Original paper Open Access

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

Jan Bocianowski[1]*, Kamila Nowosad[2], Agnieszka Tomkowiak[3]

[1] Department of Mathematical and Statistical Methods, Poznań University of Life Sciences, Wojska Polskiego 28, 60-637 Poznań, Poland

[2] Department of Genetics, Plant Breeding and Seed Production, Wrocław University of Environmental and Life Sciences, Grunwaldzki 24A, 53-363 Wrocław, Poland

[3] Department of Genetics and Plant Breeding, Poznań University of Life Sciences, Wojska Polskiego 28, 60-637 Poznań, Poland

* Corresponding author:Jan Bocianowski, Department of Mathematical and Statistical Methods,Poznań University of Life Sciences, Wojska Polskiego 28, 60-637 Poznań, Poland, tel.: 48618487143, fax.: 48618487140 E-mail: jan.bocianowski@up.poznan.pl

ORCID: Jan Bocianowski: 0000-0002-0102-0084, Kamila Nowosad: 0000-0001-6837-7806, Agnieszka Tomkowiak: 0000-0001-9516-8911

KeyWords *adaptability; AMMI; biplot; maize; seed yield; stability*

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 F_1 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 Łagiewniki 2013) to 18.31 t/ha (Popis in Łagiewniki 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 Łagiewniki 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 F_1 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-m^2 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

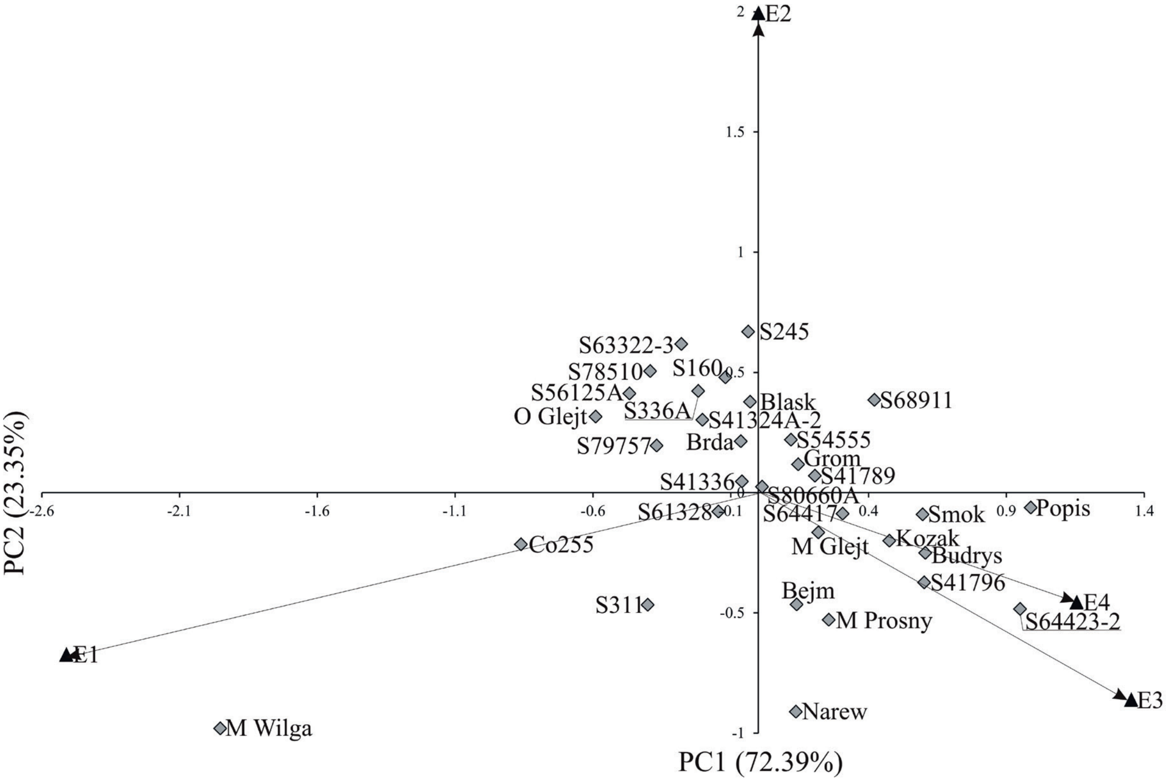

Fig. 1 -Biplot for genotype by environment interaction of maize (*Zea mays* L.) hybrids and inbred lines in four environments, showing the effects of primary and secondary components, respectively (E1 – Smolice 2013, E2 – Łagiewniki 2013, E3 – Smolice 2014, E4 – Łagiewniki 2014)

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)

	2013		2014						
Genotype	**Smolice**	**Łagiewniki**	**Smolice**	**Łagiewniki**	**Mean**	**$IPCA_1$**	**$IPCA_2$**	**ASV**	**GSI**
	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 Prosny	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 Gołębiowska (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

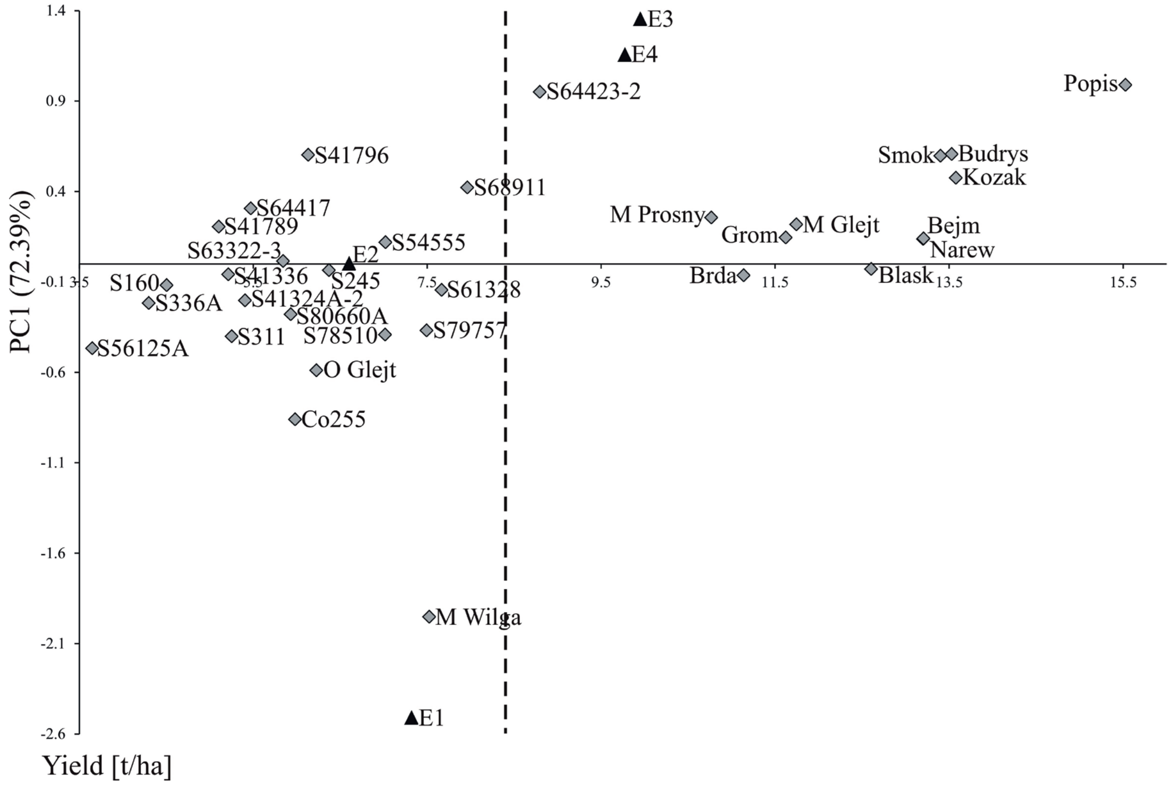

Fig. 2 -Biplot for the principal component of interaction (IPCA1) and average maize (*Zea mays* L.) seed yield (t/ha). Vertical line in the center of the biplot is the general grand mean.

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.

References

Abakemal D, Shimelis H, Derera J, 2016. Genotype-by-environment interaction and yield stability of quality protein maize hybrids developed from tropical-highland adapted inbred lines. Euphytica 209:757-769 https://doi.org/10.1007/s10681-016-1673-7

Acosta-Pech R, Crossa J, de los Campos G, Pérez-Rodríguez P, 2017. Genomic models with genotype × environment interaction for predicting hybrid performance: an application in maize hybrids. Theor Appl Genet 130:1431-1440 https://doi.org/10.1007/s00122-017-2898-0

Bernardo Júnior LAY, da Silva CP, de Oliveira LA, Nuvunga JJ, Pires LPM, Von Pinho RG, Balestre M, 2018. AMMI Bayesian Models to Study Stability and Adaptability in Maize. Agron J 110(5):1765-1776 doi:10.2134/agronj2017.11.0668

Bisawas A, Sarker U, Banik BR, Rohman MM, Talukder MZA, 2014. Genotype x environment interaction for grain yield of maize (*Zea mays* L.) inbreds under salinity stress. Bangladesh J Agr Res 39:293-301 https://doi.org/10.3329/bjar.v39i2.20431

Bocianowski J, Niemann J, Nowosad K, 2019a. Genotype-by-environment interaction for seed quality traits in interspecific cross-derived *Brassica* lines using additive main effects and multiplicative interaction model. Euphytica 215:7 https://link.springer.com/article/10.1007/s10681-018-2328-7

Bocianowski J, Nowosad K, Szulc P, 2019b. Soil tillage methods by years interaction for harvest index of maize (*Zea mays* L.) using additive main effects and multiplicative interaction model. Acta Agr Scand B-S P 69:75-81 https://doi.org/10.1080/09064710.2018.1502343

Bocianowski J, Szulc P, Nowosad K, 2018. Soil tillage methods by years interaction for dry matter of plant yield of maize (*Zea mays* L.) using additive main effects and multiplicative interaction model. J Integr Agr 17:2836-2839 https://doi.org/10.1016/S2095-3119(18)62085-4

Bocianowski J, Szulc P, Tratwal A, Nowosad K, Piesik D, 2016. The influence of potassium to mineral fertilizers on the maize health. J Integr Agr 15:1286-1292 doi: 10.1016/S2095-3119(15)61243-6

Bocianowski J, Warzecha T, Nowosad K, Bathelt R, 2019c. Genotype by environment interaction using AMMI model and estimation of additive and epistasis gene effects for 1000-kernel weight in spring barley (*Hordeum vulgare* L.). J Appl Genetics 60:127-135. https://link.springer.com/article/10.1007/s13353-019-00490-2

Boote KJ, Jones JW, Pickering NB, 1996. Potential Uses and Limitations of Crop Models. Agron J 88(5):704-716 doi:10.2134/agronj1996.00021962008800050005x

Branković-Radojčić D, Babić V, Girek Z, Živanović T, Radojčic A, Filipović M., Srdić J, 2018. Evaluation of maize grain yield and yield stability by AMMI analysis. Genetika 50(3):1067-1080 doi:10.2298/GENSR1803067B

Burgueño J, de los Campos G, Weigel K, Crossa J, 2012. Genomic prediction of breeding values when modeling genotype × environment interaction using pedigree and dense molecular markers. Crop Sci 52:707-719 doi:10.2135/

cropsci2011.06.0299

Costa C, Dwyer LM, Stewart DW, Smith DL, 2002. Nitrogen Effect on Grain Yield and Yield Components of Leafy and Nonleafy Maize Genotypes. Crop Sci 42(5):1556-1563 doi:10.2135/cropsci2002.1556

Cygiert H, Królikowska Z, Kaczmarek J, Adamczyk J, 2003. The effects of genotype-environment interaction on grain yield of maize (*Zea mays* L.) hybrids. Bulletin of Plant Breeding and Acclimatization Institute 226:366-376

Das AK, Muthusamy V, Zunjare RU, Chauhan HS, Sharma PK, Bhat JS, Guleria SK, Saha S, Hossain F, 2019. Genetic variability-, genotype × environment interactions- and combining ability-analyses of kernel tocopherols among maize genotypes possessing novel allele of *γ-tocopherol methyl transferase* (ZmVTE4). J Cereal Sci 86:1-8 doi:10.1016/J.JCS.2018.12.018

Dawson JC, Endelman JB, Heslot N, Crossa J, Poland J, Dreisigacker S, Manes Y, Sorrells ME, Jannink JL, 2013. The use of unbalanced historical data for genomic selection in an international wheat breeding program. Field Crop Res 154:12-22 https://www.sciencedirect.com/science/article/pii/S0378429013002645

Dia M, Wehner TC, Perkins-Veazie P, Hassell R, Price DS, Boyhan GE, Olson SM, King SR, Davis AR, Tolla GE, Bernier J, Juarez B, 2016. Stability of fruit quality traits in diverse watermelon cultivarstested in multiple environments. Horticulture Res 3:16066 doi:10.1038/hortres.2016.66

Edwards JW, 2016. Genotype×environment interaction for plant density response in maize (*Zea mays* L.). Crop Sci 56:1493-1505 https://doi.org/10.1016/j.fcr.2013.07.020

Eriksson H, Eklundh L, Hall K, Lindroth A, 2005. Estimating LAI in deciduous forest stands. Agr Forest Meteorol 129:27-37 https://doi.org/10.1016/j.agrformet.2004.12.003

Farshadfar E, Sutka J, 2003. Locating QTLs controlling adaptation in wheat using AMMI model. Cereal Res Commun 31:249-256 https://www.jstor.org/stable/23786964?seq=1#page_scan_tab_contents

Freeman GH, 1985. The analysis and interpretation of interactions. J Appl Stat 12:3-10 https://doi.org/10.1080/02664768500000001

Gauch HG, Zobel RW, 1990. Imputing missing yield trial data. Theor Appl Genet 79:753-761 https://doi.org/10.1007/BF00224240

Jarquín D, Crossa J, Lacaze X, Cheyron PD, Daucourt J, Lorgeou J, Piraux F, Guerreiro L, Perez P, Calus M, Burgueno J, de los Campos G, 2014. A reaction norm model for genomic selection using high-dimensional genomic and environmental data. Theor Appl Genet 127:595-607 https://doi.org/10.1007/s00122-013-2243-1

Larkan NJ, Raman H, Lydiate DJ, Robinson SJ, Yu F, Barbulescu DM, Raman R, Luckett DJ, Burton W, Wratten N, Salisbury PA, Rimmer SR, Borhan MH, 2016. Multi-environment QTL studies suggest a role for cysteine-rich protein kinase genes in quantitative resistance to blackleg disease in *Brassica napus*. BMC Plant Biol 16:183 DOI 10.1186/s12870-016-0877-2

Li Z, Coffey L, Garfin J, Miller ND, White MR, Spalding EP, de Leon N, Kaeppler SM, Schnable PS, Springer NM, Hirsch CN, 2018. Genotype-by-environment interactions affecting heterosis in maize. PLoS One 13(1):e0191321 https://doi.org/10.1371/journal.pone.0191321

Nowosad K, Liersch A, Popławska W, Bocianowski J, 2016. Genotype by environment interaction for seed yield in rapeseed (*Brassica napus* L.) using additive main effects and multiplicative interaction model. Euphytica 208:187-194 https://doi.org/10.1007/s10681-015-1620-z

Nowosad K, Liersch A, Popławska W, Bocianowski J, 2017. Genotype by environment interaction for oil content in winter oilseed rape (*Brassica napus* L.) using additive main effects and multiplicative interaction model. Indian J Genet Pl Br 77(2):293-297 DOI : 10.5958/0975-6906.2017.00039.6

Nowosad K, Tratwal A, Bocianowski J, 2018. Genotype by environment interaction for grain yield in spring barley using additive main effects and multiplicative interaction model. Cereal Res Commun 46:729-738 https://akademiai.com/doi/abs/10.1556/0806.46.2018.046

Pandey RK, Maranville JW, Chetima MM, 2000. Deficit irrigation and nitrogen effects on maize in a Sahelian environment: II. Shoot growth, nitrogen uptake and water extraction. Agr Water Manage 46:15-27 https://doi.org/10.1016/S0378-3774(00)00074-3

Parent B, Bonneau J, Maphosa L, Kovalchuk A, Langridge P, Fleury D, 2017. Quantifying Wheat Sensitivities to Environmental Constraints to Dissect Genotype × Environment Interactions in the Field. Plant Physiol 174:1669–1682 DOI: https://doi.org/10.1104/pp.17.00372

Purchase JL, Hatting H, van Deventer CS, 2000. Genotype × environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II.

Stability analysis of yield performance. South African J Pl Soil 17:101-107 https://doi.org/10.1080/02571862.2000.10634878

Szulc P, Bocianowski J, 2011. Hierarchy of mineral uptake in the creation of generative yield. Fresen Environ Bull 20:2135-2140

Szulc P, Bocianowski J, Kruczek A, Szymańska G, Roszkiewicz R, 2013. Response of two cultivar types of maize (*Zea mays* L.) expressed in protein content and its yield to varied soil resources of N and Mg and a form of nitrogen fertilizer. Pol J Environ Stud 22:1845-1853 https://www.researchgate.net/profile/Jan_Bocianowski/publication/259077299_Response_of_Two_Cultivar_Types_of_Maize_Zea_mays_L_Expressed_in_Protein_Content_and_Its_Yield_to_Varied_Soil_Resources_of_N_and_Mg_and_a_Form_of_Nitrogen_Fertilizer/links/0c96053839984acf9c000000/Response-of-Two-Cultivar-Types-of-Maize-Zea-mays-L-Expressed-in-Protein-Content-and-Its-Yield-to-Varied-Soil-Resources-of-N-and-Mg-and-a-Form-of-Nitrogen-Fertilizer.pdf

Szulc P, Bocianowski J, Nowosad K, Michalski T, Waligóra H, Olejarski P, 2018. Assessment of the influence of fertilisation and environmental conditions on maize health. Plant Protect Sci 54:174-182 https://doi.org/10.17221/22/2017-PPS

Szulc P, Bocianowski J, Rybus-Zając M, 2011. The reaction of „stay-green" maize hybrid (*Zea mays* L.) to various methods of magnesium application. Fresen Environ Bull 20:2126-2134

Weber R, Gołębiowska H, 2009. Effect of herbicide Titus 25 WG on variability of maize cultivars yield under Lower Silesia. Fragmenta Agronomica 26(4):181-188 [In Polish]

Zobel RW, Wright MJ, Gauch HG, 1988. Statistical analysis of a yield trial. Agron J 80:388-393 doi:10.2134/agronj1988.00021962008000030002x