GGE Biplot-Based Evaluation of Yield Performance of Barley Genotypes across Different Environments in China

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ABSTRACT

The yield performance of 23 barley (*Hordeum vulgare* L.) genotypes in sixteen test environments across a barley growing region of China was evaluated. The experiment was conducted using a randomized complete block design with three replicates, in two cropping seasons (2010-2011, in the South; 2012-2013, in the North). The GGE biplot was applied to analyze the data obtained in the multi-environment trials. The results indicated that either the North or South test sites could be grouped into three possible mega-environments, the best- performing and candidate genotypes for the North and South were G7 (Zhongsimai1), G5 (08B26), G17 (G231M004M), and G13 (Zhe3521), respectively. Among the sixteen test environments, E6 (Shihezi) and E12 (Yancheng) had the greatest discriminating ability, while E1 (Haerbing), E4 (Shang kuli), E8 (Wuhan), and E16 (Chengdu) could be dismissed from the future trials due to the similarity of their ability of discrimination and representation.

Keywords: Discriminating ability, Genotype main effect, Multi-environment trial, Stability.

INTRODUCTION

Barley (*Hordeum vulgare* L.) is the fourth cereal crop following wheat, rice, and maize in the world (Lai and Feng, 2012). It is widely cultivated around the world because of its moderate resistance to barren soil, salinity and drought conditions. Barley is used as a raw material in processing, as forage grain, as well as staple food. With the rapid rise and development of malt barley and beer malt industries, feed barley, and animal husbandry industries, the importance of barley production has already been highlighted in China. However, the planting area of barley in China has been reduced from 1.7 million hectares in the 1990s to around 650,000 hectares due to the impact of economic benefits in recent years (Li, 2012). What's worse, with the arable land gradually decreasing, barley has to compete with wheat, corn, and potato for the limited land. Therefore, it is necessary to increase the barley gross production mostly through breeding new varieties with both high and stable yield, as well as wide adaptation. In order to identify the high and stable yielding cultivars, it is important to conduct Multi-Environment Trials (MET). The high stable yield and adaptability of varieties are mainly evaluated by arithmetic mean method in regional tests, which are generally conducted as multi-location two-year experiments and the data is used for joint variance analysis, estimating pooled error,

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and comparing significant differences among varieties (Gao, 2008; Rezene *et al.*, 2014; Rahnejat and Farshadfar, 2015). Usually, the candidate genotypes, which were integrated with good and comprehensive character, can be chosen directly by multi-trait in the typical test (Jin and Bai, 1999; Lin, 2000; Bai *et al.*, 2014; Yan *et al.*, 2007a), In addition, the representativeness and discernment of test sites (the sites ability to distinguish various species) was also an essential part of analyzing yield stability and variety adaptability.

Additive Main Effects and Multiplicative Interaction (AMMI) model has been widely applied in analysis of data obtained from MET (Zhang *et al.*, 1997; Mortazavian *et al.*, 2014; Yan *et al.*, 2007b; Rezene *et al.*, 2014; Lule *et al.*, 2014), however, it only allows one to study the interaction between Genotype and Environment (GE). The yield of each cultivar in each test environment is a sum of Environment main effect (E), Genotype main effect (G), and Genotype×Environment interaction (GE). Moreover, G and GE must be considered simultaneously when making cultivar selection decisions. For this reason, instead of trying to separate G and GE, Yan *et al.* (2000) combined G and GE and referred to Genotype main effect (G) and Genotype by Environment interaction (GGE) model. The methodology based on this model, called the GGE biplot methodology, has been recommended and used widely by many scientists (Akbarpour *et al.*, 2014; Yan *et al.*, 2001; Yan, 2002; Yan and Tinker, 2005; Sha *et al.*, 2006).

In this study, GGE-biplot methodology was adopted to illustrate its usefulness in evaluating the national multi-location barley trials. The main objectives were: (1) To evaluate the performance stability of 23 barley genotypes under sixteen environmental conditions; (2) To examine the representativeness and discriminating ability of the sixteen test environments, and (3) To evaluate the yield performance of 23

genotypes through comparisons with an ideal genotype.

MATERIALS AND METHODS

Barley Varieties and Experimental Design

In this study, a total of 23 barley cultivars varieties were studied during the growing season of 2010 and 2011 (11 entries) in national barley regional test of South China winter barley (10 sites), and 2012 and 2013 (12 entries) North China spring barley region (6 sites). Geographic, agricultural and weather characteristics of the testing environments are summarized in Table 1. The cultivars were planted in a randomized complete block design with three replicates in plots of 5×2 m². The plot area included eight rows of 5 m long and 20 cm spacing and the seeds were sown using hand drill. Sowing dates ranged from 25 March to 10 April in North China depending on the onset of the growing season, and the seeding rate was 375 kg ha⁻¹; in South China, the sowing dates ranged from 13 October to 15 November depending on the onset of the growing season, and the seeding rate was 225 kg ha⁻¹. Among other test sites, E5 and E6 were irrigated farming land, the water was supplied twice during the growing season (2×120 mm), and all agronomic managements were implemented equally as per the recommendation.

Statistical Analysis

Combined Analysis Of Variance (ANOVA) was conducted for average yields of the barley varieties tested separately for each region. (Yield data was shown in Table 2 & 3). The main effects of Environment (E), Genotype (G), and GE interaction were determined with the software of statistical package for social sciences (SPSS, Version 17; SPSS Inc., Chicago, USA) (Tables 4 and 5). After detecting the GE interaction (P test

Table 1. Geographic, agricultural and weather characteristics of the testing environments in China.

Location	Code	Longitude	Latitude	Altitude	Annual average temperature	Annual rainfall (mm)
North 2012-2013 Haerbing	E1	E130°10'	N 46°40'	127.95	5.2	523
Hohhot	E2	E111°4'77.69"	N40°29'28.01"	1040.0	7.9	331.1
Hong Xinglong	E3	E134°35'	N47°17'	232.9	3.6	525.3
Shang Kuli	E4	E121°49'	N53°26'	1100.0	-3.5	300
Huang Yangzhen	E5	E103°5'	N 37°30'	1776.0	7.2	160
Shihezi	E6	E86°00'	N 44°18'	450.8	8.1	225
South 2010-2011 Hangzhou	E7	E 120°12'	N30°16'	60.0	17.2	1473
Wuhan	E8	E 113°41'	N 29°58'	23.3	16.3	1256
Baoshan	E9	E99°10'12.01"	N 25°0.08'	1635.0	15.5	700
Yuxi	E10	E101°16'	N 23°19'	1630.0	19.8	667.3
Xiangyang	E11	E112°00'	N 31°54'	77.0	16.0	831.3
Yancheng	E12	E119°57'	N 32°0.85'	5.0	15.1	970
Taizhou	E13	E 119°38'24"	N 32°01'0.57"	5.0	16.0	990
Zhumadian	E14	E 115°12'	N 32°18'	90.0	15.3	971
Hefei	E15	E116°25'0.01"	N39°55'0.01"	50.19	16.3	1015
Chengdu	E16	E104°06'	N 30°67'	500.0	16.0	1003.2

Table 2. Yields (kg ha^{-1}) of barley cultivars evaluated at various locations of North China in the growing season 2012-2013.

Cultivar	Season	Code	Environment					
			Haerbing	Hohhot	Hong Xinglong	Shang Kuli	Huang Yangzhen	Shihezi
			E1	E2	E3	E4	E5	E6
Kenpi7	12-13	G1	4191	6498	4059	1477	7863	10900
Ganpi7	12-13	G2	4662	5119	3987	2778	7967	6800
10PJ-24	12-13	G3	4282	6618	3507	3583	7313	5966
Hong08-764	12-13	G4	4669	7181	3996	1914	7823	5600
08B26	12-13	G5	4863	6503	4401	3111	7450	6500
P10-6	12-13	G6	4428	4758	3462	1027	7900	4100
Zhongsimai1	12-13	G7	4609	6676	2880	2094	7113	7533
09GW-01	12-13	G8	3849	7431	3646	1956	6923	6400
9821	12-13	G9	4653	4509	3946	1441	7953	7066
Hong 00-801	12-13	G10	4444	6101	3825	2925	6723	5266
P11-1	12-13	G11	3951	5583	3588	708	5780	4266
Ganpi6	12-13	G12	4017	5151	3752	1989	7640	5466

Table 3. Yields (kg ha^{-1}) of barley cultivars evaluated at various locations of South China in the growing season 2010-2011.

Cultivar	Season	Code	Hangzhou E7	Wuhan E8	Baoshan E9	Yuxi E10	Xiangyang E11	Yancheng E12	Taizhou E13	Zhumadian E14	Hefei E15	Chengdu E16
											Environment	
Zhe3521	10-11	G13	6070	4786	4263	5002	6300	6571	7266	6093	5262	3988
Zhe0892	10-11	G14	6012	5644	2787	4446	6436	5544	6466	6055	5913	4456
Yangnongpi5	10-11	G15	6049	5410	4249	3597	6625	5892	7366	5703	6525	4089
2008pin22	10-11	G16	5350	5185	4587	5188	6219	7156	6900	5445	6475	4083
G231M004M	10-11	G17	6637	5682	4467	5535	7384	7518	6733	6721	6799	3427
Zhudamai7	10-11	G18	5287	5398	2403	3600	6492	5736	5833	6519	6400	3741
Supi3	10-11	G19	5974	5464	3862	3784	6243	6669	6666	6204	6438	4191
Yan99175	10-11	G20	6124	5431	3195	3549	6052	6384	6133	6073	5662	3619
Edamai83	10-11	G21	5763	5548	5118	3708	6405	5229	5433	5130	5850	3822
Fen18-11	10-11	G22	6138	3757	4075	4738	6924	7975	6567	6426	6312	3409
Hua2759	10-11	G23	5287	5322	2062	4234	6726	5910	6466	4981	5838	3921

significance), the data were graphically analyzed to interpret adaptability and stability using the GGE biplot software (Yan *et al.*, 2000). The GGE biplot methodology is composed of two components: the biplot concept (Gabriel, 1971) and the GGE concept (Yan *et al.*, 2000). The detailed description of the principles of GGE-biplot can be found in the review of Yan and Tinker (2006). The graphs were generated based on: (1) "Which wins-where" (which is best for where) pattern; (2) Ranking of genotypes on the basis of yield and stability; (3) Comparing test environments on the basis of discriminating ability and representativeness, and (4) Ranking of genotypes with respect to the highest yielding environment and an ideal genotype, respectively.

RESULTS AND DISCUSSION

Polygon View of the GGE Biplot Analysis

The results of the combined ANOVA for barley yield indicated that the effects of all sources of variations were highly significant (P< 0.01) for both North and South China (Tables 4 and 5). The GE interaction explained about one-fifth of the total yield variation among G×E combinations, and the environments contributed more to the total variation in North and South regional tests. To explore the possible existence of mega-environments within the regions, a polygon graph for North and South was constructed to visualize the interaction patterns between genotypes and the test environments (Figure 1). The genotypes that had the longest vectors were connected with straight lines. The yields of these genotypes were either the highest or lowest in one or more test environments. The vertices of the polygon were G1 (Kenpi7), G9 (9821), G6 (P10-6), G11 (P11-1), G3 (10PJ-24), and G7 (Zhongsimai1) for North China (Figure 1A). The rest of genotypes were contained within the polygon and had shorter vectors,

Table 4. Combined analysis of variance of grain yield in 11 barley cultivars tested across 10 test sites within South China in the season 2010-2011.

Source	df	SS	MS	F
Environment	9	1599311.86	177701.32	282.37**
Genotype	10	116412.51	11641.25	18.50**
GE interaction	90	391533.52	4350.37	6.91**
Error	200	125864.55	629.32	
Total	329	2298621.69		

** Denotes significant effects at $P< 0.01$.

Table 5. Combined analysis of variance of grain yield in 12 barley cultivars tested across 6 test sites within North China in the season 2012-2013.

Source	df	SS	MS	F
Environment	5	3012110.16	602422.03	602254.74**
Genotype	11	220639.45	20058.13	20052.56**
GE interaction	55	592486.40	10772.48	10769.49**
Error	144	144.04	1.00	
Total	216	27709087.90		

** Denotes significant effects at $P< 0.01$.
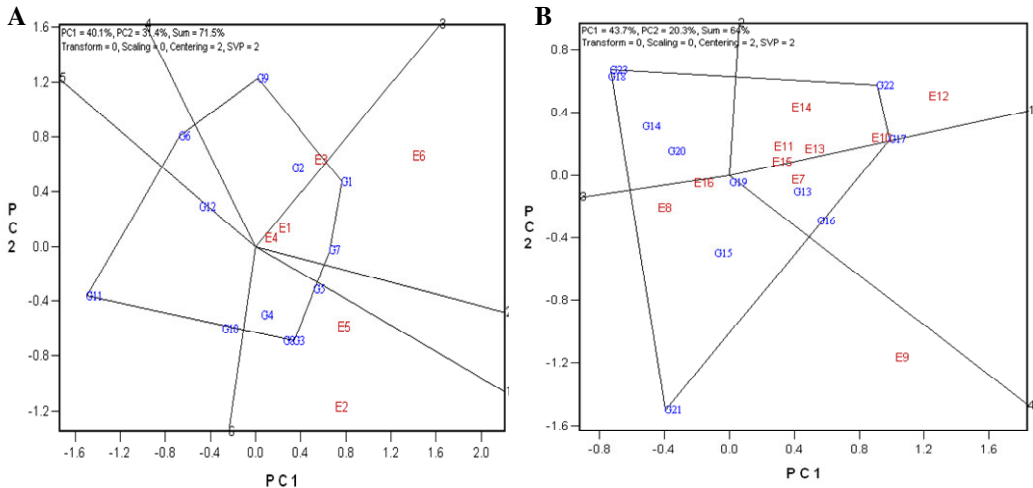
Figure 1. The GGE biplot analysis to show the yields of different barley genotypes with the best performance in different testing environments. Symbols E1-16 represent the sixteen environments and G1-23 represents the 23 barley genotypes. The plot is based on an environment-centered (Center= 2) G by E table without any scaling and transforming of data (Scaling= 0, Transform= 0), and it is Environment-Metric Preserving (SVP= 2). (A) North China, (B) South China.

suggesting that they were relatively less responsive to the interaction with the environments. The equality lines, which originate from the center of biplot and are perpendicular to the sides of polygon, divide the graph into six sectors. The partitioning of GE interaction through GGE biplot analysis showed that the first and second Principal Components (PC1 and PC2) together could explain 71.5% of the total variation. From the polygon view of biplot analysis, the genotypes fell into six sections and the test environments could be grouped into three sections (Sections 2, 3 and 6), suggesting that North trial regions could be divided into three environments and that the

preferred genotypes probably that adapt to each environment could be evaluated. The genotype G1 (Kenpi7), G9 (9821), and G3 (10PJ-24) were the winner in Section 2, 3 and 6, respectively. Thus, G1 (Kenpi7), G9 (9821) and G3 (10PJ-24) could be considered as the adaptable genotypes for E6 (E1 and E4), E3, as well as the mega-environment E2 (E5). The vertices of the polygon for South (Figure 1B) were G17 (G231M004M), G22 (Fen18-11), G23 (Hua2759), and G21 (E damai83). The equality line divided the graph into four sectors, and ten test environments fell into three groups. Thus, G22 (Fen18-11), G21 (Edamai83) and G17 (G231M004M) could be considered as the adaptable genotypes for E12 (E10, E11, E13, E14, and E15), E8 (E16), and E7.

Average Yield and Stability Performance of Barley Genotypes

The yield and stability of the genotypes were evaluated with the Average Environment Coordination (AEC) (Figure 2). The abscissa of AEC is defined by a line that passes through the origin of biplot and the average of all test environments (small circle on the line) (Yan and Rajcan, 2002). The ranking of 12 barley genotypes from North regional trial was based on their average yields and stability performance (Figure 2-A). The direction of AEC abscissa pointed to the higher average yield across different environments. Thus, the yield of G1 (Kenpi7) was the highest and that of G11 (P11-1) was the lowest among others. The ordinate of AEC was the double arrowed line that passes through the biplot origin and perpendicular to AEC abscissa. It was used to determine the stability of the genotypes and both arrows pointed to poorer stability. Therefore, the genotype stability was higher and environment had less influence on the yield performance if the vector of genotype on AEC abscissa was shorter. For a potential elite genotype, the high mean yield and high stability are preferred. In Figure 2-A, the potential genotypes should be those which are close to the average environment (the center of the small circle in Figure 2-A) and have the shortest vector from AEC abscissa. Although G1 (Kenpi7) has the highest yield among all environments (Figures 1-A and 2-A), it is less stable when compared to G7 (Zhongsimai1) and G5 (08B26). In addition, the mean yield of G7 (Zhongsimai1) and G5 (08B26) is very close to the average environment. It suggests that the GE interaction somehow impacts the yield stability of G1 (Kenpi7), while both G7 (Zhongsimai1) and G5 (08B26) could be
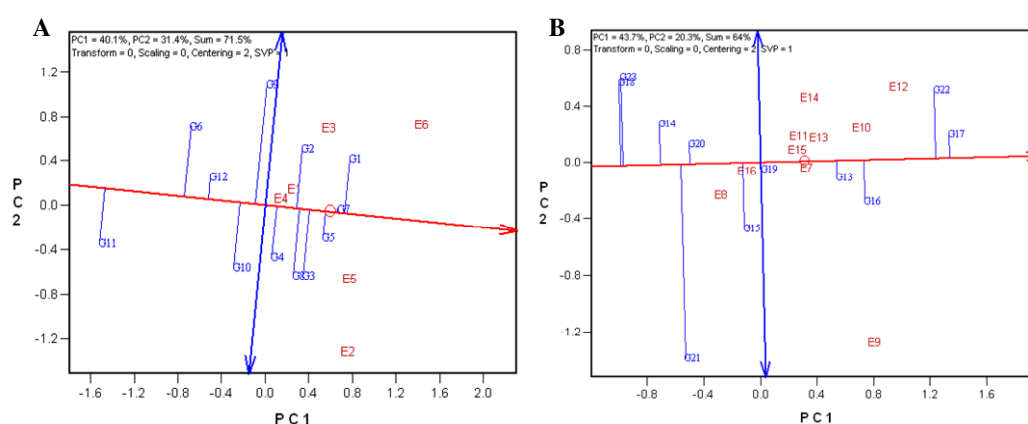

Figure 2. The ranking of 23 barley genotypes for both the yield and stability performance over sixteen environments during the experiments of 2010-2011 and 2012-2013 in China. Symbols E1-16 represent the six environments and G1-23 represents the 23 barley genotypes. (A) North China, (B) South China.

selected as the candidate genotypes for North China for the purpose of high and stable yield. For the South China, the mean yield of G17 (G231M004M), G22 (Fen18-11), G16 (2008pin22), and G13 (Zhe3521) was higher than the value of average environment (Figure 2B). The value of G17 is the highest among all environments. The vectors of G17 (G231M004M) and G13 (Zhe3521) are relatively shorter than those of G16 (2008pin22) and G22 (Fen18-11), indicating that the GE interaction had less impact on the yield of G17 (G231M004M) and G13 (Zhe3521). Therefore, for South China, G17 (G231M004M) and G13 (Zhe3521) might be the candidate barley genotype for production.

Discriminating Ability and Representativeness of Test Environments

In the biplot graph, the relationships among test environments are determined by the angles between the environmental vectors, which are the lines that connect each environment point with the origin point of the biplot (Figure 3). The cosine of the angle between vectors approximately represents the correlation between two environments, and an acute angle indicates a positive correlation, otherwise a negative correlation between the two test

environments (Yan and Tinker, 2006). All of the six Northern test environments are positively correlated because of the acute angles among their vectors (Figure 3-A), suggesting that all test environments in North China are very similar in discriminating the genotypes in yield performance. The angle between vectors of E1 (Haerbing), E4 (Shang kuli), and E6 (Shihezi) is very small, suggesting that very similar trial data could be obtained from the three locations. In addition, the vectors of E1 (Haerbing) and E4 (Shang kuli) are much shorter than others, indicating that the two locations have very limited discriminating ability on genotype evaluation, therefore, these two sites might be eliminated without losing too much information about the genotypes for the future trials. The distribution of test environments on biplot is more complicated for South China than that for North China (Figure 3-B). Except E8 (Wuhan) and E16 (Chengdu), all other test environments are positively correlated. The angle between vectors of E11 (Xiangyang), E12 (Yancheng), E13 (Taizhou), E10 (Yuxi) and E15 (Hefei) is very small, suggesting that some of these Southern sites could be removed from future trials as well.

The concept of 'ideal test environment' is defined as the environment that is most discriminating and also representative among all test environments (Yan and
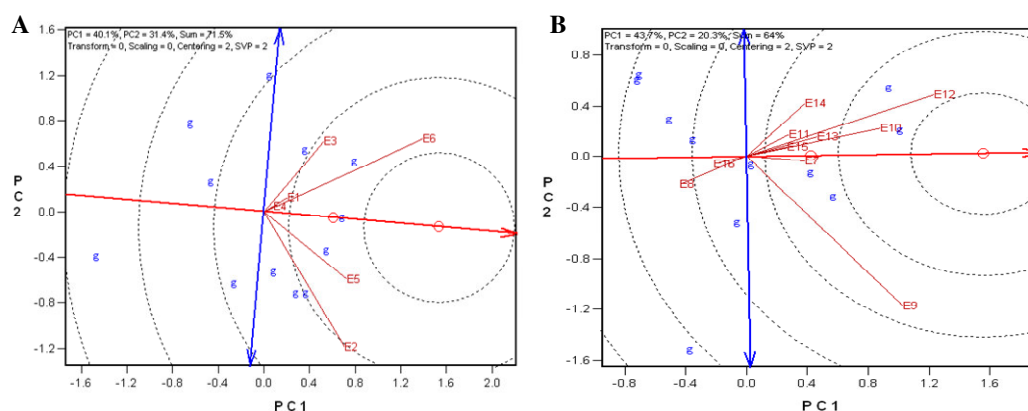

Figure 3. Sixteen test environments in relation to the ideal environment (the center of concentric circles). Symbols E1-16 represent the sixteen environments. 'g' is used to show the distribution of genotypes on the GGE biplot graph. See similar remarks in graph 2. (A) North China, (B) South China.

Tinker, 2006). The center of concentric circles on the AEC indicates the ideal test environment (Figures 3-A and -B). The distance from the ideal test environment to the biplot origin is equal to the longest vector of all environments, which is E6 (Shihezi) for North and E9 (Baoshan) for South. Thus, the site of E9 (Baoshan) might not be used in selecting superior genotypes, but it could be useful in culling unstable genotypes for South China. The site of E6 (Shihezi) and E12 (Yancheng) is closest to the center of concentric circles and can be considered as one of the best test sites for evaluating superior genotypes in North and South China, respectively, while the site of E8 (Wuhan) and E16 (Chengdu) were relatively poor for selecting cultivars adapted to the whole region.

Evaluation of Cultivars Relative to a Highest Yield Environment

Since the site of E6 (Shihezi) was the test environment with the highest yield in North China, the performance of all genotypes in North China was evaluated in E6 (Figure 4-A). The E6-axis, which is the line passing through point E6 and the origin of biplot, is called the axis of this environment. The

perpendicular lines indicate the ranking of yields of 12 genotypes along the E6-axis. Genotypes of G1 (Kenpi7), G2 (Ganpi7), G7 (Zhongsimai1), G9 (9821), G5 (08B26), and G3 (10PJ-24) had yields higher than the average, while all others had lower yields than the average. The genotype of G1 (Kenpi7) had the highest yield in the site of E6 (Shihezi) and G11 (P11-1) had the lowest one in North China. The site of E9 (Baoshan) was the highest yield environment in South China (Figure 4-B). Genotypes G21 (Edamai83), G16 (2008pin22), G17 (G231M004M), G13 (Zhe3521), G15 (Yangnongpi5), G22 (Fen18-11), and G19 (Supi3) had yields higher than the average, while all others had lower yields than the average. Genotype G21 (Edamai83) had the highest yield in the site of E9 (Baoshan) and G23 (Hua2759) had the lowest one.

Evaluation of Genotypes with Respect to the Ideal Genotype

The concept of 'ideal genotype' is the 'genotype' that is most stable and also has the highest yield among all test environments (Yan and Tinker, 2006; Mustapha *et al.*, 2014). It has been shown
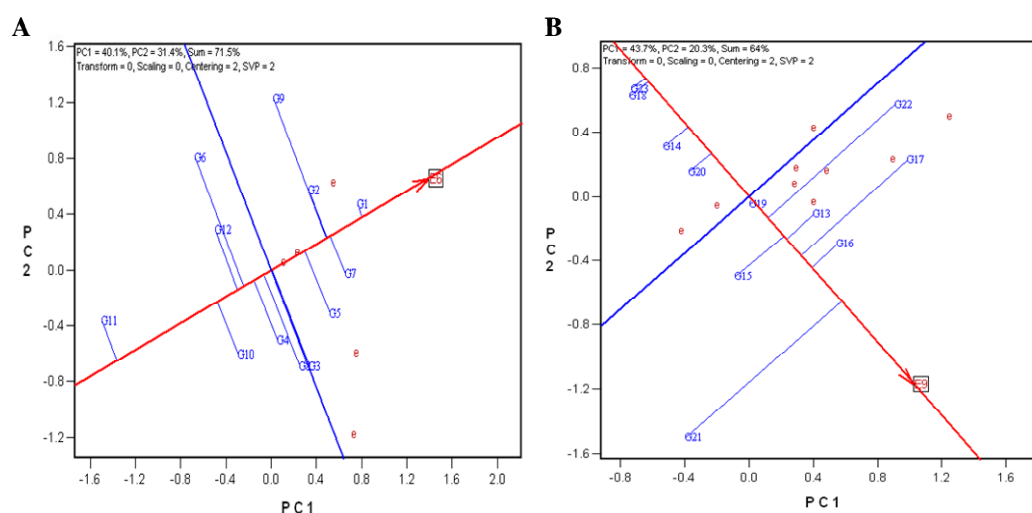

Figure 4. Comparison and ranking of 23 genotypes in a specific environment (E6, Shihezi and E9, Baoshan). 'e' is used to show the distribution of environments other than E6 or E9 on the GGE biplot graph. Symbols G1-23 represent the 23 barley genotypes. (A) North China, (B) South China.

that the distance between one genotype and the ideal genotype is a more repeatable parameter to evaluate the genotype performance than either mean performance or stability. In a GGE biplot graph, the center of the concentric circles on the AEC indicates the ideal genotype (Figures 5-A and -B), which is equal to the length of genotype vector with the highest yield. Therefore, the distance between the ideal genotype and the biplot origin is equal to the longest vector among all genotypes. Genotypes G1 (Kenpi7), G7 (Zhongsimai1), G5 (08B26), and G3 (10PJ-24) are included in the second inner cycle (Figure 5-A). Therefore, they can be considered as the candidate genotypes for the North China, while G11 (P11-1) is the poorest for the region. As shown in Figure 5B, genotype G17 (G231M004M) is included in the first inner cycle, suggesting that it could be a superior genotype for South China, while G14 (Zhe0892), G21 (Edamai83), G18 (Zhudamai7), and G23 (Hua2759) were not necessarily selected for the future trial in South China.

CONCLUSIONS

The results indicated that the genotype G17 (G231M004M) showed the best yield performance across the test environments in South China, while genotypes G1 (Kenpi7), G7 (Zhongsimai1), and G5 (08B26) could be considered as the candidate genotypes for North China. All test environments can be grouped in three environments in North and South China, respectively. The site of E6 (Shihezi) showed the greatest discriminating ability in North China and E12 (Yancheng) exhibited better discriminating ability than other sites in South China while the sites E2 (Hohhot) and E9 (Baoshan) were relatively poor in their ability to select adaptable cultivars for North and South, respectively. The sites E1 (Haerbing), E4 (Shang kuli), E11 (Xiangyang), E13 (Taizhou), and E15 (Hefei) could be eliminated from the future trials due to the similarity in their discrimination and representation abilities.

Abbreviations

AEC: Average Environment Coordination, AMMI: Additive Main effects and Multiplicative Interaction; ANOVA: Analysis Of Variance, GE: Interaction between Genotype and Environment, GGE: Genotype main effect (G) and Genotype by Environment interaction (GE), MET: Multi-Environment Trial.
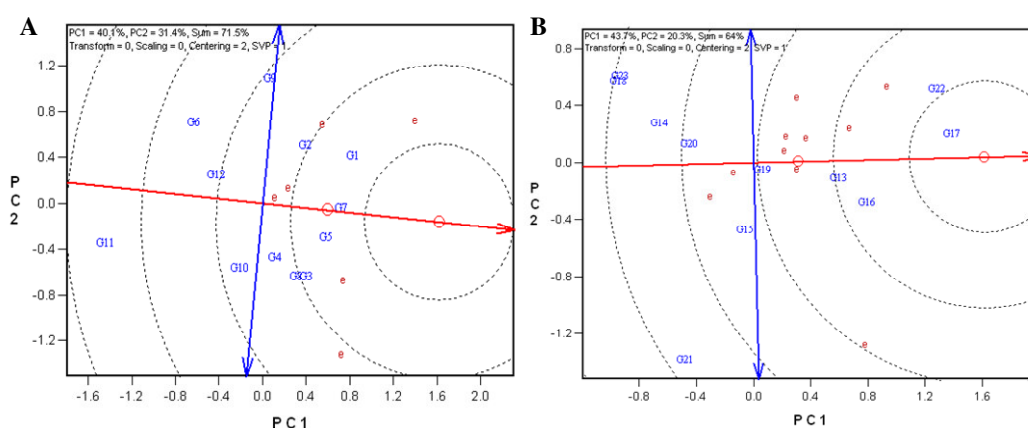

Figure 5. Ranking of the mean yield of 23 genotypes relative to the ideal genotype (the center of concentric circles). Symbols G1-23 represent the 23 barley genotypes. 'e' is used to show the distribution of environments. (A) North China, (B) South China.

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ارزیابی عملکرد ژنوتیپ های جو مبتنی بر بای پلات GGE درمحیط های مختلف درچین

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چکیده

عملکرد ۲۳ ژنوتیپ جو (.Hordeum vulgare L)در ۱۶ محل ومحیط آزمون در مناطق کاشت جو در چین ارزیابی شد. آزمایش با طرح بلوک های کامل تصادفی در سه تکرار در دو فصل زراعی (۱۱-۲۰۱۰ در جنوب چین و ۱۳-۲۰۱۲ در شمال) اجرا شد. برای تحلیل داده های به دست آمده از آزمایش های سراسری از روش بای پلات GGEاستفاده شد. نتایج حاکی از آن بود که هر کدام از مناطق آزمون شده در شمال یا جنوب کشور را می توان در در سه محیط بزرگ (mega-environment) گروه بندی کرد و بهترین عملکرد و مناسب ترین ژنوتیپ ها برای مناطق شمال و جنوب به ترتیب کولتیوار G7 (Zhongsimai1) ، G5 (08B26)، G17 (G231M004M) و G13 (Zhe3521) بودند. در میان ۱۶ محل ومحیط آزمایشی، منطقه E6 (Shihezi) وE12 (Yancheng) بیشترین توانایی فرق گذاری وتمایز دهی (discriminating ability) راداشتند در حالی که در آزمون های آینده می توان مناطق E1 (Haerbing)، E4 (Shang kuli)، E8 (Wuhan) ، و E16 (Chengdu) را به علت شباهت توان فرق گذاری ومعرف بودنشان حذف کرد.