SELECTING THE SUPERIOR GENOTYPE OF SUMMER MAIZE HYBRIDS IN MEGA-ENVIRONMENTS USING AMMI MODEL AND GGE BIPLOT IN CHINA

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(Received 12th Dec 2019; accepted 23rd Mar 2020)

Abstract. Effective analysis of genotype by environment interactions (GEI) is helpful to screen stable genotypes in a variety of environments. Therefore, the purpose of this study is to test the stability and adaptability of the agronomic traits of maize hybrids from different ecological environments. Thirteen maize hybrids in twenty-six locations over two years (2017-2018) in Huanghuaihai region was conducted to compare the performance and stability of six agronomic traits using AMMI (additive main effect and multiplicative interaction) model and GGE (genotype, genotype × environment) biplot. The analysis of variance through AMMI model showed that genotype (G), environment (E), and GEI had significant effects on agronomic traits. E explains a larger portion of the total variation in grain yield (GY), ear weight (EW) and 100-grain weight (100-GW), to a much higher degree than GEI and G. However, compared to E and G, GEI contributed more to total variation in ear length (EL), kernel row number (KRN) and bald tip length (BTL). Comprehensive analysis of the AMMI model and the GGE biplot results showed that genotypes G2, G3, and G4 had better agronomic performance and stability than other genotypes and are ideal for planting.

Keywords: *genotype by environment interaction, stability, adaptability, agronomic traits, yield, agronomic traits*

Introduction

Maize (*Zea mays* L.) originated in Central and South America and is an important food crop in the world, widely distributed in the United States, China, Brazil and other countries. In China, maize is used as an important food, feed and industrial raw material. The domestic maize cultivation area was 42 million ha with the annual maize production was 260 million tons in 2017 (Wang et al., 2019). Since 2012, maize has surpassed rice and became China's largest food crop variety (Yang et al., 2019). The Huanghuaihai summer maize region is China's largest concentrated maize production area. The annual planting area accounts for more than 40% of the country's total area, and the planting area accounts for about 32% of the country's total planting area, the total output accounts for about 34% of the country's total output. In recent years, the planting area and yield of summer maize in this region have shown a gradual increasing trend, which plays an important role in ensuring national food security (Yue et al., 2018a). The farming system, soil, fertilizer, variety, cultivation management and climatic factors all have different effects on maize yield (Li et al.,

DOI: http://dx.doi.org/10.15666/aeer/1802_35933614

2019). There is a wide difference in maize yield between the Huanghuaihai region, with an average yield of 5.3 tons/ha, a large area with a high yield of 7.5-9 tons, and a small area with a high yield of 15 tons. For most regions, there is a huge potential for increased production (Huang et al., 2019). High yielding and stable yielding of summer maize has always been one of the research goals of scientists all over the world, and it is also one of the difficulties. Analysis of the high yielding and stability of the representative hybrids, as well as the contribution of various yield components to yield, can effectively guide the production and breeding of maize in the Huanghuaihai region.

Screening and identifying good genotypes are very difficult due to the genotype (G) by environment (E) interaction (GEI). But assessing this interaction is important because it is the primary factor in genotypic performance changes under different environments. The GEI can weaken the association between maize phenotypes and genotype values, and leading to bias in the terms of genotypic effect assessment (Farshadfar et al., 2011; Mohamed, 2013). The GEI can make summer maize genotypes behave differently in different environments, especially in the Huanghuaihai region where the climate is complex and variable (Yue et al., 2019). The selection and breeding of important traits of maize genotypes is complicated by the cross-interaction between hybrids in different environments, and the result is that high-yielding and stable genotypes are easily overlooked (Mulema et al., 2008; Nzuve et al., 2013). In order to breed hybrids that meet people’s living needs, it is necessary to systematically evaluate the yield, resistance and quality of the tested genotypes, and obtain basic data on adaptability, high yielding and stability in different ecological regions, comprehensive evaluation and screen out hybrids with excellent yield traits. At the same time, the discriminative power and representativeness of each testing site are evaluated, and the basis for selecting the ideal site for resource and hybrid screening is provided. Multi-environment trials (Mets) is a well-established method for identifying the high yielding and adaptability of different crop varieties. In the Mets, the newly bred varieties were tested according to uniform specifications, and their important characteristics such as high yield, stability, adaptability, stress resistance and quality were comprehensively identified (Navas-Lopeza et al., 2019).

There were many statistical methods for evaluating the GEI, such as, scientists have earlier proposed the coefficient of variation (CV) (Döring and Reckling, 2018), analysis of variance (ANOVA) (Fry, 1992), principal component analysis (PCA) (Perkins, 1972) and linear regression analysis (LRA) (Kang, 1993), but each method has its shortcomings. The coefficient of variation method describes the stability of genotypes, this method can only explain the difference in genotype effects, and does not explain the environmental effects and the interaction between genotypes and the environment. The study of the stability of the variety by linear regression does not reflect the adaptability of the genotype to the environment. The application of analysis of variance to evaluate the adaptability of genotypes cannot analyze the relationship between environmental effects and interaction effects (Blouin et al., 2015). In recent years, with the deepening of research methods, scientists have proposed two analysis methods of the additive main effects and multiplicative interaction (AMMI) model (Gauch, 1988) and the genotype plus genotype by environment (GGE) biplot (Yan et al., 2000) for GEI research. The AMMI model is a graphically unique linear-bilinear model based on a biplot, combining both the ANOVA and the multiplicative model (Yan et al., 2007). The AMMI model is an effective tool for studying genotypic stability analysis and distinguishing the environment, and has been successfully applied to the research of various crops (Suwaero et al., 2011; Mortazavian et al., 2014; Ndhlela et al., 2014; Raggi et al., 2017; Mehdipour et al., 2019). The GGE biplot takes into account the G and GE effects and can simultaneously evaluate genotypes and the environments. At the same time, the GGE biplot gives information on the genotype and environment and their relationship, including determining the best variety in a particular environment, the most appropriate environment for a particular variety, and the performance of any two varieties in different environments. Which variety is a high yielding and stable yield. Which environment is conducive to the screening the varieties with high yielding and stable yield (Yan, 2001; Kaya et al., 2006; Dehghani et al., 2017; Oral et al., 2018).

In this study, the multi-environment test was conducted to analyze the yield and yield component traits of 13 tested maize hybrids using the AMMI model and GGE biplot data through the data of 26 test sites for 2 consecutive years, and the genotype-environment interaction effect was evaluated. The actual effect of maize grain yield and yield components, and the comprehensive yield components screen out excellent hybrids. At the same time, the GGE biplot is used to analyze the representativeness and discriminative power of the test sites.

Material and methods

Data of 13 tested genotypes used were maize hybrids recently approved by the National Crop Variety Approval Committee (NCVAC), including one check hybrid Zhengdan958 (G13), were evaluated in 26 locations during two consecutive years (2017-2018 growing seasons) in Huanghuaihai region, and the basic information of tested genotypes is given in *Table 1*. In this study, there were 26 testing sites in the multi-environment trials (Mets), which were derived from seven provinces of Hebei province, Shanxi province, Henan province, Shandong province, Anhui province, Jiangsu province and Shanxi Province. Agro-climatic description and the code of testing sites is given in *Table 2*.

Table 1. *The description of the tested maize hybrids and its code in this study*

Cultivars	Code	Plant type	Female	Male	Ear axis color	Year
Weike702	G1	Compact	WK858	WK798-2	White	2017-18
Liyu86	G2	Semi-compact	L5895	L5012	Red	2017-18
Nonghua101	G3	Compact	NH60	S121	Red	2017-18
Liangyu99	G4	Compact	M03	M5972	Red	2017-18
Meiyu5	G5	Compact	M2325	M1826	Red	2017-18
Nonghua032	G6	Semi-compact	7P402	LS121	Red	2017-18
Wugu704	G7	Compact	6320	WG5603	Red	2017-18
Mingyu19	G8	Semi-compact	M84	M71	White	2017-18
Tunyu808	G9	Semi-compact	T88	T172	White	2017-18
Luyu36	G10	Semi-compact	LZM2-18	LZF4	White	2017-18
Xianyu335	G11	Compact	PH6WC	PH4CV	Red	2017-18
Denghai605	G12	Compact	DH351	DH382	Red	2017-18
Zhengdan958	G13	Compact	Z58	C7-2	White	2017-18

Table 2. *The agro-climatic description of the sites in the trials in 2017-2018*

Sites	Province	Code	Longitude	Latitude	Altitude (m)	Sowing date	Harvest date
Luquan	Hebei	E1	114°18′	38°05′	155	12 June	10 Oct.
Xingtai	Hebei	E2	114°30′	37°08′	102	13 June	11 Oct.
Anping	Hebei	E3	115°21′	38°18′	25	11 June	10 Oct.
Wuqiang	Hebei	E4	115°15′	38°16′	18	13 June	11 Oct.
Wuqiao	Hebei	E5	116°20′	37°43′	55	13 June	11 Oct.
Yuanshi	Hebei	E6	114°49′	37°77′	165	14 June	12 Oct.
Gaoyang	Hebei	E7	115°38′	38°30′	408	15 June	13 Oct.
Yuncheng	Shanxi	E8	110°35′	35°29′	226	9 June	4 Oct.
Yongqiao	Anhui	E9	116°95′	33°65′	48	6 June	1 Oct.
Taihe	Anhui	E10	115°30′	33°10′	12	5 June	30 Sep.
Qianxian	Shanxi	E11	108°12′	34°26′	520	4 June	1 Oct.
Xinxiang	Henan	E12	113°92′	35°30′	70	5 June	2 Oct.
Zhoukou	Henan	E13	114°69′	33°62′	49	3 June	1 Oct.
Runan	Henan	E14	114°23′	33°10′	80	3 June	30 Sep.
Fangcheng	Henan	E15	113°12′	33°29′	155	2 June	3 Oct.
Fugou	Henan	E16	114°75′	33°60′	52	2 June	1 Oct.
Wenxian	Henan	E17	112°51′	34°52′	105	3 June	2 Oct.
Anyang	Henan	E18	113°45′	36°02′	68	7 June	5 Oct.
Ningjin	Shandong	E19	116°38′	37°41′	35	11 June	9 Oct.
Linqing	Shandong	E20	115°59′	36°36′	35	8 June	7 Oct.
Laizhou	Shandong	E21	119°95′	37°17′	56	8 June	5 Oct.
Weishan	Shandong	E22	116°35′	34°28′	38	4 June	2 Oct.
Lanling	Shandong	E23	117°48′	34°57′	75	7 June	5 Oct.
Dongping	Shandong	E24	116°12′	35°76′	56	8 June	5 Oct.
Peixian	Jiangsu	E25	116°57′	34°38′	35	1 June	30 Sep.
Siyang	Jiangsu	E26	118°29′	33°26′	15	1 June	1 Oct.

We used the randomized block design with three repetitions in each testing site, and the experimental plot contained five lines (6.7 m long). The width between each line is 0.7 m, and the sowing density was used 7,5000 plants in per hectare which is widely used in local agricultural production. The grain yield (GY) was calculated in the middle three rows of each plot when harvested by manual harvesting. The two side rows were used to sample the ear length (EL), ear row number (ERN), bald tip (BT), kernel weight (KW) and 100-grain weight (100-GW). The fertilization situation of each plot depends on the soil nutrient analysis results of the plot.

Statistical analysis

AMMI model

The formula for the AMMI model was used (Gauch, 1992):

$$y_{ge} = \mu + \alpha_g + \beta_e + \sum_{n=1}^{N} \lambda_n \gamma_{gn} \delta_{en} + \theta_{ge} \qquad \text{(Eq.1)}$$

where y_{ge} represents the value of the genotype (g) in the environment (e); μ is the grand mean; is the average deviation of the *g*th genotype from the grand mean; is the average deviation of the *e*th environment from the grand mean; is the *n*th eigenvalue of interaction principal component axis (IPCA); and are the genotypic and environmental principal component score representing the *n*th principal component, respectively; is the error term. The AMMI model can also be used to rank genotypes in accordance with yield stability of the tested varieties. The AMMI stability values (ASVs) calculation can be performed according to the formula of Purchase (Purchase et al., 2000).

$$\mathrm{ASV} = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}}(IPCA_1)\right]^2 + (\mathrm{IPCA}_2)^2} \qquad \text{(Eq.2)}$$

In the formula, SS_{IPCA1} and SS_{IPCA2} are the sum of squares of interaction principal component analysis 1 (IPCA1) and IPCA2, respectively.

GGE biplot

The GGE biplot is called the principal component analysis of environmental centralization. After subtracting the average value of the environment from the original data, the genotype is singularly decomposed in the interaction effect, and the formula as follows:

$$Y_{ge} - y_e = \lambda_1 \xi_{g1} \eta_{e1} + \lambda_2 \xi_{g2} \eta_{e2} + \varepsilon_{ge} \qquad \text{(Eq.3)}$$

where Y_{ge} is the value of the *g*th genotype in the *e*th environment; y_e is the yield performance of all genotypes in the *e*th environment; ξ_{g1} and ξ_{g2} are the first and second principal component scores of the *g*th genotype in the *e*th environment, respectively; λ_1 andλ_2 are the eigenvectors of the first and second principal components, respectively; η_{e1} andη_{e2} represent the first and second eigenvector scores of the *e*th environment, respectively; ε_{ge} is the residuals in the model (Balestre et al., 2009).

Data analysis

In this study, the effects of the genotypes, environments and their interactions were calculated by analysis of variance (ANOVA) using Data Processing System (DPS) software (Tang and Zhang, 2013) in the AMMI model. The GGE biplot analysis using the Genstat 64-bit Release (Payne et al., 2013) to select the optimal environments and superior genotypes.

Results

Variations in six agronomic traits

It can be seen from *Figure 1* that the agronomic traits are significantly different. The coefficient of variation of the six agronomic traits is between 5.08 and 77.97%, with an average of 20.18%, and the coefficient of variation of the bald tip length is the largest. Statistics on six agronomic traits of thirteen hybrids in the twenty-six tested environments are shown in *Table 3*. The grain weight varied between 7227.91 and 12321.56 kg/t across environments, the ear length and bald tip length are between 12.85-21.35 cm and 0.00-9.90 cm, respectively. The change range of ear weight and 100-grain weight are between 103.00-214.25 g and 24.25-42.30 g, respectively. The minimum and maximum values of the kernel row number are 12.00 and 17.60, respectively. Further statistical values for six agronomic traits can also be seen from *Table 3*.

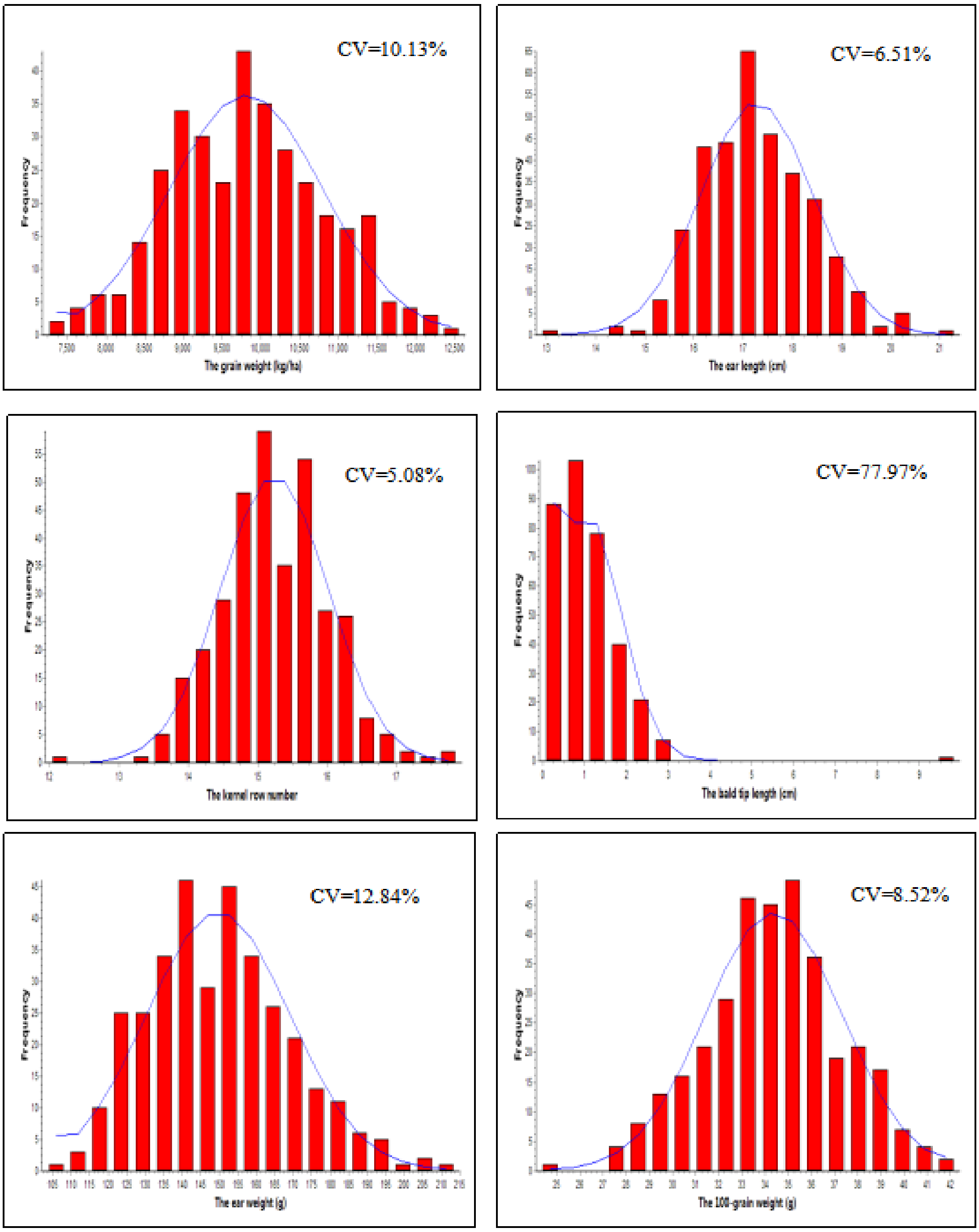

***Figure 1.** Normal distribution map of agronomic traits of tested hybrids. CV: coefficient of variation*

DOI: http://dx.doi.org/10.15666/aeer/1802_35933614

Table 3. *Statistical value of each agronomic trait*

Agronomic traits	NS	Min	Max	Mean	AD	R	V	STD	SEM
Grain weight (kg/ha)	338	7227.91	12321.56	9807.43	804.05	5093.64	987716.60	993.84	54.06
Ear length (cm)	338	12.85	21.35	17.27	0.88	8.50	1.27	1.13	0.07
Kernel row number	338	12.00	17.60	15.24	0.61	5.60	0.60	0.77	0.04
Bald tip length (cm)	338	0.00	9.90	1.04	0.56	9.90	0.65	0.81	0.04
Ear weight (g)	338	103.00	214.25	149.70	15.36	111.25	369.71	19.22	1.05
100-grain weight (g)	338	24.25	42.30	34.38	2.31	18.05	8.58	2.93	0.16

NS: Number of samples; Min: minimum; Max: Maximum; AD: Average deviation; R: range; V: variance; STD: Standard deviation; SEM: Standard error of mean

The AMMI model analysis

The results of AMMI model analysis exhibited the variations across mega-environments and genotype by environment interaction (GEI) had a significantly differences ($P < 0.001$, $P < 0.01$ and $P < 0.05$) for tested maize hybrid agronomic traits in 2017-2018 (*Table 4*). The genotype (G) and environment (E) of each agronomic trait had very highly significant effects ($P < 0.001$). The GEI effects on grain yield, bald tip length and 100-grain weight also reached very highly significant effects ($P < 0.001$). The GEI effects on ear length exhibited highly significant effects ($P < 0.01$), and there are significant differences ($P < 0.05$) were observed for kernel row number and ear weight. Furthermore, the AMMI model analysis decomposed the SS of GEI into eight interaction principal component axes (IPCAs), of which the first four IPCAs exhibited very highly significant differences ($P < 0.001$) for all agronomic traits. In terms of the ratio of the variance to the total SS, among the three agronomic traits of grain yield, ear weight and 100-grain weight, environmental effects accounted for 57.48%, 66.62% and 50.52% of the total sum of squares, respectively. The GEI as a second main effect contributed to 47.89%, 54.74% and 44.48% of the total sum of squares of ear length, kernel row number and bald tip length, respectively. Among all the six agronomic traits, genotype effects accounted for the lowest proportion. The first four IPCAs explained 64.62%, 70.71%, 65.22%, 84.41%, 69.72% and 62.97% of the interaction sum of squares of grain yield, ear length, kernel row number, bald tip length, ear weight and 100- grain weight, respectively, with IPCA1 contributing 22.23%, 30.82%, 21.30%, 60.42%, 25.74% and 19.71%, in which greater than other IPCAs.

The IPCA values, average performance of the agronomic traits and the ASV values of the tested maize hybrids are presented in *Table 4*. The IPCA value for a specific genotype in the AMMI model indicates the stability of this genotype throughout the environment. The difference in IPCA values (positive or negative) shows the genotype adapted to the specific environment, and the closer the IPCA value is to zero, the more stable the adaptation to the environment (Gerrano et al., 2019). Genotypes vary widely in yield performance between traits. The average grain yield of the genotypes G7 and

G9 was the lowest and highest in different environments, 9304 kg/ha and 10222 kg/ha, respectively. Other genotypes such as G1, G2, G3, G4, G5 and G8 have higher grain yields. Genotypes G8 and G10 are 16.11 cm and 18.20 cm, which are the worst and best hyrids of ear length, respectively. The performance range of the kernel row number of the tested hybrids was 14.36 to 15.66, which belonged to G4 and G3, respectively. The lightest of the bald tip length is G12, which is 0.38 cm. In contrast, bald tip length of genotype G6 has the highest value of 1.65 cm. Genotypes such as G10 and G5 is the champion of ear weight and 100-grain weight, respectively, and the yield performance is 159.00 g and 36.56 g, respectively.

Table 4. *The performances of IPCA1 to IPCA8 for interaction effect components of 6 agronomic traits of 13 maize hybrids*

Trait	Genotype code	Trait yield	IPCA1	IPCA2	IPCA3	IPCA4	IPCA5	IPCA6	IPCA7	IPCA8	ASV
Grain yield (kg/ha)	G1	9803	8.78	24.00	-27.02	18.61	-2.09	5.57	-29.72	-7.43	27.08
	G2	10237	-2.72	16.29	-8.32	3.01	-25.97	5.99	16.79	14.07	16.74
	G3	10088	9.25	1.47	-15.11	-5.32	21.55	10.44	16.20	-13.33	13.29
	G4	10208	4.02	-12.05	16.54	-13.49	-10.46	-3.34	-20.94	16.01	13.35
	G5	10112	-23.60	17.49	-12.64	-24.14	17.63	-28.38	4.22	6.68	37.97
	G6	9736	1.98	1.33	23.78	-18.90	-11.98	-6.96	-8.68	-29.05	3.12
	G7	9304	10.66	-18.14	-17.84	-16.81	5.14	6.88	-8.35	7.09	23.68
	G8	10157	-10.17	-11.36	9.07	-9.73	15.86	31.43	1.26	3.63	18.44
	G9	10222	-46.17	-21.51	2.09	29.58	3.03	-4.80	-3.48	-3.70	69.34
	G10	9204	26.09	12.69	28.50	22.56	25.78	-9.11	1.24	11.11	39.35
	G11	9417	2.45	8.89	6.04	7.35	-9.74	2.02	14.70	-14.88	9.55
	G12	9257	26.45	-33.56	-14.12	9.15	-11.18	-17.41	10.40	-0.49	50.53
	G13	9753	-7.03	14.46	9.03	-1.89	-17.57	7.68	6.36	10.29	17.6
Ear length (cm)	G1	16.87	0.38	0.50	0.69	-0.57	-0.67	0.21	0.56	-0.46	0.84
	G2	17.28	0.00	0.51	-0.15	0.03	-0.34	0.81	0.43	0.07	0.51
	G3	17.33	0.22	-0.18	0.72	0.09	0.77	-0.59	0.50	0.58	0.43
	G4	17.47	1.30	-0.97	-0.03	0.43	-1.12	-0.52	-0.44	0.30	2.50
	G5	17.69	0.86	-0.01	0.54	0.26	0.59	-0.01	-0.37	-0.77	1.53
	G6	17.19	-0.42	1.15	0.09	0.17	-0.57	0.30	-0.47	0.23	1.37
	G7	17.00	0.21	0.99	-0.11	1.16	0.41	-0.38	0.30	0.10	1.06
	G8	16.11	1.20	-0.25	-0.99	-0.86	0.50	0.23	0.29	-0.24	2.16
	G9	17.63	-0.44	0.09	0.39	-0.48	0.47	0.10	-1.24	-0.07	0.79
	G10	18.20	-0.72	0.14	0.11	-1.10	-0.12	-0.69	0.15	0.53	1.28
	G11	17.56	-0.79	-1.35	0.67	0.37	0.14	0.94	0.25	0.22	1.94
	G12	17.16	-1.50	-0.49	-0.52	0.25	-0.27	-0.69	0.23	-0.88	2.72
	G13	17.08	-0.29	-0.14	-1.41	0.25	0.22	0.29	-0.20	0.39	0.53
Kernel row number	G1	15.30	0.16	-0.43	-0.13	-1.11	0.24	0.22	-0.14	0.60	0.83
	G2	15.52	-0.44	0.45	0.76	0.58	0.74	-0.29	0.18	-0.34	0.98
	G3	15.66	0.73	-0.55	0.13	0.10	-0.34	-0.83	-0.20	0.22	1.25
	G4	14.36	0.64	-0.78	-0.49	0.89	0.23	0.84	0.49	0.06	0.59
	G5	15.01	0.26	0.01	0.14	-0.14	0.63	-0.04	0.06	-0.22	1.60
	G6	15.43	0.17	-0.66	0.55	-0.69	-0.27	0.29	-0.08	-1.00	1.73
	G7	15.51	0.23	-0.35	0.42	0.56	-0.49	-0.10	-0.30	0.36	9.48

	G8	15.11	-0.13	0.07	0.07	0.09	0.24	-0.83	-0.11	0.17	0.89
	G9	15.63	0.28	0.57	-1.15	-0.35	0.13	-0.46	0.66	-0.19	2.28
	G10	15.07	-0.32	0.61	0.75	-0.31	0.25	0.60	0.28	0.59	2.21
	G11	15.38	-1.79	-0.61	-0.42	0.09	-0.51	-0.05	0.19	0.02	3.83
	G12	15.21	-0.16	0.53	-0.76	0.21	0.30	0.41	-1.17	-0.16	3.35
	G13	14.94	0.35	1.14	0.12	0.06	-1.15	0.25	0.15	-0.09	1.43
Bald tip length	G1	1.48	-2.61	0.22	0.06	0.03	0.12	0.05	0.07	0.03	15.90
	G2	0.85	0.08	-0.34	0.11	-0.49	0.20	0.02	-0.09	-0.64	0.62
	G3	0.74	0.22	0.15	0.31	-0.51	-0.10	-0.97	0.56	0.08	1.37
	G4	1.13	0.49	0.85	-0.29	0.03	0.23	-0.13	-0.36	0.13	3.08
	G5	1.56	0.11	0.24	-0.68	0.40	-0.14	-0.19	-0.21	-0.69	0.69
	G6	1.65	0.01	-0.61	-0.64	-0.10	-0.95	0.25	0.30	0.13	0.61
	G7	0.82	0.15	-0.44	0.20	0.17	0.32	0.50	0.09	0.13	0.99
	G8	1.08	0.33	0.72	0.64	0.82	-0.48	0.13	0.20	0.05	2.15
	G9	0.69	0.35	0.28	-0.08	-0.52	-0.03	0.47	-0.13	0.16	2.13
	G10	1.20	0.01	-0.92	0.50	0.42	-0.08	-0.47	-0.67	0.18	0.92
	G11	1.23	0.20	-0.12	-0.89	0.22	0.54	-0.20	0.10	0.49	1.22
	G12	0.38	0.15	0.26	0.39	-0.68	-0.18	0.23	-0.40	0.16	0.98
	G13	0.66	0.52	-0.27	0.37	0.21	0.54	0.30	0.55	-0.20	3.17
Ear weight (g)	G1	149.00	3.03	3.54	2.49	0.33	-1.24	-1.63	1.46	-0.41	5.48
	G2	151.90	4.09	-4.60	-1.76	-2.15	1.00	-2.17	-1.77	-0.15	7.27
	G3	149.10	1.55	0.32	1.72	-0.37	2.77	0.49	0.54	-1.92	2.17
	G4	155.90	-0.88	-3.51	3.57	2.27	1.33	-0.06	-0.04	3.32	3.71
	G5	152.30	-4.74	0.26	0.58	-0.44	-2.04	0.34	-1.86	1.53	6.54
	G6	150.50	1.46	0.12	-2.15	-4.41	-2.33	0.65	1.15	1.87	2.02
	G7	144.20	0.48	1.67	-4.62	2.78	0.52	0.77	2.35	1.74	1.80
	G8	142.70	0.02	2.44	1.56	-2.07	3.57	2.32	0.31	0.65	2.44
	G9	153.1	-2.11	2.47	-3.18	1.53	2.08	-2.42	-2.65	-0.57	3.82
	G10	159.00	-5.07	-3.01	-0.87	-1.33	0.17	1.01	2.08	-2.79	7.61
	G11	143.30	-1.05	2.62	2.10	-1.38	-1.92	-1.25	-1.33	-0.70	2.99
	G12	148.90	2.94	-0.72	-0.33	2.63	-2.15	4.28	-2.30	-1.50	4.12
	G13	146.30	0.28	-1.61	0.88	2.62	-1.76	-2.31	2.06	-1.08	1.65
100-grain weight (g)	G1	32.86	1.23	-0.67	0.62	-1.13	0.03	-1.64	-0.12	1.09	1.66
	G2	33.49	1.05	-0.85	0.48	1.28	1.13	-0.33	-0.24	-0.87	1.56
	G3	34.57	-1.67	0.20	0.42	0.02	-0.14	0.07	-1.97	0.01	2.09
	G4	36.47	-0.37	-0.94	-2.21	0.66	0.72	-0.14	-0.18	0.95	1.05
	G5	36.56	0.78	-0.40	-0.02	-1.15	-0.13	1.93	-0.13	0.69	1.05
	G6	34.35	0.63	0.86	1.51	0.72	0.46	0.19	0.18	0.29	1.17
	G7	32.54	0.63	0.09	-0.26	0.36	0.35	0.48	-0.43	-0.89	0.79
	G8	35.68	0.18	-0.76	-0.83	-0.90	-0.52	-0.07	0.69	-1.38	0.79
	G9	35.27	0.35	-0.57	0.62	0.13	-1.34	0.50	0.06	0.06	0.71
	G10	34.11	-2.07	-1.14	0.86	0.02	-0.46	-0.45	0.79	-0.16	2.81
	G11	32.57	0.24	1.90	-0.76	-1.02	-0.35	-0.80	-0.39	-0.58	1.93
	G12	35.24	-1.11	1.11	0.17	-0.64	1.55	0.36	1.09	0.22	1.77
	G13	33.16	0.14	1.16	-0.58	1.65	-1.30	-0.10	0.66	0.56	1.17

IPCA: Interaction principal component axes; ASV: AMMI stability value

In the AMMI model, genotypes with lower ASV values are considered to be more stable. Therefore, genotypes G6 and G11 have better stability of grain yield than other maize hybrids. By the same method and so on, the genotypes G3, G2, and G13 have better stability in ear length performance, G4, G1, G8, and G2 belong to the genotypes with better stability of ear row number, genotypes G6, G2, and G5 belong to the hybrids with better stability in bald tip length. We can also see from *Table 4* that genotype G13 followed by G7 and G9 followed by G8, G7, which belong to the hybrids with better stability of ear weight and 100-grain weight, respectively.

The adaptive analysis using GGE biplot

The “who-wins-where” views of the GGE biplot of grain yield, ear length, kernel row number, bald tip length, ear weight and 100-grain weight are shown in *Figure 2a, b, c, d, e* and *f*. The biplot consists of genotypes that are furthest from the origin in the same direction, and all genotypes are included. The biplot is divided into several sectors by vertical lines from the origin to the sides of the polygon, and the test sites fall in different areas in the sector. Test sites in the same sector are considered to have similar yield performance to genotypes, and these sites also belong to the same ecological group. In the same way, genotypes located in the same sector are considered to have similar performance to the environments of this sector. In the biplot, the genotype at the “vertex” position is considered to be the best-performing genotype in this sector (Duma et al., 2019).

GGE biplot analysis showed that the first two principal components (PC1 + PC2) accounted for 54.27%, 54.88%, 46.62%, 77.56%, 49.65% and 59.14% of the total variation in GEI of grain yield, ear length, kernel row number, bald tip length, ear weight and 100-grain weight, respectively. For grain yield, G9, G12, G10, G1, and G2 are connected into a polygon, and the five rays divide the polygon into 5 sectors. The first sector contains the test sites E1, E2, E5, E9, E10, E14, E15, E16, E17, E18, E20, E21, E23, E24 and E25, genotype G9 has the highest yield performance. There are no sites in the second, third, and fourth sectors, indicating that the “vertex” genotypes G12, G10, and G1 of these sectors did not perform well in all the sites. The fifth sector contains the remaining sites, with G2 performing best (*Fig. 1a*). For ear length, PC1 and PC2 in the GGE biplot explained 36.60% and 18.28% of the total variation of GEI, respectively. In this biplot, it can be divided into four ecological groups. The first ecological group contains twelve test sites, environments E2, E4, E5, E6, E7, E8, E10, E12, E14, E16, E19, and E23 fell into the first ecological group, environments E1, E11, E15, E20, E21 and E24 belong to the second ecological group, E13 fell into the third ecological group, and E3 and E9 belong to the fourth ecological group. The genotypes G10, G4, G8 and G12 belong to the champion hybrids of the first to fourth ecological regions, respectively (*Fig. 1b*). For kernel row number, PC1 contributed 31.48% while PC2 accounted for 15.14% of the total variation. This biplot consisted of three ecological group; where E1, E2, E5, E6, E8, E9, E10, E13, E15, E16, E19, E20, E22, E24 and E26 belong to the first ecological group; E23 fell in one group; the remaining sites are combined belong to the third ecological group. Genotype G11 had the highest yielding performance in the first ecological group, G12 was the winner in the second ecological group, whereas genotype G7 was the vertex hybrid in the third group (*Fig. 1c*). For bald tip length, the percentages of 53.10% and 24.46% are attributed to PC1 and PC2, respectively. In this biplot, only two ecological groups were found;

where E10 and E18 belong to one group; the remaining sites were divided into another group. Genotype G1 and G6 in the first and second ecological group are the vertex genotypes, respectively, which had the most bald performance (*Fig. 1d*). For ear weight, PC1 and PC2 accounted 30.63% and 19.02% of GEI, respectively. GGE biplot for ear weight grouped E2, E4, E12, E13, E14, E15, E16, E18, E19, E21, E24 and E25 as the first group and E1, E5, E6, E7, E8, E10, E20 and E22 belong to the second group. E26 and E1, E9, E9 were found in the third and fourth group, respectively. Genotypes G10, G2, G1 and G5 were found suited for the first to fourth group, respectively (*Fig. 1e*). For 100-grain weight, PC1 accounted for 48.16% of the variation caused by GEI, while PC2 accounted for 10.98% (*Fig. 1f*). Genotype G4 had the highest 100-grain weight performance in E1, E2, E5, E7, E9, E11, E12, E14, E16, E17, E18 and E22. No genotypes fell on E16, indicating that all genotypes did not perform well on E16. Genotype G5 was the top-ranking hybrid at the remaining sites.

Mean performance and stability analysis of the tested genotypes using GGE biplot

The use of the first two principal components axises formed a biplot related to genotypic performance. GGE biplot is an effective tool for assessing two aspects (mean performance and genotypic stability). The longer the vertical line of the genotype relative to axis 1, the lower the stability, and the longer the distance between the genotype and axis 2 (vertical to axis 1), indicated the higher yield (Badu-Apraku et al., 2012). *Figure 3* showed the average environment coordinate (AEC) of the GGE biplot of the agronomic traits of the tested hybrids. Thus, the genotypes G3, G4, G5, G8 and G13 had high grain yield combined with high stability. Genotypes G6 and G11 had good stability, however, these genotypes had no promising performance with grain yield. Based on these interpretations, although G9 has a high grain yield, it has poor stability and is not an ideal genotype (*Fig. 3a*). Genotypes G3, G9, G10 and G11 had longer ear length and good stability, whereas G4, G5 and G12 were highly unstable with longer ear length performance. Genotypes G4 and G5 had higher ear length performance, but had poor stability (*Fig. 3b*). The mean kernel row number of tested genotypes were arranged in the following order: G11 > G5 > G3 > G10 > G2 > G7 > G1 > G4 > G8 > G6 > G13 > G9 > G12. The performance of genotypes G7 and G11 had the worst stability, whereas genotypes G5, G3 and G10 were highly stable with high kernel row number (*Fig. 3c*). Genotype G6 had the highest mean bald tip length, followed by G5, G1, G11, etc.; and G12 had the lowest mean bald tip length. In terms of stability, genotype G2 was the most stable hybrid whereas, G1 was the least stable genotype (*Fig. 3d*). G13 was the most stable genotype with an average ear weight performance. Genotypes G2, G5 and G10 were the most unstable with a high average performance of ear weight (*Fig. 3e*). The biplot showed the ranking of 13 tested maize genotypes based on their average 100-grain weight and stability performance (*Fig. 3f*). The 100-grain weight performance of genotype G5 was the highest and that of G11 was the lowest among all 13 tested genotypes. From the perspective of crop breeding, breeders prefer genotypes with high average yield and high stability as potential ideal genotypes. In the biplot, the more stable genotype should be close to the average environment (the center of the small circle), and it should also have the shortest vector (Bai et al., 2014). Based on this information, although G5 had the highest 100-grain yield performance among all the genotypes, it is still less stable compared with genotypes G7, G8 and G9.

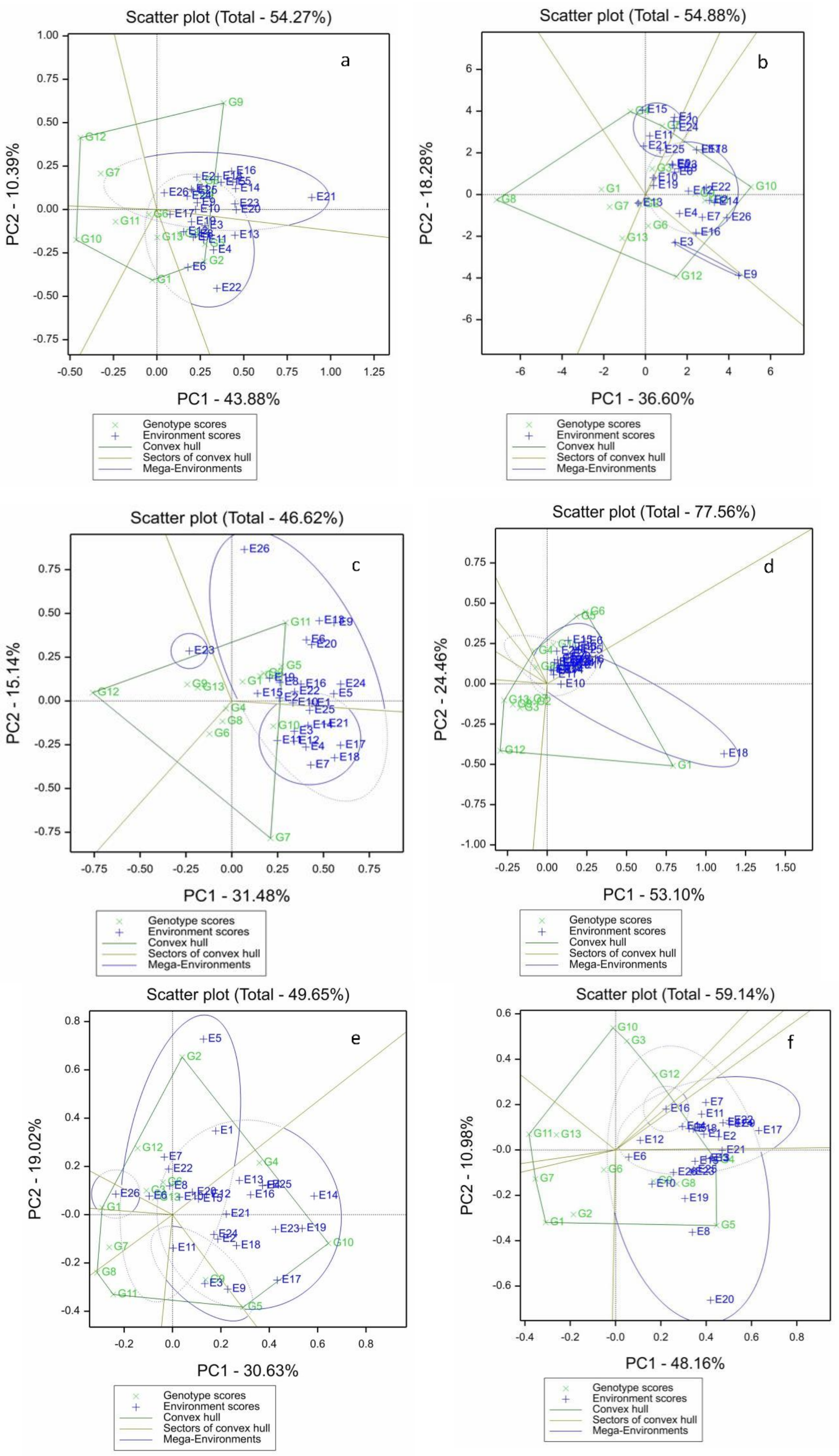

Figure 2. *The "who-wins-where" view for agronomic traits of the GGE biplot of 13 maize hybrids in 26 environments to display which genotype performs best in which environment. See Table 1 for genotypes and Table 2 for environments codes. a: grain yield; b: ear length; c: kernel row number; d: bald tip length; e: ear weight; f: 100-grain weight (the same as below)*

DOI: http://dx.doi.org/10.15666/aeer/1802_35933614

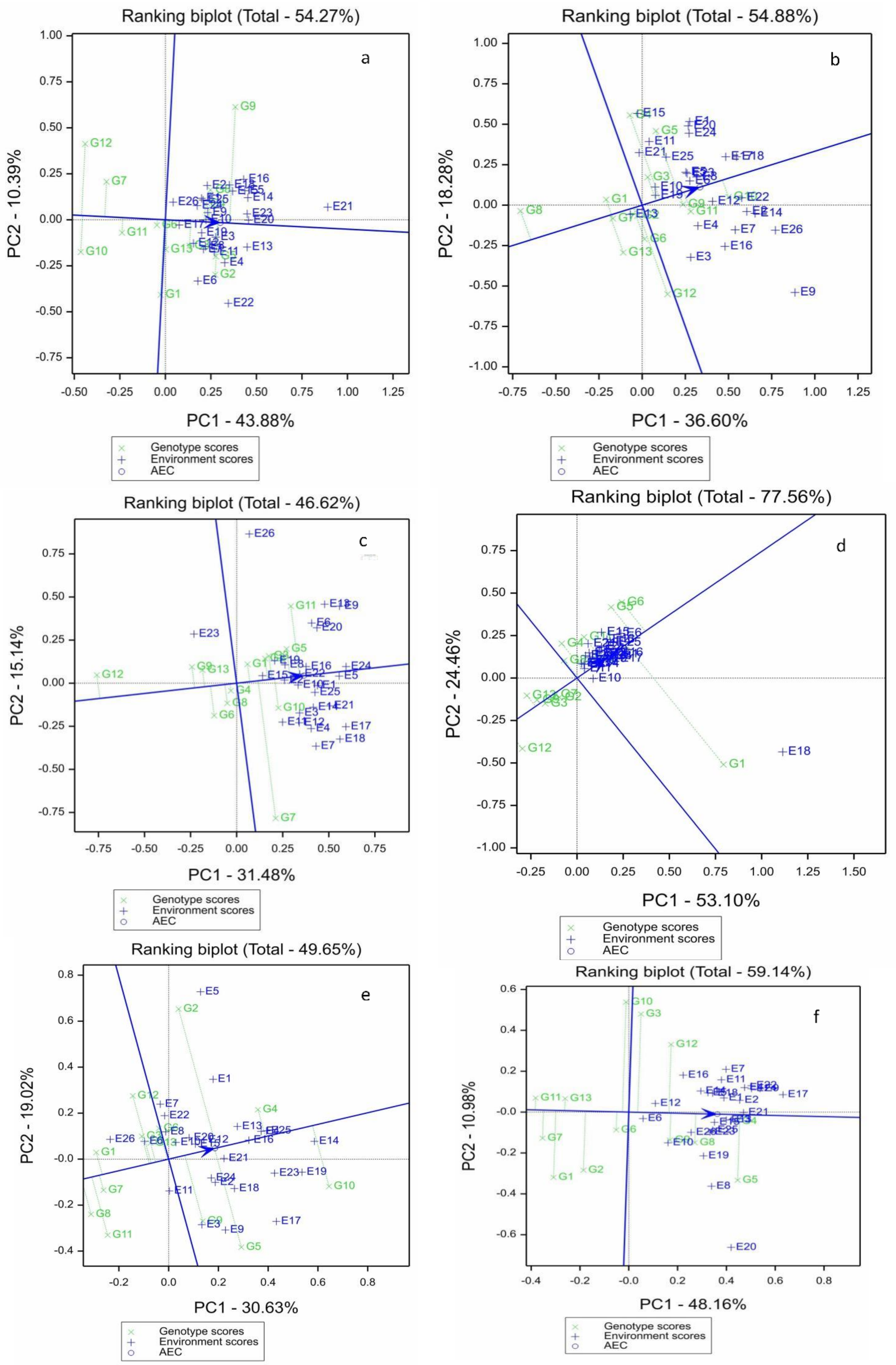

Figure 3. *The mean performance and stability of the tested 13 maize hybrids evaluated in 26 environments using GGE biplot*

Judging the best genotypes based on the GGE biplot

The concept of 'ideal genotypes' should show high yielding and stability within a mega- environments (Yan and Tinker, 2006). However, we know that ideal genotypes do not exist in reality. Studies have also shown that, compared to average performance and stability, different concentric circles were drawn to help clearly distinguish the distance between each genotype and the ideal genotype, the distance between a genotype and an ideal genotype is also an important parameter for evaluating genotype performance. The closer the genotype is to the center of the circle (the position of ideal genotype), the better the average yield and stability of this genotype. On the contrary, being far away from the center of the circle represents the worst performance of this genotype is defined as the undesired genotype (Erdemci et al., 2018). Based on these, the genotypes G5 and G2 were located on the innermost concentric circle of the biplot, and are closer to the center of the circle than other genotypes. Therefore, these two genotypes (G5 and G2) can be considered as the genotypes closest to the ideal genotypes. In addition, genotypes G6 and G8 were located on the next concentric circle, and these two genotypes were considered desirable genotypes in terms of grain yield. In contrast, genotypes G10 and G12 were located on the outermost concentric circles, which are farther from the center of the concentric circles than other genotypes, may be regarded as undesirable genotypes (*Fig. 4a*). Given that the genotype G10 was located near the first concentric circle and closer to the ideal genotype position, it can be used as the genotype closest to the ideal genotype for evaluation in terms of ear length. Next to genotype G10, compared to other maize hybrids, G9 and G11 were the more desirable genotypes. On the other side, genotype G8 belong to the undesirable hybrid and implying poor performance in all environments (*Fig. 4b*). Genotype G5 belong to the most favorable genotype owing to was closest to the center of the concentric circle, whereas, G12 had the worst performance of kernel row number (*Fig. 4c*).

In the first circle, genotype G15 was found. Therefore, this was an ideal genotype in terms of obtaining a higher average bald tip length and good stability in the tested environments. Genotype G12 was located in the last circle, with the worst average baldness length and general stability compared to other tested maize genotypes (*Fig. 4d*). According to *Fig. 4e*, genotype G10 was highly "ideal", followed by genotypes G4, G5, G9, etc., and these genotypes can be considered as desirable genotypes. On the other hand, G1, G7, G11 and G8 were very poorest for average ear weight, classify them as undesirable genotypes in all environments. Compared with other maize genotypes, G4 fell into the center of concentric circles was ideal genotype, with higher 100-grain weight and good stability. In addition, next to G4 were the genotypes G5, G8 and G9, which were considered as the promising genotypes. In contrast, G11 was the furthest from the center of the circle, followed by genotypes G7, G1, G13, and G2, which were considered the least promising genotypes (*Fig. 4f*).

Discussion

In view of the vast area of the Huang-Huai-Hai region and as the largest area of centralized maize cultivation in China, it is particularly important to test and evaluate the stability and adaptability of different maize genotypes before large-scale planting (Yue et al., 2018). The performance of maize agronomic traits was affected by multiple factors, such as the genotype itself, environmental conditions, and the interaction between genotype and environment. Compared with genotype (G) and environment (E), the genotype by environment interaction (GEI) was the most difficult to grasp and control due to its uncertainty. The expression of many traits, such as crop yield, ear length, 100-grain, etc., were significantly affected by the GEI, and it effects on yield will affected yield stability directly. If the GEI effect was greater, the genotypes' stability was worse. Genotypes with high yielding and stable under multi-environmental trials (Mets) generally had broad adaptability and great value for promotion and utilization, genotypes with poor yielding and unstable but had special adaptability to local environments also had high recommendation. Screening and evaluating high-yielding and stable genotypes in various of environments has been an ongoing challenge for agronomy breeders worldwide (Lin et al., 1992; Alwala et al., 2010). The analysis of the Mets data of most genotypes were based on the data of a single trait (such as yield, quality or resistance), but multiple traits need to be considered simultaneously during the breeding practice. The conclusion based on the comprehensive analysis of single trait components is more important than the conclusion of single trait analysis (Kendal et al., 2016a). According to the analysis of single-yield traits of hybrid maize, only genotype total yield data can be obtained. ear length, ear row number, bald tip length, ear weight and 100-grain weight data and the main factors affecting these data cannot be obtained from the total yield. The purpose of Mets was to identify superior genotypes under different environments. Because of the existence of unpredictable environmental factors, researchers have developed different analytical models (GE, GEI, GGE, AMMI) to explain the effects of genotype, environment, and their interactions. So far, the AMMI model and the GGE biplot were the recommended methods for analyzing the GEI effect across the mega-environments (Kendal et al., 2019). According to reports, the AMMI model was a comprehensive and effective method because it can classify genotypes based on the genotype level combined with the target environment and classify them according to their advantages and disadvantages in different environments. Compared with other methods (such as joint regression methods), this model was a valuable statistical tool for identifying genotypes with specific or broad adaptability, which may be an important advantage of this method. On the other hand, the GGE biplot has been successfully used in Mets of various crops, which can concisely and effectively distinguish the best performing genotypes in the entire environment, so that specific genotypes can be recommended to specific large environments and the yield and stability were fully evaluated (Kendal et al., 2016b).

In this study, the AMMI model analysis indicated that the main effect of G, E and GEI were important among agronomic traits (*Table 5*). By analyzing the proportions of G, E, and GEI of the total variation, the six traits can be divided into two categories. The first category was grain yield (GY), ear weight (EW) and 100-grain weight (100-GW). These three agronomic indicators reflect a phenomenon that the proportion of environment effect was the greatest, followed by GEI and G, which ranged from 3.89-, 11.37- and 2.37-fold the genotype effect for GY, EW and 100-GW, respectively. This suggesting that maize breeders can either choose to set a specific genotype for each environment, or can choose excellent genotypes in a wide range of environments. Correspondingly, ear length (EL), kernel row number (KRN) and bald tip length (BTL) belong to the second category. This type of agronomic traits reflected the largest proportion of the total variation was GEI effect, followed by E and G, which ranged from 2.68-, 6.00- and 2.10- fold the genotype effect for EL, KRN and BTL. It has often been shown in the Mets that agronomic traits variations due to GEI effect exceed that due to genotypes effects (Dehghani et al., 2016).

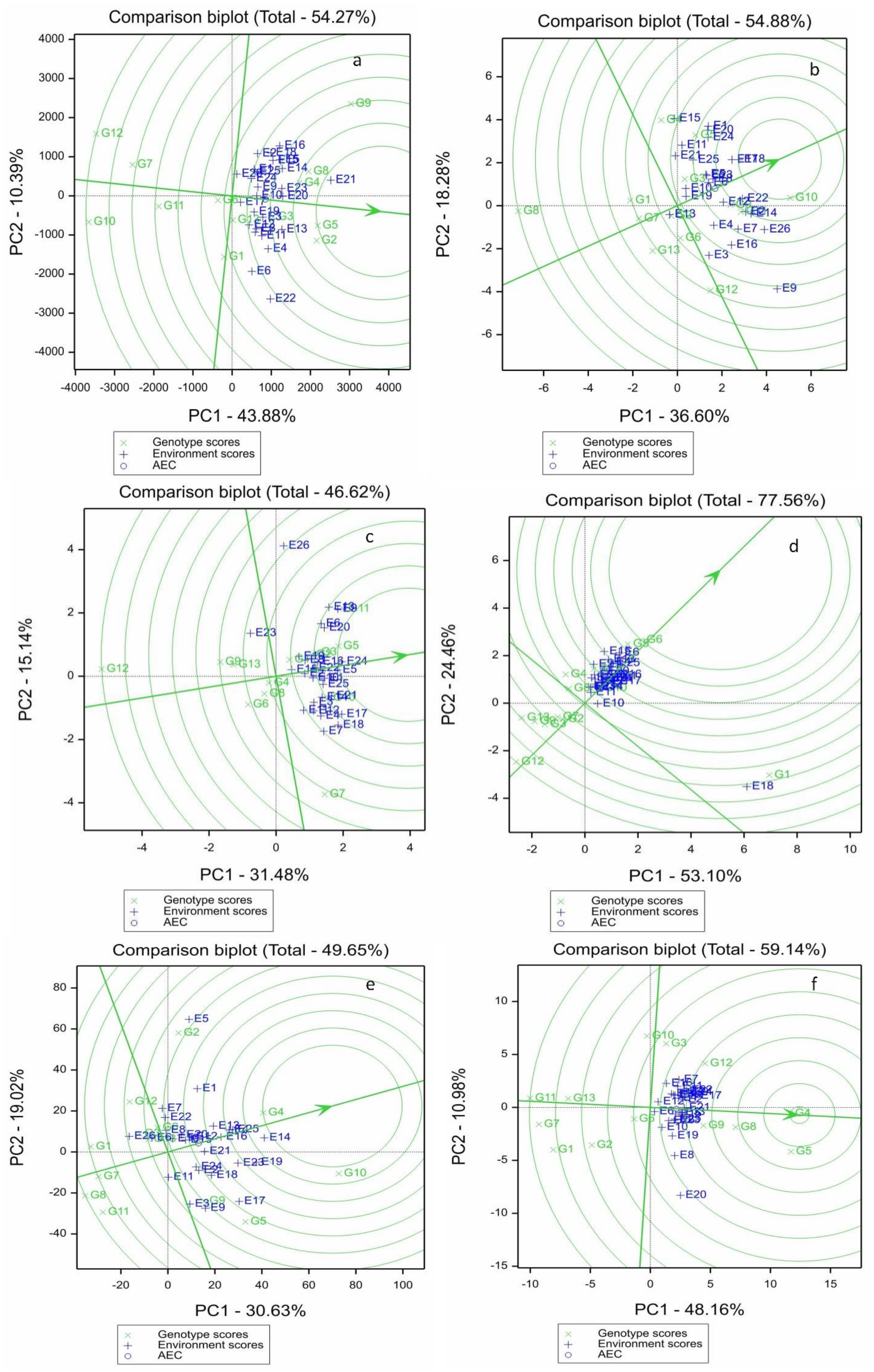

***Figure 4.** Comparison of distance between tested genotypes and ideal genotype in GGE biplot*

Table 5. *Analysis of variance of 13 maize hybrids in 26 environments for agronomic traits using the additive main effects and multiplicative interaction (AMMI) model analysis in China*

Traits	Source	DF	SS	MS	*F*	%SS	*P* value
Grain yield (kg/ha)	Total	337	332860498	987716.6			
	Genotype (G)	12	49171359	4097613	13.31***	14.77^{a}	< .001
	Environment (E)	25	191327413	7653097	24.86***	57.48^{a}	< .001
	Genotype and environment interaction (GEI)	300	92361726	307872	1.15***	27.75^{a}	< .001
	IPCA 1	36	20532503	570347	6.19***	22.23^{b}	< .001
	IPCA 2	34	14379975	422940	4.59***	15.57^{b}	< .001
	IPCA 3	32	12681392	396293	4.30***	13.73^{b}	< .001
	IPCA 4	30	11615878	387196	4.20***	12.58^{b}	< .001
	IPCA 5	28	10161779	362921	3.94***	11.00^{b}	< .001
	IPCA 6	26	6494016	249770	2.71***	7.03^{b}	< .001
	IPCA 7	24	5800433	241685	2.62**	6.28^{b}	0.0012
	IPCA 8	22	4426879	201222	2.18**	4.79^{b}	0.0076
	Residuals	68	6268872	92189		6.79^{b}	
	Error	262	70130640	267674.2			
Ear length (cm)	Total	337	426.73	1.2662			
	Genotype (G)	12	76.17	6.347	9.32***	17.85^{a}	< .001
	Environment (E)	25	146.19	5.848	8.58***	34.26^{a}	< .001
	Genotype and environment interaction (GEI)	300	204.36	0.681	1.34**	47.89^{a}	0.0072
	IPCA 1	36	62.98	1.749	7.85***	30.82^{b}	< .001
	IPCA 2	34	35.38	1.041	4.67***	17.31^{b}	< .001
	IPCA 3	32	26.89	0.84	3.77***	13.16^{b}	< .001
	IPCA 4	30	19.26	0.642	2.88***	9.42^{b}	< .001
	IPCA 5	28	15.14	0.541	2.43**	7.41^{b}	0.0016
	IPCA 6	26	12.56	0.483	2.17**	6.15^{b}	0.0058
	IPCA 7	24	10.14	0.422	1.89*	4.96^{b}	0.0211
	IPCA 8	22	6.84	0.311	1.39^{ns}	3.35^{b}	0.1495
	Residuals	68	15.16	0.223		7.42^{b}	
	Error	262	132.89	0.5072			
Kernel row number	Total	337	202.15	0.5998			
	Genotype (G)	12	38.92	3.2437	8.79***	9.12^{a}	< .001
	Environment (E)	25	51.22	2.0489	5.55***	12.00^{a}	< .001
	Genotype and environment interaction (GEI)	300	110.66	0.3689	1.16*	54.74^{a}	0.0270
	IPCA 1	36	23.57	0.6547	5.76***	21.30^{b}	< .001
	IPCA 2	34	20.53	0.6038	5.31***	18.55^{b}	< .001
	IPCA 3	32	16.07	0.5021	4.42***	14.52^{b}	< .001
	IPCA 4	30	12.01	0.4005	3.52***	10.85^{b}	< .001
	IPCA 5	28	10.83	0.3867	3.40***	9.79^{b}	< .001
	IPCA 6	26	9.7	0.3732	3.28***	8.77^{b}	< .001
	IPCA 7	24	5.63	0.2344	2.06*	5.09^{b}	0.0105
	IPCA 8	22	4.60	0.2091	1.84*	4.16^{b}	0.0294
	Residuals	68	7.73	0.1136		6.99^{b}	
	Error	262	83.9685	0.3205			

Bald tip length (cm)	Total	337	219.9935	0.6528			
	Genotype (G)	12	46.65	3.8874	11.92^{***}	21.21^{a}	< .001
	Environment (E)	25	75.49	3.0195	9.26^{***}	34.31^{a}	< .001
	Genotype and environment interaction (GEI)	300	97.86	0.3262	2.30^{***}	44.48^{a}	< .001
	IPCA 1	36	59.13	1.6424	34.09^{***}	60.42^{b}	< .001
	IPCA 2	34	9.70	0.2852	5.92^{***}	9.91^{b}	< .001
	IPCA 3	32	8.14	0.2544	5.28^{***}	8.32^{b}	< .001
	IPCA 4	30	5.64	0.1882	3.9^{***}	5.76^{b}	< .001
	IPCA 5	28	3.95	0.1412	2.93^{***}	4.04^{b}	< .001
	IPCA 6	26	3.82	0.1471	3.05^{***}	3.90^{b}	< .001
	IPCA 7	24	2.48	0.1033	2.14^{**}	2.53^{b}	0.0075
	IPCA 8	22	1.71	0.0778	1.61^{ns}	1.75^{b}	0.0688
	Residuals	68	3.28	0.0482		3.35^{b}	
	Error	262	37.17	0.1419			
Ear weight (g)	Total	337	124591.40	369.71			
	Genotype (G)	12	7297	608.10	5.32^{***}	5.86^{a}	< .001
	Environment (E)	25	83004	3320.20	29.05^{***}	66.62^{a}	< .001
	Genotype and environment interaction (GEI)	300	34290	114.30	1.2501^{*}	27.52^{a}	0.0318
	IPCA 1	36	8826	245.20	5.73^{***}	25.74^{b}	< .001
	IPCA 2	34	6403	188.30	4.40^{***}	18.67^{b}	< .001
	IPCA 3	32	4895	153.00	3.58^{***}	14.28^{b}	< .001
	IPCA 4	30	3783	126.10	2.95^{***}	11.03^{b}	< .001
	IPCA 5	28	2540	90.70	2.12^{**}	7.41^{b}	0.0062
	IPCA 6	26	2132	82.00	1.92^{*}	6.22^{b}	0.0171
	IPCA 7	24	1492	62.20	1.45^{ns}	4.35^{b}	0.1165
	IPCA 8	22	1310	59.60	1.39^{ns}	3.82^{b}	0.1506
	Residuals	68	2908	42.80		8.48^{b}	
	Error	262	23956.31	91.44			
100-grain weight (g)	Total	337	2892.55	8.58			
	Genotype (G)	12	616.2	51.35	18.90^{***}	21.30^{a}	< .001
	Environment (E)	25	1461.4	58.45	21.52^{***}	50.52^{a}	< .001
	Genotype and environment interaction (GEI)	300	815	2.72	1.01^{***}	28.18^{a}	< .001
	IPCA 1	36	161.1	4.48	4.66^{***}	19.77^{b}	< .001
	IPCA 2	34	129.5	3.81	3.97^{***}	15.89^{b}	< .001
	IPCA 3	32	116.1	3.63	3.78^{***}	14.25^{b}	< .001
	IPCA 4	30	106.4	3.55	3.70^{***}	13.06^{b}	< .001
	IPCA 5	28	75.2	2.68	2.80^{***}	9.23^{b}	< .001
	IPCA 6	26	64.7	2.49	2.60^{***}	7.94^{b}	< .001
	IPCA 7	24	50.7	2.11	2.20^{**}	6.22^{b}	0.0059
	IPCA 8	22	46.1	2.09	2.18^{**}	5.66^{b}	0.0076
	Residuals	68	65.2	0.96		8.00^{b}	
	Error	262	640.43	2.44			

df: degree of freedom; SS: sum of squares, a: Percentage of total SS; b: Percentage of sum of squares of GEI; MS: mean square; IPCA, Interaction principal component axes; *, **, *** significant at $P < 0.05$, $P < 0.01$ and $P < 0.001$, respectively; ns: non-significant ($P > .05$)

The effect of GEI on agronomic traits can be confirmed by the ear length of each genotype varied from 12.85 cm (corresponding to G8 at environment E26) to 21.35 cm (corresponding to G11 at environment E18) (*Table 3*), it was shown that the ear length performance of 13 genotypes in 26 environments had considerable variation. Further analysis of the AMMI model, in the face of different parameters, because of the stability analysis using multiple IPCA numbers, it was better than the stability analysis using the first IPCA score. Hence, combined with the ASV results in this study, G9 had a higher performance of GY, but the worst stability. However, G6 had the best stability, the GY was moderate. According to comprehensive analysis, genotypes G2, G3, G4 and G8 were high yielding with outstanding stable in GY. Similarly, genotypes G2, G3 and G4 also showed better agronomic performance and stability in agronomic traits, like EL, KN, GTL, EW and 100-WG compared with other genotypes. In production practice, genotypes with showing good adaptability in agronomic traits across all the environments were favored by plant breeders. Conceptually, successful genotypes not only had high agronomic trait values, but also showed good stable performance in different ecological environments (Mohammadi et al., 2017). However, we should not ignore those genotypes that had special adaptability to individual environments. For instance, genotypes showed higher EL (i.e. G8 at environment E13 and G12 at environments E3, E9), genotype G5 showed higher EW at environments E3, E9 and E11. Because of the existence of GEI, both the AMMI model and GGE biplot could well explore the variations in Mets data, and the two methods had proven to be similar in practice, which leads to basically the same conclusion (Mitrovic et al., 2012; Vaezi et al., 2017; Yue et al., 2020).

Conclusions

This result of research revealed that agronomic traits like GY, EW and 100-GW of tested maize hybrids were highly influenced by E effect, followed by GEI effect and G contributed the least, other agronomic traits EL, KRN and BTL were highly influenced by GEI effect, followed by E effect and G. For the maize agronomic traits GY, EL, KRN, EW and 100-GW, the larger the field performance value, the more the breeder likes, but the BTL was just the opposite. The results of the GEI study indicated that the environments in this research had an opposite effect on genotypes performance. For instance, genotypes G2 and G5 had opposite results for 100-KW in the tested environments. Genotypes G2, G3 and G4 showed the best performance and stability in agronomic traits. These genotypes could be considered as the desirable hybrids with similar ecological region. It turns out that the AMMI model and GGE biplot were approximately equal for the analysis results of this study, and thus the conclusions of the genotypes with the highest agronomic performance and stability were basically the same. Considering the enormous impact of environment and genotype by environment interactions on agronomic traits of summer maize hybrids, maize breeders across China are encouraged to conduct further experiments in more seasons and elsewhere in agro-climatic regions.

Acknowledgements. This research was supported by the National Natural Science Foundation of China (31601386).

Conflict of interests. The authors declare no conflict of interests.

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