

AMMI and GGE biplot analyses of adaptability and yield stability of advantage varieties of common winter wheat

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Abstract

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The creation of varieties that can be adapted to a wide range of environments is the crucial goal of plant breeders in wheat improvement programs. The primary objective of this study was to identify high-yielding, stable, and adaptive common winter wheat genotypes for breeding purposes by applying various statistical analyses. The study was conducted over four growing seasons in the experimental field of IPGR-Sadovo, Southern Bulgaria. In the study, 46 common winter wheat cultivars with different geographical origins were included. The experiments were arranged in a completely randomized block design with three replications on plots of 10 m². Combined analysis of variance (ANOVA) revealed that grain yield was significantly affected by the sources of variance: genotype (G), environment (E), and the genotype × environment interaction (GEI) ($p < 0.001$). Genotypes G16, G31, G14, G24, and G1 emerged as the most stable according to the parametric stability estimates analysis. Genotypes G14, G33, and G19 were considered generally adaptable to each environment according to AMMI1 analysis, while G19, G2, G35, G21, G4, and G32 were assessed as the most stable according to AMMI2 analysis. GGE biplot analyses identified G33, G14, G16, and G9 as the most favorable and adaptable to a wide range of environments that could be included in the standard winter wheat breeding programs.

Keywords: wheat; AMMI analysis; GGE analysis; stability parameters; yield

Introduction

The creation of varieties that can be adapted to a wide range of environments is the crucial goal of plant breeders in wheat improvement programs (Wardofa and Ararsa, 2020). Identifying stable, high-yielding genotypes is significant in the current climate change scenario, which is leading to increasingly frequent occurrences of adverse conditions (Mansour et al., 2018). Knowledge of the pattern and magnitude of GEI, as well as stability analysis, is essential for understanding the response of different genotypes to various environments and for identifying stable and broadly adapted genotypes, as well as unstable but specifically adapted genotypes (Amare et al., 2020). It can help plant breeders to reduce the cost of extensive

genotype evaluation by eliminating unnecessary testing sites (Wardofa and Ararsa, 2020). Stability in grain yield among genotypes can be described as the linear response to environmental yield and the deviation from that response (Sial et al., 2007). An ideal genotype generally shows low G×E interaction variance, above-average response to environmental yield potential, and lower deviations from the expected response within a target environment (Arain et al., 2011). Tollenaar and Lee (2002) and Altay (2012) noted that the yield stability is generally grouped as static or dynamic stability. Static stability is defined as the lack of response to environmental variations, and it is an absolute value independent of the performance of other cultivars in the trials. The dynamic stability is defined as the average response. Therefore, the dynamic stability of

a cultivar depends on the mean response of all the cultivars. Yield experiments conducted in different environments can be analyzed to extract more information about the stability, adaptability, and efficiency of yield using various statistical methods and software (Wardofa and Ararsa, 2020). Several statistical methods have been proposed to investigate genotype-by-environment interactions, including both parametric and non-parametric approaches. The most widely used parametric stability estimates are: regression coefficient (b_i) (Finlay and Wilkinson, 1963), deviation from regression (S^2_{di}) proposed by Eberhart and Russel (1966), coefficient of determination (R_i^2) (Pinthus, 1973), coefficient of variance (CV_i) (Francis and Kannenberg, 1978), Wricke's ecovalence (W_i^2) (Wricke's, 1962), Shukla's stability variance (σ_i^2) (Shukla, 1972), mean variance component (θ_i) (Plaisted and Peterson, 1959), GE variance component ($\theta_{(i)}$) (Plaisted, 1960), stability criterion (YSi) by Kang (1988) and AMMI Stability Value (ASV) of Purchase (1997). Nonparametric stability methods are based on ranking the genotypes in each environment. Genotypes with close ranking across environments are classified as stable. The following four nonparametric measures of phenotypic stability have been proposed by Huhn (1990) and Nassar and Huhn (1987): $Si^{(1)}$, the genotype absolute rank difference mean as tested over n environments; $Si^{(2)}$, the between-ranks variance over the n environments; $Si^{(3)}$, the sum of the absolute deviations of the squares of ranks for each genotype; and $Si^{(6)}$, the sum of the squares of ranks for each genotype relative to the mean of ranks (Akcura and Kaya, 2008).

Recently, as a method of evaluating stability in multi-location varietal trials, many researchers have used the AMMI method (Additive Main Effects and Multiplicative Interactions) and the Site Regression Model (SREG), generally known as GGE biplot analysis (Genotype Main Effects and Genotype $\times$ Environment Interaction). The AMMI mod-

el integrates combined analysis of variance (ANOVA) with principal component analysis (PCA) of the GE interaction in a unified approach. The model is a valuable tool for identifying environments that optimize genotypic performance, therefore, making better use of limited available resources in breeding programs (Mohammadi et al., 2016; Neisse et al., 2018; Obsa, 2019; Khan et al., 2020). The GGE biplot is an effective method based on principal component analysis (PCA) for fully exploring multi-location performance evaluation trial data (Singh et al., 2018; Tulu and Wondimu, 2019; Khan et al., 2020). It is helpful for summarizing data from biplots obtained by graphing the first two components of the multiplicative part (Ram et al., 2020). Yang et al. (2009) reported that a biplot, whether based on AMMI, GGE, or any other linear-bilinear model, is a proper visualization technique for identifying similarity or dissimilarity among genotypes or environments.

The primary objective of this study was to identify high-yielding, stable, and adaptive common winter wheat genotypes for breeding purposes by employing various statistical analyses.

Materials and Methods

The field experimental conditions and design

The study was conducted over four growing seasons, from 2016-2017 to 2019-2020, in the experimental field of IPGR "K. Malkov" in Sadovo, Southern Bulgaria, at the locality "Dolusene", on a meadow-cinnamon resin-like soil type. The climate of the area is transitional-continental with weak Mediterranean influence. The area is characterised by warm and long autumns, mild and often snowy winters. Spring is short with an almost abrupt transition to summer temperatures. For the conditions of the area, the low temperatures in December and January, which often occur in snowless winters, and

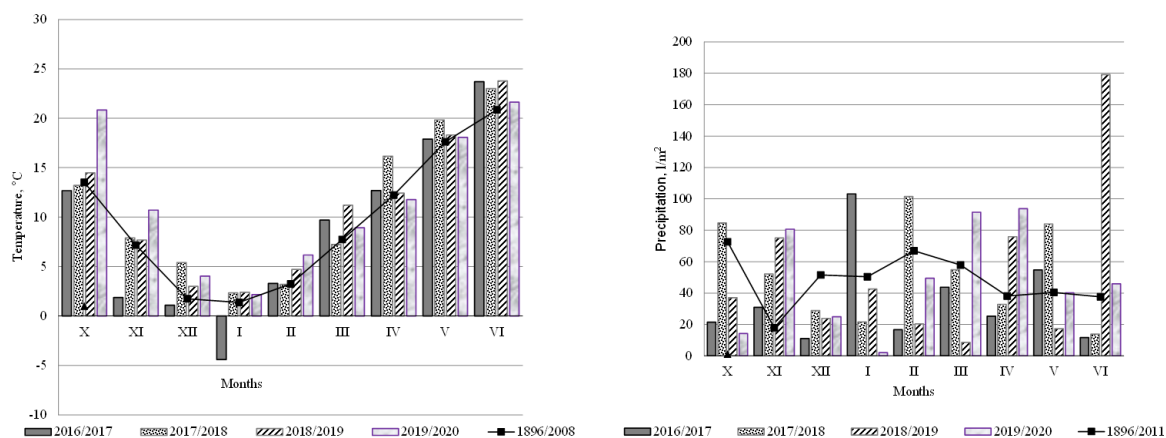


Fig. 1. Average monthly air temperatures ($^{\circ}\text{C}$) and average monthly precipitation (l/m^2) for the IPGR-Sadovo area

Table 1. The list of 46 genotypes included in the study

Number of genotype	Species	Subspecies	Name of cultivar	Origin
G1	<i>Triticum aestivum</i> L.	<i>var. erythrospermum</i> (Koern.) Mansf.	Enola	BGR
G2	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Ines	CZE
G3	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Bohemia	CZE
G4	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Baletka	CZE
G5	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Secese	CZE
G6	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Seladon	CZE
G7	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Silueta	CZE
G8	<i>Triticum aestivum</i> L.	<i>var. erythrospermum</i> (Koern.) Mansf.	Coa	PRT
G9	<i>Triticum aestivum</i> L.	<i>var. erythrospermum</i> (Koern.) Mansf.	Jordao	PRT
G10	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Andalou	FRA
G11	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Muza	POL
G12	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Kobra Plus	POL
G13	<i>Triticum aestivum</i> L.	<i>var. erythrospermum</i> (Koern.) Mansf.	Alcione	ITA
G14	<i>Triticum aestivum</i> L.	<i>var. erythrospermum</i> (Koern.) Mansf.	Bilancia	ITA
G15	<i>Triticum aestivum</i> L.	<i>var. erythrospermum</i> (Koern.) Mansf.	Carisma	ITA
G16	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Delfino (P 204 A)	ITA
G17	<i>Triticum aestivum</i> L.	<i>var. erythrospermum</i> (Koern.) Mansf.	Esperia	ITA
G18	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Gemini	ITA
G19	<i>Triticum aestivum</i> L.	<i>var. militurum</i> (Alef.) Mansf.	Primoasi	ITA
G20	<i>Triticum aestivum</i> L.	<i>var. erythrospermum</i> (Koern.) Mansf.	Accor	FRA
G21	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Allister	FRA
G22	<i>Triticum aestivum</i> L.	<i>var. erythrospermum</i> (Koern.) Mansf.	Autan	FRA
G23	<i>Triticum aestivum</i> L.	<i>var. erythrospermum</i> (Koern.) Mansf.	Colfiorito	ITA
G24	<i>Triticum aestivum</i> L.	<i>var. erythrospermum</i> (Koern.) Mansf.	Collerosso	ITA
G25	<i>Triticum aestivum</i> L.	<i>var. erythrospermum</i> (Koern.) Mansf.	Vittorio	ITA
G26	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Bardotka	CZE
G27	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Bazilika	CZE
G28	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Nikol	CZE
G29	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Bodycek	CZE
G30	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Elly	CZE
G31	<i>Triticum aestivum</i> L.	<i>var. erythrospermum</i> (Koern.) Mansf.	Jindra	CZE
G32	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	RW Nadal	CZE
G33	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Matylda	CZE
G34	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Canadair	FRA
G35	<i>Triticum aestivum</i> L.	<i>var. ferrugineum</i> (Alef.) Mansf.	Oropos	GRC
G36	<i>Triticum aestivum</i> L.	<i>var. aureum</i> (Link) Mansf.	Nestor	GRC
G37	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Altigo	FRA
G38	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Aldric	FRA
G39	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Acienda	FRA
G40	<i>Triticum aestivum</i> L.	<i>var. erythrospermum</i> (Koern.) Mansf.	Saturnus	AUT
G41	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Mahissa-1	ESP
G42	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Dimas	ESP
G43	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Estrella	ESP
G44	<i>Triticum aestivum</i> L.	<i>var. lutescens</i> (Alef.) Mansf.	Navarro 150	ESP
G45	<i>Triticum aestivum</i> L.	<i>var. ferrugineum</i> (Alef.) Mansf.	Albimonte	ESP
G46	<i>Triticum aestivum</i> L.	<i>var. erythrospermum</i> (Koern.) Mansf.	Amarok	FRA

the high temperatures in June, combined with dry spells, are essential for the overwintering of autumn crops. The average monthly temperatures and precipitation during the experimental periods are shown in Figure 1.

In the study, 46 common winter wheat cultivars with different geographical origins were included (Table 1). Sowing was carried out in the optimal period for Southern Bulgaria, from 10 to 20 October, following the pea precursor. The experiments were arranged in a completely randomized block design with three replications on plots of 10 m². Standard agronomic and plant protection practices were applied during the growing seasons to ensure plant development under uniform conditions.

Data Analysis

Different statistical software packages were used to analyze the data of grain yield (t/ha) from the multi-year trial. Duncan's multiple range test was used to explain the significant differences among means of genotypes, and combined analyses of variance were performed using SPSS. Stabilitysoft software was used for calculation of following phenotype stability parameters: regression coefficient (b_i) (Finlay and Wilkinson, 1963), deviation from regression (S^2_{di}) proposed by Eberhart and Russel (1966), coefficient of determination (R_i^2) (Pinthus, 1973), coefficient of variation (CV_i) (Francis and Kannenberg, 1978), Wricke's ecovalence (W_i^2) (Wricke's, 1962), Shukla's stability variance (σ_i^2) (Shukla, 1972), mean variance component (θ_i) (Plaisted and Peterson, 1959), GE variance component ($\theta_{(i)}$) (Plaisted, 1960).

The additive main effect and multiplicative interaction (AMMI) analysis and GGE biplot analysis were performed using PBTools software. AMMI stability value (ASV) and Yield stability index (YSI) were calculated using the formulas developed by Purchase et al. (2000) and Farshadfar (2008), respectively, in Microsoft Excel 2010. The genotype selection index (GSI), calculated as the sum of the ASV and yield stability index (YSI) ranking positions, was also determined.

Results and Discussion

Combined analysis of variance (ANOVA) revealed that grain yield was significantly affected by the sources of variance: genotype (G), environment (E), and the genotype $\times$ environment interaction (GEI) ($p < 0.001$). 36.56% of the total sum of squares (SS) for grain yield was explained by the effect of environment (E), 30.42% by genotype $\times$ environment interaction (GEI), and only 18.52% of the total SS was due to the effect of genotype (G) (Table 2). This indicates that genotypes exhibited different behaviour in the various environments, and that there was a change in the magnitude of the responses for GY due to environmental variation. Similar results were observed by Melkamu et al. (2015), Baktash (2016), Krupal et al. (2018), Singh et al. (2018), Thakur et al. (2019), Amare et al. (2020), Kamini et al. (2020), Wardofa and Ararsa (2020), Tanin et al. (2022).

Several studies highlight the use of phenotype stability parameters to identify widely adapted wheat genotypes (van Eeuwijk et al., 2016; Knapp et al., 2017; Hayder et al., 2018; Cheshkova et al., 2020; Subedi et al., 2021; Kyratzis et al., 2022; Pour-Aboughadareh et al., 2022). In this study, the results of average grain yield per hectare and yield phenotypic stability parameters for 46 common winter wheat genotypes studied over four years are presented in Table 3. The Duncan's multiple range test, applied at a 0.05 level of probability, showed that the G16 and G21 genotypes differed significantly from the others in the study. G16 genotype with an average yield of 6.61 t ha⁻¹ had the highest average yield, while G21 genotype with an average yield of 3.72 t ha⁻¹ had the lowest mean yield among genotypes.

GE interaction is equivalent to genotypic variation in terms of phenotypic plasticity (Tanin et al., 2022). The regression coefficient (b_i) best expresses this quality. According to Pour-Aboughadareh et al. (2019), if the value of the coefficient is not significantly different from 1, then the genotype is adaptive to all environments. If $b_i > 1$, genotypes

Table 2. Combined analysis of variance (ANOVA) for yield and the percentage sum of squares (%SS) of the 46 genotypes tested over a period of four years (2016-2020)

Source	Sum of Squares	df	Mean Square	F	Sig.	%SS
Corrected Model	557.43	183.00	3.05	5.93	0.000	
Intercept	10287.89	1.00	10287.89	20028.00	0.000	
Genotype	120.72	45.00	2.68	5.22	0.000	18.52
Environment	238.36	3.00	79.45	154.67	0.000	36.56
Genotype X Environment Interaction	198.35	135.00	1.47	2.86	0.000	30.42
Error	94.52	184.00	0.51			14.50
Total	10939.83	368.00				
Corrected Total	651.94	367.00				

RSquare = 0.855 (Adjusted RSquare = 0.711)

are more sensitive to changing environmental conditions and have greater specific adaptability to high-diversity environments. When $b_i < 1$ genotypes are more stable to environmental changes, they increase their specific adaptability to low-yielding environments. In our study, the values of the regression coefficient (β_i) varied from -0.77 for the G15 genotype to 1.92 for the G3 genotype, indicating that genotypes had different responses to environmental changes (Kamini et al., 2020). Genotypes G8, G9, and G14 with coefficient of regression (b_i) values equal to 1.0 and grain yields above the mean were the most adaptive to all environmental conditions. In nineteen genotypes, the b_i values ranged between -0.77 and 0.84. The genotypes with the lowest b_i coefficient were G15, G17, G11, and G37, and were therefore regarded as more adapted to marginal environments. In contrast, genotypes G5, G6, G23, G25, and G41 had regression coefficients significantly greater than one and grain yields above the grand mean. They are considered sensitive to environmental changes and would be recommended for growing under suitable conditions.

Genotypes G2, G7, G30, G31, G16, G12, G24, G14, and G42 were relatively stable, as they had small deviations from regression values (S^2_{di}) between 0.01 and 0.05 (Table 3).

According to the model of Eberhart and Russell (1966), genotypes characterized by regression coefficients (b_i) close to 1.0 and S^2_{di} equal to zero, in combination with high average grain yield, exhibit general adaptability. In our case, only genotype G14 has general adaptability.

Based on the coefficient of variation stability statistic (CV_i), G12, G30, G31, G37, and G16 with CV_i between 8.09 and 10.56 were considered to be desirable and stable (Table 3).

According to the mean variance component (θ_i) of Plaisted and Peterson (1959), and the GE component ($\theta_{(i)}$), genotypes that show lower values for θ_i and higher values for $\theta_{(i)}$ are considered more stable. In our study, the genotypes G2, G14, G16, and G24 were identified, while G8 and G15 were found to be the more unstable (Table 3). The parameters based on Wricke's ecovalence (W_i^2) and Shukla's stability variance (σ_i^2) also defined G2, G14, G16, and

Table 3. Average grain yield (tha⁻¹) and phenotype stability parameters in 46 common winter wheat genotypes

Geno-type	Yield	W_i^2	σ_i^2	S^2_{di}	b_i	CV_i	$\theta_{(i)}$	θ_i
G1	5.44 ^{c-h}	0.73	0.24	0.07	0.70	14.07	0.74	0.50
G2	4.81 ^{a-f}	0.10	0.02	0.01	1.14	22.14	0.74	0.39
G3	5.63 ^{c-h}	1.76	0.60	0.23	1.25	24.36	0.73	0.67
G4	5.97 ^{f-h}	2.56	0.88	0.34	1.28	24.83	0.73	0.81
G5	6.06 ^{f-h}	2.32	0.79	0.23	1.52	26.26	0.73	0.77
G6	5.56 ^{c-h}	2.05	0.70	0.07	1.77	30.51	0.73	0.72
G7	4.99 ^{b-g}	1.15	0.38	0.01	1.64	30.79	0.74	0.57
G8	5.31 ^{b-g}	6.75	2.34	0.96	1.05	33.68	0.69	1.52
G9	5.88 ^{f-h}	3.83	1.32	0.54	1.07	25.56	0.72	1.02
G10	4.93 ^{b-g}	1.12	0.37	0.16	1.06	23.54	0.74	0.56
G11	5.06 ^{b-g}	5.07	1.75	0.27	-0.11	15.82	0.71	1.24
G12	5.25 ^{b-g}	1.27	0.43	0.03	0.36	8.09	0.74	0.59
G13	5.04 ^{b-g}	1.20	0.40	0.13	0.68	16.73	0.74	0.58
G14	6.12 ^{gh}	0.31	0.09	0.04	1.05	16.75	0.74	0.43
G15	5.79 ^{c-h}	9.10	3.16	0.15	-0.77	15.90	0.67	1.92
G16	6.61 ^h	0.41	0.13	0.03	0.70	10.56	0.74	0.44
G17	5.27 ^{b-g}	6.14	2.12	0.09	-0.46	11.96	0.70	1.42
G18	4.84 ^{a-f}	1.64	0.56	0.12	0.45	14.07	0.73	0.65
G19	6.01 ^{f-h}	1.60	0.54	0.21	0.80	17.00	0.73	0.64
G20	5.92 ^{f-h}	1.21	0.41	0.11	1.42	23.81	0.74	0.58
G21	3.72 ^a	1.25	0.42	0.18	1.02	30.84	0.74	0.58
G22	4.98 ^{b-g}	3.89	1.34	0.28	1.86	38.35	0.72	1.04
G23	5.49 ^{c-h}	2.89	0.99	0.13	1.88	33.34	0.72	0.87
G24	5.31 ^{b-g}	0.52	0.17	0.04	0.70	13.75	0.74	0.46
G25	5.42 ^{c-h}	2.31	0.79	0.19	1.62	30.32	0.73	0.77
G26	5.23 ^{b-g}	0.78	0.25	0.06	1.38	25.49	0.74	0.51
G27	4.99 ^{b-g}	1.70	0.58	0.17	0.56	16.38	0.73	0.66
G28	5.54 ^{d-h}	2.42	0.83	0.30	1.35	27.24	0.73	0.78
G29	5.83 ^{c-h}	0.91	0.30	0.12	0.82	15.88	0.74	0.53
G30	5.26 ^{b-g}	0.95	0.31	0.01	0.43	8.38	0.74	0.53
G31	6.18 ^{gh}	0.69	0.22	0.01	0.51	8.13	0.74	0.49
G32	4.99 ^{b-g}	0.61	0.20	0.07	1.19	23.60	0.74	0.48
G33	6.05 ^{f-h}	1.55	0.52	0.22	1.13	20.89	0.73	0.64
G34	5.04 ^{b-g}	1.46	0.49	0.20	0.84	20.47	0.73	0.62
G35	5.09 ^{b-g}	0.90	0.30	0.13	1.01	21.28	0.74	0.53
G36	5.59 ^{c-h}	2.54	0.87	0.35	0.79	20.71	0.73	0.81
G37	5.02 ^{b-g}	2.91	1.00	0.09	0.06	8.67	0.72	0.87
G38	4.62 ^{a-c}	3.24	1.11	0.35	0.44	22.17	0.72	0.92
G39	4.99 ^{b-g}	2.25	0.77	0.15	1.67	33.86	0.73	0.76
G40	4.24 ^{abc}	1.43	0.48	0.11	0.50	16.30	0.73	0.62
G41	5.35 ^{c-g}	1.53	0.52	0.10	1.58	28.77	0.73	0.63
G42	5.24 ^{b-g}	1.18	0.40	0.05	1.56	28.47	0.74	0.57
G43	4.85 ^{a-f}	3.00	1.03	0.11	1.92	38.34	0.72	0.88
G44	4.08 ^{ab}	1.98	0.67	0.23	1.38	36.29	0.73	0.71
G45	4.30 ^{a-d}	3.42	1.17	0.22	1.85	43.33	0.72	0.95
G46	5.39 ^{c-g}	1.75	0.59	0.20	1.36	26.68	0.73	0.67

Different letters within the same column indicate significant differences between genotypes ($p \leq 0.05$) according to Duncan multiple range test

W_i^2 – Wricke's ecovalence, σ_i^2 – Shukla's stability variance, S^2_{di} – deviation from regression, b_i – regression coefficient, CV_i – coefficient of variation, $\theta_{(i)}$ – GE variance component, θ_i – mean variance component

G24 as the most stable genotypes, while G15, G8, G17, G11, and G9 provided the lowest contribution to total GE interaction.

Summarizing the data from the parametric stability assessments, genotypes G16, G31, G14, G24, and G1 were identified as the most stable, while genotypes G22, G45, G8, and G38 were found to be the most unstable.

ASV is the stability of genotypes considering their distance from the IPCA1 and IPCA2 axes. The genotype with the least ASV score is the most stable (Farshadfar et al., 2011; Kyratzis et al., 2022). Our result showed that G35 was the most stable, followed by G19 and G2. On the other hand, the genotype with the smallest YSI is considered the most stable and has a high grain yield. Based on YSI, the most stable genotypes with high grain yields above 6 tha⁻¹ are G19,

G14, G16, and G5. The Genotype Selection Index (GSI) enables the ranking and creation of clear classifications of the breeding value of genotypes. Genotypes with the lowest GSI coefficient had the broad adaptation (Jędzura et al., 2023). In our study, the genotypes were G19 (GSI = 3), G4 (GSI = 9), and G14 (GSI = 9) (Table 4).

Analysis of variance for the AMMI model of grain yield showed that the three main components (IPCA) of the genotype-environment interactions accounted for 44.00%, 31.60%, and 24.40%, respectively. Furthermore, the first two components explain 75.60% of the interaction effects, indicating that the AMMI model is beneficial for analyzing genotype-by-environment interactions (Table 5).

The AMMI1 biplot facilitated the interpretation of interaction effects among genotypes and environments, as well

Table 4. Mean performance of common winter genotypes based on AMMI Stability Value (ASV), Yield stability index (YSI) and Genotype Selection Index (GSI)

Genotype	Yield	Rank	ASV	Rank	YSI	Rank	GSI
G1	5.44	17	0.379	14	31	13	27
G2	4.81	36	0.133	3	39	15	18
G3	5.63	12	0.206	6	18	6	12
G4	5.97	7	0.170	5	12	4	9
G5	6.06	4	0.366	13	17	5	18
G6	5.56	14	0.703	35	49	22	57
G7	4.99	31	0.551	25	56	26	51
G8	5.31	21	1.101	43	64	28	71
G9	5.88	9	0.831	38	47	20	58
G10	4.93	33	0.294	11	44	17	28
G11	5.06	29	1.028	42	71	32	74
G12	5.25	24	0.579	28	52	24	52
G13	5.04	30	0.473	19	49	22	41
G14	6.12	3	0.229	7	10	2	9
G15	5.79	11	1.577	45	56	26	71
G16	6.61	1	0.277	10	11	3	13
G17	5.27	22	1.327	44	66	29	73
G18	4.84	35	0.517	24	59	27	51
G19	6.01	6	0.102	2	8	1	3
G20	5.92	8	0.491	22	30	12	34
G21	3.72	41	0.153	4	45	18	22
G22	4.98	32	0.999	41	73	34	75
G23	5.49	16	0.797	37	53	25	62

Genotype	Yield	Rank	ASV	Rank	YSI	Rank	GSI
G24	5.27	22	0.277	10	32	14	24
G25	5.42	18	0.598	30	48	21	51
G26	5.23	27	0.386	16	43	16	32
G27	4.99	31	0.482	21	52	24	45
G28	5.54	15	0.606	31	46	19	50
G29	5.83	10	0.331	12	22	8	20
G30	5.26	23	0.505	23	46	19	42
G31	6.18	2	0.434	17	19	7	24
G32	4.99	31	0.243	8	39	15	23
G33	6.05	5	0.479	20	25	9	29
G34	5.04	30	0.470	18	48	21	39
G35	5.09	28	0.092	1	29	11	12
G36	5.59	13	0.384	15	28	10	25
G37	5.23	26	0.687	33	59	27	60
G38	4.47	37	0.904	39	76	36	75
G39	4.93	33	0.771	36	69	31	67
G40	4.24	39	0.580	29	68	30	59
G41	5.35	20	0.565	26	46	19	45
G42	5.24	25	0.573	27	52	24	51
G43	4.85	34	0.917	40	74	35	75
G44	4.08	40	0.260	9	49	22	31
G45	4.30	38	0.690	34	72	33	67
G46	5.39	19	0.622	32	51	23	55

Table 5. Analysis of variance for AMMI model of grain yield

Sources of variation	df	Sum of Squares	Mean Square	F	Sig.	percent	acum
PC1	47	65.41	1.39	5.99	0.00	44.00	44.00
PC2	45	47.06	1.05	4.50	0.00	31.60	75.60
PC3	43	36.28	0.84	3.61	0.00	24.40	100.00
PC4	41	0.00	0.00	0.00	1.00	0.00	100.00

as the assessment of genotype adaptability (Temesgen et al., 2015; Awoke and Sharma, 2016; Amare et al., 2020; Tanin et al., 2022; Jędzura et al., 2023). Bishwas et al. (2021) noted that vectors of genotypes with PC1 close to the origin (zero) have a general adaptive capacity, while vectors with larger PC1 values are specifically adapted to their environment. In our study, genotypes G14, G33, and G19 had mean values greater than the overall mean and near-zero PC1 scores; therefore, they were considered generally adaptable to each environment (Figure 2).

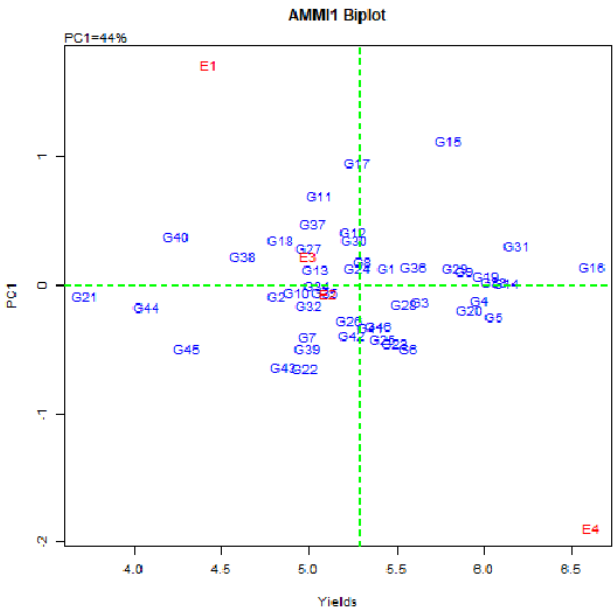


Fig. 2. The AMMI1 biplot of PC1 against yield for 46 genotypes and 4 growing seasons

According to AMMI2-based analysis, genotypes and environments with lower PC1 and PC2 values, which are closer to the origin, are considered the most stable (Tanin et al., 2022). In our cases, genotypes G19, G2, G35, G21, G4 and G32 were assessed as most stable (Figure 3). Several researchers have utilised the AMMI biplot to distinguish

between stable and unstable wheat genotypes across various environments (Ali et al., 2015; Singh et al., 2018; Singh et al., 2019; Amare et al., 2020; Munjal et al., 2020; Poudel et al., 2020; Ram et al., 2020; Regmi et al., 2021; Bishwas et al., 2021; Adil et al., 2022; Gupta et al., 2022; Tanin et al., 2022; Gupta et al., 2023; Jędzura et al., 2023).

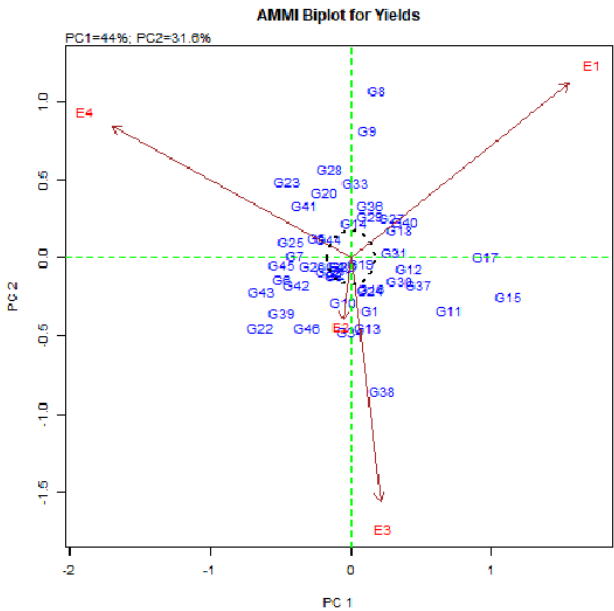


Fig. 3. The AMMI2 based analysis of 46 genotypes and 4 growing seasons for PC1, PC2 and grain yield

Roostaei et al. (2014) compared various statistical methods for ranking 20 winter wheat genotypes based on yield, stability, and yield-stability. They found that AMMI analysis and GGE biplot were the most similar in ranking genotypes for yield. Additionally, they noted that the GGE biplot was more comprehensive and versatile, providing a better understanding of GGE interaction than other methods. In this study, the GGE biplot analysis revealed that the total GGE variation for grain yield of the genotypes evaluated at four growing seasons was 73.38%, of which 41.2% was explained by principal component 1 (PC1) and 26.7% by PC2. The „Which-won-where” model of GGE biplot polygonal view showed the main effect of genotype plus the $G \times E$ interaction effect of the 46 studied genotypes in four seasons for grain yield. According to the polygon view, the investigated 46 advantage cultivars fall under four sectors, while four environments fall under three sectors in the polygon. The genotype G15 was recorded as high-yielding and stable across environments E1 (growing season 2016-2017) and E3 (growing season 2018-2019), while genotypes G16 and

G23, respectively, showed high yields in environments E2 (growing season 2017-2018) and E4 (growing season 2019-2020). According to Poudel et al. (2020), these vertex/winning genotypes, being the most responsive, exhibit specific adaptation. In addition, genotypes found in the sector with no test environment were classified as poorly adapted to all environments (Poudel et al., 2020; Regmi et al., 2021). Furthermore, genotype G2, located at the top of the polygon in a section of the biplot where no environmental indicator was present, exhibited the worst performance in all environments tested (Figure 4).

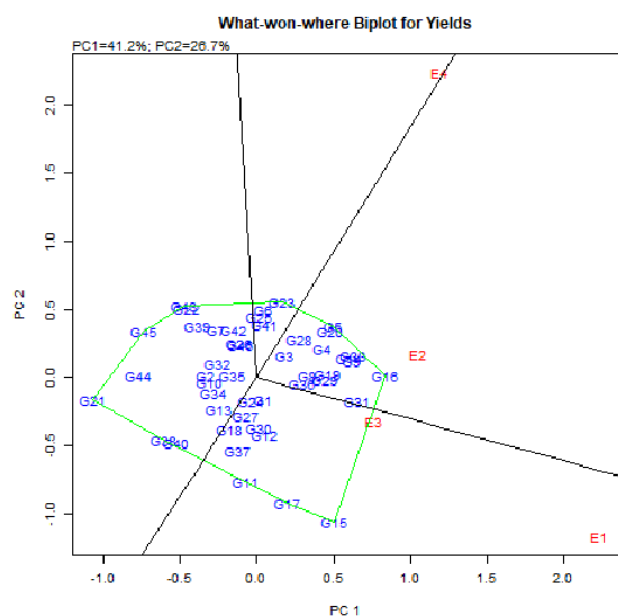


Fig. 4. GGE biplot of polygon view displaying 46 genotypes and 4 environments for grain yield

Many breeders use the concept of the ideal genotype as a reference in their programs (Mehari et al., 2015; Chimdesa et al., 2019; Wardofa et al., 2019; Omrani et al., 2022; Ahakpaz et al., 2023; Dabi et al., 2023; Kebede et al., 2023; Mohammadi et al., 2023). Genotypes that deviate from the ideal genotype can be eliminated in early breeding cycles, while those that are closer to it can be further tested. (Wardofa et al., 2019). In this study, G16 was located closest to the first concentric circle in the biplot, therefore, to the ideal genotype, followed by the genotypes in the following sequence: G33, G14, G9, G5, G20, G31, G4, G29, and G19. At the same time, G21 was the most unstable genotype because it was located far from the ideal genotypes (Figure 5). The GGE biplot for genotypes also showed the stability of genotypes as a function of environments. Productive genotypes are those

located to the right of the average climate abscissa (AEA) vector, and stable genotypes are those located closest to the AEA axis. Genotype G16 had the highest average yield, followed by G31, G14, and G33, while G21 had the lowest, followed by G44 and G45. Genotypes G33, G14, and G9 were the most stable genotypes, because they showed the shortest distance from the average environment abscissa. Genotypes G15 and G11 were less stable, having the longest distance from the AEA. However, considering the stability of yield about the average yield and the location of the genotypes relative to the ideal genotype, genotypes G33, G14, G16, and G9 could be considered the most favourable and adaptable to a wide range of environments (Figure 5).

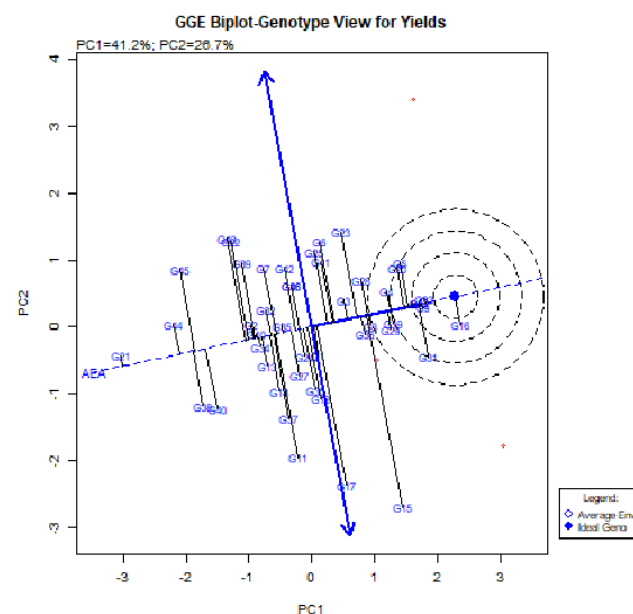


Fig. 5. GGE biplot genotype view for mean yield, stability and ideal genotypes 3 assessment

Conclusions

Grain yield of 46 common winter cultivars was significantly ($p < 0.001$) affected by the sources of variance: genotype (G), environment (E), and genotype $\times$ environment interaction (GEI) during four growing seasons in Southern Bulgaria. The magnitude of environment and genotype-by-environment interaction for grain yield was larger than that of the genotype effect. According to the parametric stability estimates, genotypes G16, G31, G14, G24, and G1 were identified as the most stable. The AMMI1 biplot analysis determined that the G14, G33, and G19 genotypes were

generally adaptive to each environment. According to the AMMI2-based analysis, the genotypes G19, G2, G35, G21, G4, and G32 were assessed as the most stable. The GGE biplot analysis revealed that the total GGE variation for grain yield of the genotypes evaluated at four growing seasons was 73.38%, of which 41.2% was explained by principal component 1 (PC1) and 26.7% by PC2. GGE biplot genotype view analysis for mean yield, stability, and ideal genotypes assessment identified G33, G14, G16, and G9 as the most stable and high-yielding genotypes, close to the ideal genotype. Therefore, they could be included in breeding programs and used as controls when evaluating the performance of other genotypes in Southern Bulgaria.

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