INTERNATIONAL JOURNAL OF AGRICULTURE & BIOLOGY
ISSN Print: 1560–8530; ISSN Online: 1814–9596
19F–113/2019/22–6–1573–1580
DOI: 10.17957/IJAB/15.1237
http://www.fspublishers.org

Full Length Article

Genotype by Environment Interaction Analysis in Summer Maize Hybrids for Grain Yield under Multi-Environment Trials in Huang-Huai-Hai Area, China

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Abstract

Maize is one of the most important cereal crops supporting millions of people in China. The main purpose of this research was to assess the genotype by environment interaction (GEI) and yield performance of 20 maize genotypes in 16 different environments of Huang-Huai-Hai area, China. In this research, the additive main effects and multiplicative interactions (AMMI) model was applied to analyze the GEI effect and to evaluate the suitability and yield stability of 20 different maize genotypes. The AMMI model analysis indicated that genotype (G), environment (E) and GEI had significant effects on grain yield and the contribution to the total sum of squares difference was 3.10%, 35.05% and 42.25%, respectively, suggesting that GEI was the primary factor affecting grain yield. The AMMI model analysis partitioned sum of squares of GEI into fourteen interaction principal components axes (IPCA), of which all the IPCA were significant ($P < 0.01$) and the first five IPCA (IPCA1, IPCA2, IPCA3, IPCA4 and IPCA5) explained 77.7% of variation. The AMMI model analysis using IPCA1 scores and G main effect indicated that two genotypes Hengyu147 and Hengyu321 had relatively stable performance across the environments. Among the locations, Quwo was the most productive site in distinguishing genotypes and the most representative environment. In conclusion, this study suggested that genotype and environment interactions were the major source of variation in maize yield, and use of AMMI model seemed useful for screening and identifying the response of summer maize genotypes in different environments. © 2019 Friends Science Publishers

Keywords: AMMI model; *Zea mays* L.; Stability; Interaction principal component axes; Biplot

Introduction

Maize (*Zea mays* L.) is one of the most important cereal crops around the word and nearly 25% of world's total production comes from China (Zhou *et al*., 2017; Yue *et al*., 2018a). With ongoing rapid demographic, social and economic changes, maize demand is expected to be greater than wheat (*Triticum aestivum* L.) and rice (*Oryza sativa* L.) by 2020 (Li *et al*., 2015). China is the 2nd largest maize producer in the world after United States. In China during 2017, maize was cultivated on an area of 42 million ha with total production of 260 million tons and an average yield of 6.1 tons ha^{-1}. Therefore, continuously increasing maize production and accelerating the development of the maize industry have important strategic significance for ensuring China's food security (Yue *et al*., 2019).

The Huang-Huai-Hai summer maize area is one of China's dominant maize producing areas. The meteorological conditions of the maize growing period are complex, often encountering extreme natural weather such as strong wind and heavy rainfall (Yue *et al*., 2018b). Multi-environment trials (MET) of maize hybrids refers to the selection of test sites in different ecological types that can represent various agricultural production environments such as climate, soil, temperature and humidity and illumination in the region. The main purpose of the MET is to evaluate the yield and stability of the tested maize hybrids, which is a comprehensive comparison and evaluation of the tested hybrids in multiple environments (Smith and Cullis, 2018). This includes accurate estimates of genotypic effects, environmental effects, as well as interactions between genotypes and environments. Hybrids with significant genotype effects and small cross-effects

To cite this paper: Wang, S., X. Jiang, S. Wang, J. Bu, J. Wei, S. Chen, H. Peng, J. Xie, H. Yue and H. Li, 2019. Genotype by environment interaction analysis in summer maize hybrids for grain yield under multi-environment trials in Huang-Huai-Hai area, China. *Intl. J. Agric. Biol*., 22: 1573–1580

are suitable for large-scale promotion. On the contrary, the interaction effect significantly indicates that the hybrids have special requirements for the environment, and can only be promoted in specific regions to give play to advantages (Dolatabad *et al*., 2010; Crossa *et al*., 2011).

The high-yielding and stability of maize hybrids are the most concerned issues for maize breeders. The formation of maize yield is often affected by environmental changes, and there is a phenomenon in which genotypes interact with the environments (Farfan *et al*., 2013). The phenotypic values of crop yield and agronomic traits are determined by genotype (G), environment (E) and the interaction between genotype and environment (GE). The changes between different test sites and years reflect the interaction between genotypes and environments. Interaction effects can occur when different hybrids respond to different environmental conditions.

GEI is a major focus of plant breeders as large interactions reduce yield and complicate the identification of elite genotypes (Ma'ali, 2008). Therefore, understanding and mastering the structure and nature of interaction effects is very useful in deciding whether to continue to promote planting or breeding varieties adapted to specific regional environments (Yang *et al.*, 2005; Piepho *et al*., 2008). The GEI analysis method is crucial for the correct evaluation of the stability of the genotype (Sabaghnia *et al*., 2012). With the deepening of scientific research requirements, more and more genotype and environment interaction evaluation methods have emerged, such as Perkins-Jinks model (Freeman and Perkins, 1970), coefficient of variation method (Francis and Kannenberg, 1978), principal component analysis (PCA) (Kroonenberg and Basford, 1989) and linear regression model (Kang, 1997), *etc*., however, these methods generally only explain a small part of the interaction and cannot make full use of the information obtained by the experiment.

The additional main effect and multiplicative interaction model (AMMI) combines ANOVA and PCA to effectively analyze the interaction between genotype and environment and then visualizes it through the AMMI double-label map, which can comprehensively evaluate the stability and adaptability of crop varieties in different regions (Tekdal and Kendal, 2018). There have been many AMMI model reports on maize analyzed the stability of yield and agronomic traits in previous reports (Badu-Apraku *et al*., 2003; Morenogonzalez *et al.*, 2004; Ndhlela *et al*., 2014; Acorsi *et al*., 2016; Ye *et al*., 2019), but three consecutive years of fixed-point trials in the same test sites have not been reported. In this study, AMMI model was used to analyze the MET data of summer maize in the Huang-Huai-Hai area from 2016 to 2018 to evaluate the suitability and yield stability of 20 different maize genotypes in multi-environment locations. The findings of this study will enable the plant breeders and farmers to select good genotypes for specific areas and to understand the GET in order to provide the more reliable advice to maize produces.

Materials and Methods

Experimental Materials

In this study, Zhengdan 958 (as check cultivar) and 19 other maize hybrids were used as test materials. The detailed information of the hybrids is shown in Table 1. The seeds of all tested hybrids were provided by Dryland Farming Institute, Hebei Academy of Agriculture and Forestry Sciences. The multi-environment trials were carried out at 16 different ecological sites which distributed in Hebei Province, Henan Province, Shandong Province, Shanxi Province and Anhui Province for three consecutive years (2016-2018). The geographical and climate conditions of 16 experimental sites are shown in Table 2.

Experiment Design

The field trials were established using a randomized complete block design (RCBD) with three replicates at each location with net plot size of 6 m × 3 m. Maize was sown in 60 cm spaced rows with plant to plat distance of 22 cm. Crop was fertilized with compound fertilizer Anhui Liuguo (N 22%, P_2O_5 12% and K_2O 14%) at 460 kg ha^{-1} before sowing and additional 180 kg N ha^{-1} was applied at 12th leaf stage (V12). Weeds were controlled manually and crop was irrigated to avoid any moisture stress according to the rainfall. Grain yield was recorded from three central rows in each plot.

Stability Analysis

Analysis of variance (ANOVA) was used to examine the statistical significance of grain yield, the stability analysis of each trait was carried out based on genotype (G) ×environment (E) interaction according to the AMMI model (Gauch, 1988). The formula for the AMMI model is as follows:

$$y_{ijn}=\mu+\alpha_i+\beta_i+\sum_n \lambda_n \gamma_{in}\delta_{jn}+\rho_{ij}+\varepsilon_{ijn} \qquad (1)$$

Where y_{ijn} is the yield of the *i*th genotype in the *j*th environment in block *n*; μ is the grand mean;

α_i is the mean deviation of genotype *i* (the main effect of genotype); β_i is the mean deviation of environment *j* (the main effect of environment); λ_n is the singular value of the *n*th interaction principal component axis (IPCA); γ_{in} is the eigenvector value of genotype *i* and component *n*; δ_{jn} is is the eigenvector value of environment *j* and component *n*; ρ_{ij} is the residual; and ε_{ijn} is the error (Fabio *et al*., 2016).

In this study, the stability factor $D_{i(j)}$ value is used to indicate the distance from a genotype (environment) to the origin in the first three IPCA spaces for accurate determine the stability. The stability coefficient $D_{i(j)}$ is calculated as follows:

$$D_{i(j)}=\sqrt{\sum_{n=1}^{c} r_{i(j)n}^2} \quad \text{i(j)=1,2,…20(16)} \qquad (2)$$

Table 1: Description the basic information of the 20 tested genotypes in 2016-2018

Genotype	Genotype Code	Mother	Father	Plant type
Zhengdan958	G1	Zheng58	Chang7-2	Semi-Compact
Hengyu147	G2	H58	H59	Compact
Hengyu321	G3	H14	H13	Compact
Nongda108	G4	HuangC	178	Flat
Qiule218	G5	NK05	NK07	Semi-compact
Yufeng303	G6	CT1669	CT3354	Semi-compact
Huayu168	G7	HF2458-1	MC712-2111	Compact
Lianchuang808	G8	CT3566	CT3354	Semi-compact
Zhengdan1002	G9	Zheng588	ZhengH71	Compact
Xudan606	G10	YuA9241	XinA3	Semi-compact
Yuyu30	G11	XX1132-2	SX3821	Compact
Liangyu918	G12	LiangyuM53	LiangyuS127	Semi-compact
Anzao10	G13	J12	ZJ01	Compact
Longping208	G14	L238	L72-6	Semi-compact
Jinhua150	G15	5H558	B8328	Semi-compact
Deyu977	G16	LK910	LK122	Semi-compact
Dacheng168	G17	802	6107A	Compact
Qiangsheng369	G18	6143	997	Compact
Mengyu908	G19	DK58-2	Jing772-2	Compact
Shengrui999	G20	Sheng68	Sheng62	Semi-compact

Table 2: Basic information of the locations in the multi-environment trials in 2016-2018

Province	Location	Code	Longitude	Latitude	Elevation /m	Annual average rainfall /mm	Soil type
Anhui	Suzhou	E1	116°97′	33°64′	28	832	Red clay loams
Anhui	Guzhen	E2	117°31′	33°32′	20	801	Yellow brown soil
Hebei	Handan	E3	114°54′	36°63′	55	347	Cinnamon soil
Hebei	Lixian	E4	115°58′	38°48′	18	338	Brown soil
Hebei	Zhaoxian	E5	114°78′	37°76′	44	420	Brown soil
Hebei	Hengshui	E6	115°67′	37°73′	27	642	Brown soil
Hebei	Cangzhou	E7	116°84′	38°30′	16	485	Brown soil
Henan	Changge	E8	113°82′	34°19′	88	711	Cinnamon soil
Henan	Shangqiu	E9	115°65′	34°41′	50	705	Cinnamon soil
Henan	Zhengzhou	E10	113°62′	34°74′	144	542	Cinnamon soil
Henan	Luoyang	E11	112°46′	34°61′	140	608	Cinnamon soil
Shandong	Shanghe	E12	117°14′	37°30′	17	591	Brown soil
Shandong	Zaozhuang	E13	117°32′	34°81′	76	684	Brown soil
Shandong	Qihe	E14	116°76′	36°79′	36	576	Brown soil
Shanxi	Yuncheng	E15	111°01′	35°03′	369	525	Cinnamon soil
Shanxi	Quwo	E16	111°47′	35°64′	512	501	Cinnamon soil

In the formula, D_i and D_j represents the stability coefficient of genotype and environment, respectively; *c* represents the number of significant IPCAs (Zhang *et al*., 2017). It is inferred that genotypes with lower D_i value were considered relatively stable (Abakemal *et al*., 2016). The larger the D_j value is, the larger the genetic difference that the genotype shows in the environment, and the greater the pilot resolution of the environment (Alizadeh *et al*., 2017).

SAS software v.9.1 (SAS, 2011) was used for analysis of variance and AMMI model was analyzed using Data Processing System 17.0 (Tang and Zhang, 2013).

Results

Climatic Data, Yield Performance and Analysis of Variance

Among the environments, annual average rainfall (January-December) varied from 338 mm at E4 (Lixian) to 801 mm at E2 (Guzhen), the elevation ranged from 16 m at E7 (Cangzhou) to 369 m at E15 (Yuncheng). In this study, the selected pilot climate conditions represent different ecological types of the Huanghuaihai area (Table 2).

The grain yield performance data of these genotypes across sixteen environments is presented in Table 3. Genotype 1 (Zhengdan958) was the check cultivar. G2 was the best performing hybrid with the highest yield, followed by G3, G12, G10 and G9. Compared with the check cultivar G1, G2, G3, G12, G10 and G9 genotypes observed 6.05%, 5.81%, 4.80%, 3.02% and 3.01% more yield, respectively. G15 was the lowest one among all the tested hybrids, and its yield was reduced by 4.35% compared with the genotype G1 (Table 3).

All the sources showed highly significant effect ($P < 0.01$) on grain yield except genotype × year and genotype × environment × year (Table 4). The significant difference of variance analysis between years indicated that the performance of hybrids was different each year. The same

Table 3: The mean grain yield (t ha^{-1}) for 20 maize genotypes across 16 environments in 2016-2018

Genotype Code	Location Code																Mean (t ha^{-1})	Increasing rate (%)
	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11	E12	E13	E14	E15	E16		
G1(CK)	7.76	7.95	8.67	9.25	9.65	10.39	9.74	9.88	11.52	9.92	11.18	10.54	9.00	9.14	13.37	10.97	9.93	-
G2	8.85	9.83	10.95	11.17	11.63	10.16	12.06	10.60	11.49	10.78	10.03	7.71	11.78	9.71	11.41	10.95	10.57	6.05
G3	8.13	9.25	10.45	11.72	11.26	10.34	11.36	10.82	10.84	12.48	10.03	8.80	8.37	10.85	12.44	11.56	10.54	5.81
G4	8.11	8.38	9.34	10.87	11.02	9.69	9.80	11.00	12.46	10.52	10.66	10.37	9.70	9.21	11.19	8.40	10.05	1.16
G5	8.19	9.76	11.35	9.04	11.34	9.35	11.71	10.80	12.11	10.57	10.28	10.88	8.34	9.60	10.11	9.60	10.19	2.55
G6	8.64	9.15	10.58	7.55	12.36	8.99	10.94	10.38	11.23	10.55	10.63	10.34	8.89	11.02	9.91	8.40	9.97	0.41
G7	8.07	9.09	9.70	9.58	11.27	8.19	11.66	10.81	10.74	8.42	10.16	10.84	12.59	10.77	10.77	9.39	10.13	1.97
G8	7.53	9.34	12.47	10.79	12.13	8.77	10.71	9.21	11.53	9.63	10.32	10.43	8.37	10.77	10.83	10.20	10.19	2.55
G9	6.83	8.11	10.95	9.93	10.77	10.02	10.89	10.56	12.15	8.93	8.75	10.35	11.96	11.56	11.85	10.19	10.24	3.01
G10	7.86	9.21	11.02	10.72	10.98	10.01	10.83	10.58	11.45	9.45	9.22	9.95	11.26	9.67	12.08	9.51	10.24	3.02
G11	6.79	7.95	10.55	10.93	9.71	9.61	9.23	11.25	11.68	6.70	9.03	12.10	12.00	10.48	11.52	10.25	9.99	0.57
G12	7.55	8.93	10.02	11.97	9.95	9.49	10.90	10.50	11.30	9.21	10.41	9.98	10.93	12.30	11.92	11.53	10.43	4.80
G13	8.33	8.42	9.66	9.52	10.35	9.58	9.92	10.23	12.37	7.81	10.05	11.44	9.97	12.16	11.94	5.19	9.81	-1.23
G14	8.16	9.48	10.75	10.24	11.17	10.27	11.19	8.57	10.87	8.46	9.70	11.86	9.96	9.34	11.91	6.99	9.93	0.03
G15	7.32	9.63	9.62	10.61	11.57	10.03	9.27	8.70	11.19	6.98	9.93	8.48	10.15	9.29	12.91	6.57	9.52	-4.35
G16	5.99	8.79	10.90	10.49	9.09	9.80	10.81	9.77	11.24	6.28	12.40	9.43	9.81	9.30	11.40	9.10	9.66	-2.76
G17	6.83	9.27	11.62	10.90	9.54	10.31	9.95	9.41	11.14	8.48	10.56	9.80	8.88	10.68	10.38	9.74	9.84	-0.88
G18	6.94	8.99	8.78	8.68	10.01	8.75	10.55	9.32	11.70	8.03	10.38	10.01	9.22	10.89	11.27	11.57	9.69	-2.44
G19	7.60	9.21	12.00	9.34	9.77	8.66	10.74	9.05	12.40	8.97	10.45	9.96	8.34	10.85	11.99	10.20	9.97	0.41
G20	6.51	8.64	11.41	10.18	9.71	8.71	10.83	10.12	10.77	10.62	10.57	13.09	9.48	10.53	7.18	12.02	10.02	0.93

Table 4: The variance of AMMI analysis on grain yield of 20 maize genotypes in 2016-2018

Source of Variation	DF	SS	MS	F value	G +E +GE SS Explained (%)	GE SS Explained (%)
Total	2879	6888.29	2.39			
Treatment	319	5538.25	17.36	32.92**		
Genotype (G)	19	213.23	11.22	21.28**	3.10	
Environment (E)	15	2414.50	160.97	305.23**	35.05	
Genotype × Environment	285	2910.53	10.21	19.37**	42.25	
Year (Y)	2	558.33	279.16	6374.78**		
Environment ×Year	30	4.37	0.15	3.33**		
Genotype × Year	38	0.42	0.01	0.26^{ns}		
Genotype × Environment × Year	570	5.62	0.01	0.23^{ns}		
Joint-Regression	1	41.311	41.311	78.34**		1.42
Genotype-regression	18	94.0945	5.2275	9.91**		3.23
Environment-regression	14	304.5973	21.7569	41.26**		10.47
IPCA1	33	743.26	22.52	42.71**		25.54
IPCA2	31	509.60	16.44	31.17**		17.51
IPCA3	29	457.28	15.77	29.90**		15.71
IPCA4	27	308.66	11.43	21.68**		10.60
IPCA5	25	242.02	9.68	18.36**		8.32
IPCA6	23	172.34	7.49	14.21**		5.92
IPCA7	21	150.64	7.17	13.60**		5.18
IPCA8	19	102.14	5.38	10.19**		3.51
IPCA9	17	74.36	4.37	8.29**		2.55
IPCA10	15	50.46	3.36	6.38**		1.73
IPCA11	13	33.53	2.58	4.89**		1.15
IPCA12	11	25.51	2.32	4.40**		0.88
IPCA13	9	20.66	2.30	4.35**		0.71
IPCA14	7	15.75	2.25	4.27**		0.54
Residuals	5	4.33	0.87			0.15
Error	2560	1350.03	0.53			

DF: degrees of freedom; SS: sum of squares; MS: means squares; **: $P < 0.01$; ns: non-significant; IPCA: interaction principal component axes

interpretation can be expressed for environments. ANOVA for grain yield of 20 maize genotypes across 16 environments in 2016–2018 showed highly significant effect ($P < 0.01$) of genotype, environment and GEI, which explained about 3.10%, 35.05% and 42.25% of the total sum of squares, respectively. The magnitude of the environment and GEI were 11.63 times and 13.63 times larger than that for genotypes in terms of the treatment combination and sum of squares, respectively (Table 4). This clearly demonstrated that the differences in genotypes across the environment were significant and that resistance was determined by the GEI effect. The genotype effect seems to be negligible (Table 4).

The AMMI model analysis divided the square of the GEI into fourteen interaction principal component axes (IPCA) and the first fourteen IPCAs were highly significant ($P < 0.01$). IPCA1-14 were accounted for 25.5, 17.5, 15.7, 10.6, 8.3, 5.9, 5.2, 3.5, 2.6, 1.7, 1.2, 0.9,

Table 5: Average grain yield (AGY), interaction principal component analysis (IPCAs) values of 20 maize hybrids, AMMI stability value (ASV) and genotype stability factor (D_i)

Genotype	AGY (kg ha^{-1})	IPCA1	IPCA2	IPCA3	IPCA4	IPCA5	IPCA6	IPCA7	IPCA8	IPCA9	IPCA10	IPCA11	IPCA12	IPCA13	IPCA14	ASV	D_i
G1	9.93	0.13	0.08	0.72	-0.42	-1.41	0.29	-0.52	0.45	-0.11	0.14	-0.16	0.17	0.36	0.24	0.18	1.88
G2	10.57	0.27	0.38	0.97	0.90	0.75	-0.14	-0.40	-0.13	0.26	0.23	0.03	-0.44	0.19	0.21	0.50	0.98
G3	10.54	0.87	0.74	1.04	0.13	-0.18	0.37	0.63	-0.25	-0.30	0.20	0.01	0.48	-0.37	-0.12	1.31	1.19
G4	10.05	-0.14	0.49	0.02	0.27	-0.54	0.90	-0.23	-0.50	0.43	-0.52	0.35	-0.28	0.24	-0.27	0.52	1.59
G5	10.19	0.62	0.71	-0.59	-0.02	0.02	0.03	-0.34	0.24	0.50	0.08	0.20	-0.09	-0.71	-0.16	1.05	1.50
G6	9.97	0.33	1.00	-0.88	0.43	-0.25	-0.63	-0.15	-0.18	0.15	-0.14	-0.59	0.35	0.11	0.32	1.08	1.79
G7	10.13	-0.28	-0.46	-0.36	1.06	0.12	-0.57	-0.57	-0.18	-0.43	-0.02	0.42	0.32	0.04	0.12	0.58	1.65
G8	10.19	0.50	0.39	-0.25	-0.48	0.67	-0.12	0.52	0.31	-0.19	-0.74	0.22	0.35	0.30	-0.13	0.73	1.54
G9	10.24	-0.22	-0.62	0.11	0.62	0.01	-0.26	0.59	0.45	0.51	0.31	-0.47	0.09	0.31	-0.63	0.68	1.59
G10	10.24	-0.26	0.00	0.33	0.49	0.32	0.32	0.01	0.45	0.24	0.16	0.08	0.05	-0.10	0.15	0.32	0.97
G11	9.99	-0.53	-1.44	-0.15	0.22	-0.14	0.47	0.23	0.43	0.35	-0.43	0.01	0.20	-0.37	0.39	1.58	1.88
G12	10.43	0.18	-0.72	0.61	0.12	-0.09	-0.21	0.56	-0.62	-0.52	0.07	0.24	-0.05	-0.01	0.05	0.75	1.42
G13	9.81	-1.32	0.29	-0.95	-0.04	-0.60	-0.08	0.69	-0.66	0.08	0.35	0.13	-0.12	-0.02	0.02	1.67	2.04
G14	9.93	-0.77	0.46	-0.55	-0.16	0.32	0.53	-0.21	0.69	-0.84	0.55	0.07	-0.08	-0.02	-0.14	1.06	1.76
G15	9.52	-1.35	0.52	0.49	-0.22	0.45	0.02	-0.10	0.03	-0.31	-0.63	-0.35	-0.21	-0.01	-0.03	1.75	1.81
G16	9.66	-0.43	-0.57	0.26	-1.07	0.48	-0.15	-0.95	-0.58	0.34	0.25	0.02	0.49	0.00	-0.28	0.78	1.92
G17	9.84	0.19	-0.19	0.06	-0.76	0.54	0.23	0.30	-0.36	0.10	0.21	-0.54	-0.27	-0.10	0.38	0.31	1.34
G18	9.69	0.36	-0.43	0.24	-0.24	-0.66	-0.97	-0.24	0.16	-0.35	-0.32	-0.15	-0.51	-0.37	-0.29	0.62	1.62
G19	9.97	0.28	0.16	-0.02	-0.84	0.03	-0.67	0.39	0.45	0.40	0.23	0.63	-0.20	0.29	0.25	0.39	1.55
G20	10.02	1.54	-0.79	-1.08	0.02	0.17	0.63	-0.19	-0.19	-0.32	0.04	-0.16	-0.24	0.25	-0.07	2.07	2.22

0.7 and 0.5% of the GEI sum of squares, respectively, and the residuals effect contributed 0.2% of the interaction sum of squares (Table 4).

AMMI Stability Performance of Tested Genotypes and Environments

The lowest values of D_i was observed for G10, followed by G2, G3 and G5, which demonstrated a higher stability of these genotypes than others across the 16 environments (Table 5). Among these genotypes, G2 and G3 had higher grain yield in all tested environments. The highest D_i belongs to G20, followed by the descending order of G13, G16, G1, G11 and G6 (Table 6). The values of the D_j parameter could be useful in identifying environment stability, and E16, E12 and E13 were the most unstable environments, this showed that E16 and E12 had the strongest resolution, whereas E2 and E1 had the weakest resolution (Table 6).

AMMI-1 Biplot Stability

In the AMMI-1 biplot, X axis indicates the main effects (means) and Y axis indicates the effects of interaction (IPCA1). The icon of the environment in the horizontal axis direction is far more dispersed than the genotype icon, indicating that the variation of the environment was far greater than the variation of the genotypes. It means that the yield difference of the same genotype in different places was large (Fig. 1). This pattern clearly demonstrated the linear relationship between interaction scores and genotype main effects. Specifically, the upper and lower genotypes showed opposite interactions (Fig. 1). For example, genotype G20 and minimally expressed genotype G15 differed significantly in their interactions.

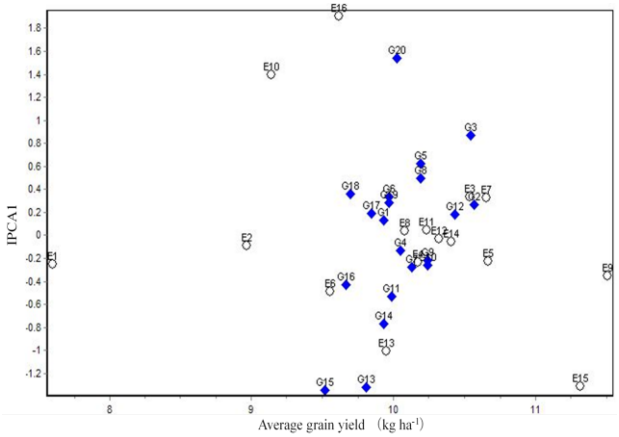

Fig. 1: AMMI-1 biplot for the average grain yield and the first component of interaction (IPCA1) of 20 maize genotypes in 16 environments

Genotype G20 had a larger positive interaction score of IPCA1 (1.54), while G15 had a smaller negative score (-1.35). Therefore, the upper and lower genotypes in the AMMI-1 biplot were adapted to different environments. An environment with a fraction near zero has almost no GE interaction between genotypes and provides a low distinction between genotypes. This pattern was observed some test environments, namely E8, E11, E12 and E14 (Fig. 1). In contrast, the environments E16 and E10 have high interactions across genotypes, providing the highest distinction between genotypes (Fig. 1).

The AMMI-2 Biplot for Genotypes (IPCA1 vs IPCA2)

The AMMI-2 biplot provided a good model explanation for the first two AMMI multiplicative components to evaluate

Table 6: Average grain yield (AGY), interaction principal component analysis (IPCAs) values of 16 tested sites, AMMI stability value (ASV) and environment stability factor (D_j)

Environment	AGY (kg ha^{-1})	Deviation	IPCA1	IPCA2	IPCA3	IPCA4	IPCA5	IPCA6	IPCA7	IPCA8	IPCA9	IPCA10	IPCA11	IPCA12	IPCA13	IPCA14	D_j
E1	7.60	-2.45	-0.25	-0.83	-0.15	-0.41	-0.28	0.12	0.09	0.01	-0.15	0.08	-0.35	0.30	-0.01	0.73	1.35
E2	8.97	-1.08	-0.09	-0.46	-0.06	0.29	0.61	0.34	0.32	0.03	-0.36	-0.13	0.06	0.51	-0.56	0.20	1.29
E3	10.54	0.49	0.33	-0.02	-0.55	0.69	1.33	-0.01	-0.41	0.50	0.66	0.20	-0.04	-0.33	0.26	0.29	1.95
E4	10.17	0.13	-0.24	0.45	0.79	0.25	0.76	-1.10	-0.50	-0.60	-0.44	-0.28	-0.45	0.09	-0.05	-0.15	1.96
E5	10.67	0.62	-0.22	-1.00	-0.28	-0.60	0.39	0.25	0.04	0.32	-0.26	-0.97	0.36	-0.33	0.04	-0.30	1.77
E6	9.56	-0.49	-0.49	-0.14	0.43	0.38	-0.09	-0.67	0.09	0.08	0.11	0.49	1.03	0.18	-0.17	-0.05	1.56
E7	10.66	0.61	0.32	-0.24	-0.13	-0.25	0.45	0.56	0.49	0.02	-0.22	0.83	-0.37	-0.14	-0.26	-0.56	1.51
E8	10.08	0.03	0.04	0.29	-0.09	-0.65	-0.43	-0.27	0.13	-0.53	0.84	-0.14	-0.08	-0.52	-0.65	0.14	1.58
E9	11.51	1.46	-0.35	-0.04	-0.22	0.37	-0.44	0.19	-0.14	0.09	0.93	-0.31	-0.27	0.73	0.12	-0.43	1.52
E10	9.14	-0.91	1.40	-1.23	0.15	-0.69	-0.47	-0.63	-0.29	-0.11	0.00	0.30	-0.01	0.05	0.41	-0.08	2.22
E11	10.24	0.19	0.04	-0.10	-0.11	1.09	-0.26	0.23	1.07	-0.90	-0.08	-0.15	0.05	-0.24	0.45	0.07	1.89
E12	10.32	0.27	-0.03	0.79	-1.73	0.30	-0.71	-0.70	0.07	0.57	-0.52	-0.01	-0.12	-0.07	-0.06	-0.05	2.31
E13	9.95	-0.10	-1.01	1.21	0.14	-1.39	0.39	0.10	0.47	0.04	0.03	0.14	0.10	0.15	0.47	0.08	2.26
E14	10.41	0.36	-0.05	0.44	-0.47	0.02	-0.27	0.97	-1.31	-0.71	-0.30	0.14	0.29	-0.02	0.04	0.01	1.96
E15	11.32	1.27	-1.31	-0.29	1.25	0.50	-0.75	0.25	-0.28	0.68	-0.13	0.12	-0.29	-0.41	0.05	0.01	2.25
E16	9.62	-0.43	1.91	1.17	1.01	0.11	-0.24	0.39	0.16	0.50	-0.11	-0.30	0.10	0.07	-0.06	0.10	2.58

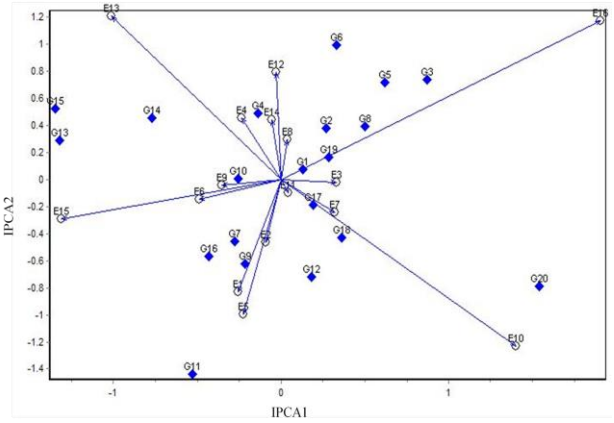

Fig 2: AMMI-2 biplot for genotype by environment interaction of 20 maize genotypes in 16 environments

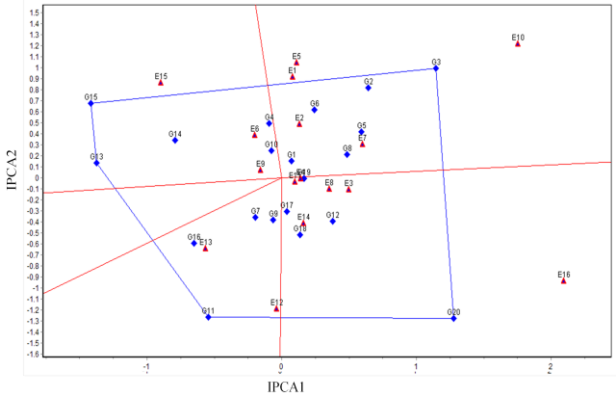

Fig 3: The biplot of first two IPCA components of AMMI model showing "which-won-where" results of 20 maize genotypes in 16 environments

the interaction pattern of the 20 maize genotypes within 16 environments (Fig. 2). AMMI-2 biplot displayed E15, E13, E16, E10, E5 and E1 were the most discriminating tested environments; however, G6, G3, G20, G12, G16, G13 and G15 were the most insensitive genotypes (Fig. 2).

"Which-won-where" View of the AMMI Model to Show the Adaptability of Tested Genotypes

The AMMI biplot can visually identify the best performing genotypes in different test environments. The marking points of each genotype are connected by a straight line to form a polygon containing all the genotypes (Fig. 3). The vertical line of each side is started from the origin and the whole double-marking is divided into several fan-shaped areas. The grain yield of each test hybrids naturally falls within a certain fan-shaped area. In a sectoral area, the "apex angle" hybrid of each area is the best performing genotype in the area. The AMMI biplot analyses of the 20 summer maize genotypes tested it sixteen environments are presented in Fig. 3. The AMMI biplot is divided into five zones, but sixteen test sites are divided into five sectors. The first zone contains 3 pilots (E6, E9 and E15), which performed better with G13 and G15. There were 4 pilots (E1, E2, E7 and E10) in the second sector and the best performing hybrids in the region was G3 (Fig. 3). The third sector contains five pilots, E3, E8, E11, E14 and E16 and genotype G20 was the champion in this region. The two pilots E12 and E13 belonged to the fourth sector, and G11 performed best in this region. No genotypes and environments were found in the fifth sector (Fig. 3).

Discussion

In this study, GEI accounted for 42% of the total squared sum, higher than the environment effect (35%) and much higher than the genotype effect (about 13-fold the genotype effect). All of which reached extremely significant levels suggesting that there may be differences in the

environmental group and GEI was the main factor affecting the grain yield of the tested hybrids. Multi-environment trials data is very common in a mixture of cross-type and non-cross-type of GE. In the current study, large-scale GE interactions lead to more diverse physiological processes that control yield stability in different environments in the genetic system (Sharifi *et al*., 2017). The results of this study indicate that due to the presence of GET, there were differences in yield performance interactions between genotypes across the test environments. The relative contribution of GEI to grain yield in this study was consistent with the findings by other studies (Beleggia *et al*., 2013; Mostafavi *et al*., 2014; Muthoni *et al*., 2015; Dehghani *et al*., 2016).

Compared to other methods (such as joint regression analysis), AMMI model analysis is a very valuable statistical tool for screening for specific or broadly adapted genotypes (Aslam *et al*., 2015; Kumar and Singh, 2015). The combination of regression, genotype regression and environment regression in the linear regression model explained 15.1% of the GEI, and the residual is still large, accounting for 84.9%, indicating that the interaction model explained by the regression model was less, and the regression model is not ideal for fitting the data of this experiment. Among the many genotype and environment interaction analysis models, AMMI-1 is considered to be the best model for accurately assessing changes in GEI data. This shows that the AMMI-1 estimate is closer to the true value production forecast. Therefore, in this dataset, AMMI-1 was a better model for estimating the average genotype yield in each environment (Gauch, 2013). The IPCA1 effect was 3.5 times than that of genotype effect, indicating the importance of IPCA1 in the total GEI. The AMMI biplot can select stable and productive genotypes for different environments and can screen out genotypes with specific suitability (Li *et al*., 2006).

The AMMI-1 biplot depicted a symmetric distribution to evaluate the GEI model and interpret grain yield data. G20 showed a larger positive IPCA1 score and was found to be more adaptable to environment E16 with a larger and identical IPCA1 marker score. According to the D_i stability statistic, G1, G2, G3, G17 and G12 are the most stable genotypes, combination with grain yield performance, genotypes G2 and G3 are among the hybrids with good yield and stability. Their relative rankings vary greatly with the environment, so these genotypes were poorly adaptable (Dehghani *et al*., 2016).

Each test environment also played an important role in the selection of hybrids; as the environments had different discriminative powers for the genotypes (Bose *et al*., 2014). Environment E16 had the strongest resolution and had a good discriminating power for the genotypes. Environment E2 had the weakest discrimination for the genotypes. Each test hybrid had its special adaptability to the test site, and there were also hybrids that were not suitable for planting on different test sites.

The MET of maize are the main way to identify the characteristics, application value and adaptation area of new hybrids and thus provide important basis for the examination and approval of other crop varieties. However, the GET is an interaction between biological characteristics and natural laws. The introduction of the AMMI model and its application in this field indicated that the AMMI model provides a better analytical method for the study of GET and regional trials of varieties (Nzuve *et al*., 2013; Rasul *et al*., 2017). The results of this study further confirmed that the AMMI model not only well explain the interaction between the genotypes and environments on tested maize grain yield but and can also explain the reasons for the differences on grain yield between the tested sites.

Conclusion

Stability analysis helps to identify and screen the most stable and high yielding genotypes that are more suitable for specific environmental conditions. In this study, genotypes Hengyu 147 (H58× H59) and Hengyu321 (H14 × H13) were identified as promising hybrids with average grain yields of 10.57 and 10.54 t ha^{-1}, respectively. Moreover, AMMI model seemed successful to assess the yield performance of different genotypes and recommended in the multi-years and multi-environments in future as well.

Acknowledgement

This research was supported by Appropriate Mechanization of New Summer Maize Variety Breeding, Demonstration and Promotion in North Huanghuaihai (Beijing-Tianjin-Hebei) (2017YFD0101202); Special Fund for National System (Maize) of Modern Industrial Technology (nycytx-02); Science and Technology Support Program of Hebei Province (16226323D-X).

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[Received 14 Jun 2019; Accepted 10 Jul 2019; Published (online) 22 Dec 2019]