



Comprehensive Analysis of Genotype by Environment Interaction of Maize Cultivars under Multi-Environment Conditions in North China

Haiwang Yue^{1,2}, Jianwei Wei^{1,2}, Junzhou Bu^{1,2}, Jie Li^{1,2}, Xiuguo Wang^{1,2}, Shuhong Zheng^{1,2}, Juexue Xie^{1,2}, Shuping Chen^{1,2}, Haicheng Peng^{1,2}, Xuwen Jiang^{3*} and Junliang Xie^{1,2*}

¹Dryland Farming Institute, Hebei Academy of Agriculture and Forestry Sciences, Hengshui 053000, China

²Hebei Provincial Key Laboratory of Crops Drought Resistance Research, Hengshui 053000, China

³College of Agronomy, Qingdao Agricultural University, Qingdao, China

*For correspondence: mjxw888@163.com; yanjiu1982@163.com

Abstract

A multi-environment trial of maize cultivars in the north of China was conducted at 17 sites to assess the agronomic traits and test location representativeness. An additive main effects and multiplicative interaction (AMMI) model and a genotype main effect (G) and genotype and environment interaction (GE), (GGE) biplot were used to analyze the data. Results showed that the grain yields of summer maize cultivars were remarkably influenced by environment (E), genotype (G), and genotype by environment interaction (GEI). The effect of GEI was 1.53 times higher than that of genotypes. The cultivars Hengyu1182, Longhua369 and J1302 exhibited good yield and stability. Among sites Baoding, Xinle, Yutian and Zhengding showed good discriminating ability while Langfang, Gaoyang and Tanchang sites displayed good representativeness. In correlation analysis, agronomic traits, such as ear length, kernel row number, and 1000-grain weight were positively correlated with maize yield. Conversely, barren ear tip was negatively correlated with yield. This study confirmed that the AMMI model and GGE biplot are effective methods for exploring the stability and adaptability of genotypes and representative patterns of biplots in crop breeding and subsequent cultivar recommendations. © 2019 Friends Science Publishers

Keywords: Agronomic traits; AMMI model; Correlation; GGE biplot; Stability analysis

Introduction

Maize (Zea mays L.), which can be used as grain, feed, and raw material, is an important cereal cultivated for millions of people worldwide (Hussain et al., 2013; Lu et al., 2015; Ofori et al., 2015). Hebei Province located in North China, the annual acreage and yield of maize account for approximately one-tenth of the total values in China. The region covered by maize in Hebei Province is wide and yield differences are great (Yue et al., 2018). The selection of high yield, stable yield, and good adaptable cultivars needs time (Meng et al., 2010; Ullah et al., 2010) and the application of classical quantitative genetics in maize breeding programs promotes the development of elite genotypes, thereby maximizing the benefit of selection. Maize growth is also affected by external environmental conditions, such as temperature, water, and latitude (Oyekunle et al., 2017). The interaction between genotype and environment is inevitable in maize breeding programs (Chai and Mu, 2016). Differences are hereditary and can be measured by statistical methods. Studies on genotype and environment interaction have been considered an important progress in contemporary statistical genetics. As such, the

adaptability of maize cultivars should be evaluated before they are produced and promoted. The main purpose of mutienvironment trial is to evaluate the adaptability, yield and stability of tested cultivars and to provide a scientific basis for maximizing the value of cultivars. These trials are keys to demonstrating and popularizing new crop cultivars (Correa *et al.*, 2016; Tao *et al.*, 2016). The promotion and development of high-yielding crop genotypes requires a comprehensive understanding of the genetic variation of yield and its components (Mohammad *et al.*, 2008; Zare *et al.*, 2017). Grain yield is a complex quantitative trait that is greatly affected by the environment. It is important to determine the traits that have the greatest impact on grain yield (Khan and Naqvi, 2012; Desheva, 2016).

When the interaction effect of genotype \times environment (GEI) is remarkable, it will reduce the association between phenotype and genotype values, and lead to bias in the estimation of gene effects, as well as the ability to combine various characteristics sensitive to environmental fluctuations, these factors are not suitable for selection (Mitrovic *et al.*, 2012). Few breeders have influenced the combination of multi-environment trials without considering the GEI effects (Liang *et al.*, 2015; Aruna *et al.*,

To cite this paper: Yue, H., J. Wei, J. Bu, J. Li, X. Wang, S. Zheng, J. Xie, S. Chen, H. Peng, X. Jiang and J. Xie, 2019. Comprehensive analysis of genotype by environment interaction of maize cultivars under multi-environment conditions in North China. *Intl. J. Agric. Biol.*, 21: 289–299

2016). If by using basic analysis of variance (ANOVA), only can the results that GE interaction effects are significant or not be parsed, but the effect of variance components contributed by some combinations of parameters or by the environment cannot be explained (Lopes et al., 2015). Therefore, some experts proposed various analytical methods, including additive main effects and multiplicative interaction (AMMI) model (Zobel et al., 1988; Gauch and Zobel, 1997; Najafian et al., 2010) and genotype (G) plus GE (GGE) biplot analysis system (Dimitrios et al., 2008; Akçura et al., 2011), to evaluate genotype and environment interaction. The AMMI model is more reliable than other methods, and it is widely used to evaluate cultivars from different environmental conditions. This model also reflects the interaction variation to the maximum extent by using experimental data and by combining variance analysis with principal component analysis (PCA) (Abay and Bjørnstad, 2009; Miranda et al., 2009). GGE biplot analysis is another important method that analyzes data after environmental centralization. GGE biplot and graphic axes can distinguish superior cultivars in multienvironments because the data contain the genotype (G) effect and genotype-environment (GE) interaction effect in the evaluation of cultivars (Yan et al., 2000). However, AMMI model or GGE biplot have disadvantages. For example, the AMMI model focuses on the interaction effect between genotype and environment, and a less comprehensive evaluation of genotypes is observed from the perspective of breeding and extension. The AMMI model is selected for high-yielding or stable-lowyielding cultivars and some high-yielding but less stable cultivars are disregarded (Yan et al., 2007; Gauch et al., 2008; Jin and Xu, 2012). In GGE biplot analysis, a part of GEI variation information is often lost if the information is based only on a two-dimensional plane diagram. As such, this information has a certain risk (Chang and Chai, 2010).

Two models with complementary advantages and disadvantages can be compared for the comprehensive analysis of AMMI models and GGE biplots. Using these models can be conducive to improve the scientific accuracy of data analysis and to explain the stability of cultivars in suitable areas. These models can also provide a reference for applications in the regional screening of suitable cultivars to create an excellent cultivar system layout (Wang *et al.*, 2016).

In this study, the AMMI model and GGE-biplot, two popular methodologies, were used to illustrate their usefulness in assessing multi-environment trials in North China. The main objectives were to: (i) assess the performance stability of 13 different maize genotypes; (ii) evaluate the representativeness and discriminability of 17 environmental conditions; (iii) evaluate the best quality among 13 maize genotypes by comparison of ideal genotypes and (iv) analyze the important agronomic traits associated with yield in a multi-environment trial.

Materials and Methods

Test Material

The 13 summer maize cultivars (coded G1 to G13) planted in 17 testing sites (coded E1 to E17) in North China was tested instead of the control cultivar Zhengdan958. The name of each cultivar, the information of the location, and the average yield are shown in Table 1 and 2.

Experimental Design and Data Collected

All the tests followed a randomized complete block design with three replications at a planting density of 75,000 plants ha⁻¹. A plot size of 20.1 m² (6.7 m length and 3 m width) was set, and each plot consisted of five rows and a row distance of 60.0 cm. At maturity, the middle three lines were harvested in each plot, and the yield was calculated. All agricultural operations were conducted in accordance with the recommendations.

Seeds of each cultivar were sown on 12 June 2015 in Gucheng, Xianxian, Shenzhou, Feixiang, Handan and Yutian, 13 June 2015 in Zunhua, Luquan, Gaoyang, Wuji, Zhengding, Yongqing and Baoding, 15 June 2015 in Xinle, Langfang, Xinhe and Qingxian, respectively. Before sowing, each location was finely cultivated and irrigated, and basal fertilizer was applied as described by Anhui Liuguo. Compound fertilizer (containing 22-12-14% as N-P-K, respectively) and nitrogen fertilizer (180 kg N ha⁻¹) were applied at the 12th leaf stage (V12) of maize growth. Irrigation was conducted 2–3 times depending on rainfall at each location. Agronomic trait records, including grain yield, ear length, kernel row number, barren ear tip and 1000-grain weight, were evaluated for each cultivar in each plot after harvest.

Statistical Analysis

Microsoft Excel version 2007 (Microsoft Corporation, Redmond, WA, USA, 2007) was used for data processing. SAS software (SAS Institute, 2008) was used for analysis of variance. Genotype \times environment interaction was analyzed using the AMMI model and the GGE biplot analysis embedded in the program Genstat release 16.1(Copyright 2013, VSN International Ltd.).

AMMI Model

Genstat 16.1 was used to statistically analyze the mean and standard deviation of agronomic traits, and ANOVA was performed to examine the stability of the AMMI model based on the significant interaction between genotype and environment.

Table 1: Basic information of the cultivars

Cultivars	Code	Supplier organization and institution	Cultivar type	Mean yield (t ha ⁻¹)
Xinyan218	Gı	Shandong Xinfeng Seed Industry Co., Ltd.	Compact	10.88
ZX14-4	G_2	Henan Xiandai Seed Industry Co., Ltd.	Compact	10.56
Yuanyu305	G_3	Shijiazhuang Shengyu Technology Development Co., Ltd.	Flat	10.93
Xianyu1453	G_4	Pioneer seed industry CO., Ltd.	Compact	10.57
Quanyu18	G ₅	Anhui Quanyin High-tech Co., Ltd.	Semi-compact	10.73
JF33	G_6	Hebei Jifeng Agricultural Development Co., Ltd.	Compact	9.80
Zhengdan958CK	G_7	Henan Academy of Agriculture and Forestry Sciences	Compact	10.22
YS1402	G_8	Hebei Yuansheng Agricultural Development Co., Ltd.	Semi-compact	10.43
Longhua369	G ₉	Hebei Kelier Seed Industry Co., Ltd.	Semi-compact	11.32
Hengyu1182	G_{10}	Dryland Farming Institute, Hebei Academy of Agriculture and Forestry Sciences	Compact	11.28
Tang13-B127	G11	Tangshan Academy of Agricultural Sciences	Semi-compact	10.27
J1302	G12	Hebei Guanhu Agricultural Technology Co., Ltd.	Compact	11.06
Aoyu698	G ₁₃	Hebei Aosheng Seed Industry Co., Ltd.	Flat	9.17

Table 2: Description of the locations for the evaluation of maize cultivars

Location	Code	Longitude (E)	Latitude (N)	Altitude (m)	Annual Rainfall (mm)	Mean annual temperature (°C)	Mean yield (t ha ⁻¹)
Gucheng	E_1	115°96′	37°34′	301	437	18.2	11.43
Zunhua	E_2	117°97′	40°19′	290	724	10.9	13.07
Xinle	E_3	114°40′	38°19′	32	458	13.5	10.78
Xianxian	E_4	116°11′	38°27′	27	435	12.4	10.39
Luquan	E_5	114°28′	38°01′	215	542	13.3	10.16
Gaoyang	E_6	115°81′	38°79′	125	486	11.9	10.72
Wuji	E_7	114°97′	38°23′	52	412	12.3	8.50
Shenzhou	E_8	115°72′	37°89′	25	480	13.4	8.778
Handan	E ₉	114°53′	36°60′	45	534	14.1	11.10
Zhengding	E_{10}	116°31′	38°07′	74	544	13.2	10.77
Feixiang	E11	114°35′	36°29′	55	326	13.4	10.74
Yongqing	E ₁₂	116°31′	39°19′	31	540	11.2	7.73
Yutian	E_{13}	117°79′	39°96′	168	693	10.8	11.59
Baoding	E ₁₄	115°31′	38°52′	52	498	13.5	11.17
Langfang	E15	116°41′	39°32′	17	556	12.0	11.33
Xinhe	E ₁₆	115°18′	37°54′	32	458	13.5	10.02
Qingxian	E17	116°47′	38°35′	7	620	12.0	11.20

Its mathematical model was described as follows (Nzuve *et al.*, 2013):

$$Y_{ij} = \mu + G_i + E_j + \sum_{n=1}^N \lambda_k lpha_{ik} \gamma_{jk} + heta_k$$

Where Y_{ij} is the yield of *i*th genotype in the *e*th environment; μ is the grand mean; G_i is the *i*th genotypic effect; E_j is the *j*th environment effect; λ_k is the characteristic value of the interaction principal component axis (IPCA) of the *k*th interaction effect; α_{ik} is the kth principal component genotype principal component score; γ_{jk} is the principal component score; γ_{ik} is the total number of principal component axes, and θ_{ij} is the residual.

Stability Parameter Calculation

The stability parameter of testing sites and the cultivars is the distance $D_{g(e)}$ from the IPCA's K-dimensional space in the plot or product category to the origin.

The calculation formula is as follows:

$$D_{g(e)} = \sqrt{\sum_{i=1}^{n} (IPCA_{g(e)i})^2}$$

Where D_g is the stability parameter of the cultivar, and a small D_g corresponds to a stable cultivar; D_e is the stability parameter of the testing site, and a large D_e indicates a strong resolution of the testing site. In other words, a high D_e suggests that a great difference in the inheritance of the genotype is shown in the environment, and it is favorable to the full utilization of the characteristics of the genotype.

GGE Biplot Analysis

GGE biplot theory consists of a biplot and a GGE (Yan *et al.*, 2000). The biplot belonged to a 2-dimensional matrix. The regional test data set was a genotype–environment interaction matrix that included the year of the test, the number of cultivars, and the number of plots. The table could be approximated as a 2-dimensional matrix. Therefore, bi-labeling could be used to perform singular value decomposition and represent a 2-dimensional matrix containing the cultivar and the environment. Principal component analysis was performed on the data set of the regional test. The principal component that accounted for the highest variation was called the first principal component (PC1). The second-highest variation was named the second principal component (PC2).

The GGE biplot is a tool that considers the total effects of genotype (G) and genotype \times environment interactions (GEI) during cultivar evaluation. The yield (mathematical model) of multiple cultivars and multiple environmental tests can generally be decomposed into the following (Yan and Rajcan, 2002):

$$\mathbf{Y}_{ij} = \mu + \beta_{ij} + \lambda_1 \xi_{il} \eta_{jl} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

Where Y_{ij} is the yield of genotype *i* in the environment *j*; μ is the grand mean; β_j is the yield performance of all genotypes in environment *j*; ξ_{i1} and ξ_{i2} are the genotype *i* scores on PC1 and PC2, respectively; η_{j1} and η_{j2} are the scores of environment *j* in PC1 and PC2, respectively; and ϵ_{ij} is the residual in the model.

The GGE biplot in this study was composed of ξ_{il} , η_{i1} , ξ_{i2} , and η_{i2} to easily and comprehensively display the information results in the two-way data table. In the GGE biplot, the average environment coordinate (AEC) method was used. The PC1 and PC2 scores of the AEC were equal to the average PC1 and PC2 scores of all the indicators. The over-origin and AEC (i.e., the average value of the environment with a small circle) were also utilized. The AEC's averaging-axis (AEA) axis was the vertical axis of the AEC. The AEA represented the average yield of a cultivar, and several genotypes projected to the right in the positive direction (arrow direction) of the AEA corresponded to a high yield. The vertical axis represented the GE effect (*i.e.*, the stability of the cultivar), and the short vertical line of each genotype on the AEA indicated the good stability of the table.

Results

Analysis of the Joint Variance and the Linear Regression Model

The analysis of the joint variance showed that the sum of squares of the testing site accounted for 53.70% of the total sum of squares. GEI constituted 17.94%, whereas the cultivars corresponded to 11.75%. This finding also revealed the remarkable effects on genotype, environment, and their interaction. This result suggested that the tested cultivars significantly differed. The variations in the interaction were greater than those in the cultivars because the variation in the environments accounted for the major part. Therefore, the stability of cultivars should be analyzed.

The regression analysis (Table 3) indicated that the joint regression, the genetic regression, and the environmental regression could explain 22.11% of the sum of squares, and the residuals remained notable and high instead of large, accounting for 77.89%. This finding implied that the interpretation of the regression models was less interactive and the regression models did not fit well with the experimental data. As such, this observation should be further examined using the AMMI model.

AMMI Analysis of Variance

The GE of maize before multi-environment trials was further analyzed with the AMMI model, including the interaction principal component axis (IPCA1–IPCA6), which accounted for 88.28% of the sum of the square of the interaction. The F value of the PC1–PC5 interaction axis showed that it was highly significant (P < 0.01), and PCA6 reached a significant level (P < 0.05). This result also fully explained that the AMMI model could be used to thoroughly analyze the GE information, and the AMMI model was superior to traditional regression models. This model could effectively overcome the linear regression analysis method in terms of evaluating cultivar stability.

Analysis of the Yield Stability and Testing Site Discrimination of Maize Cultivars by using the AMMI Model

For each cultivar, the distance between the projection points and the origin of the corresponding coordinates in the PCA1–PCA3 space (D_g) was sorted on the basis of D_g of PCA1–PCA3 (Table 4). A small D_g indicated that the origin was close to the projection points, indicating that the stability of the cultivar was enhanced. The rank of the cultivar stability performance was J1302 > Hengyu1182 > Zhengdan958 > Longhua369 > Quanyu18 > ZX14-4 > YS1402 > Yuanyu305 > JF33 > Aoyu698 > Xianyu1453 > Tang13-B127 > Xinyan218. This result implied that J1302, Hengyu1182, Zhengdan958, Longhua369 and Quanyu18 had good stability; ZX14-4, YS1402, Yuanyu305 and JF33 had moderate stability; and Aoyu698, Xianyu1453, Tang13-B127 and Xinyan218 had poor stability. The yield data revealed that cultivars J1302, Hengyu1182 and Longhua369 had good stability and high yields. Zhengdan958 and Quanyu18 belonged to cultivars with good stability and moderate yields. Tang13-B127 and Aoyu698 showed poor yield and stability. De of each testing site in the PCA1-PCA3 score was sorted. For the testing sites, a high De indicated a high discrimination (Table 5). The testing sites with a high spot discrimination were Baoding, Xianxian, Zhegnding, Yutian, Xinle, Luquan, Langfang, Zunhua, Gaoyang, Shenzhou, Yongqing, Gucheng, Feixiang, Xinhe, Handan, Qingxian and Wuji.

Yield and Related Traits

The cultivars of the polygon were JF33, Xianyu1453, Yuanyu305, Hengyu1182, Longhua369, Tang13-B127 and Aoyu698. Hengyu1182 had the highest average yield at Gucheng, Gaoyang, Qingxian, Shenzhou, Zhegnding, Feixiang, Yongqing, Yutian, and Xinhe. Yuanyu305 had the highest average yield at Xianxian. Longhua369 had the highest average yield at Xinle, Luquan and Handan. Tang13-B127 showed the highest average yield at Zunhua, Baoding and Qingxian.

Methods	Source of Variance	d.f.	S.S.	M.S.	G+E+GE SS explained /%	Explained % of GEI SS	F value
Analysis of Variance	Total variance	662	1877.24	2.84			
	Treatment	220	1565.39	7.12			10.09^{**}
	Genotype	12	220.49	18.37	11.75		26.04**
	Environment	16	1008.11	63.01	53.70		89.30**
	Genotype and environment Interaction	192	336.79	1.75	17.94		2.49^{**}
	Error	442	311.85	0.71			
Linear regression analysis	Joint regression	1	0.25	0.25		0.07	0.35
	Genetic regression	11	30.39	2.76		9.02	3.92**
	Environmental regression	15	43.85	2.92		13.02	4.14^{**}
	Residual	165	262.31	1.59		77.89	2.25^{**}
AMMI Model	PCA1	27	103.18	3.82		30.63	6.38^{**}
	PCA2	25	77.42	3.10		22.99	5.19^{**}
	PCA3	23	45.91	2.00		13.63	3.34**
	PCA4	21	30.50	1.50		9.06	2.51^{**}
	PCA5	19	24.76	1.26		7.35	2.31^{**}
	PCA6	17	15.56	0.95		4.62	1.61^{*}
	Residual	60	35.91	0.94		11.72	

Table 3: Analysis of variance, linear regression analysis and AMMI model analysis of the grain yield of maize cultivars

Note: * and ** significant at the 5% and 1% levels, respectively

Table 4: The score and stability parameter of cultivars on the axle

Cultivar	Mean yield t ha ⁻¹	Deviation	PCA1	PCA2	PCA3	Stability parameter (Dg)	Rank
Xinyan218	10.88	0.33	0.12	1.75	0.56	1.84	13
ZX14-4	10.56	0.01	0.56	-0.04	-0.74	0.93	6
Yuanyu305	10.93	0.37	0.58	0.25	-0.93	1.13	8
Xianyu1453	10.57	0.02	0.91	0.01	0.84	1.24	11
Quanyu18	10.73	0.17	-0.46	0.04	-0.43	0.63	5
JF33	9.80	-0.75	0.97	-0.39	0.51	1.16	9
Zhengdan958CK	10.22	-0.34	-0.17	-0.38	-0.33	0.53	3
YS1402	10.43	-0.12	-0.77	-0.68	0.36	1.08	7
Longhua369	11.32	0.76	-0.35	-0.23	-0.46	0.62	4
Hengyu1182	11.28	0.72	0.00	0.38	-0.29	0.48	2
Tang13-B127	10.27	-0.28	-1.52	0.16	0.48	1.60	12
J1302	11.06	0.50	-0.23	0.11	-0.08	0.27	1
Aoyu698	9.17	-1.39	0.36	-0.99	0.51	1.17	10

Table 5: The score and stability parameter of testing sites on the significant interact axle

Testing site	Mean yield (t ha ⁻¹)	Deviation	PCA1	PCA2	PCA3	Stability parameter (D _e)	Rank
Gucheng	11.43	0.87	0.25	-0.25	0.23	0.42	12
Zunhua	10.16	-0.40	-0.54	0.39	-0.21	0.70	8
Xinle	10.39	-0.17	1.25	-0.02	-0.04	1.25	5
Xianxian	10.78	0.22	-0.95	0.61	-0.95	1.47	2
Luquan	11.59	1.04	0.24	0.65	-0.39	0.80	6
Gaoyang	10.72	0.16	0.09	-0.33	0.50	0.61	9
Wuji	8.50	-2.06	0.09	0.03	0.24	0.26	17
Shenzhou	8.77	-1.79	0.12	0.48	-0.27	0.57	10
Handan	11.10	0.54	-0.10	-0.22	0.24	0.34	15
Zhengding	11.17	0.61	-1.34	0.04	0.33	1.39	3
Feixiang	10.74	0.18	0.15	0.25	-0.27	0.39	13
Yongqing	7.73	-2.82	0.48	0.18	0.08	0.52	11
Yutian	13.07	2.51	-0.61	-0.47	1.00	1.26	4
Baoding	11.20	0.64	-0.06	-1.80	-0.99	2.06	1
Langfang	10.77	0.21	0.65	0.31	-0.02	0.72	7
Xinhe	10.02	-0.53	0.29	-0.01	0.23	0.36	14
Qingxian	11.33	0.78	0.00	0.17	0.28	0.33	16

Quanyu18 and J1302 also displayed strong adaptability. No plots were observed in Xianyu1453, JF33 and Aoyu698 sectors, indicating that the yield of these three cultivars was not excellent among all the experimental results (Fig. 1A). Yuanyu305 was more adapted at Handan, Zhegnding, Gucheng and Xinle. Aoyu698 performed well at Qingxian, Qingxian, Baoding and Xianyu1453 was adapted at Zunhua, Yongqing, Langfang and Shenzhou. Quanyu18 showed high adaptation to environments such as Xinhe, Xianxian and Gaoyang; however, in contrast, ZX14-4 was not good under all environments (Fig. 1B).



Fig. 1: Adaptability of maize cultivars based on GGE-biplot analysis A: grain yield; B: ear length; C: kernel row number; D: barren ear tip; E: 1000-grain weight, the same as below

According to the polygon view of GGE biplot analysis, the cultivars were divided into seven parts and the test environments fell in two sections. The first section includes the test environments Ongging, Yutian and Xinhe which had the cultivar Hengyu1182 as the winner, while Quanyu18 was more adapted at the other environments (Fig. 1C). The vertex cultivars were Xianyu1453, Aoyu698, JF33, J1302, Zhengdan958 and YS1402. According to the biplot in Fig. 1D, environments were divided into three sectors. The first section represents Oingxian and Shenzhou, with genotype Xianyu1453 as the best cultivar for barren ear tip and the second sector represents Gucheng, Zunhua, Xinle, Xianxian, Luquan, Gaoyang, Wuji, Handan, Zhengding, Feixiang, Yutian, Baoding, Langfang and Xinhe, with genotype Aoyu698 as the most favorable while the third section represents Yongqing, with genotype JF33 as the winner genotype for barren ear tip. By contrast, J1302 and Zhengdan958 yielded a light barren ear tip at all the environments (Fig. 1D). In Gucheng and Xianxian, Tang13-B127 had the highest 1000-grain weight and was considered the superior cultivars in these test environments. In the rest of the test environments, Hengyu1182 was superior to other cultivars in 1000 grain weight (Fig. 1E).

Discriminating Ability and Representativeness of Testing Sites

Fig. 2 shows the analysis of the similarity between the testing sites during the cultivar evaluation. The angle between the vectors of Feixiang and Shenzhou was very small, suggesting that similar trial data could be obtained

from Feixiang and Shenzhou (Fig. 2A). Therefore, one of them could be eliminated without losing much information about the genotypes for future trials. In this study, the long lines at Baoding, Xinle, Yutian and Zhengding showed good discrimination. In terms of ear length, the discriminating powers were high for Yutian and Qingxian, but low for Gucheng, Xianxian and Gaoyang (Fig. 2B). That means good performance for ear length could be effectively selected at Yutian and Qingxian. From the perspective of ear length, three environment sites, namely, Zunhua, Yongqing and Langfang were highly representative environments, the same as to four environment sites, namely, Xinle, Wuji, Feixiang and Baoding. In terms of kernel row number, the discriminating powers were high for Zunhua, Wuji, Yongqing and Qingxian, but low for Zhengding and Xinle (Fig. 2C). From the perspective of kernel row number, Zunhua and Xinle, Wuji and Baoding, Shenzhou and Handan were highly representative environments, respectively. According to the length of the environment vectors (Fig. 2D), Wuji, Feixiang and Yongging had long vectors, and these environments had good discriminating performance for barren ear tip. Conversely, belonged to Qingxian the poorest discriminating environment. Xianxian and Zhengding, Luquan and Gaoyang, Handan and Langfang were highly representative environments, respectively.

The environment vectors of Gucheng and Xianxian were much longer than others (Fig. 2E), indicating that the two sites had strong discriminating ability on genotype evaluation. All of the seventeen environment tests were positively correlated because the angles between all



Fig. 2: Representation and discrimination of testing sites based on GGE-biplot analysis

environments were acute angles, and indicating that all environment tests were very similar in representativeness the genotypes in 1000-grain weight performance.

Analysis of the Mean Performance and Stability of Maize Cultivars by using the GGE Biplot Method

A vertical line was made between the cultivar point and the average environmental axis to analyze the high yield and stability of the cultivars. The ranking of the 13 maize cultivars was based on their high yield and stability performance (Fig. 3). The yield of Hengyu1182 was the highest, whereas the yield of Aoyu698 was the lowest among the 13 cultivars. The line perpendicular to the mean axis through the center (origin) represented the trend of each cultivar that interacted with each environment. A long vertical line between the cultivar and the average environment axis indicated that the cultivar was weakly stable. Thus, the stability of Aoyu698 was the highest and the stability of Tang13-B127 was the lowest among the 13 cultivars. In terms of maize breeding, the cultivars, such as Aoyu698, with high stability but poor yield could not be promoted in the production. The cultivars, such as Hengyu1182, with both high yield and high stability were ideal cultivars (Fig. 3A).

From the perspective of ear length (Fig. 3B), Aoyu698 and Hengyu1182 were higher than that of the other cultivars, by contrast, ZX14-4 and Quanyu18 were lower than that of the other cultivars. In terms of stability, Hengyu1182 and YS1402 were good, Yuanyu305 and Xianyu1453 were poor.

According to Fig. 3C, cultivar Quanyu18 had high yield but with poor stability in terms of kernel row number, whereas Tang13-B127 had the poorest performance and good stability. Generally, it seems that cultivar J1302 was a cultivar with a high and stable kernel row number. In this study, the greatest stability and high yielding performance in terms of barren ear tip was cultivar Aoyu698. By contrast, J1302 baldness was the lightest, but its stability was good (Fig. 3D). Cultivar Hengyu1182, Longhua369 and J1302 had higher performance in 1000-grain weight than that of the other cultivars, and the cultivars that had poor 1000-grain weight were ZX14-4, Quanyu18, Aoyu698 and Jf33 and the most unstable cultivar was Tang13-B127 (Fig. 3E).

Comparative Evaluation of Ideal Cultivars

An ideal cultivar refers to the highest average yielding and the most stable yield in all environments. As the cultivars moves closely to the center, the average yield and stability of the cultivars are enhanced (Fig. 4). Hengyu1182 and Longhua369 were included in the first inner cycle and closer to the center of the concentric circle than the other cultivars. Therefore, they could be considered as the best cultivars for the region. Conversely, Aoyu698 was the poorest cultivar for the region (Fig. 4A). Aoyu698 was closer to the center than the other cultivars and belonged to the best performance cultivar in terms of ear length. Quanyu18 was the most undesirable cultivar in terms of ear length (Fig. 4B). Because of placed closer to the first circle than the other cultivars, cultivar Xinyan218 could be used as desirable genotype in terms of kernel row number,

Yue et al. / Intl. J. Agric. Biol., Vol. 21, No. 2, 2019



Fig. 3: Analysis of high yield and stable yield maize cultivars based on GGE-biplot analysis



Fig. 4: Relationship between maize cultivars and ideal cultivar based on GGE-biplot analysis

and Tang13-B127 was the most undesirable cultivar in terms of kernel row number (Fig. 4C). Cultivar Aoyu698 had proximity to the ideal genotype in terms of barren ear tip, while J1302 was the poorest for the region (Fig. 4D). As shown in Fig. 4E, cultivar Hengyu1182 was included in the first inner cycle than the other cultivars. Therefore, Hengyu1182 could be considered as the best for the region in terms of 1000-grain weight. By contrast, JF33 was the poorest for the region.

Correlation Analysis of Grain Yield and Agronomic Traits

The correlation analysis of the agronomic traits and components of maize yield showed a significantly negative correlation between the barren ear tip and yield, and the correlation coefficient was -0.68 (Table 6). The yield was positively correlated with ear length and kernel row number, and their correlation coefficients were 0.25 and 0.16,

Items	Ear length (cm)	Kernel row number (row)	Barren ear tip (cm)	1000-grain weight (g)	Yield (t ha ⁻¹)
Ear length	1.00				
Kernel row number	0.45	1.00			
Barren ear tip	0.26	0.4514	1.00		
1000-grain weight	0.28	-0.02	-0.50	1.00	
Yield	0.25	0.16	-0.68**	0.74^{**}	1.00

Table 6: The correlation of yield and agronomic traits

respectively. The 1000-grain weight was significantly and positively correlated with yield, with a correlation coefficient of 0.74. The positive correlation coefficient between the 1000-grain weight and the yield was the highest, and the negative correlation coefficient between the barren ear tip and the yield was the highest. This result indicated that 1000-grain weight and barren ear tip performance were the main factors affecting maize yield.

Discussion

In the correlation analysis, the 1000-grain weight exhibited a highly significant positive correlation with yield, and the correlation coefficient was the highest, indicating that the 1000-grain weight had major contribution and had the greatest effect on the maize yield. Moreover, the barren ear tip exhibited a significantly negative correlation with the maize yield, suggesting that the barren ear tip was the key factor limiting the maize production. The correlation coefficient between yield and traits suggested that high grain weight and grain plumpness were the important characteristics of high-yielding maize cultivars. When selecting materials, breeders must control the selection of 1000-grain weight trait and should strictly control the selection of grain plumpness. When selecting other traits, such as ear length and kernel row number, breeders may choose appropriate requirements based on their breeding goal (Chen et al., 2017).

The environmental change has an important influence on the growth and yield of crops because of the interaction between genotype and environment (Rao et al., 2011; Dan et al., 2015; Nowosad et al., 2016). In the experimental analysis of the crop cultivars, simple two-dimensional data expression could not easily show the relationship between genotype and environment. These factors needed the requisition of the interaction effect (Luo et al., 2012; Klomsa-ard et al., 2013). The effects of genotype, environment, and GE interaction determined the extension value and the suitable planting area of a new cultivar to a large extent. Using the GGE biplot, we could comprehensively display the original data in the form of an atlas. The goals of three aspects could be achieved by comparing and analyzing the multiyear and multipoint identification test of cultivars for many years through a GGE double graph. First, the plot was divided into several zones, which could intuitively reflect the specific adaptation area of the cultivar. Second, the image showed the discriminating ability and representativeness of each plot. Third, the ideal cultivar was screened on the basis of the distance from the center of the concentric circle (Badu-Apraku *et al.*, 2012). The AMMI model could well integrate ANOVA and principal component analysis. This model could be used to analyze the interaction between the cultivar and the plot and between cultivars and plots. Therefore, the AMMI model has been gradually accepted by breeders (Tekdal and Kendal, 2018). In our study, the AMMI model and the GGE biplot method were used to analyze the regional data of summer maize cultivars in North China in 2015. The two methods complemented each other, and the conclusions obtained were scientific and objective.

The analysis of the yield and stability of crop cultivars is a key to producing a large area before planting. This step is also an important basis for testing the best quality of cultivars (Tonk et al., 2011). In our study, stability and adaptability were important factors in determining the popularization and application of maize cultivars. Ideal maize cultivars should have a high and stable yield and wide adaptability. Under different environmental conditions, the stability of the cultivars could be combined with their high yield. Thus, maize cultivars with a high and stable yield are the main promotion targets. For low-yielding cultivars, even if they were stable, they were unsuitable for extensive planting. The analysis of the GGE double plotting revealed that the cultivars with high yield and stability were Hengvu1182, followed by Longhua369, However, in certain regions, the cultivars, such as Tang13-b127, with high fertility and good adaptability had the highest yield in two plots in E2 (Zunhua) and E14 (Baoding). Tang13-B127 had good adaptability in these two pilots and had a moderate performance in the 15 remaining pilots. The stability of Aoyu698 was the best in this study, but the yield was the worst. Thus, it was not popularized in production. The cultivars with a high yield should still be considered in specific areas with special adaptability.

The ANOVA of the AMMI model showed the significant effects on genotypes, environment, and genotype by environment interaction (GEI). This finding indicated that suitable cultivars could be screened from different environments (Derera *et al.*, 2008; Sandoya *et al.*, 2010). The environmental effect (E) was more than that between genotype (G) by environment (E) interaction (GEI) and genotype effect (G), and GEI was 1.53 times higher than G. This result was consistent with the findings of other researchers (Jaruchai *et al.*, 2018). In the selection and demonstration of maize cultivars, we should initially consider the influence of environmental factors and the

interaction between genotype and environment. We should also choose suitable cultivars for local environments (Fantie *et al.*, 2013). The AMMI model focused on analyzing the stability and the interaction effects between cultivars and environments, whereas GGE biplot analysis revealed the adaptability and fertility of the cultivars. Combining the AMMI model and the GGE biplot, we could easily and quickly analyze the yield, adaptability, and stability of cultivars and provide a reliable basis for the scientific layout of cultivars (Luo *et al.*, 2015).

How to choose the right testing site is also a key concern for maize breeders. In our study, E14 (Baoding), E3 (Xinle), E13 (Yutian), and E10 (Zhengding) had a strong identification of yield characteristics. E15 (Langfang), E6 and exhibited (Gaoyang), E7 (Jifeng) strong representativeness. The factors resulting in the discrimination of the test points and the poor representativeness were environmental and human factors. If the yield of the tested cultivars was low and the difference was not significant, weather, disaster, or human factor was the main cause. To save the test cost, we should not set too many plots in an area with a high similarity of environmental conditions. When identifying a site for the plot representative and distinguishing between good and bad, we should obtain long-term data, strengthen the field investigation of a test site, and reduce the influence of human factors on test results (Dia et al., 2016; Vaezi et al., 2017).

When used alone, any analysis method of genotype and environment interaction has limitations. For example, if GGE analysis was based only on the two-dimensional plane mapping, a part of GE variation information would be lost, which could be inferred as a certain risk. The AMMI model adopted bidirectional central data. Our research focused on the interaction between genotype and environment, evaluated the stability of cultivars, and disregarded some high-yielding but stable cultivars. When some of the highly stable cultivars had no popularization value because of their low yield, the use of the AMMI model was limited. The GGE biplot and the AMMI model could compensate for each other's defects compared with the AMMI model alone. The GGE biplot provided further information, such as cultivar adaptability region and plot representativeness. It also uses relevant information obtained from regional experiments (Baxevanos et al., 2008; Forkman and Piepho, 2014). In the future, GGE biplots and AMMI models can be comprehensively applied to reasonably arrange cultivars and achieve the maximum yield of cultivars.

Conclusion

With respect to yield performance of the maize cultivars at 17 testing sites, the highest was observed in Hengyu1182 followed by Longhua369 and J1302. Among sites, Baoding, Xinle, Yutian, and Zhengding had a good discriminating ability; whereas Langfang, Gaoyang and Tanchang showed

good representativeness. Correlation analysis disclosed that 1000-grain weight was positively correlated with yield while barren ear tip was negatively correlated with yield.

Acknowledgments

This research was supported by Special Fund for the National Natural Science Foundation of China (31601386); National System (Maize) of Modern Industrial Technology (nycytx-02); Appropriate Mechanization of New Summer Maize Variety Breeding, Demonstration and Promotion in North Huanghuaihai (Beijing-Tianjin-Hebei) (2017YFD0101202); Science and Technology Support Program of Hebei Province (16226323D-X); Shandong Key Research and Development Plan (Public Welfare Special Project, 2017GNC11103), the National Key Research and Development Program of China (2017YFD0701203).

References

- Abay, F. and A. Bjørnstad, 2009. Specific adaptation of barley varieties in different locations in Ethiopia. *Euphytica*, 167: 181–195
- Akçura, M., S. Taner and Y. Kaya, 2011. Evaluation of bread wheat genotypes under irrigated multi-environment conditions using GGE biplot analyses. *Zemdirbyste*, 98: 35–40
- Aruna, C., S. Rakshit, P.K. Shrotria, S.K. Pahuja, S.K. Jain, S. Sivakumar, N.D. Modi, D.T. Deshmukh, R. Kapoor and J.V. Patil, 2016. Assessing genotype-by-environment interactions and trait associations in forage sorghum using GGE biplot analysis. J. Agric. Sci., 154: 73–86
- Badu-Apraku, B., M. Oyekunle, K. Obeng-Antwi, A.S. Osuman, S.G. Ado, N. Coulibay, C.G. Yallou, M. Abdulai, G.A. Boakyewaa and A. Didjeira, 2012. Performance of extra-early maize cultivars based on GGE biplot and AMMI analysis. J. Agrest. Sci., 150: 473–483
- Baxevanos, D., C. Goulas, J. Rossi and E. Braojos, 2008. Separation of cotton cultivar testing sites based on representativeness and discriminating ability using GGE biplots. Agron. J., 100: 1230–1236
- Chai, J.P. and Z.G. Mu, 2016. Study on yield stability and test site representativeness of eight oat varieties in Gansu province. Acta Agrest. Sin., 24: 1100–1107
- Chang, L. and S. Chai, 2010. Application of GGE biplot in spring wheat yield stability analysis in rainfed areas of China. *Chin. J. Eco-Agric.*, 18: 988–994
- Chen, K., J.J. Camberato and T.J. Vyn, 2017. Maize grain yield and kernel component relationships to morphophysiological traits in commercial hybrids separated by four decades. *Crop Sci.*, 57: 1641–1657
- Correa, A.M., M.C. Gonçalves and P.E. Teodoro, 2016. Pattern analysis of multi-environment trials in common bean genotypes. *Biosci. J.*, 32: 328–336
- Dan, M., A. Diallo, F. Kanampiu, S. Mugo and H. Karaya, 2015. Agronomic performance and genotype environment interaction of herbicideresistant maize varieties in Eastern Africa. Crop Sci., 55: 540–555
- Derera, J., P. Tongoona, K.V. Pixley, B. Vivek, M.D. Laing and N.C. Rij, 2008. Gene action controlling grey leaf spot resistance in Southern African maize germplasm. Crop Sci., 48: 93–98
- Desheva, G., 2016. Correlation and path-coefficient analysis of quantitative characters in winter bread wheat varieties. *Trakia J. Sci.*, 1: 24–29
- Dia, M., T. Wehner, R. Hassell, D.S. Price, G.E. Boyhan, S. Olson, S. King, R.A. Davis and E.G. Tolla, 2016. Genotype × environment interaction and stability analysis for watermelon fruit yield in the United States. *Crop Sci.*, 56: 1645–1661
- Dimitrios, B., G. Christos, R. Jesus and B. Eva, 2008. Separation of cotton cultivar testing sites based on representativeness and discriminating ability using GGE biplots. *Agron. J.*, 100: 1230–1236

- Fantie, M., A. Assefa and K. Belete, 2013. AMMI analysis of yield performance and stability of finger millet genotypes across different environments. *World J. Agric. Sci.*, 9: 231–237
- Forkman, J. and H.P. Piepho, 2014. Parametric bootstrap methods for testing multiplicative terms in GGE and AMMI models. *Biometrics*, 70: 639–647
- Gauch, J.G.H. and R.W. Zobel, 1997. Interpreting mega-environments and targeting genotypes. Crop Sci., 37: 311–326
- Gauch, J.H.G., H.P. Piepho and P. Annicchiarico, 2008. Statistical analysis of yield trials by AMMI and GGE: further considerations. *Crop Sci.*, 48: 866–889
- Genstat, 2013. Genstat for Windows. Release 16.1. VSN International Ltd. http://www.vsni.co.uk
- Hussain, M., W. Bashir, S. Farooq and A. Rehim, 2013. Root development, allometry and productivity of maize hybrids under terminal drought sown by varying method. *Intl. J. Agric. Biol.*, 15: 1243–1250
- Jaruchai, W., T. Monkham, S. Chankaew, B. Suriham and J. Sanitchon, 2018. Evaluation of stability and yield potential of upland rice genotypes in North and Northeast Thailand. J. Integr. Agric., 17: 28–36
- Jin, S. and N.Y. Xu, 2012. The discuss of necessity about GGE double labeling chart applied in crop variety experiment in China. Seed, 31: 89–92
- Khan, N. and F.N. Naqvi, 2012. Correlation and path coefficient analysis in wheat genotypes under irrigated and non-irrigated conditions. *Asian J. Agric. Sci.*, 4: 346–351
- Klomsa-ard, P., A. Patanothaia and P. Jaisila, 2013. Efficient test sites for multi-environment evaluation of sugarcane genotypes in Thailand. *Intl. J. Plant Prod.*, 7: 763–790
- Liang, S.S., G.J. Ren, J.P. Liu, X.Q. Zhao, M.X. Zhou, D.N. Neil and G.Y. Ye, 2015. Genotype-by-environment interaction is important for grain yield in irrigated lowland rice. *Field Crops Res.*, 180: 90–99
- Lopes, M.S., S. Dreisigacker, R.J. Peña, S. Sukumaran and M.P. Reynolds, 2015. Genetic characterization of the wheat association mapping initiative (WAMI) panel for dissection of complex traits in spring wheat. *Theor. Appl. Genet.*, 128: 453–464
- Lu, W., C. Kang, Y. Wang and Z. Xie, 2015. Influence of biochar on the moisture of dark brown soil and yield of maize in Northern China. *Intl. J. Agric. Biol.*, 17: 1007–1012
- Luo, J., Y.B. Pan, Y. Que, H. Zhang, M.P. Grisham and L. Xu, 2015. Biplot evaluation of test environments and identification of megaenvironment for sugarcane cultivars in China. Sci. Rep., 5: 1–11
- Luo, J., H. Zhang and Z. Deng, 2012. Trait stability and test site representativeness of sugarcane varieties based on GGE-biplot analysis. *Chin. J. Appl. Ecol.*, 23: 1319–1325
- Meng, J., H. Wei, L. Yang and Z. Gu, 2010. Analysis on the regional comparative advantages of maize production in Hebei province. B. *Chin. Agric. Sci.*, 26: 343–348
- Miranda, G.V., L.V.D. Souza, L.J.M. Guimarães, H.L. Namorato, L.R. Oliveira and M.O. Soares, 2009. Multivariate analyses of genotype × environment interaction of popcorn. *Pesg. Agropec. Bras.*, 44: 45–50
- Mitrovic, B., D. Stanisavljevic, S. Treskic, M. Stojakovic, M. Ivanovic, G. Bekavac and M. Rajkovic, 2012. Evaluation of Experimental Maize Hybrids Tested in Multi-Location Trials Using Ammi and GGE Biplot Analyses. *Turk. J. Field Crops*, 17: 35–40
- Mohammad, T., M. Amin, M. Irfaq, M.I. Khan and A.J. Khan, 2008. Identification of traits in bread wheat genotypes (*Triticum Aestivum* L.) contributing to grain yield through correlation and path coefficient analysis. *Pak. J. Bot.*, 40: 2393–2402
- Najafian, G., A.K. Kaffashi and A. Jafar-Nezhad, 2010. Analysis of Grain Yield Stability in Hexaploid Wheat Genotypes Grown in Temperate Regions of Iran Using Additive Main Effects and Multiplicative Interaction. J. Agric. Sci. Technol., 12: 213–222

- Nowosad, K., A. Liersch, W. Popławska and J. Bocianowski, 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
- Nzuve, F., S. Githiri, D.M. Mukunya and J. Gethi, 2013. Analysis of genotype × environment interaction for grain yield in maize hybrids. *J. Agric. Sci.*, 5: 75–85
- Ofori, A.P., K. Ofori, K. Obeng-Antwi, K.M.L. Tengan, A. Agyeman and B. Badu-Apraku, 2015. Genetic analysis of single cross quality protein maize (QPM) hybrids. J. Plant Breed. Crop Sci., 7: 251–255
- Oyekunle, M., A. Haruna, B. Badu-Apraku, I.S. Usman, H. Mani, S.G. Ado, G. Olaoye, K. Obeng-Antwi, R.O. Abdulmalik and H.O. Ahmed, 2017. Assessment of Early-Maturing Maize Hybrids and Testing Sites Using GGE Biplot Analysis. *Crop Sci.*, 57: 1–9
- Rao, P.S., P.S. Reddy and A. Rathore, 2011. Application GGE biplot and AMMI model to evaluate sweet sorghum (*Sorghum bicolor*) hybrids for genotype × environment interaction and seasonal adaptation. *Ind. J. Agric. Sci.*, 81: 438–444
- Sandoya, G., R.A. Malvar, R. Santiago, A. Alvarez, P. Revilla and A. Butrón, 2010. Effects of selection for resistance to Sesamia nonagrioides on maize yield, performance and stability under infestation with Sesamia nonagrioides and Ostrinia nubilalis in Spain. Ann. Appl. Biol., 156: 377–386
- Statistical Analysis System (SAS), 2008. Version SAS/STAT 9.2; SAS Institute Inc.: Cary, North Carolina, USA
- Tao, L., J. Ali, M. Marcaida, O. Angeles, N.J. Franje, J.E. Revilleza, E. Manalo, E. Redoña, J.L. Xu and Z.K. Li, 2016. Combining Limited Multiple Environment Trials Data with Crop Modeling to Identify Widely Adaptable Rice Varieties. *Plos One*, 11: e0164456
- Tekdal, S. and E. Kendal, 2018. AMMI model to assess durum wheat genotypes in multi-environment trials. J. Agric. Sci. Technol., 20: 153–166
- Tonk, F.A., E. Ilker and M. tosun, 2011. Evaluation of genotype × environment interactions in maize hybrids using GGE biplot analysis. *Crop Breed. Appl. Biotechnol.*, 11: 1–9
- Ullah, S., A.S. Khan, A. Raza and S. Sadique, 2010. Gene Action analysis of yield and yield related traits in spring wheat (*Triticum aestivum*). *Intl. J. Agric. Biol.*, 12: 125–128
- Vaezi, B., A. Pour-Aboughadareh, R. Mohammadi, M. Armion, A. Mehraban, T. Hossein-Pour and M. Dorii, 2017. GGE biplot and AMMI analysis of barley yield performance in Iran. *Cereal Res. Commun.*, 45: 500–511
- Wang, Z.T., Zhou, W.H. Su, Y.X. Que, L.P. Xu, H. Zhang and J. Luo, 2016. Analysis of yield stability and test site representativeness of sugarcane trials using combined AMMI and HA-GGE biplot models. *Chin. J. Eco-Agric.*, 24: 790–800
- Yan, W.K. and I. Rajcan, 2002. Biplot analysis of test sites and trait relations of soybean in Ontario. Crop Sci., 42: 11–20
- Yan, W.K., M.S. Kang and B.L. Ma, 2007. GGE biplot vs. AMMI analysis of genotype-by-environment data. Crop Sci., 47: 643–653
- Yan, W.K., L.A. Hunt and Q. Sheng, 2000. Cultivar evaluation and megaenvironment investigation based on the GGE biplot. *Crop Sci.*, 40: 597–605
- Yue, H., Y. Li, C. Li, J. Bu, J. Wei, A. Guo, S. Chen, H. Peng, J. Xie and X. Jiang, 2018. Grain filling characteristics of maize hybrids with different maturity periods. *Intl. J. Agric. Biol.*, 20: 1650–1656
- Zare, M., M. Shokrpour and S.E.H. Nejad, 2017. Correlation and path coeffeicient analysis in wheat (*Triticum aestivum* L.) under various drought stress conditions. *Bangl. J. Bot.*, 46: 1309–1315
- Zobel, R.W., M.J. Wright and H.G. Gauch, 1988. Statistical analysis of a yield trial. Agron. J., 80: 388–393

(Received 21 June 2018; Accepted 10 September 2018)