



**Full Length Article**

## Application of AMMI Model to Assess Spring Maize Genotypes under Multi-environment Trials in Hebei Province

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### Abstract

The genotype (G) by environment (E) interaction (GEI) determines the stability of maize grain yield in multi-environment trials (METs). This study evaluated the high-yielding and promising maize genotypes over years and locations by the additive main effects and multiplicative interaction (AMMI) model. The grain yield of 13 spring maize genotypes was evaluated for two consecutive years (2012-2013) when planted in six and eight ecological environments, respectively, using a randomized complete block design (RCBD) with three replications. The AMMI model explained 77.49% and 75.57% of total observed genotypic variation, respectively. A comprehensive analysis of variances showed a highly significant impact of environment, genotype and genotype×environment (GE) interaction on grain yield ( $P < 0.01$ ). The AMMI model analysis of variance showed that the environment contributed the most to variations in grain yield (55.58% and 72.50% of the total variation, respectively), followed by GE interaction (24.61% and 10.71% of the total variation, respectively) and genotype (3.01% and 3.01% of the total variation, respectively). Among the interaction effects, first interaction principal component axis (IPCA1), IPCA2 and IPCA3 explained the vast majority of genetic and environmental interaction information. Two years of experimental data showed that the genotype with high yield and stability was G4 (Zhongdi175) while G3 (C807) and G8 (LY10) of poor yield and unstable. The check genotype G6 (Nongda108) had good stability and general high-yielding. The best and worst discriminative environments for each of the locations in 2012-2013 were XT (Xingtai) and LH (Longhua), WA (Wuan) and PQ (Pingquan), respectively. © 2019 Friends Science Publishers

**Keywords:** Adaptability; Grain yield; Stability parameters; *Zea mays* L.

### Introduction

Maize (*Zea mays* L.) is the most important cereal crop with the largest acreage and total yield in China. Therefore, increasing maize yield per unit area is of great significance in ensuring national food security (Tao *et al.*, 2016; Yue *et al.*, 2018a). In China, the dominant areas of maize planting are mainly distributed extending northeast through the Huanghuaihai to the southwest, including the northern spring maize area, the Huanghuaihai summer maize area and the southwest mountain maize area (Yue *et al.*, 2018b). According to Food and Agriculture Organization of the United Nations (FAO), the national maize planting area and total output accounted for about 38% of the cereal crop planting area and total production in 2016 (FAOSTAT, 2017). Due to the potential use for maize as a feedstock for food, livestock feed and industrial products, the demand for

maize have increased significantly (Oyekunle *et al.*, 2017).

The spring maize area of Hebei Province includes the northern spring and the western spring, and the planting area of the spring in Hebei Province is stable at around 1 million hectares. The spring sowing area in Hebei Province is wide with adverse conditions, such as high temperature stress, seedling stage drought, late growth frost, etc., combined with the deterioration of genotype characteristics and the yield levels vary greatly between different genotypes (Kang and Zhang, 2016; Chen *et al.*, 2017). Therefore, to select genotypes with high yield, stability and adaptability to serve local production is a difficult problem that maize breeding researchers urgently need to solve.

The interaction between factors is widespread in nature, especially in the agricultural production, the expression of crop yield, quality, resistance and many other traits are significantly affected by genotype (G) and environment (E)

interaction effects (GEI) (Akter *et al.*, 2014). Acting on production directly affects yield stability, the greater the interaction effect is, the worse is the stability (Chang and Chai, 2010). Therefore, GEI research and further analysis of the stability of traits can provide a direct basis for the evaluation of the utilization value of the genotype, the selection of the environment, the determination of the cultivation measures and the formulation of the target trait breeding program (Escobar *et al.*, 2011; Xu *et al.*, 2013).

Multi-environment trials (MET) is an effective method for identifying and evaluating the high yield, stability and adaptability of crop genotypes, and also an important way to improve crop productivity (Akcura *et al.*, 2011; Badu-Apraku *et al.*, 2011; Haider *et al.*, 2017; Mohammadi *et al.*, 2017). In the MET, the difference in yield between genotypes is usually compared by ANOVA, and the stability of the genotype is mainly determined by the interaction between genotype and environment (GEI). Therefore, the use of effective  $G \times E$  analysis method is crucial for the correct evaluation of the stability of the genotype. In the past few decades, researchers have proposed many mathematical models for studying  $G \times E$ , among which linear regression models are the most widely used (Burdon, 1977; Kang, 1997), but the shortcoming of linear regression is that only a small part of the interaction can be explained, and the information obtained from the use of the test is not sufficient (Purchase *et al.*, 2000). In some cases, the AMMI (additive main effects and multiplicative interaction, AMMI) model seems to be able to extract a large portion of GEI, so it is more efficient in analyzing GEI patterns (Ebdon and Gauch, 2002; Mohammadi and Amri, 2013; Kilic, 2014). The AMMI model was first proposed by Gauch (1988), which combines principal component analysis with analysis of variance to add the interaction of product forms to the additive model of conventional genotypes and environments. The analysis results of the AMMI model can be expressed and interpreted using straightforward and simple graphs, AMMI model can not only help to achieve more reliable stability analysis of the genotypes, and it can be used to identify some specific types of genotype by environment interaction (GEI). Compared with the variance analysis and the linear regression models, the AMMI model is wider and more effective (Hassanpanah, 2010; Mohammed *et al.*, 2016).

The main purpose of this study was to analyze the yield data of different maize genotypes using the AMMI model, in order to analyse the genotype and environment interaction (GEI) effect on the yield of the tested maize genotypes and investigate the stability.

## Materials and Methods

### Experimental Materials

Thirteen maize genotypes (Coded G1 to G13) used in this study are listed in Table 1. Seeds of each genotype were provided by Hebei seed management station (HSMS).

**Table 1:** Code, name and type of tested maize genotypes

Code	Genotype	Plant type	Year
G1	HC0901	Flat	2012-2013
G2	J1108	Compact	2012-2013
G3	C807	Semi-compact	2012-2013
G4	ZD175	Semi-compact	2012-2013
G5	JD152	Compact	2012-2013
G6	ND108CK	Flat	2012-2013
G7	KS7074	Flat	2012-2013
G8	LY10	Compact	2012-2013
G9	T2143	Flat	2012-2013
G10	XBS7801	Semi-compact	2012-2013
G11	Y9077	Semi-compact	2012-2013
G12	ZY101	Compact	2012-2013
G13	JWP340	Flat	2012-2013

The maize multi-environmental trials were conducted at fourteen environments throughout two crop seasons, 2012-2013 (Table 2).

### Experiment Design

The tested genotypes were arranged in randomized complete block design (RCBD) with three replications. The test plot has a length of 6.7 m, a row spacing of 0.6 m and a plot area of 20.1 m<sup>2</sup>, and the planting density per hectare of 60,000 plants. At maturity, three intermediate rows were harvested in each plot, naturally dried and weighed after harvest at moisture contents of 14%.

### Statistical Analysis

The mean and standard deviation of grain yield were statistically analyzed using Genstat 15.0 software (Payne *et al.*, 2012) for analysis of variance. Based on the significant interaction between genotype and environment, the AMMI model was used for stability analysis. The mathematical model was:

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

Where  $y_{ge}$  is the yield of genotype (g) in environment e;  $\mu$  is the population mean;  $\alpha_g$  is the average deviation of genotypes;  $\beta_e$  is the average deviation of the environment;  $\lambda_n$  is the  $n$ th interaction principal component analysis axis (IPCA);  $\gamma_{gn}$  is the first genotype principal component scores of  $n$  principal components;  $\delta_{en}$  is the environmental principal component score of the  $n$ th principal component;  $N$  is the total number of principal component axes;  $\theta_{ge}$  is the residual (Gauch, 2013).

The relative stability parameters of the genotype and the environment are the distance  $D_{g(e)}$  (Euclidean distance) of the genotype or environment from the origin in the  $k$ -dimensional space of IPCA. The 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 genotype and  $D_e$  is the stability parameter of the environment.

**Table 2:** Description of the locations for the evaluation of maize cultivars in 2012–2013

Location	Code	Longitude (E)	Latitude (N)	Altitude (m)	Annual Rainfall (mm)	Mean annual temperature (°C)	Year
Laiyuan	LY	114°41'	39°22'	859	517.3	12.1	2012
Zanhuang	ZH	114°38'	37°66'	124	568.1	12.2	2012
Xingtai	XT	114°51'	37°07'	73	256.2	12.9	2012
Laishui	LS	115°71'	39°39'	43	553.4	11.5	2012
Pingshan	PS	114°19'	38°24'	138	157.2	12.7	2012
Wuan	WA	114°20'	36°69'	194	560.2	12.4	2012
Xuanhua	XH	115°10'	40°60'	648	364.6	7.8	2013
Longhua	LH	117°74'	41°31'	567	563.9	7.3	2013
Chengde	CD	117°96'	40°95'	325	624.6	7.8	2013
Luannan	LN	118°68'	39°52'	25	162.7	13.8	2013
Qingxian	QX	116°83'	38°58'	12	618.2	12.1	2013
Wanquan	WQ	114°74'	40°77'	750	464.5	6.9	2013
Pingquan	PQ	118°70'	41°02'	507	540.1	7.2	2013
Zunhua	ZH	117°95'	40°18'	53	674.7	10.9	2013

The genotype with the lowest value of the  $D_g$  would be more stable and the larger the  $D_e$ , the stronger the resolution of the environment, that is, the larger the  $D_e$  value, the greater the genetic difference exhibited by the genotype in the environment, and the more favorable it is to fully carry out the genotype characteristics (Alizadeh *et al.*, 2017).

## Results

### Meteorological Data at Trial Sites

According to meteorological data, different spring maize genotypes have experienced low annual average temperatures below 13°C and low rainfall of less than 700 mm for all pilots during the test period (Table 2). The annual rainfall of each pilot varied between 157.2 mm in 2012 at Pingshan and 674.7 mm in 2013 at Zunhua. Meteorological data indicates that maize genotypes can be planted in a wide range of altitudes from 12 m at Qingxian to 859 m at Laiyuan. The climate characteristics of the northern and western parts of Hebei province coincide with this feature (Chen *et al.*, 2017).

### Genotype by Environment Analysis

Analysis of variance showed that variation among environment (E), genotype (G) and  $G \times E$  was highly significant ( $P < 0.01$ ), and accounting for 55.58%, 10.71% and 24.61% of the total sum of squares (SS), respectively (Table 3). The partitioning of total SS indicated that environment effect was a predominant source of variation followed by GE and genotype effect. The environment effect was approximately 5.2 and 2.3 times higher than genotype and GE, respectively, implying variations between environments account for the majority, and the variation of  $G \times E$  is greater than genotypes. Therefore, it is necessary to carry out the stability analysis of the genotype. The linear regression analysis showed that the joint regression, genetic regression and environmental regression add up to explain 25.36% of the total GE interaction, however, the residual

accounting for 74.64% of the total GE interaction (GEI), indicating regression model explains less interaction and regression model has a poor fit to the experimental data in this study. Decomposition of GE interaction by the AMMI model showed that the first third significant IPCAs explained 94.21% of the GEI sum of squares for grain yield, and the residual effect explained 5.79% of the total GEI (Table 3).

The variance analysis, regression analysis and AMMI model analysis in 2013 showed that all factors, including genotype, environment, GEI, IPC1, IPC2 and IPC3 had highly significant main effects ( $P < 0.01$ ) on maize grain yield of thirteen genotypes tested in eight environments and total SS explained 72.50% for environment, 9.18% for GEI effects, and only 3.01% for genotype (Table 4). The AMMI model analysis also indicated that the IPC1, IPC2 and IPC3 explained 43.93%, 22.77% and 16.34% of GEI sum of squares, respectively.

### AMMI Analysis of Maize Genotypes

The mean yield and IPCA1-IPCA3 scores of maize genotypes and stability parameter ( $D_g$ ) for each genotype in 2012-2013 are displayed in Table 5 and 6, respectively. The grain yield of different maize genotypes in 2012 varied in the mean yield of each plot. The genotypes G4, followed by G9, G13 and G2 had the highest mean yield performance across environments, while the genotypes G1 followed by G11, G3 and G6 had the lowest yield performance (Table 5). The genotypes G4, followed by G9, G7 and G2 showed the highest mean yield performance, while the genotypes G1 followed by G10, G6 and G11 had the lowest yield performance (Table 6).

The distance (D) value of the projection point in the space of each genotype IPCA1-IPCA3 and the corresponding coordinate origin, that is, the stability  $D_g$  of each genotype based on IPCA1-IPCA3 is arranged. The genotypes G4, followed by G5, G1 and G11 had the best stability performance across environments, while the genotypes G7 followed by G8, G13 and G2 had the worst stability performance in 2012.

**Table 3:** Analysis of variance, linear regression analysis and AMMI model analysis in 2012

Methods	Source	DF	SS	MS	Percentage of total SS/%	Percentage of SS of interaction/%	F value
Analysis of variance	Total variance	233	530.3540	2.2762	-	-	
	Treatment	77	482.0678	6.2606	-	-	20.22**
	Genotype	12	56.7889	4.7324	10.71	-	15.29**
	Environment	5	294.7761	58.9552	55.58	-	190.47*
	Genotype and environment interaction	60	130.5028	2.1750	24.61	-	7.03**
Linear regression analysis	Error	156	48.2861	0.3095	9.10	-	-
	Joint regression	1	1.0564	2.1750	-	0.81	3.41 <sup>ns</sup>
	Genetic regression	11	28.2446	1.0564	-	21.64	8.30**
	Environmental regression	4	3.7925	2.5677	-	2.91	3.06*
	Residual	44	97.4093	0.9481	-	74.64	7.15**
AMMI model	IPCA1	16	74.5705	4.6607	-	57.14	11.10**
	IPCA2	14	35.1427	2.5102	-	26.93	5.98**
	IPCA3	12	13.2315	1.1026	-	10.14	2.63**
	Residual	18	7.5582	0.4199	-	5.79	-

DF: degree of freedom, MS: mean squares, SS: sum of squares, MS: mean squares, \*, \*\*: significant at 5% and 1% probability level, respectively, ns: non-significant, the same as below

**Table 4:** Analysis of variance, linear regression analysis and AMMI model analysis in 2013

Methods	Source	DF	SS	MS	Percentage of total SS/%	Percentage of SS of interaction/%	F value
Analysis of variance	Total variance	311	808.8572	2.6008	-	-	
	Treatment	103	684.9871	6.6504	-	-	11.17**
	Genotype	12	24.3426	2.0285	3.01	-	3.41**
	Environment	7	586.4074	83.7725	72.50	-	140.67**
	Genotype and environment interaction	84	74.2371	0.8838	9.18	-	1.48*
Linear regression analysis	Error	208	123.8701	0.5955	15.31	-	-
	Joint regression	1	0.1001	0.1001	-	0.13	0.17 <sup>ns</sup>
	Genetic regression	11	8.8079	0.8007	-	11.86	1.34 <sup>ns</sup>
	Environmental regression	6	6.2980	1.0497	-	8.48	1.76 <sup>ns</sup>
	Residual	66	59.0311	0.8944	-	79.52	1.50*
AMMI model	IPCA1	18	32.6092	1.8116	-	43.93	5.18**
	IPCA2	16	16.9041	1.0565	-	22.77	3.02**
	IPCA3	14	12.1336	0.8667	-	16.34	2.48**
	Residual	36	12.5901	0.3497	-	16.96	-

**Table 5:** Score and stability parameter of maize genotypes in the principle components axis of significant interaction in 2012

Genotype Code	Mean yield (t ha <sup>-1</sup> )	Deviation	IPCA1	IPCA2	IPCA3	Stability parameter (D <sub>e</sub> )	Rank
G1	9.0162	0.5118	-0.1376	-0.7679	-0.0574	0.7822	3
G2	10.3360	0.3400	0.5189	-0.7743	-0.4184	1.0217	10
G3	9.7167	1.0257	-0.7840	0.0242	0.4389	0.8988	7
G4	11.0218	-0.1011	-0.0595	-0.0005	0.0703	0.0921	1
G5	9.8949	-0.2381	-0.1908	-0.2782	-0.0805	0.3468	2
G6	9.7579	-0.0146	0.1475	0.5740	-0.5817	0.8305	6
G7	9.9604	-0.1858	1.1411	0.1810	-0.0728	1.1576	13
G8	9.9283	-0.0677	0.6060	0.7728	0.6129	1.1576	12
G9	10.5465	-0.5261	0.8874	-0.0232	0.4783	1.0084	9
G10	9.8103	-0.2793	-0.3347	0.4128	-0.6147	0.8126	5
G11	9.4700	-0.0356	-0.1339	-0.7813	0.0591	0.7948	4
G12	9.9814	0.5505	-0.6629	0.6437	-0.3497	0.9880	8
G13	10.5078	-0.9798	-0.9975	0.0168	0.5158	1.1231	11

The results of AMMI model analysis indicated that G4, G2, G7, G13 and G6 had the best performance for grain yield in all environments, while the genotypes G5, followed by G3, G1 and G12 with poor stability performance in 2013. Combined with two years of data analysis, G4 belongs to both high-yielding and stable-yielding genotype, G3 and G8 were neither high-yielding nor stable.

#### AMMI Analysis of Experimental Locations

The average grain yield, IPCA1-IPCA3 score and stability parameters for each environment in 2012-2013 are shown in Table 7 and 8. The environments Wuan, Xingtai and Laishui showed the highest performance in the mean grain yield, Pingshan followed by LY with the lowest performance.

**Table 6:** Score and stability parameter of maize genotypes in the principle components axis of significant interaction in 2013

Genotype Code	Mean yield (t ha <sup>-1</sup> )	Deviation	IPCA1	IPCA2	IPCA3	Stability parameter (D <sub>e</sub> )	Rank
G1	9.6130	-0.3322	0.4523	0.7981	-0.4802	1.0355	11
G2	10.0767	0.1315	0.2502	-0.3900	-0.2469	0.5250	2
G3	9.8581	-0.0871	0.6917	-0.5353	0.6658	1.0992	12
G4	10.5872	-0.0886	0.1567	-0.0665	0.1439	0.2229	1
G5	9.7868	-0.1584	-1.0672	-0.4958	-0.4435	1.2575	13
G6	9.6588	-0.2864	0.2163	-0.5256	0.0478	0.5703	5
G7	10.2442	0.2990	-0.0598	0.3923	0.3587	0.5349	3
G8	9.9727	0.0275	-0.5462	-0.0027	0.3892	0.6707	7
G9	10.2945	0.3493	-0.2507	0.6722	0.0168	0.7176	8
G10	9.6168	-0.3284	0.5569	-0.1537	-0.4995	0.7638	9
G11	9.7668	-0.1784	0.0594	-0.1504	-0.5760	0.5983	6
G12	9.9556	0.0103	-0.7576	0.1416	0.3060	0.8292	10
G13	9.8566	0.6420	0.2980	0.3159	0.3180	0.5382	4

**Table 7:** Score and stability parameters of locations in the principle components axis of significant interaction in 2012

Location code	Mean yield/(t ha <sup>-1</sup> )	Deviation	IPCA1	IPCA2	IPCA3	Stability parameter (D <sub>e</sub> )	Rank
LY	8.9893	1.5029	1.4386	0.0721	0.5984	1.5598	2
ZH	9.0679	0.8886	0.7223	-0.5028	-1.0803	1.3934	4
XT	10.8927	0.8966	-1.0761	-1.1340	0.0697	1.5649	1
LS	10.8846	-1.0067	-0.4044	1.3052	-0.4401	1.4356	3
PS	8.6428	-0.9281	-0.9888	0.3955	0.3442	1.1192	5
WA	11.4989	-1.3532	0.3084	-0.1360	0.5080	0.6096	6

**Table 8:** Score and stability parameters of locations in the principle components axis of significant interaction in 2013

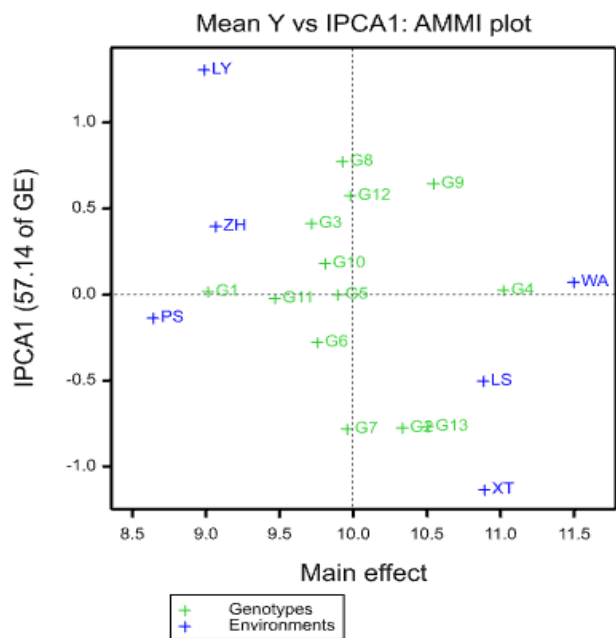
Location code	Mean yield/(t ha <sup>-1</sup> )	Deviation	IPCA1	IPCA2	IPCA3	Stability parameter (D <sub>e</sub> )	Rank
XH	9.4296	-0.5156	-0.6804	0.1489	-0.6490	0.9520	5
LH	11.7707	1.8255	1.5433	0.0640	0.0811	1.5467	1
CD	11.6595	1.7143	-0.2288	-0.9223	0.1876	0.9686	3
LN	11.2403	1.2950	-0.5857	0.4658	0.6041	0.9617	4
QX	9.2240	-0.7212	-0.1614	-0.6796	0.5355	0.8802	6
WQ	7.5986	-2.3466	0.1191	-0.2868	-0.9179	0.9690	2
PQ	9.3981	-0.5471	0.0882	0.5630	0.2230	0.6120	8
ZH	9.2408	-0.7044	-0.0942	0.6472	-0.0645	0.6571	7

In the view of the stability (D<sub>e</sub>), the environments Xingtai, Laiyuan and Laishui showed the highest value among 6 environments. While the environments Wuan, Pingshan and Zhanhuang with the lowest in D<sub>e</sub> (Table 7). Xingtai and Laishui are environments with good-yielding and discriminative performance, whereas Laiyuan belongs to poor-yielding and discriminative. Results showed that the environments Longhua, followed by Chengde and Luannan showed good performance, that meant these environments were high yielding. On the other hand, Wanquan, Qingxian and Zhanhuang demonstrated the lowest performance. With regards to D<sub>e</sub>, Longhua has the highest stability parameter and has the best discrimination among the 8 environments. Wanquan, Chengde and Luannan showed average, Pingquan and Zhanhuang were the lowest (Table 8). Longhua demonstrated good-yielding and good-discriminative performance, whereas Zhanhuang belongs to poor-yielding and poor-discriminative.

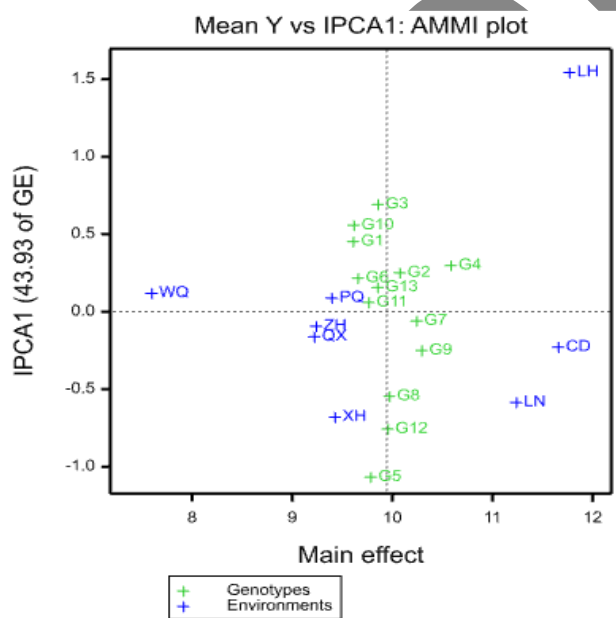
#### Adaptability Analysis of Genotypes in Different Environments

A graphical representation of maize grain yield demonstrated

in AMMI biplot (Fig. 1 and 2), showed that the x-coordinate represents grain mean yield, whereas y-coordinate represents the effects of first interaction principal component axis (IPCA1). It can be seen from Fig. 1 and 2 that the environment in the horizontal direction is more dispersed than the genotype, implying that the variation of the environment is much larger than of genotype, indicating that the 13 genotypes tested are generally more adaptable. The average yield of G12 and G7, G9 and G13 in the vertical direction are not much different, but the difference in IPCA1 values is large, indicating that the four genotypes have different performances in different locations. The closer the genotype position is to the IPCA1 zero value, the better the stability of the genotype. It can be seen from Fig. 1 that the IPCA1 values of G4, G5, G11 and G1 are close to zero, and the performance of the tested genotypes are relatively stable. The genotypes G2 and G4 had a positive interaction with the environment LH, *i.e.*, the LH had a positive effect on the yield increase of G2 and G4 genotypes, and the genotypes close to the horizontal line are more stable genotypes. The genotypes near the right and the horizontal line are high-yielding and stable genotypes as G4 and G7.



**Fig. 1:** AMMI biplot for seed yield in 13 spring maize genotypes and 6 environments against their respective IPCA 1 scores in 2012



**Fig. 2:** AMMI biplot for seed yield in 13 spring maize genotypes and 8 environments against their respective IPCA 1 scores in 2013

## Discussion

Significant differences in the environments of present study indicated that each environment is unique and needs to be evaluated to determine the best environment for the

widespread promotion of high-yielding and stable-yielding maize genotypes in Hebei province. The significant impact of the interaction between genotype and environment reflects the differential response of genotypes in different environments. This indicated that the GE interaction (GEI) was very significant and had a significant impact on genotype performance in various environments. The more the interaction between the genotype and environment, the worse is the stability of the genotypes. Therefore, stability analysis of genotype and environment interaction was necessary (Sharifi *et al.*, 2017). In this study, GEI had a large effect on spring maize grain yield ( $P < 0.01$ ), which explains 24.61% and 9.18% of the total sum of squares in 2012-2013 (about 2.30 and 3.05 times larger than that for genotype effect, respectively). Previous studies have also reported that genotype and environmental interaction lead to yield changes exceeded genotype in multi-environment trials. (Luo *et al.*, 2015; Mohammed *et al.*, 2016; Mohammadi *et al.*, 2017). This indicated that in the selection of maize genotypes and regional adaptation, it is necessary to fully consider the interaction between genotype and the environment, and select maize genotypes suitable for the local climate.

In the past, regression model analysis was often used to evaluate the environmental stability of genotypes. However, the interaction between genotype and environment is not a simple linear superposition estimation, but the AMMI model can effectively estimate the interaction between genotype, environment and interaction between these. The AMMI model combines ANOVA, linear regression analysis and principal component analysis to combine the advantages of these three analytical methods. It can not only analyze the significance of genotype and environment interaction, but also help to establish an interpretable nonlinear biological model, which had important reference significance for the rational use of maize genotypes and the correct selection of new genotypes testing sites (Oliveira *et al.*, 2009; Akter *et al.*, 2014). Because of the AMMI model lacks of quantitative stability measurements, and this measurement is critical for quantifying and ranking genotypes based on yield stability (Gauch, 2013; Fikre *et al.*, 2017). Therefore, genotype stability parameter was proposed by researcher to rank genotypes according to yield stability (Purchase *et al.*, 2000; Kulsum *et al.*, 2013). In the vertical direction, the closer the projection on the ordinate is to the origin, the more stable the yield is, and in the direction, the farther the projection on the abscissa is from the origin, the better the yielding of the genotypes (Silveira *et al.*, 2013). Analysis of the results of the two-year trial by the AMMI model showed that G4 is the most high and stable-yielding genotype, with relatively higher yield than other genotypes, and the stability parameter of the genotype is relatively small. In 2012, genotypes G1, G10 and G11 showed better genotype stability, but these three genotypes were less productive. In 2013, genotypes G1, G10 and G11 were less productive, and G1 and G10 were also unstable. The check genotype G6 belongs to the genotype with good stability and general high-yielding.

In the AMMI model, IPCA1 is closely related to genotypes stability and the smaller the IPCA1 score means that the genotype is the most stable in its environment (Vita *et al.*, 2010; Dia *et al.*, 2016). For the explanation of the AMMI model, the magnitude of the IPCA1 value was observed, and the fraction close to zero was the typical genotype and environment, which contributes little to the GE interaction showing their stability. This was consistent with the results of Tarakanovas and Ruzgas (2006) which suggests that genotype and environment interaction are mainly from IPCA1. This study showed that different trial locations had a large difference in the resolution of maize genotypes. In the six locations in 2012, the environments XT stability parameter ( $D_e$ ) was the highest (1.5649), WA was the lowest (0.6096) and the two locations was 2.57 times different. Among the eight locations in 2013, the highest and lowest stability parameter ( $D_e$ ) of the location LH and PQ was 1.5467 and 0.6120, respectively, with a difference of 2.53 times. Based on stability parameter ( $D_e$ ), environments XT and LH showed higher genotype discriminating ability than other environments in 2012-2013. On the other hand, WA and PQ locations exhibited relatively small genotype discriminating power and proved to be more environmentally characterized than the rest of the environments. The AMMI model thoroughly analyzes the GEI information and is significantly better than the traditional regression model, which can effectively overcome the limitations of the linear regression analysis method in evaluating the stability of the genotypes (Tekdal and Kendal, 2018).

## Conclusion

This study showed that AMMI model could be successfully used to evaluate the performance of different genotypes of spring maize in several test locations. AMMI model indicated that there were a large number of complex GE interactions, which means that some entries are inhibitory to different environments, while others are not inhibitory, which can be used to improve selection and evaluation. The AMMI model identified genotype G4 (Zhongdi175) as the high-yielding and stable genotypes across environments, and the genotypes G3 (C807) and G8 (LY10) as unstable with low-yielding performance.

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