

Genotype – environment interaction for seed yield of maize hybrids and lines using the AMMI model

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Abstract

The objective of this study was to assess genotype by environment interaction for seed yield in maize hybrids and lines growing in Western Poland using the additive main effects and multiplicative interaction model (AMMI). The study comprised 32 maize genotypes (13 F₁ hybrids and their 19 parental lines), evaluated in four environments (two locations in two years). Seed yield ranged from 2.50 t/ha (S311 in Łągiewniki 2013) to 18.31 t/ha (Popis in Łągiewniki 2014), with an average of 8.41 t/ha. The Popis hybrid had the highest average seed yield (15.53 t/ha), and the S56125A line had the lowest (3.65 t/ha). The average seed yield per environments also varied from 6.60 t/ha in Łągiewniki 2013, to 9.95 t/ha in Smolice 2013. AMMI analyses revealed significant genotype (G) and environmental (E) effects as well as GE interaction effect with respect to seed yield. The analysis of variance explained 14.59% of the total seed yield variation by environment, 77.41% by differences between genotypes, 6.50% by GE interaction, and 1.50% by error. The Blask, Brda and Bejm hybrids are recommended for further inclusion in the breeding program because of their stability and high averages of seed yields.

Introduction

Maize (*Zea mays* L.) is the most important grain crop in the world and is produced nationwide in various environments. Maize ranks first in the global grain production (<https://www.statista.com/statistics/263977/world-grain-production-by-type/> accessed 30.11.2018). Successful maize production depends on the correct application of production inputs that will sustain the environment as well as agricultural production (Boote et al., 1996; Eriksson et al., 2005; Bocianowski et al., 2016). These inputs include adapted cultivars, plant population, soil tillage, fertilization, insect and disease control, harvesting (Pandey et al., 2000; Costa et al., 2002; Szulc and Bocianowski, 2011; Szulc et al., 2011, 2013, 2018; Bocianowski et al., 2019b). Maize is one of the most economically important cultivated plants in the world and is the main energy source for animal feed. Yield of maize is determined by the genotype and environmental effects as well as by genotype-environment (GE) interaction (Bocianowski et al., 2018; Branković-Radojčić et al., 2018; Das et al., 2019).

Analysis of GE interaction becomes indispensable for breeders and varietal experimentation. Each cultivar reacts specifically to changing climatic and soil conditions; some of them exhibit high GE interaction, while in others it is low. Quantitative and qualitative interactions may occur between cultivars and the environment (Dia et al. 2016; Larkan et al., 2016; Parent et al., 2017). Qualitative interaction occurs when the yield curves intersect and the order of cultivars in the yield ranking changes. Differences between cultivars increase significantly with quantitative interaction, but curves do not intersect. An assessment of the stability of cultivars' yield provides valuable information about their behavior in specific environments (Bernardo Júnior et al., 2018). This information is the basic criterion for micro- and macro-regionalization of cultivars.

One of the primary objectives in maize breeding has always been to increase seed yield as a way of maximizing yield. Better knowledge of the genetic determinism of seed yield can help breeders to control the genetic advance for the crop. Seed yield is a very complex quantitative trait, whose expression is the result of the genotype, environment as well as

GE interaction. The complexity of seed yield is the result of different genotype reactions to changing environmental conditions during plant development. GE interaction is often analyzed by the additive main effects and multiplicative interaction (AMMI) model (Zobel et al., 1988; Bocianowski et al., 2019c). The AMMI model combines the analysis of variance for the genotype and environment main effects and the principal component analysis (PCA) with multiplicative parameters in a single analysis (Zobel et al., 1988).

The objective of this study was to assess genotype by environment interaction for seed yield in maize (*Zea mays* L.) hybrids and lines grown in Western Poland using the AMMI model.

Materials and Methods

Plant material

As plant material, 32 maize (*Zea mays* L.) genotypes (19 inbred lines and their 13 F₁ hybrids) were used from the maize collections belonging to the Plant Breeding Smolice and the Plant Breeding and Acclimatization Institute (PBAI) – National Research Institute (NRI) Group.

Field trials

Two-year (2012, 2013) field experiment with inbred lines and hybrids was established on 10-m² experimental plots in a set of complete random block design in three replicates in two Polish breeding stations in Plant Breeding Smolice the PBAI – NRI Group: in Smolice (51°42'20.813"N, 17°9'57.405"E) and Łagiewniki (50°47'27"N, 16°50'40"E). Point sowing was used and each plot consisted of three rows. The row spacing was 70 cm and the distance between plants in a row was 18 cm; 278 plants were sown in the row; 83,400 seeds were sown per 1 ha. The yield of plants from the plot was calculated based on the yield of plants from ha in tonnes. Measurements of seed yield were performed on 20 randomly selected cobs from three replicates of each genotype.

Statistical analyses

A two-way fixed effect model was fitted to determine the magnitude of the main variation effects and their interactions on seed yield. Least-squares means were simultaneously generated for the AMMI model. The model first fits additive effects for the main effects of genotypes and environments followed by multiplicative effects for GE interaction using principal component analysis. The AMMI model (Gauch and Zobel, 1990; Nowosad et al., 2016) is presented as the following formula:

$$y_{ge} = \mu + \alpha_g + \beta_e + \sum_{n=1}^N \lambda_n \gamma_{gn} \delta_{en} + Q_{ge}$$

where y_{ge} is the mean of seed yield for genotype g in the environment e , μ – grand mean, α_g – genotypic mean deviations, β_e – environmental mean deviations, N – number of PCA axis retained in the adjusted model, λ_n – eigenvalue of the PCA axis n , γ_{gn} – genotype score for PCA axis n , δ_{en} – score eigenvector for PCA axis n , Q_{ge} – residual, including AMMI noise and pooled experimental error. Expected distribution of Q_{ge} is normal. The AMMI stability value (ASV) was used to compare the stability of the genotypes as described by Purchase et al. (2000):

$$ASV = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}} (IPCA_1) \right]^2 + (IPCA_2)^2},$$

where SS – sum of squares, $IPCA^1$ and $IPCA^2$ – first and second interaction principal component axes, respectively. Genotype selection index (GSI), which incorporates both the ASV index and mean seed yield in single criteria (GSI_{*i*}) was calculated for each genotype (Farshadfar and Sutka, 2003):

$$GSI_i = RY_i + RASV_i,$$

where GSI_{*i*} is genotype selection index for i -th genotype, RY_i is the rank of mean seed yield for the i -th genotype, $RASV_i$ is the rank for the AMMI stability value of the i -th genotype. All the analyses were conducted using the GenStat v. 18 statistical software package.

Results

In the analysis of variance, the sum of squares for genotype main effects represented 77.41% of the total variation, and this factor had the highest effect on seed yield. Differences between environments explained 14.59% of the total seed yield variation, while the

Table 1 - Analysis of variance of main effects and interactions for seed yield of maize (*Zea mays* L.) genotypes

Source of variation	d.f.	Sum of squares	Mean squares	F-statistic	Variability explained (%)
Genotypes	31	4430	142.91	442.56***	77.41
Environments	3	835	278.18	382.84***	14.59
Interactions	93	372	4.00	12.38***	6.50
IPCA1	33	269	8.16	25.26***	72.39
IPCA2	31	87	2.80	8.68***	23.35
Residuals	29	16	0.55	1.69*	
Error	248	80	0.32		

* P<0.05; *** P<0.001; d.f. – number of degrees of freedom

effects of GE interaction explained 6.50% (Table 1). Seed yield of the tested genotypes varied from 2.50 t/ha (S311 in Łagiewniki 2013) to 18.31 t/ha (Popis in Łagiewniki 2014) in all four locations, with an average of 8.41 t/ha (Table 2). The Popis hybrid had the highest average seed yield (15.53 t/ha), and the S56125A line had the lowest (3.65 t/ha). The average seed yield per environment also varied from 6.60 t/ha in Łagiewniki 2013 to 9.95 t/ha in Smolice 2013. The values for the two principal components were also highly significant ($P < 0.001$). The two principal components of GE interaction accounted jointly for 95.74% of the total effect it had on seed yield variation. The first principal component ($IPCA_1$) accounted for 72.39% of the variation caused by interaction, while $IPCA_2$ accounted for 23.35% (Fig. 1, Table 1).

The AMMI1 biplot (Figure 1) shows the stability of genotypes and environments as well as specific GE interactions. Among the tested genotypes, the Popis hybrid had the highest $IPCA_1$ value of 0.989, while the lowest $IPCA_1$ value of -1.952 was recorded for the M Wilga hybrid (Figure 1, Table 2). Among the tested environments, the lowest $IPCA_1$ value was observed in Smolice 2013 (-2.511), while the highest $IPCA_1$ value was 1.354 in Smolice 2014 (Figure 1). Genotype stability

is considered as a consistent reaction to changing environmental conditions, weather conditions, agronomic factors, biotic and abiotic stresses. The stability of the tested genotypes can be evaluated using the biplot for seed yield (Figure 2). ASV revealed variations in seed yield stability among the 32 genotypes (Table 2). A variety with ASV value close to zero is defined as stable. Consequently, S80660A (ASV=0.051), S41336 (0.188), Brda (0.290) and Blask (0.388) genotypes were the most stable, while M Wilga (6.131), Popis (3.066), S64423-2 (2.985) and Co255 (2.677) genotypes were the least stable ones (Table 2). Genotypes at the highest point in certain sections of the graph have the best results in environments located in the same section (Figure 2). The M Wilga hybrid showed a specific adaptation to the conditions in E1 – Smolice 2013 (Figures 1 and 2). The S64423-2 line interacted positively with 2014 – both locations. The S64423-2 and S68911 lines, with an average seed yield of 8.80 t/ha and 7.96 t/ha, respectively, close to the general mean of 4.41 t/ha, are distinguished on the biplot. The group of hybrids: Popis, Kozak, Budrys, Smok, Bejm, Narew and Blask had the highest averages of seed yield, but with different adaptations (Figures 1 and 2). These hybrids showed a specific adaptation to the conditions in 2014 (Smolice and Łagiewniki). The

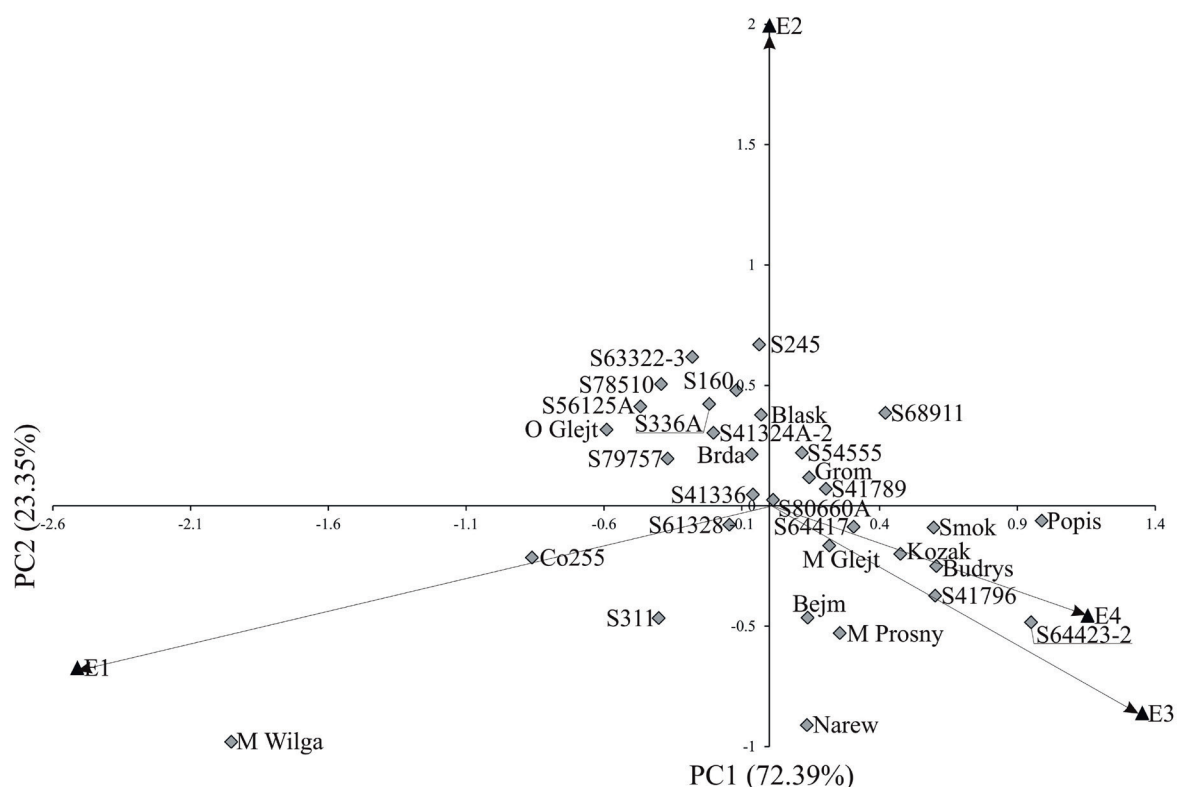


Fig. 1 - Biplot for genotype by environment interaction of maize (*Zea mays* L.) hybrids and inbred lines in four environments, showing the effects of primary and secondary components, respectively (E1 – Smolice 2013, E2 – Łagiewniki 2013, E3 – Smolice 2014, E4 – Łagiewniki 2014)

Table 2 - Average seed yield (t/ha) for genotypes and environments, principal component analysis values of tested maize (*Zea mays* L.) hybrids and lines, AMMI stability value (ASV) and genotype selection index (GSI)

Genotype	2013		2014		Mean	IPCA ₁	IPCA ₂	ASV	GSI
	Smolice	Łagiewniki	Smolice	Łagiewniki					
	E1	E2	E3	E4					
S160	3.39	3.67	5.57	5.40	4.51	-0.119	0.479	0.604	38
S41336	4.24	3.55	6.96	6.11	5.21	-0.059	0.046	0.188	30
S78510	6.57	6.27	7.96	7.26	7.02	-0.392	0.505	1.316	38
S54555	5.48	5.61	8.32	8.67	7.02	0.119	0.219	0.429	22
S245	4.92	5.91	7.35	7.31	6.37	-0.036	0.669	0.678	30
S311	5.48	2.50	6.58	6.45	5.25	-0.401	-0.467	1.328	48
S64417	3.67	3.44	7.22	7.56	5.47	0.306	-0.088	0.953	40
S41796	3.78	3.59	8.88	8.29	6.13	0.602	-0.374	1.903	49
S41789	3.45	3.41	6.74	6.82	5.11	0.206	0.069	0.641	39
S56125A	3.45	2.60	3.81	4.74	3.65	-0.467	0.412	1.505	56
S63322-3	5.12	5.35	6.55	6.70	5.93	-0.279	0.617	1.063	41
S64423-2	5.65	6.00	11.90	11.64	8.80	0.950	-0.484	2.985	42
S68911	5.55	6.90	9.62	9.78	7.96	0.421	0.385	1.361	35
S336A	3.47	3.29	4.95	5.49	4.30	-0.218	0.422	0.796	45
S41324A-2	4.62	4.17	6.23	6.61	5.41	-0.202	0.302	0.696	38
S80660A	4.70	4.09	7.45	7.13	5.84	0.015	0.024	0.051	25
S79757	7.20	6.07	8.35	8.36	7.49	-0.369	0.195	1.16	35
Co255	7.20	3.70	6.31	6.71	5.98	-0.861	-0.216	2.677	51
S61328	6.99	5.72	9.22	8.74	7.67	-0.145	-0.079	0.455	20
M Proсны	9.39	8.06	14.08	11.54	10.77	0.256	-0.530	0.954	27
O Glejt	6.40	5.07	6.82	6.62	6.23	-0.589	0.315	1.854	46
Budrys	11.09	11.22	16.12	15.69	13.53	0.606	-0.251	1.896	30
Popis	12.00	13.56	18.25	18.31	15.53	0.989	-0.063	3.066	32
M Glejt	10.22	9.53	13.30	13.93	11.75	0.218	-0.166	0.697	21
M Wilga	12.00	3.75	7.24	7.11	7.53	-1.952	-0.981	6.131	47
Narew	12.38	9.55	15.58	15.30	13.20	0.137	-0.912	1.005	23
Blask	11.33	11.60	14.12	13.36	12.61	-0.029	0.377	0.388	11
Grom	10.09	10.03	13.19	13.18	11.62	0.145	0.117	0.465	16
Brda	10.06	9.80	12.67	12.03	11.14	-0.063	0.213	0.29	13
Kozak	11.43	11.39	16.06	15.43	13.58	0.476	-0.200	1.488	25
Bejm	12.08	10.44	15.15	15.16	13.21	0.140	-0.466	0.636	14
Smok	10.87	11.43	15.93	15.38	13.40	0.597	-0.091	1.852	29
Mean	7.32	6.60	9.95	9.78	8.41				
IPCAe1	-2.511	0.001	1.354	1.156					
IPCAe2	-0.675	1.993	-0.862	-0.457					

Blask, Brda and Bejm hybrids had the best genotype selection index of 11, 13 and 14, respectively (Table 2).

Discussion

GE interaction is very important in the analysis of the results of a series of varietal experiments in terms of assessing the stability and adaptability of genotypes (Freeman, 1985). This is a phenomenon in which phenotypic plant reactions to environmental changes vary for different genotypes. The observed differences between genotypes depend on the environment in which they are compared. It is important to identify genotypes that are very efficient. This means that they are productive and stable genotypes, *i.e.* those whose yielding is proportional to the efficiency of environmental conditions. Analyses of GE interaction may prove valuable in recommending a change of agricultural practice, *i.e.* its regionalization.

Acosta-Pech et al. (2017) developed a new genomic statistical model. When selecting parental components for interbreeding, their general and specific combinatorial abilities should be considered.

The proposed model assumes the inclusion of GE interaction when creating a hybrid formula. This model is universal and can be used for different parental lines in any species. The latter authors evaluated the predictive power of two HP prediction models using a cross-validation approach on the extensive maize hybrid data. The experiment was conducted for 12 years in 58 environments. The experiment included 2724 hybrids, which were created by crossing 507 dent lines and 24 flint lines. Three traits were evaluated, and the analyses were performed for each year. In most, genomic models that included the interaction of general and specific combinatorial ability with environments showed a higher predictive ability compared to genomic models without interaction with environments (ranging from 12 to 22%, depending on the trait). The authors concluded that GE interaction increased the accuracy of genomic models in predicting untested maize hybrids.

Weber and Gołębiewska (2009) analyzed in 2003-2005 the variability of the yield of five maize varieties in relation to the method of weed control, locality and year of research. The yielding of maize hybrids was

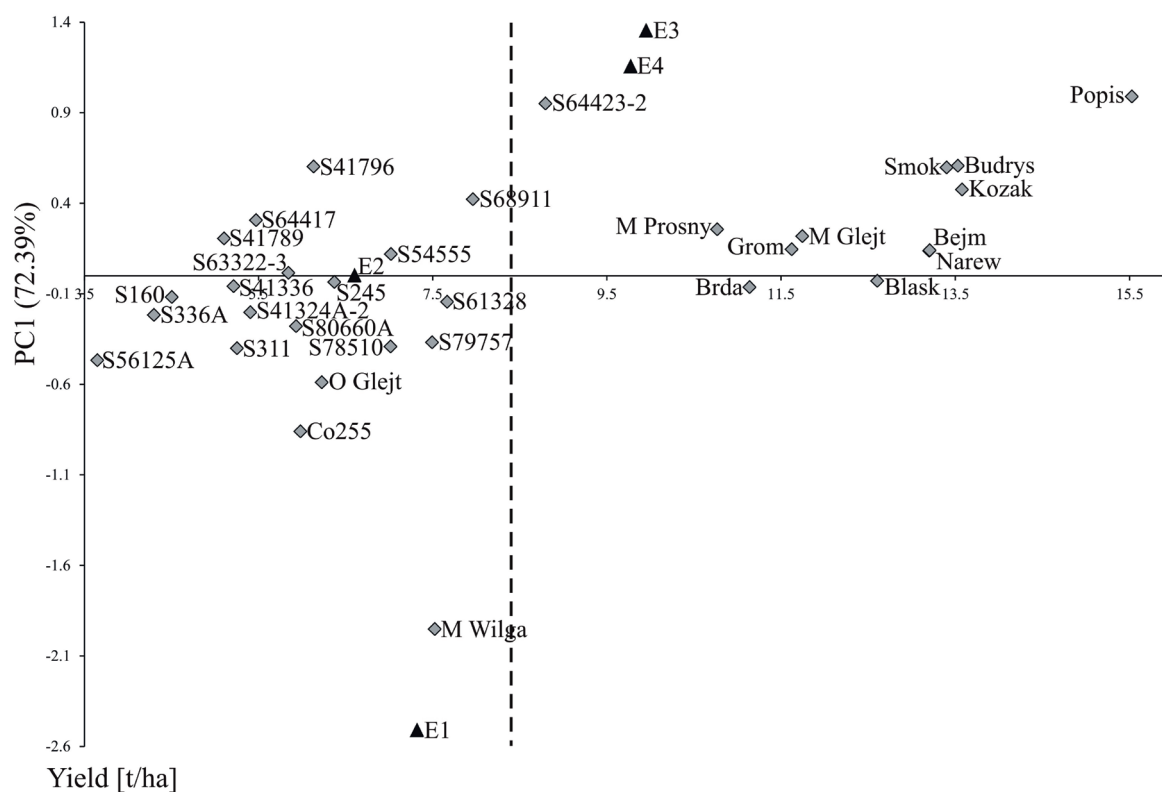


Fig. 2 -Biplot for the principal component of interaction (IPCA1) and average maize (*Zea mays* L.) seed yield (t/ha). Vertical line in the center of the biplot is the general grand mean.

compared under chemical protection conditions and mechanical weed destruction. It was shown that the yield of the analyzed varieties was highly dependent on the size and distribution of precipitation as well as the forecrop in individual towns and years of research. According to these authors, the high value of GE interaction has indicated that studies on the effectiveness of individual active substances should be an indispensable element in the registration of new maize hybrids.

Cygiert et al. (2003) assessed the impact of environmental conditions on yield stability of 10 maize hybrids. The experiment was established in 1999-2000 in various locations. The authors found the interaction of hybrids with locations, however, no interactions of hybrids with years. The highest performance was recorded for Electra, and the interaction with locations was demonstrated only in its case. Electra is a hybrid recommended for cultivation in less favorable conditions. For five hybrids: SMH 1177-9910, KOC 9939, KOC 9943, KOCKOSZ 99301 and KOCSWS 971104 no interaction with years, locations and environments was found; the aforementioned hybrids belong to the most stable ones recommended for cultivation in the whole Poland.

Bisawas et al. (2014) investigated the yielding of inbred maize lines under conditions of salinity stress. The research was conducted in many environments with different soil salinity. The aim of the analyses was to assess the stability of maize yielding in various cultivation conditions. From CYMITTY in India, 13 inbred lines were obtained that were previously tested and evaluated for their phenotypic traits. The lines were evaluated in salinity conditions and normal environment. The average for the environment and genotype mean ranged from 10.3 to 49.7 g and from 10.9 to 52.8 g, respectively. The values of regression coefficients of these genotypes ranged from 0.44 to 1.66. Genotypes P43, CZ29 and CZ33 reached higher grain yields and were very sensitive at different levels of salinity. On the other hand, considering the phenotypic index, regression coefficient, deviation from regression and AMMI biplot analysis, genotypes E32, P29 and P35 were characterized by almost stable performance under different salinity conditions. On the basis of phenotypic index, regression coefficient and deviation from regression, it is evident that all genotypes showed different adaptability responses under varied conditions, and genotypes E32, P29 and P35 exhibited almost constant stability under various salinity conditions. According to the authors, a similar

trend in the stability of the three previous genotypes was obtained in the AMMI biplot analysis, which could be used in a breeding program to obtain a more efficient maize variety tolerant to salinity.

Li et al. (2018) showed that the heterosis effect value in hybrid forms depended on the analyzed trait and the environment in which they were located. It was found that the value of the heterosis effect was not constant for a given hybrid, but varied depending on environmental conditions. Several studies have documented the benefits of using genomic multi-environmental models for assessing the performance of genotypes across different environmental conditions (Burgueño et al., 2012; Dawson et al., 2013; Jarquín et al., 2014). Analyses of multi-environment trials can include GE interactions using genomic covariance functions (Burgueño et al., 2012).

The AMMI model is frequently utilized in the studies on various species (Abakemal et al., 2016; Edwards, 2016; Nowosad et al., 2017; Bocianowski et al., 2018). Genotypes best suited to precise environmental conditions can be detected based on AMMI analysis which permits estimation of the genotype interaction effect in each environment (Nowosad et al., 2018; Bocianowski et al., 2019a). Significant GE interaction of seed yield was demonstrated using the AMMI analysis. High genotype stability was related to the AMMI stability value. Determination of the main effect of the genotype, environment, and the most meaningful GE interactions could be assessed based on the AMMI results displayed on the GE biplot. AMMI models are able to measure the weight of environments, genotypes and their interactions using a value that measures genotype stability in all environments, taking into account seed yield.

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