. The second cluster consisted of three sub-clusters with CV_i and b_i parameters in the first sub-cluster, S^2d_i, D_i, W_i and Stabvar parameters in the second sub-cluster and $S_i^{(3)}$, $S_i^{(6)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(1)}$, $NP_i^{(4)}$, $S_i^{(1)}$ and $S_i^{(2)}$ were placed in the third sub-cluster. According to previous reports, $S_i^{(3)}$, $S_i^{(6)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ criteria have shown similar stability ranking patterns in various crop species (Mohammadi et al. 2009; Farshadfar et al. 2012; Khalili & Pour-Aboughadareh 2016; Vaezi et al. 2018).

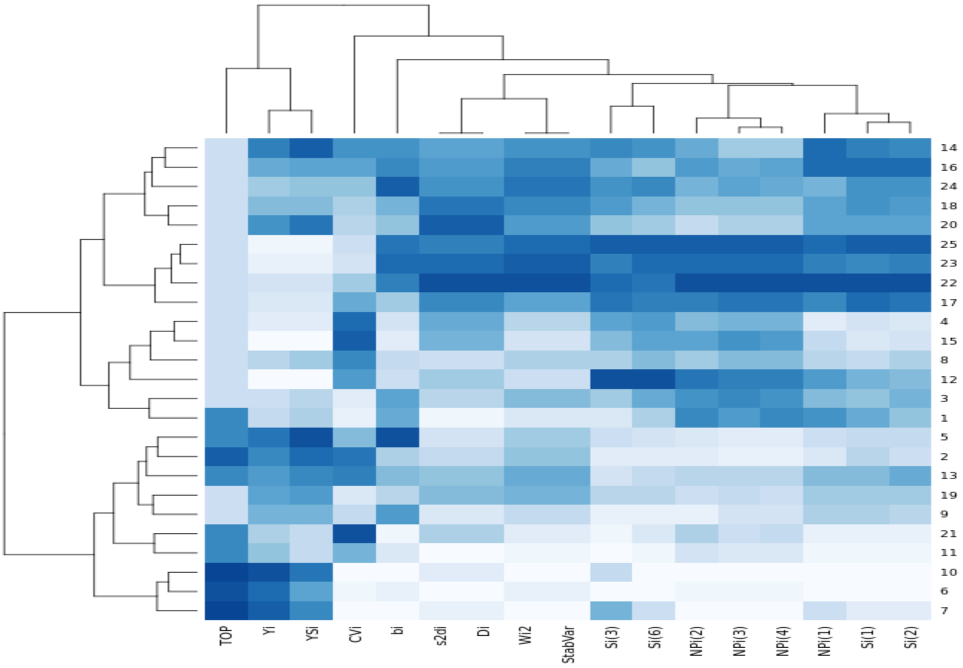

Figure 4- Heatmap of wheat genotypes distribution and stability parameters

3.4. AMMI analysis

The main effects of genotype, environment and G × E interaction were very significant ($P < 0.001$) (Table 6). The magnitude of the SSGE was 3.59 times more than that for genotype effect, demonstrating there were considerable deferential response among the genotypes to change of environment and the differential discriminating ability of the test environment (Shukla et al. 2015; Heidari et al. 2017; Bavandpori et al. 2018; Tekdal & Kendal 2018; Mekonnen et al. 2020). The value of the GEI is mostly due to variations in environmental conditions from supplementary irrigated to rainfed and from year to year. Furthermore, part of the GEI is due to genetic diversities among the studied genotypes. Analysis of GEI showed that only the first interaction principal component (IPC1) was highly significant ($P < 0.01$) and explained 58.6% of variability of GE. In the current study, the first two principal components (IPC1 and IPC2) explained about 77.8% of SSGE (Table 6). Thus, investigation of the distribution of environments and genotypes based on these two IPCs can prepare useful information for visualizing the response patterns of environments and genotypes. Hagos & Abay (2013) and Khan et al. (2020) affirmed that the first two IPCs were enough to justify the GEI. The G6, G7 and G10 genotypes showed the highest GEI while, the lowest interaction were obtained for G12, G15 and G25 genotypes.

Table 6- Combined analysis of variance for grain yield using AMMI model in wheat genotypes across six environments

Source	*Df*	*SS*	*MS*	*Prob.*	*GE expl. (%)*	*Cum. (%)*
Environment (E)	5	832512628	166502526	0.000		
Genotype (G)	24	28449331	3268722	0.000		
G × E	120	102238124	406174	0.000		
IPC1	28	59911540.7	2139697.9	0.007	58.6	58.6
IPC2	26	19629719.8	754989.2	0.148	19.2	77.8
IPC3	24	13393194.2	558049.8	0.506	13.1	90.9
IPC4	22	7054430.6	320655.9	0.922	6.9	97.8
IPC5	20	2249238.7	112461.9	0.957	2.2	100
Residuals	288	29196262	101375.9	0.989		

AMMI$_1$ model biplot shows the distribution of environments and genotypes based on IPC1 values and mean yields (Figure 5). A genotype that has a higher value of yield (horizontal axis) and a smaller amount (near zero) of IPC1 (vertical axis), will be a more desirable genotype, because this genotype has both high yield and stability. The G14, G5, G13, G16 and G20 genotypes appear to have high performance stability. The highest yield differences between genotypes were G10 and G12 and among environments were E1 (highest mean yield) and E4 (lowest mean yield). The correlation between the mean of genotypes and their IPC1 values was positive and highly significant ($r = 0.76$, $P < 0.01$), which revealed that medium-yield genotypes are stable, while high-yield and low-yield genotypes are relatively unstable. These results make it possible to use both aspects of adaptability, namely general and specific adaptability of genotypes, which is the main approach of plant breeders in selecting genotypes during MET (Gauch 2013).

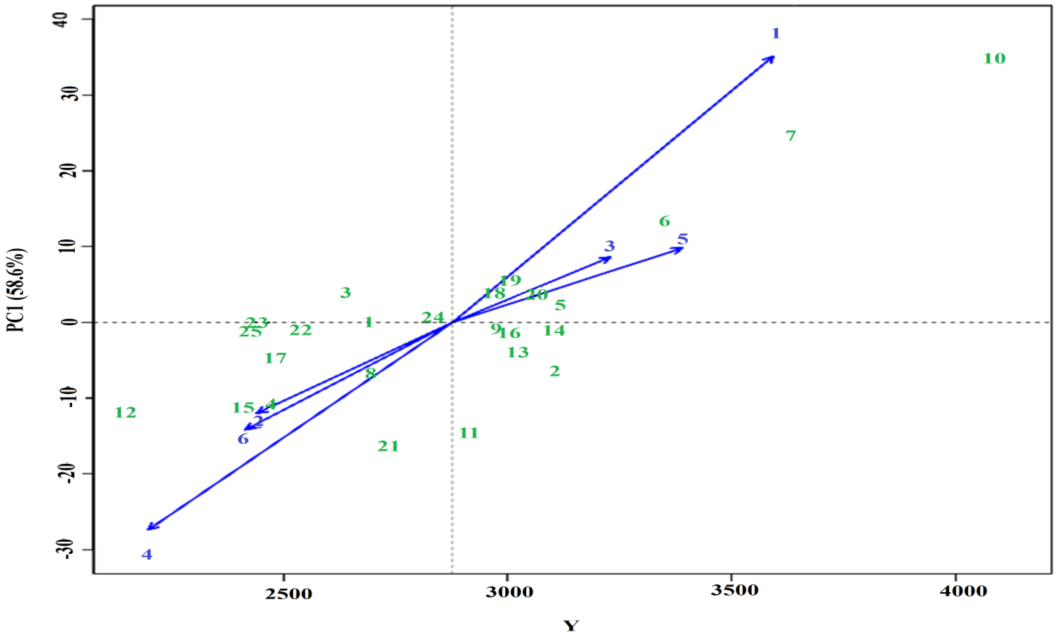

Figure 5- Biplot of yield and first principle component for wheat genotypes and environments (AMMI$_1$ model) [Genotype numbers are green and environment numbers are blue]

The AMMI$_2$ model biplot shows the position of genotypes and environments in terms of the first two IPCs, which accounted for about 77.8% of GEI variations (Figure 6). Genotypes and environments close to the origin have less impact and those far from the origin have a greater role in GEI (Lai et al. 2012). Thus, genotypes G6, G10, G11, G7 and almost G8 and G21, far from the origin, have the most fluctuation in environmental changes, while genotypes G13, G14, G16, G17, G18, G19, G20, G22, G23, G24, G25 and G5 within the orient and close to the biplot origin had a smaller share of the GEI and were generally adaptable with all environments. In addition to stability, high yielding criteria must also be considered for the final choice. Accordingly, G14, G13, G16, G19, G18, G20 and G5 genotypes can be introduced as genotypes with higher yield and general stability. The discriminating ability of the environments can be clarified by the magnitude of IPC1 and IPC2. Among the environments, E1 with the highest IPC1 and the lowest IPC2, was the most discriminatory and had the greatest effect on the GEI (Figure 6). The high distribution of environments compared to the genotypes indicated a high environmental diversity compared to the genotypes (Oliveira et al. 2014). The AMMI$_2$ biplot has better fit and accuracy for studying the complex GEI pattern. Also, the AMMI$_2$ with two main components justifies the highest rate of GEI changes (Khan et al. 2020).

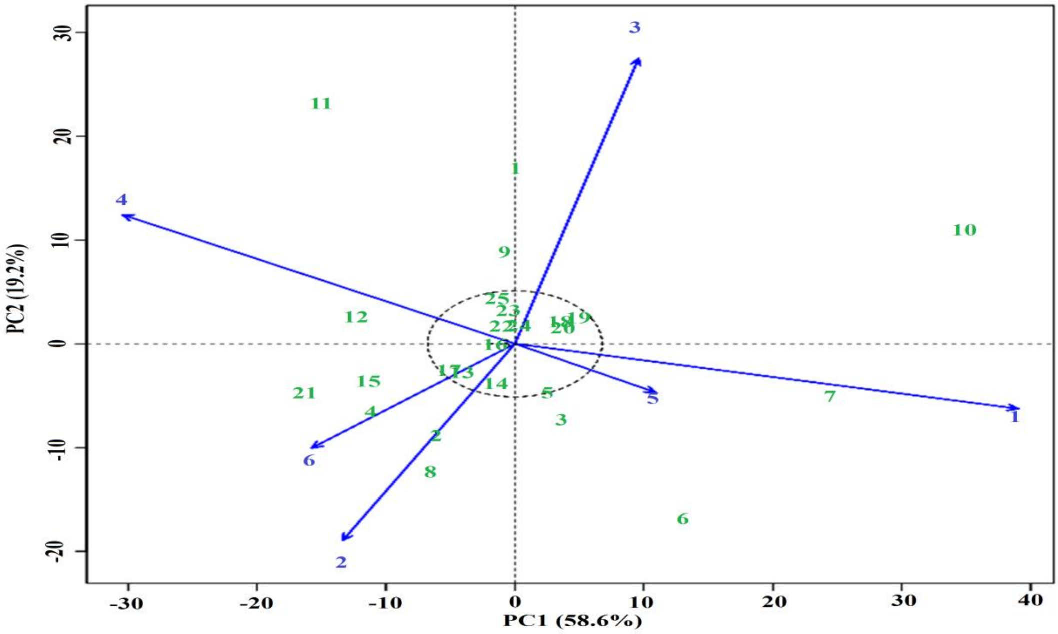

Figure 6- Biplot of the first two principal components of wheat genotypes and environments (AMMI$_2$ model) [Genotype numbers are green and environment numbers are blue]

Some researchers have reported $AMMI_2$ as a better model than $AMMI_1$ for the GEI investigation (Rodrigues et al. 2016; Kumar et al. 2018). A genotype is suitable for a specific environment when it is able to adapt well to and close to that environment. Thus, G7 genotype had specific adaptation to E1 and E5 environments, G8 and G2 genotypes to E2 environment, G12 genotype to E4 environment, G1 genotype to E3 environment and G4, G21 and G15 genotypes to E6 environment (Figure 6). In general, AMMI clarifies GEI and provides a summary of patterns and relationships between genotypes and environments.

3.5. GGE biplot analysis

The GGE biplot method is able to analyze Which-Won-Where Pattern of genotypes in which GEI, differentiation of MEs and recommendation of specific genotypes for each MEs are presented graphically (Rakshit et al. 2014; Oral et al. 2018). GGE biplot polygon view of yield for the studied genotypes in six environments is shown in Figure 7, which is formed by connecting the farthest genotypes from the biplot origin with straight lines and the rest of the genotypes within the polygon. The results show that GGE biplot justifies 85.1% of the total GEI changes by the first two IPCs. According to Yan & Kang (2003), it can be used to extract MEs if this biplot justifies at least 60% of GEI changes. By investigation the polygon diagram, the G8, G6, G10, G11, G11, and G12 genotypes at the vertex of the polygon were identified as superior or weak genotypes in some or all environments. By examining Figure 7, five MEs were identified that ME I including E1, E2, E3, E4, E5 and E6 environments, of which G7, G5, G14, G13, G16, G18 and G20 were the top ME I genotypes. Therefore, these genotypes were suitable for both SI and RF conditions. A ME refers to a group of environments in which one or more genotypes have the best performance (environmental response) (Yan et al. 2000). The G11, G12 and G8 genotypes at the top of the polygon were not included in any of the MEs, indicating low performance of these genotypes under all environments. The rest of the studied genotypes in the other four MEs did not show any specific adaptability with any of the environments (Figure 7). GGE biplot enables simultaneous visualization of the performance and stability of genotypes as well as the discriminating power and representativeness of environments. On the other hand, this procedure allows the ranking of cultivars based on yield in a specific environment and the comparison of them with the ideal cultivar (Yan et al. 2007; Aktas 2016). Due to the simplicity of graphical interpretation of GGE biplot results, this method is widely used in GEI analysis. In Ethiopia, to evaluate the stability of 22 bread wheat genotypes in six environments, using polygonal diagram, two MEs and five superior genotypes were identified (Temesgen et al. 2015). In one ME, genotypes must be evaluated for mean yield and stability over environments. Yield and stability of genotypes are assessed by Average Tester Coordinate (ATC) method in a biplot (Yan et al. 2007; Mehari et al. 2015; Singh et al. 2019). The line that passes through the origin of the biplot and the mean of the environments (mean scores of PC1 and PC2 environments) is called the ATC axis (Figure 8). The vertical dimension of ATC, which passes through the origin of the biplot and is perpendicular to the horizontal axis of the ATC, estimate the GEI and is an indicator of the instability of the genotypes. Genotypes located on the right side of the ATC vertical dimension have higher mean yield (Yan & Tinker 2006). According to this biplot view, it is possible to study the effect of G and GEI simultaneously. Figure 8 shows the visualization of each genotype on ATC and is an approximation of the yield rank of the genotypes. In this ranking, G10, G7, G6, G5, G20, G14, G19, G18, G2, G16, G13 and G9 genotypes had higher yield than total mean, respectively. The genotypes have a greater distance from ATC horizontal axis indicates a greater role in the GEI and they are less stable. Accordingly, the genotypes G11 followed by G6, G1 and G8 were more unstable than other genotypes. According to Yan & Tinker (2006), an ideal genotype should have both high mean yield and high stability in a ME. In fact, an ideal genotype should have the highest PC1 score (high yielding performance) and lowest PC2 score (high stability) (Yan & Tinker 2006; Oral et al. 2018). According to Figure 8, genotypes G10, G6 and G7 had high yield and low stability, and genotypes G1, G8, G11 and G3 had low yield and stability and genotypes G24, G21, G22, G23 and G15 had low yield and high stability. Breeders can select genotypes with high mean yield but low stability that have the best response to certain environments. For example, genotypes G7 and G10 had the best response to environments E1 and E5, while genotype G6 showed a weak reaction to environment E2. In addition to high stability under different environments, G20, G18, G13, G16, G14, G19 and G5 genotypes had mean yield higher than the total mean (Figure 8). Previously, GGE biplot has been used and emphasized to investigate adaptability and simultaneous combination of yield and stability in bread wheat by Naroui Rad et al. (2013), Mehari et al. (2015), Bornhofen et al. (2017), Bavandpori et al. (2018) and Singh et al. (2019). Evaluation of test environments for discriminating power vs. representativeness presented in Supplementary Figure S1. The small arrow shown on the ATC line is where there is ideal environment. This point is considered as an ideal virtual environment so, desired environment has short distance vector from the ATC axis is consider as an ideal environment (Yan et al. 2000). According to Figure 8, environments E5, E1, E3 and E6 can be considered as desired environments for wheat genotypes. The favorable conditions of these environments can be clearly seen in Figure S1. Environments close to the arrow represent ideal environments in the experiment. The small length of the environment vector, shows the less power of the environment to discriminate and diversify between genotypes. Accordingly, the E6 environment had the least ability to discriminating and representativeness genotypes. Whereas, E3 and E1 environments had the highest discriminating power and diversify between genotypes, indicating their sufficiency as test environments for multi-environmental trials. On the other hand, for selecting genotypes with general adaptability, E1 environment was the most suitable in terms of representativeness of environments, while E6 was the most suitable based on representativeness for yield (Figure S1). Generally, both the AMMI and GGE biplot methods performed the same in identifying stable and high-yielding genotypes (G20, G18, G13, G16, G14, G19 and G5). This result was in agreement with the findings of Aktas (2016), Bornhofen et al. (2017) and Singh et al. (2019). Moreover, GGE biplot has the advantage of better discriminating power and representativeness than AMMI biplot (Yan et al. 2007; Singh et al. 2019).

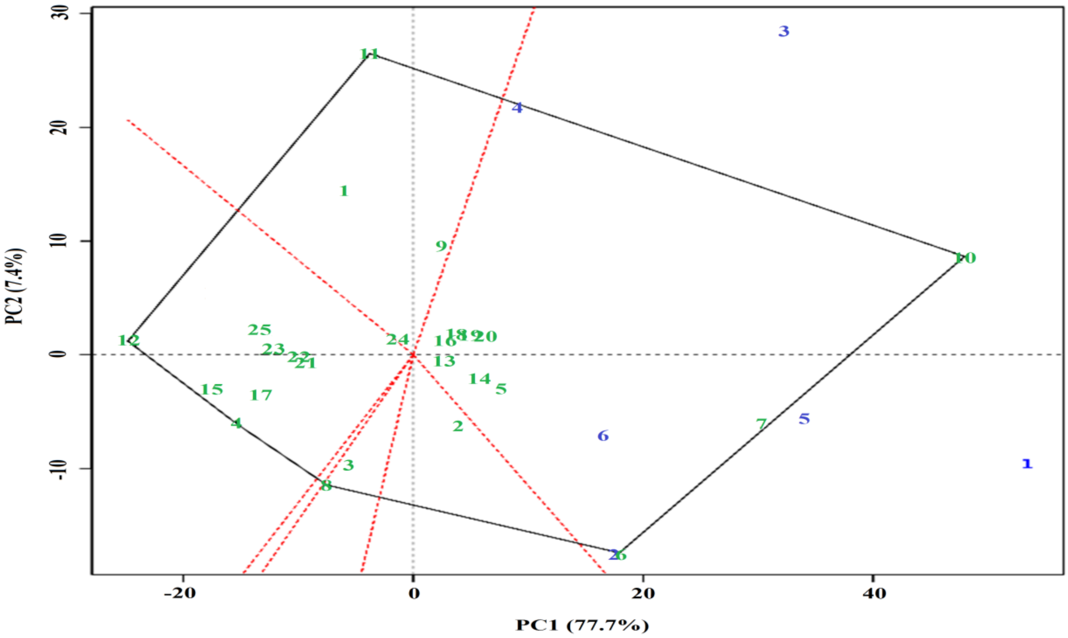

Figure 7- Graphical display for coincidence of wheat genotypes with environments and grouping test environments [Genotype numbers are green and environment number are blue]

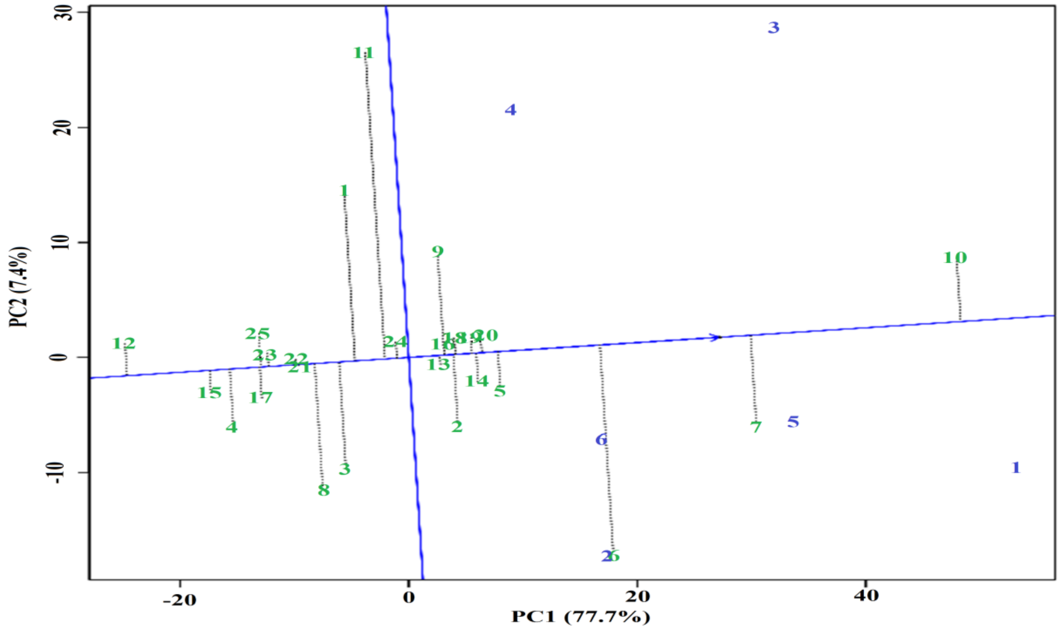

Figure 8- Average tester coordinate (ATC) view of the GGE biplot based on yield of wheat genotypes in 6 environments [Genotype number are green and environment number are blue]

4. Conclusions

Several of the univariate parametric and nonparametric stability statistics employed in the present investigation quantified stability of wheat genotypes with respect to yield, stability or both. However, both mean yield and stability should be considered simultaneously to exploit the useful effects of GEI. According to Eberhart & Russel method, G5, G14 and G16 with above-average yield, were found to be more stable than other genotypes. The results showed selection for genotypic stability based on Wi, Di and σ2i measures favors below-average-yielding over high yielding wheat genotypes. Genotypes G14, G16 and G18, with the lowest Thennarasu and Huehn non-parametric stability measures and high mean yields, were introduced as genotypes with general adaptability. The results of graphical analysis of the GEI in present study showed that the studied environments explain a large part of changes in the matrix of GEI. Therefore, the AMMI and GGE biplot methods were suitable tools for grouping diverse environments and determining stable and adaptable genotypes to different environmental conditions. Accordingly, lines G20, G18, G13, G16, G14, G19 and Saein cultivar (G5) can be considered as desirable genetic resources in wheat production programs under variable environments in Iran, due to having the appropriate combination of yield and stability. Also, G10, G7, G2, G8, G4, and G1 genotypes with specific adaptation, are only recommended for use in certain environments.

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Supplementary data:

Table S1- Some of climatic parameters from October to June at the Agricultural Research Station of Miandoab

	2013/2014				2014/2015				2015/2016			
	Average temperature			Freezing dayes[a]	Average temperature			Freezing dayes	Average temperature			Freezing dayes
	Min	Max	Mean		Min	Max	Mean		Min	Max	Mean	
OCT	7.1	25.6	16.3	0	5.5	23	14.2	2	8.4	22.1	15.2	0
NOV	4.9	16.8	10.8	3	2.7	15.7	9.2	9	0.9	13.9	7.4	12
DEC	0.7	9.3	5	13	-2.4	5.7	1.7	19	1.2	8	4.6	10
JAN	-4.4	5.7	0.6	23	-10.6	-1.5	-6	30	-2.7	8.1	2.7	24
FEB	0.4	11.2	5.8	14	-4.2	7.2	1.5	22	-1.3	11.1	4.9	23
MAR	1.3	13.8	7.6	13	2.6	15	8.8	8	-0.8	12.8	6	18
APR	3.9	19.5	11.7	2	3.7	17.8	10.8	7	4.1	21.4	10.9	3
MAY	7.3	21.4	14.4	1	9.5	25.4	17.4	0	7.4	29.6	15.5	3
JUN	11	28.6	19.8	0	12.3	29.3	20.8	0	12.8	33.4	21.8	0

[a] Days below 0°

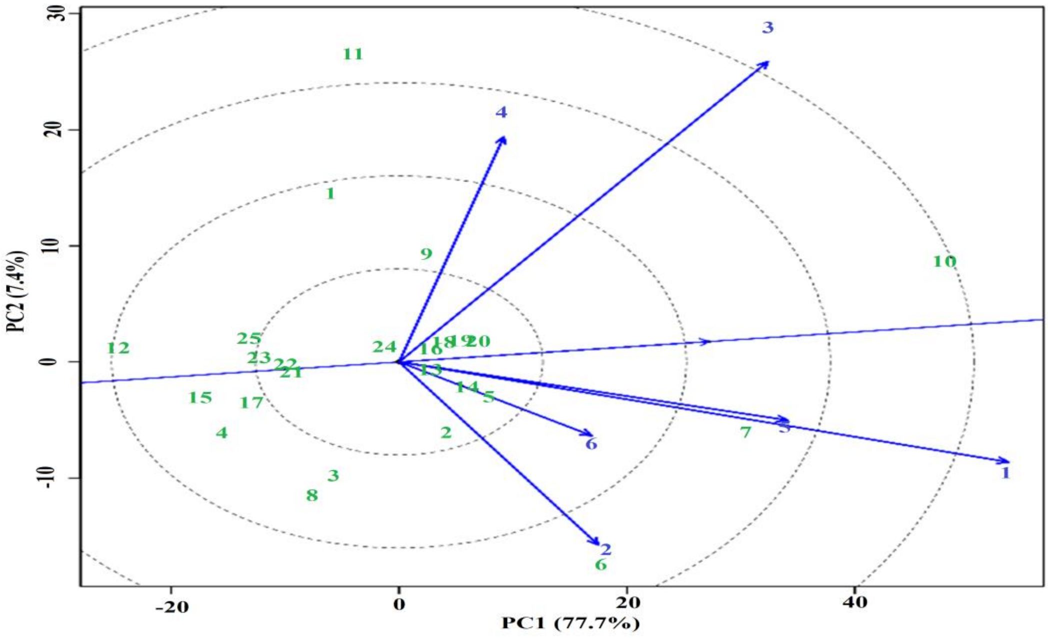
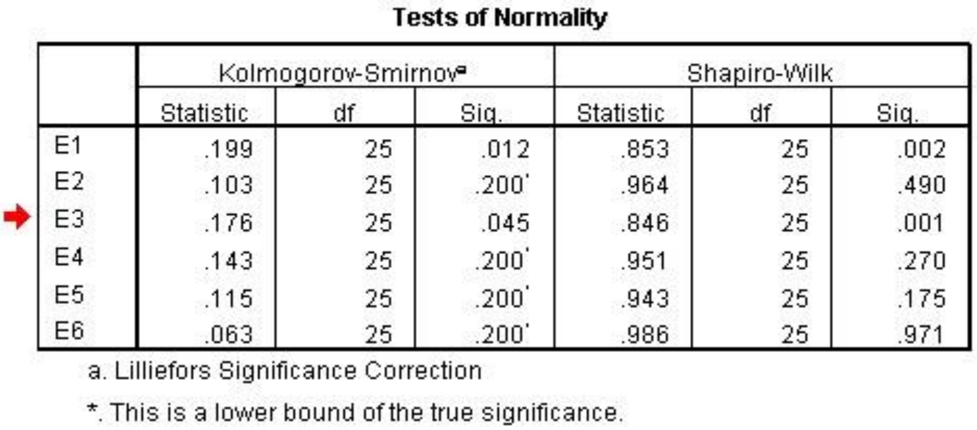


Figure S1- Evaluation of test environments in terms of their "discriminating power vs. representativeness" [Genotype number are green and environment number are blue]

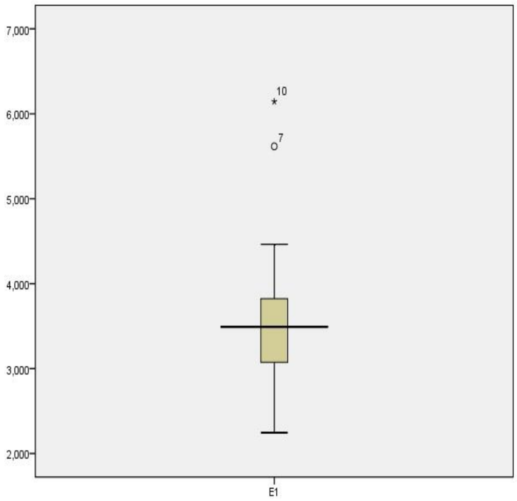


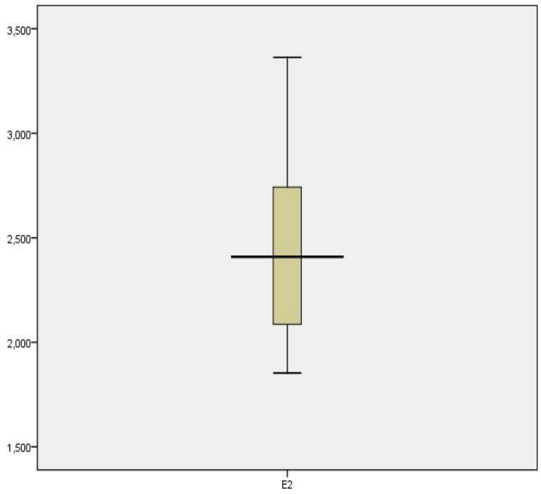
Tests of Normality

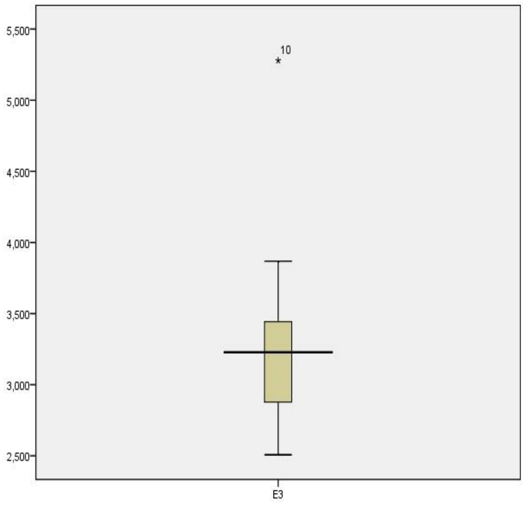
	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
	Statistic	df	Sig.	Statistic	df	Sig.
E1	.199	25	.012	.853	25	.002
E2	.103	25	.200*	.964	25	.490
E3	.176	25	.045	.846	25	.001
E4	.143	25	.200*	.951	25	.270
E5	.115	25	.200*	.943	25	.175
E6	.063	25	.200*	.986	25	.971

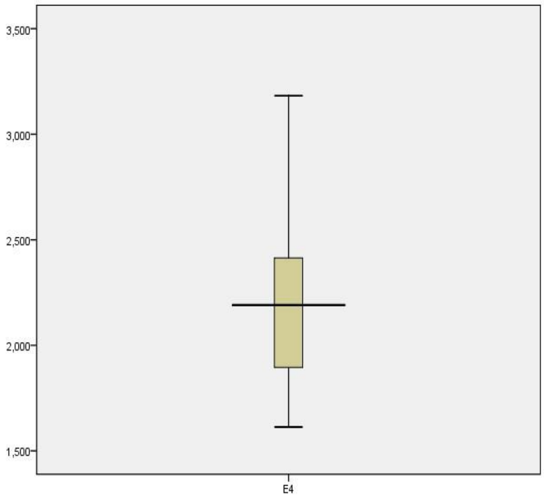
a. Lilliefors Significance Correction

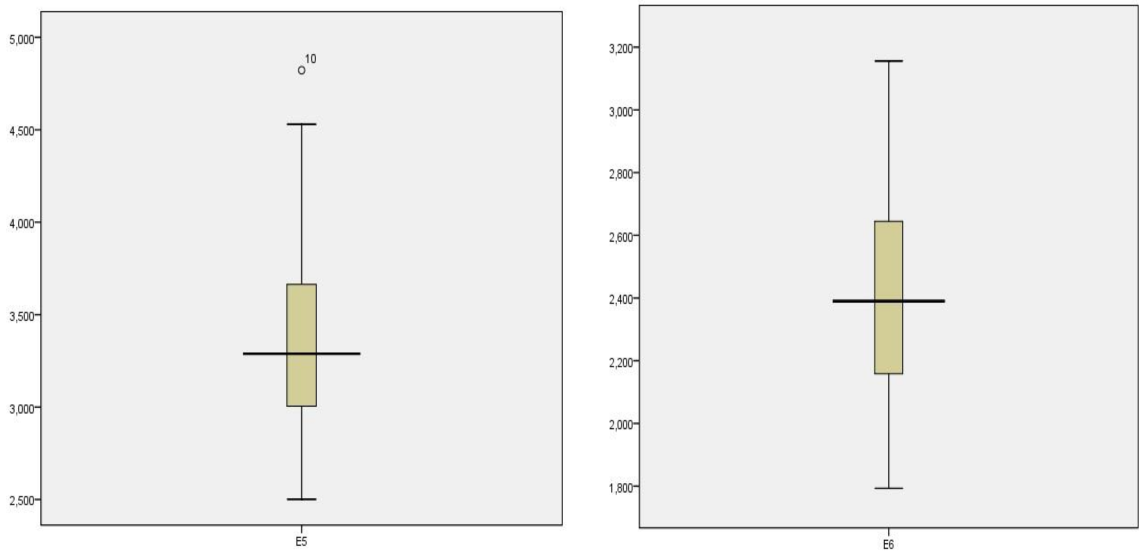
*. This is a lower bound of the true significance.







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