






Original article

Genotype × Environmental Interaction Analysis of Multi-Environment Bread Wheat Trials Using AMMI and GGE Biplot

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Abstract

This study was conducted on fifteen genotypes of bread wheat (*Triticum aestivum* L.) in three ecological sites within the first environmental area (rain-fed conditions) in Syria during 2019/2020 season. The experiment was designed according to a randomized complete block design (RCBD) in three replicates at each site, with the aim of identifying stable high-yield genotypes, the ideal environment, and the appropriate genotype for each environment, using Additive Main Effect and Multiplicative Interaction (AMMI) and GGE Biplot models. AMMI demonstrated significant interactions in G, E, and E×G. The principal components PC1 and PC2 explained 100% of the total variance, with the contribution of PC1 being 70.1% and PC2 29.9%. According to the AMMI biplot analysis, the G4, G1 and G6 genotypes were the most productive, and G3 the most stable, while the G15, G10 and G11 genotypes were the least stable. According to GGE Biplot analysis, E2 was the ideal environment compared to the rest of the tested environments, and G6 and G1 were the ideal genotypes, which indicates the importance of these two genotypes and the necessity of investing them in improving grain yield and stability. "which-won-where" analysis showed that the G4 and G8 genotypes had high yields in both E1 and E2 environment, while G1 was suitable for the E3 environment, G15 and G2 were unsuitable for any of the assessed environments.

Keywords: Yield stability, Principal components, Multiplicative interaction, AMMI stability value, Ideal genotype.

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INTRODUCTION

Bread wheat (*Triticum aestivum*, L) is the second most important cereal crop after rice, as it is an essential food source for the growing population worldwide. Increasing wheat production plays an important role in achieving food security. The development of high-yielding genotypes combined with resistance against biotic and abiotic stresses is crucial to fill the grain demand gap. Multi-environmental trials (METs) are considered as an essential step in plant breeding programs to select the stable and outstanding genotypes within different environmental conditions (Ahmadi et al., 2012; Tekdal and Kendal, 2018). Moreover, yield stability and high adaptation become more important since the climate variability is being more pronounced over the years. Thus, breeding for highly adapted genotypes to various environmental conditions is still the most important achievement for plant breeders. However, the effects on the performance and stability of the genotypes due to the interaction between the genotypes and the environment is challenging plant breeders from developing new varieties with wide adaptation (El-Morshidy et al., 2001) where the selection for the average yielding is insufficient in case of the presence of Genotype \times Environmental Interaction (Sharifi et al., 2017).

Different methods have been proposed to select the stable genotypes in different environments, using mainly regression analysis, regression deviation, principal component analysis (PCA), and additive main effect and multiplicative interaction (AMMI). AMMI model is used to test the main effects for each genotype and environment in addition, PCA is used for analyzing the remaining reaction components. Nevertheless, GGE biplot model is considered a powerful analytical method to select the best performing genotypes within diverse environments by presenting the data in graphs which facilitate the selection of highly stable and productive genotypes, in addition, to determining the optimal environment for each genotype (Yan and Kan, 2002).

Smutana et al., (2021) utilized the GGE biplot model, along with eleven stability models, to analyze 23 bread wheat genotypes over a four-year period in two fields (8 environments). The statistical analysis showed significant differences between the genotypes and the Genotype by Environmental Interaction, GGE Biplot, on the other hand, provided an effective assessment for genotypes in terms of adaptability without neglecting the ability of productivity. Furthermore, they recommended utilizing the GGE Biplot model to identify prospective genotypes for long-term performance.

In a study about bread wheat, Bishwas et al., (2021) observed that the genotypes and the Genotype by Environmental Interaction have a significant impact on yield, where 100% of the interaction effect was explained by PCA 1 in AMMI model. Meanwhile, GGE biplot analysis showed that the genotype NL 1179 was particularly adapted in the irrigated environment, while, NL 1350 was adapted in the stressed environment (which won where model). On the other hand, NL 1179 was the least stable in addition to BL 4669, and NL 1386. Additionally, NL 1420, NL 1368, NL 1350, and BL 4919 were

stable in different environmental conditions with a yield average higher than the general average. They proposed using NL1420 for breeding programs as a highly productive and stable genotype.

Furthermore, 50 bread wheat genotypes were tested in nine ecological sites, significant differences between Genotype \times Environmental Interaction were reported. AMMI model and GGE Biplot showed that the genotypes (G120, G111, G131, G135, and G112) were stable and highly productive in all the tested sites. Further, G112 and G135 were identified for their excellent productivity and stability in all the ecological sites which could be utilized for national breeding program for wheat (Singh et al., 2019).

In this study, different genotypes were evaluated from different environments to categorize bread wheat genotypes according to environmental conditions, to obtain specific recommendations. The objectives of this study were: (1) To analyze the genotype \times environment interaction using AMMI and GGE biplot models; (2) To identify the ideal and most stable genotypes and environments for bread wheat improvement.

MATERIALS and METHODS

Fifteen bread wheat genotypes were tested that consist of four approved cultivars, and eleven promising strains Table 1.

Table 1. Shows the names of the studied genotypes and their Pedigree.

Code	Genotype	Type	Pedigree
G1	Douma 6	Cultivar	SNB'S'//SHI4414/CROW'S'/3/MON'S'/CROW'S'
G2	Jolan 2	Cultivar	SHUHA-17/GHURAB-1
G3	Promising 1	Strain	-
G4	Douma 66233	Strain	4WON-IR-257/5/YMH/HYS//HYS/TUR3055/3/DGA /4/ VPM / MOS
G5	Douma 66241	Strain	ATTILA 50Y//ATTILA/BCN/3/PFAU/MILAN
G6	Douma 68017	Strain	SERI.1B//KAUZ/HEVO/3/AMAD/4/FLAG-2
G7	Douma 66981	Strain	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/TEVEE'S'/BOBWWHITE #1
G8	Douma 68010	Strain	VEE/PJN//2*KAUZ/3/SHUHA-4/FOW-2
G9	Douma 68467	Strain	ATTILA*2/PBW65//PFAU/MILAN
G10	Douma 68498	Strain	P1.861/RDWG//DAJAJ-10
G11	ACSAD 1300	Strain	ACSAD901/3/NAC/VEE'S'//TEMU196.74/TITO'S'-1IZ-1IZ-0IZ
G12	ACSAD 1302	Strain	ACSAD901/3/NAC/VEE'S'//TEMU196.74/TITO'S'-1IZ-2IZ-0IZ
G13	ACSAD 1304	Strain	ACSAD901/3/NAC/VEE'S'//TEMU196.74/TITO'S'-1IZ-3IZ-0IZ
G14	Cham 4	Cultivar	FLK'S'/HORK'S'
G15	Bohouth 6	Cultivar	FR316/3/MCM/KT//Y50/4/ZA75/5/BJY

The experiment was carried out in three different environmental sites in the first environmental area: (Homs - Al-Ghab - Gillen). The abbreviations of the environments are as follows: Homs = E1, Al-

Ghab = E2, and Gillen = E3. Table (2) presents the average temperatures (C°) and rainfall rates in the experimental sites.

Table 2. Average temperatures (C°) and rainfall rates (mm) in the studied locations during the 2019-2020 season

Site	Homs			Al-Ghab			Gillen		
Month	Average minimum temperature (C°)	Average maximum temperature (C°)	Rainfall rate (mm)	Average minimum temperature (C°)	Average maximum temperature (C°)	Rainfall rate (mm)	Average minimum temperature (C°)	Average maximum temperature (C°)	Rainfall rate (mm)
Nov	10.0	17.7	38.7	8.7	17.3	42.0	7.3	19.1	80.5
Dec	8.2	14.3	141.2	7.1	16.4	285.0	6.2	19.9	59.7
Jan	4.0	11.4	74.7	2.9	11.9	195.5	3.4	12.4	112.0
Feb	5.3	13.7	117.6	6.9	12.5	83.0	4.7	12.2	89.0
Mar	7.8	16.5	64.1	7.2	17.6	127.0	7.3	20.4	71.8
Apr	9.4	19.7	40.8	10.4	21.4	65.0	9.4	22.1	41.0
May	15.9	30.5	13.0	14.2	28.8	14.0	15.0	34.1	7.0
Total	60.4	123.8	490.1	57.4	125.8	811.5	53.3	140.1	461.0

The experiment was planted according to a randomized complete block design (RCBD) with three replicates. The seeds were planted in 16 lines of 10 m in length, spaced 20 cm apart, resulting in a total experimental plot area of approximately 32 m².

The averages were compared using the least significant difference (LSD) at the 5% level between genotypes and sites and their interaction. PBTools V1.3 software was used to analyze AMMI and GGE Biplot models.

RESULTS and DISCUSSION

Table (3) shows the average grain yield of the studied bread wheat genotypes in the first environmental area, and their average performance at different environmental sites. The overall average grain yield was (4.591) ton. ha⁻¹, where the following genotypes: (G4, G1, G6, G8, G11, G7, G9, G3, G13, G12) had a higher average performance than the overall average ($\bar{X}_i > \bar{X}$), whereas the average performance of the rest genotypes was below the overall average.

Table (3) indicates that there are significant differences at the level of 5% between the averages of the three environmental sites for the characteristic of grain yield, where site E2 significantly outperformed the other two sites with an average grain yield ($\bar{X}_{j2} = 5.260$), followed by site E1 with significant differences from Site E3, these significant differences are attributed to the different environmental sites studied in the climatic factors (rainfall rate, temperatures, altitude above sea level).

Table 3. Average grain yield (ton. ha⁻¹) for the studied genotypes in the three ecological sites and their average performance at different environmental sites.

Genotype	Homs	Al-Ghab	Gillen	\bar{X}_i
G1	5.428 ^b	5.868 ^{ab}	4.728 ^a	5.341 ^{ab}
G2	3.795 ^e	2.841 ^f	2.506 ^e	3.047 ^g
G3	5.094 ^{bc}	5.775 ^{ab}	3.686 ^{bcd}	4.852 ^{bcd}
G4	6.12 ^a	6.377 ^a	3.734 ^{abcd}	5.410 ^a
G5	4.719 ^{cd}	5.672 ^{abc}	2.802 ^{de}	4.398 ^{de}
G6	5.087 ^{bc}	6.118 ^{ab}	4.544 ^{ab}	5.250 ^{ab}
G7	5.571 ^{ab}	5.665 ^{abcd}	3.426 ^{cde}	4.887 ^{bcd}
G8	5.667 ^{ab}	6.16 ^{ab}	3.307 ^{cde}	5.045 ^{abc}
G9	5.418 ^b	5.237 ^{bcde}	3.915 ^{abc}	4.857 ^{bcd}
G10	5.268 ^{bc}	4.469 ^e	3.206 ^{cde}	4.314 ^{ef}
G11	4.644 ^{cd}	6.282 ^a	3.799 ^{abcd}	4.908 ^{abcd}
G12	5.049 ^{bcd}	4.855 ^{cde}	3.931 ^{abc}	4.612 ^{cde}
G13	4.451 ^d	6.005 ^{ab}	3.547 ^{bcd}	4.668 ^{cde}
G14	3.698 ^e	4.771 ^{ce}	3.188 ^{cde}	3.886 ^f
G15	3.617 ^e	2.804 ^f	3.741 ^{abcd}	3.387 ^g
\bar{X}_j	4.908 ^b	5.260 ^a	3.604 ^c	$\bar{X} = 4.591$
C.V	6.9	9.3	15	$G \times E = 10.6$
L.S.D	0.566	0.815	0.904	$G \times E = 0.790$
	L.S.D Geno. 5% = 0.456		L.S.D Env. 5% = 0.204	

Averages with same letter have no significant differences.

\bar{X}_i : Average grain yield of genotype i across the three ecological sites; **L.S.D Geno. 5%**: the least significant difference between the studied genotypes. \bar{X}_j : Average grain yield at each environmental site. **L.S.D Env. 5%** least significant difference between ecological sites. **G L.S.D × E 5%**: The least significant difference for the interaction between the genotypes and the environmental sites. **C.V% G × E**: coefficient of variation for the interaction between the studied genotypes and the tested environmental sites.

AMMI model analysis

The AMMI model is widely used in stability analysis because it provides a preliminary analysis of the model to suit multiple environmental assessments, allows for segmentation of the G×E interaction and elucidates genotypes and the relationships between genotypes and environments (Zobel et al., 1988, Crossa, 1990). AMMI analysis showed that 42.47% were attributable to environmental factors, 37.11% to genotypes and 20.41% to G × E effects (Table 4). This large variance in the environments boxes indicates that the environments were diverse, with large differences between the environmental conditions causing these variances, indicating that the environment has a significant effect on grain yield (Tonk et al., 2011, Munaro et al., 2014, Alam et al., 2015).

Table 4. AMMI analysis of grain yield (ton ha⁻¹)

S.O.V	DF	SS	MS	PORCENT	PORCENAC
Genotype (G)	14	59.85	4.27**	37.11	79.58
Environment (E)	2	68.50	34.25**	42.47	42.47
G × E	28	32.91	1.17**	20.41	100.00
PC1	15	23.07	1.53**	70.1	70.1
PC2	13	9.84	0.75**	29.9	100.00
Residuals	90	21.18	0.23		

*, ** Significant differences at the confidence level of 0.05 and 0.01, respectively.

The multiplicative variance was divided into two main components, which explained 100% of the total variance. The contribution of PC1 was 70.1% and PC2 29.9%. Therefore, AMMI 1 (IPCA1 vs additive main effects) and AMMI 2 (IPCA2 vs IPCA1) were created to simultaneously illuminate genotypes and environment effects.

Figure 1 indicates that environment E2 was a highly yielding site with high additive genotypes main effects, followed by environment E1, genotypes G4, G1 and G6 were the most productive, and G1 had an IPCA1 value greater than zero indicating that it is positively correlated with the environments. Whereas Figure 2 indicates that the environments E1, E2, and E3 were discriminatory and located far from the origin of the biplot. The G3 genotype was close to the origin, demonstrating its stability. Similar results were obtained (Mohammadi and Amri, 2013, Oral *et al.*, 2018) with regard to genotype stability due to lower IPCA1 values. The G10, G15 and G11 genotypes were unstable due to their distance from the ancestor and contributed significantly (positive or negative) to environmental genotype interaction.

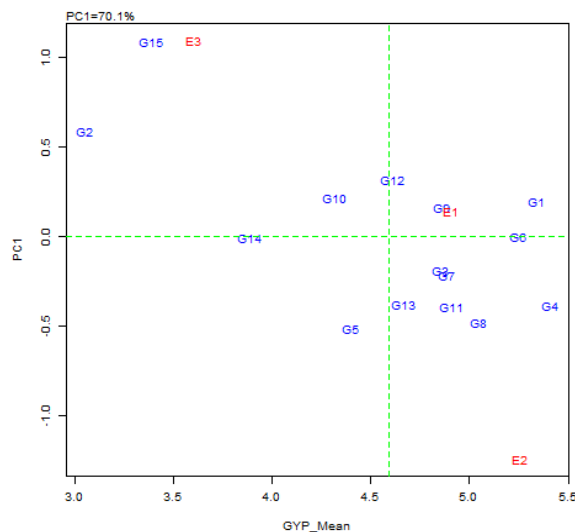


Figure 1. The relationship between the environments and the genotypes

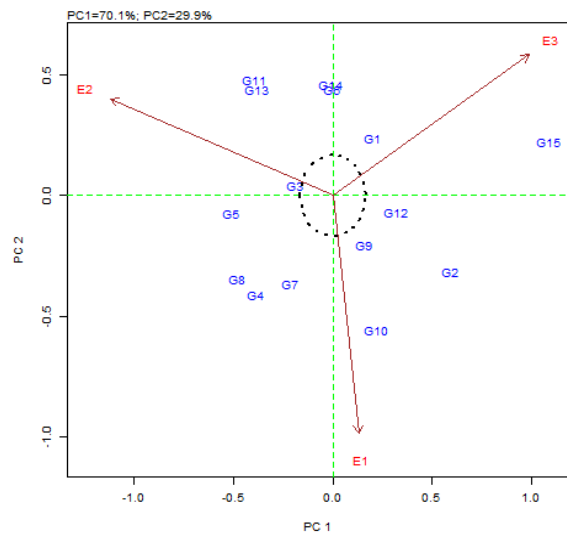


Figure 2. PC1 vs PC2 of standard values of yield stability

GGE biplot analysis

GGE biplot analysis was used to identify the best genotypes in each environment and assess their stability. The most attractive feature of the GGE biplots model is the "which-won-where" analysis, in which $G \times E$ interaction, large environmental variance, and genotype adaptation are graphically represented (Rakshit et al., 2014; Oral et al., 2018). Whereas in multi-environment experiments, "which-won-where" analysis is necessary to study the possible presence of different mega-environments in an area (Yan and Tinker, 2006). The genotypes with better or worse performance in one or all environments were considered responsive, and located within sectors (Yan and Tinker, 2006).

The GGE biplot analysis (Table 5) revealed that the first two principal components (PC1 and PC2) were statistically significant, together explaining 89.5% of the total variation in grain yield. Specifically, PC1 accounted for 77.4% of the variance, while PC2 contributed 12.1%, confirming the adequacy of the two-dimensional biplot for interpreting the genotype by environment interaction.

Table 5. GGE Biplot Analysis of Grain Yield (ton ha⁻¹)

Principal Components	DF	SS	MS	Explained (%)
PC1	15	71.7695	4.7846**	77.4
PC2	13	11.1999	0.8615**	12.1
PC3	11	9.80704	0.8915**	10.5

*, ** Significant differences at the confidence level of 0.05 and 0.01, respectively.

The graphical GGE biplot provided valuable insights into the relationships among environments and the performance of genotypes. As illustrated in Figure (3), environment E1 (Homs) was identified as the most representative and discriminative environment, being closest to the center of the concentric circles, followed by E2 (Al-Ghab). In contrast, E3 (Gillen) was positioned farther from the center, indicating a lower representativeness and less suitability for reliable genotype evaluation.

Figure 4 identifies the ideal genotypes those combining high yield with consistent performance across environments. G6 appeared closest to the biplot origin, reflecting superior stability and productivity, followed by G1. Conversely, G15 and G2 were located furthest from the ideal position, denoting lower yield potential and high instability.

Figure 5 illustrates the inter-environmental relationships as revealed by the GGE biplot. Acute angles between the environment vectors indicate positive correlations, meaning that the environments have similar discriminative ability and maintain comparable genotype rankings. All the observed angles were less than 90°, suggesting a positive association among the three environments and the absence of any major genotype re-ranking across sites. The smallest angle occurred between E1 (Homs) and E2 (Al-Ghab), implying a strong positive correlation between them. Hence, genotype performance in one of these environments can reliably predict its performance in the other. This finding highlights the

opportunity to reduce the number of test sites and the overall cost of multi-environment trials through indirect selection based on the most representative environment.

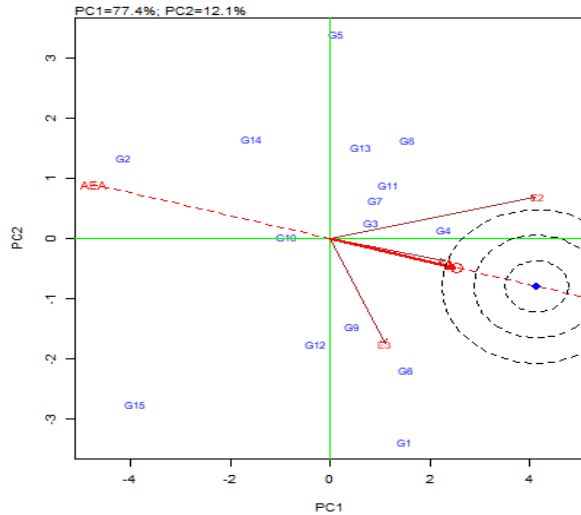


Figure 3. The ideal environment that represents the rest of the environments

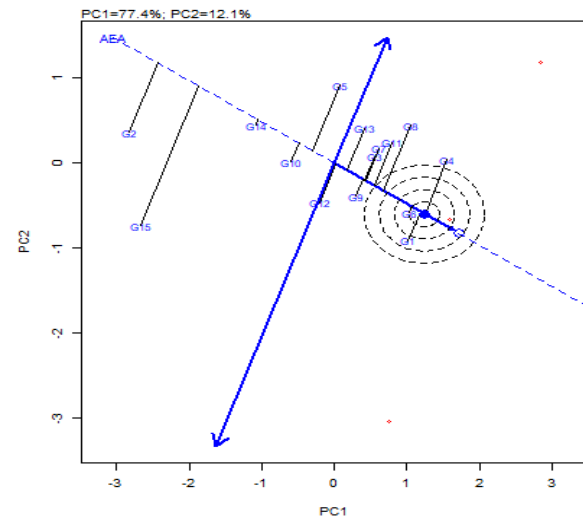


Figure 4. The ideal genotype.

Figure 6 shows the preferred genotypes for each environment depend on the formation of a polygon by connecting the genotype points far from the point of origin in the biplot diagram to include all other genotypes, as the genotypes that are located at the corners in the polygon are the highest yielding in environments located in the same direction. Figure 6 illustrates that G4 and G8 have high yields in environments located in the same direction, while G1 was suitable for the third environment.

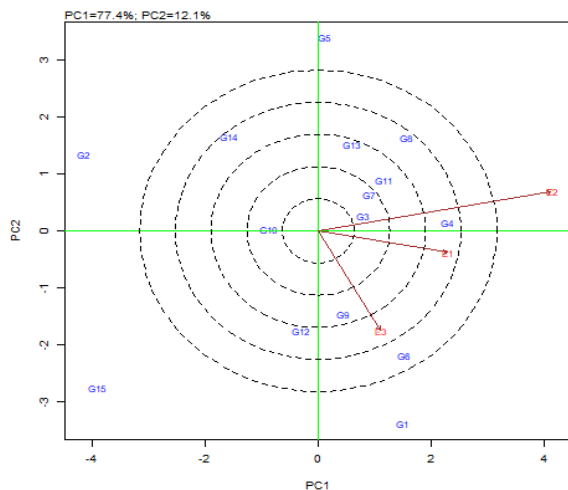


Figure 5. The relationship between the environments.

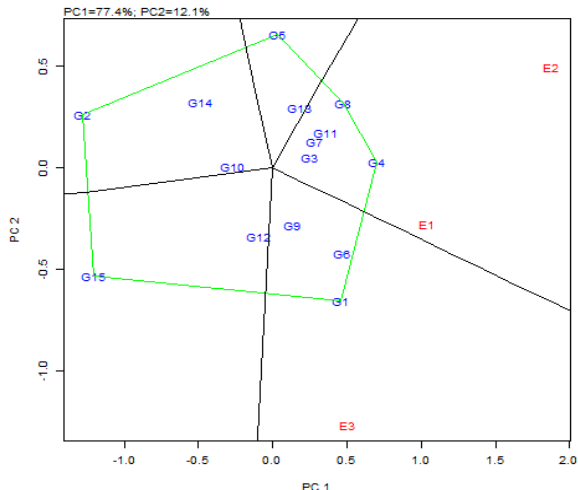


Figure 6. The preferred genotypes for each environment.

It is certain that these superior phenotypes that combined high yield and stability have a broad genetic base, and resulted from the processes of selection and genetic improvement that led to the

accumulation of desired genes responsible for the traits positively associated with high yield, or they may be resulted from harmonious and integrated parents, this indicates that they have been tested in various locations in the last stages of the breeding program before being approved. These results are consistent with the findings of (Mohammadi and Amri, 2013), which confirmed that genetic improvement of grain yield and adaptation to a wide range of environments, especially in promising strains, can be achieved through the gradual accumulation of desired genes, by conducting well-studied and specific crosses then testing them in Multiple locations, which ensures the success and progress in the breeding program.

CONCLUSION and RECOMMENDATIONS

The AMMI analysis revealed that environment E2 was the most productive, while genotypes G4, G1, and G6 exhibited superior performance, with G3 being the most stable. Conversely, G15, G10, and G11 were the least stable. The GGE Biplot analysis identified E2 as the ideal environment and G6 and G1 as the most desirable genotypes due to their high yield and stability. A strong correlation was observed between environments E1 and E2, suggesting that indirect selection could be effectively applied between these two environments.

It is therefore recommended that breeding programs should consider genotype \times environment interactions to enhance the efficiency of selection. The GGE Biplot model proved more powerful than AMMI in identifying both stable and high-yielding genotypes. Genotypes that consistently perform well across different climatic conditions should be prioritized for future breeding efforts.

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