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Evaluation of genotype × environment interactions of yield and output value in Chinese flue-cured tobacco by the additive main effects and multiplicative interaction (AMMI) model

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Additive main effects and multiplicative interaction (AMMI) model has obvious advantages of analyzing the interactions between genotypes and environment, and it can describe the differences in the stability of genotypes and the discriminability of genotypes in different locations quantitatively. The prolificacy and stability of three pilots and seven genotypes were analyzed for the north state recommendation trial of Chinese flue-cured tobacco in henan province with AMMI model. The genotypes 9808, LJ981, Y101 had high and stable yield and value with wide adaptability. Y8342 had high yield and value, but with poor stability. The yield and value of CF222 were lower than the control NC89, but its stability was inferior to the control; the output value of LJ237 was higher than the control, while the yield and stability were inferior to the control.

Key words: Additive main effects and multiplicative interaction (AMMI) model, genotype × environment (GE) interaction, multiple regression, flue-cured tobacco.

INTRODUCTION

The yield of flue-cured tobacco accounts for about 80% of the total output of tobacco in china. Henan province is a typical representative of strong aroma style of tobacco leaf and is one of the earliest area planting flue-cured tobacco in China. However, in recent years, the aroma style was not patency. Genotype plays an important role. Though, it is very urgently to strengthen the research of tobacco breeding. New elite tobacco advanced lines such as 9808 and Y101 and LJ981 had been successfully developed. An understanding of the characteristics of tobacco advanced lines could help improve their cultivation and further enhance their potential. Tobacco breeders have made a significant improvement in yield in the past few years using conventional breeding approaches. However, most of the selections were based on differences in agronomic characters. Agronomic characters represent the combined genetic and environmental effects on tobacco yield and output value. The evaluation of elite flue-cured tobacco advanced lines is essential for the further improvement of tobacco. Genotype-by-environment interactions can affect breeding progress because they often complicate the evaluation and selection of superior genotypes. Additive main effects and multiplicative interaction (AMMI) model

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Table 1. The list of genotypes.

Genotype	Breeding unit	Breeding methods	Types	Leaf	Number of leaves
Y101	Henan province	Cross breeding	Flue-cured	Long oval	20-22
LJ237	Heilongjiang province	Line breeding	Flue-cured	Oval	18-20
LJ981	Heilongjiang province	Line breeding	Flue-cured	Oval	19-21
CF222	Shandong province	Line breeding	Flue-cured	Oval	20-22
9808	Liaoning province	Line breeding	Flue-cured	Oval	18-20
Y8342	Henan province	Line breeding	Flue-cured	Oval	18-20
NC89	control	Line breeding	Flue-cured	Long oval	18-20

Table 2. The list of locations.

Names	Location	Landform types	Latitude	Rainfall	Soil type	Transplanting period
Dengzhou	In sorthwest of Henan province	Plain /upland area	N32°42′	723.8	Yellow brown soil	2010-4-29
Xuchang	In middle of Henan province	Plain area	N34°02′	735.2	Cinnamon soil	2010-5-13
Shanxian	In northwest of Henan province	Mountainous area	N34°42′	650	brown soil	2010-5-10

is an effective method in the analysis of genotype environment interaction. The AMMI model had been exploited in the genotype evaluation of barley (Minna et al., 2002) wheat (Vargas et al., 1999), rice (Liu et al., 2002), soybean (Sudari et al., 2006) and pigeonpea (Wamatu and Thomas, 2002).

The objectives of this study were to evaluate the genotype × environment interactions (GEI) of the new tobacco cultivars and advanced lines using multiple methods, to assist in their characterization in terms of yield and stability. Characterization of GEI in flue-cured tobacco should focus not only on yield but also on output value as important traits. Published data about GEI for these quality traits are still limited, and were also investigated in this study.

MATERIALS AND METHODS

The data for yield and output value were obtained from the north state recommendation trial of Chinese flue-cured tobacco in Henan province. Seven genotypes (Table 1) were evaluated at three locations (Table 2) in 2010. Except for NC89 all genotypes were of new Chinese flue-cured tobacco advanced lines. NC89 was the control genotype in north state recommendation trials. Each trial was established according to a randomized complete block design with three replications. Plot sizes were not less than 60 m^2. Trial management was same to the local production specifications. Tobacco leaves harvested from each plot was recorded as dry mass per plot. Each plot calculated value individually.

Genotype × environment interactions for yield and output value were analyzed according to the AMMI model. AMMI model was originated in the field of sociology and zoology. It was firstly used in the analysis the data of wheat region trail by Kemption. AMMI model combined with the variance analysis and the principal component. It can improve the accuracy by separating model error and interference from the residuals of the additive model. Interaction principal component analysis (IPCA) is the stability parameter in AMMI model. AMMI model analyzed GEI visually with the help of the biplot. The stability coefficient Di, the distance of interaction principal component (IPC) point with origin in space, was estimated according to the formula:

$$Di=\sqrt{\sum_{s=1}^{c} r^2{}_{is}}, \qquad i=1,2,3...,G$$

Where c is the number of the significant IPCs, and is the scores of genotype i in IPCs. Data analysis was performed using the software Data Proceeding System (DPS) version 7.05 (Tang and Feng, 2002).

RESULTS

AMMI analysis

The analysis of variance for yield and output value in 2010 showed that genotype, environment and GEI had significant effects on the yield and output value performance (Table 3). It was found that G and GE interactions were all important for yield and output value variation. On yield, the sum of squares of G and GE interactions accounted for 38.6 and 31.3% of total variation, respectively. IPCA1 accounted for 88.07 of the GE interaction, whereas the sum of squares of Joint-regression and Gene-regression and E-regression accounted for 52.65, 31.87 and 0.30% of the GE interaction, respectively.

On output value, the sum of squares of G and GE interactions accounted for 32.03 and 32.04% respectively. IPCA1 accounted for 86.85 of the GE interactions, whereas the sum of squares of

Table 3. AMMI Analysis of variance for yield and output value of seven genotypes evaluated in three environments in 2010.

Sources	Yield				Output value		
	d.f.	SS	F	SS percent	SS	F	SS percent
Total	62	10060269.83			2843601404.9		
Treatment	20	8323757.80	10.07**		1999353176.7	4.97**	
Genotype (G)	6	3885785.35	15.66**	38.63	910714092.56	7.55**	32.03
Environment (E)	2	1284970.42	15.54**	12.77	177515401.84	4.42*	6.24
G×E interaction	12	3153002.03	6.36**	31.34	911123682.27	3.78**	32.04
Joint-regression	1	1659942.43	40.15**	52.65	449117307.84	22.34**	49.29
Gene-regression	5	1004890.09	4.86**	31.87	291212824.26	2.90*	31.96
E-regression	1	9602.46	0.23	0.30	24791219.589	1.23	2.72
IPCA1	7	2776861.95	5.27**	88.07	791321997.87	4.72**	86.85
Residual	5	376140.07			119801684.39		
Error	42	1736512.04			844248228.21		

SS, sum of squares; d.f., degrees of freedom, * and **; significant at the 0.05 and 0.01 level respectively.

Table 4. Multiple comparisons of yield and output value.

Genotype	Yield (kg/ha)			Output value (yuan/ha)		
	Average	5% *	1% **	Average	5% *	1% **
Y101	2465.00	a	A	29237.15	b	AB
LJ237	1914.90	b	B	24882.50	c	B
LJ981	2402.73	a	A	32325.60	ab	A
CF222	1930.22	b	B	24180.18	c	B
9808	2501.37	a	A	33954.67	a	A
Y8342	2323.83	a	A	31202.43	ab	A
NC89	1952.27	b	B	24344.95	c	B

*The same letters are not significant at the 0.05 level; **the same letters are not significant at the 0.01 level.

Joint-regression and Gene-regression and E-regression accounted for 49.29, 31.96 and 2.72% of the GE interactions respectively. AMMI model analysis was better than linear regression analysis method. On yield and output value, most of the interactions were described by IPCA1.

Yield and output value performance

The yield of each genotype varied from 1914.90 to 2501.37 kg/ha, among which 9808 had the highest yield performance, followed by Y101, LJ981 and Y8342. Based on multiple comparisons, the yields of four flue-cured tobacco genotypes (that is, 9808, Y101, LJ981 and Y8342) were found to be significantly higher than that of the other genotypes; LJ237 and CF222 were found to be lower than NC89, but not significant (Table 4).

The output value of each genotype varied from 24180.18 to 33954.67 yuan/hm^2, among which 9808 had the highest output value performance, followed by LJ981, Y8342 and Y101. Based on multiple comparisons, the output value of four flue-cured tobacco genotypes (that is, 9808, LJ981, Y8342 and Y101) were found to be significantly higher than that of the other genotypes; CF222 were found to be lower than NC89, while LJ237 was higher than NC89, but not significant (Table 4).

Double-axes diagram of AMMI model and the analysis of stability coefficient *Di*

Most information had been graphically displayed in an AMMI biplot (Figures 1 and 2). It was found that the variation of yield and output value for each genotype was significant at different location. The *Di* (absolute *IPCA1* in this study) value of yield and output value varied among different genotypes. The estimates of *Di* for each genotype were estimated using the method described by zhang et al. (1998a, b). On yield, the *Di* value ranged from 0.97 to 22.51 on output value, the *Di* value ranged from 0.46 to 84.80.

LJ981 had the lowest *Di* value on yield and output value, whereas Y8342 had the highest *Di* value, indicating that the yield of LJ981 was more stable in different locations than that of Y8342. The

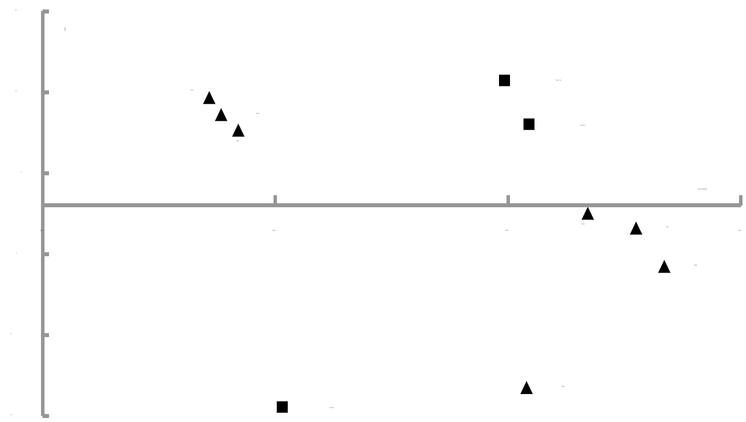

Figure 1. AMMI biplot of yield of seven genotypes in three environments in 2010.

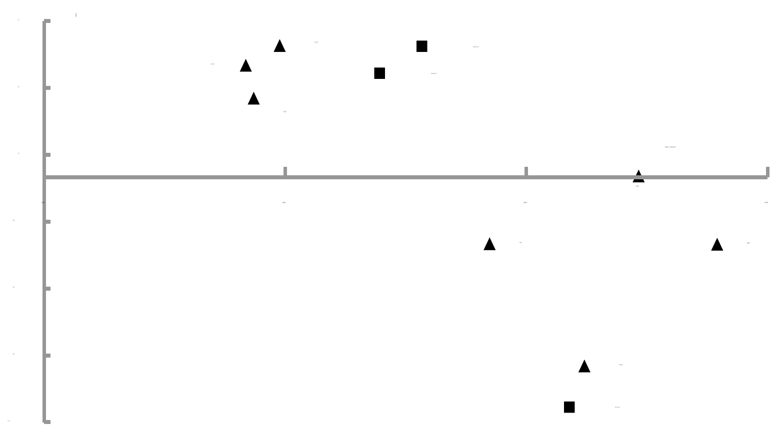

Figure 2. AMMI biplot of output value of seven genotypes in three environments in 2010.

genotypes9808, LJ981 and Y101 had high and stable yield and output value with wide adaptability. Y8342 had high yield and output value, but with poor stability. The yield and output value of CF222 were lower than the control NC89, and its stability was inferior to the control; the output value of LJ237 was higher than the control, while the yield and stability were inferior to the control. The *Di* value of yield and output value varied among different locations. Dengzhou had the lowest *Di* value, followed by Shanxian, whereas Xuchang had the highest *Di* value, indicating that Dengzhou was more stable for different genotypes than Xuchang.

DISCUSSION

GEI are important sources of variation in any crop. GEI can affect breeding progress because they often complicate the evaluation and selection of superior genotypes. GEI analysis is particularly important when the rank of lines selected for breeding changes in different environments. Understanding the causes of GEI would help in developing genotype which shows satisfactory performances in one to several environments (Yan et al., 2010). The GE biplot was applied to verify the GE interaction. In this study, it was found that the GE biplot and IPCA (*Di*) values were powerful for evaluation of Chinese flue-cured tobacco genotypes.

In this study, from the biplots and Di values, it was found that the yield and output value of genotypes varied from one location to the next. It was found that the genotypes 9808, LJ981, Y101 were better than the other genotypes. Y8342 performed general. LJ237 was good in value but poor in stability, CF222 performed worst overall in the test.

In the analysis of GEI, breeding workers are also interest for location discernment, in addition to the genotype stability. The Di values in AMMI model were better to measure the site discrimination and a criterion for judging testing location. The GE biplots not only display the GEI, but also facilitate a visual description of "which-wins-where" patterns. AMMI model analysis also helped in explaining the GEI in a given location (environment). In this study, the suitable locations for each genotype were detected. It was found that the Di value of Xuchang was larger than that of Shanxian and Dengzhou. Most of the tested genotypes had better adaptability in Dengzhou and Shanxian which had lower discernment.Y8342 adapted to Xuchang, but not adapted to shanxian and dengzhou. In the test, the genotypes play a more important role than environment due to the small differences of latitude between the three locations.

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