

Perform Stability of Fatty Acids of Soybean Cultivar Evaluated by GGE Biplot

HAN Ying-peng¹, ZHAO Xue¹, TENG Wei-li¹, SUN Ming-ming², ZHANG Hong-jian³, LI Wen-bin¹

(1. Key Laboratory of Soybean Biology in Chinese Ministry of Education, Key Laboratory of Soybean Biology and Breeding/Genetics of Chinese Agriculture Ministry, Northeast Agricultural University, Harbin 150030, China; 2. Information Center, Heilongjiang Academy of Agricultural Sciences, Harbin 150086, China; 3. Hongxing Farm of Heilongjiang Province, Beian 164022, China)

Abstract: Soybean fatty acids (FA) are major sources of vegetable oil. The objective of the present study was to select stable perform of FA of twenty-six cultivars across three environments. Three tested locations including Nanning in 2012, Harbin in 2013, and Harbin in 2012 were highly correlated. ‘Which-won where’ study partitioned the testing locations into three environments, the result showed genotypes G17 (Hefeng 52), G21 (Bei 1484), G4 (Donong 42), G20 (Heihe 45) and G20 (Heihe 45) were the best performing genotypes for palmitic acid, stearic acid, oleic acid, linoleic acid and linolenic acid content, respectively. Genotypes G9 (Kenfeng 15) and G20 (Heihe 45) located closer to the ‘ideal genotype’ are more desirable than others. The result of the present study indicated that most genotypes varied depending on the tested environment. This study was valuable to identify genotype with stable perform of fatty acid of these twenty-six cultivar for developing new cultivar.

Key words: Soybean; Fatty acid; Stability; GGE biplot

中图分类号: S565.1

文献标识码: A

DOI: 10.11861/j.issn.1000-9841.2014.04.0514

GGE 双图标法评价大豆脂肪酸表现的稳定性

韩英鹏¹, 赵雪¹, 滕卫丽¹, 孙明明², 张洪建³, 李文宾¹

(1. 东北农业大学大豆生物学教育部重点实验室, 农业部北方大豆生物学与遗传育种区域重点实验室, 黑龙江 哈尔滨 150030; 2. 黑龙江省农业科学院 信息中心, 黑龙江 哈尔滨 150086; 3. 黑龙江省红星农场, 黑龙江 北安 164022)

摘要: 分别于2012年在南宁、2012和2013年在哈尔滨利用GGE双图标法评价了26个大豆品种在3个环境条件下的稳定性。结果表明: G17(合丰52)、G21(北1484)、G4(东农42)和G20(黑河45)是棕榈酸、硬脂酸、油酸、亚油酸、亚麻酸5种脂肪酸表现最稳定的基因型; 大豆品种G9(垦丰15)和G20(黑河45)比其他大豆品种更接近理想基因型, 因此这两个大豆品种具有更大的稳定性。研究结果显示, 绝大多数的大豆品种在被测试的环境中, 具有较大的变异。

关键词: 大豆; 脂肪酸; 稳定性; GGE双标图

Soybean oil consisted of five FA including palmitic (PA), stearic (ST), oleic (OL), linoleic (LI), and linolenic acids (LN)^[1], which was approximately 20% of the seed mass^[2]. Human nutritional studies have suggested that FA might play an important role in the prevention and treatment of a number of diseases^[3-5]. These five FA content were effected by significant genotype \times environments (GE). Hence, soybean cultivars with reasonable FA content required evaluation in multiple environments, however, perform of soybean cultivar across multi-environments didn't behave stable. GGE biplot analysis offered a faster and more accurate approach for evaluating stability of cultivar, because evaluation could be based on genetic main effect than

solely on phenotype. GGE biplot analysis could remove the environment and GE interaction effect^[6]. Furthermore, GGE biplot analysis could identify ‘which-won-where’ besides identifying different mega-environments^[6-7]. It has been used to analyze many crop species' stability across multi-environments including rice^[8], wheat^[9], peanut^[10], oat^[11], sorghum^[12]. While there has no analysis on FA for soybean yet using GGE biplot.

In this study, we analyzed the fatty acid performance of twenty-six soybean cultivars from Heilongjiang province using GGE biplot.

Received: 2014-05-01

Foundation: Young Academic Backbone Support Plan in General University of Heilongjiang Province (1252G014).

Biography: HAN Ying-peng (1978-), male, PhD, professor. Major in molecular breeding. E-mail: hyp234286@aliyun.com.

Corresponding author: LI Wen-bin (1958-), male, PhD, professor. Major in molecular breeding. E-mail: wenbinli@neau.edu.cn.

1 Martial and methods

1.1 Plant materials

Twenty-six soybean cultivars from Heilongjiang

province were used to analyze, mainly from Northeast Agricultural University, Soybean Institute of HAAS, Suihua Branch of HAAS, Jiamusi Branch of HAAS and Academy of Land Reclamation Science(Table 1).

Table 1 Twenty-six tested culticans and their developing settor information

Code	Name	Developing sector	Code	Name	Developing sector
G1	Donong 50	Northeast Agricultural University	G14	Suinong 4	Suihua Branch of HAAS
G2	Donong 49	Northeast Agricultural University	G15	Hefeng 25	Jiamusi Branch of HAAS
G3	Donong 47	Northeast Agricultural University	G16	Hefeng 50	Jiamusi Branch of HAAS
G4	Donong 42	Northeast Agricultural University	G17	Hefeng 52	Jiamusi Branch of HAAS
G5	Heinong 33	Soybean Institute of HAAS	G18	Heihe 38	Jiamusi Branch of HAAS
G6	Heinong 44	Soybean Institute of HAAS	G19	Heihe 48	Jiamusi Branch of HAAS
G7	Heinong 50	Soybean Institute of HAAS	G20	Heihe 45	Jiamusi Branch of HAAS
G8	Kenfeng 22	Heilongjiang Academy of Land Reclamation Sciences	G21	Bei 1484	Beian Research Institute
G9	Kenfeng 15	Heilongjiang Academy of Land Reclamation Sciences	G22	Bei 1361	Beian Research Institute
G10	Kenfeng 18	Heilongjiang Academy of Land Reclamation Sciences	G23	Bei 1873	Beian Research Institute
G11	Suinong 14	Suihua Branch of HAAS	G24	Kangxian 1	—
G12	Suinong 28	Suihua Branch of HAAS	G25	Kangxian 2	—
G13	Suinong 20	Suihua Branch of HAAS	G26	Longxuan 1	Northeast Agriculture University

HAAS;Heilongjiang Academy of Agricultural Sciences.

1.2 Field design and evaluation of fatty acid

Those twenty-six cultivars were grown in a randomized complete block design at Harbin during 2012 and 2013 and at Nanning during 2102 in two row plots. The rows were 3 m long, 90 cm apart and there was a space of about 6 cm between two plants in a row. FA content was extracted and determined by gas chromatograph analysis^[13].

1.3 Data analysis

All analysis was done through GGE biplot^[14].

2 Results and analysis

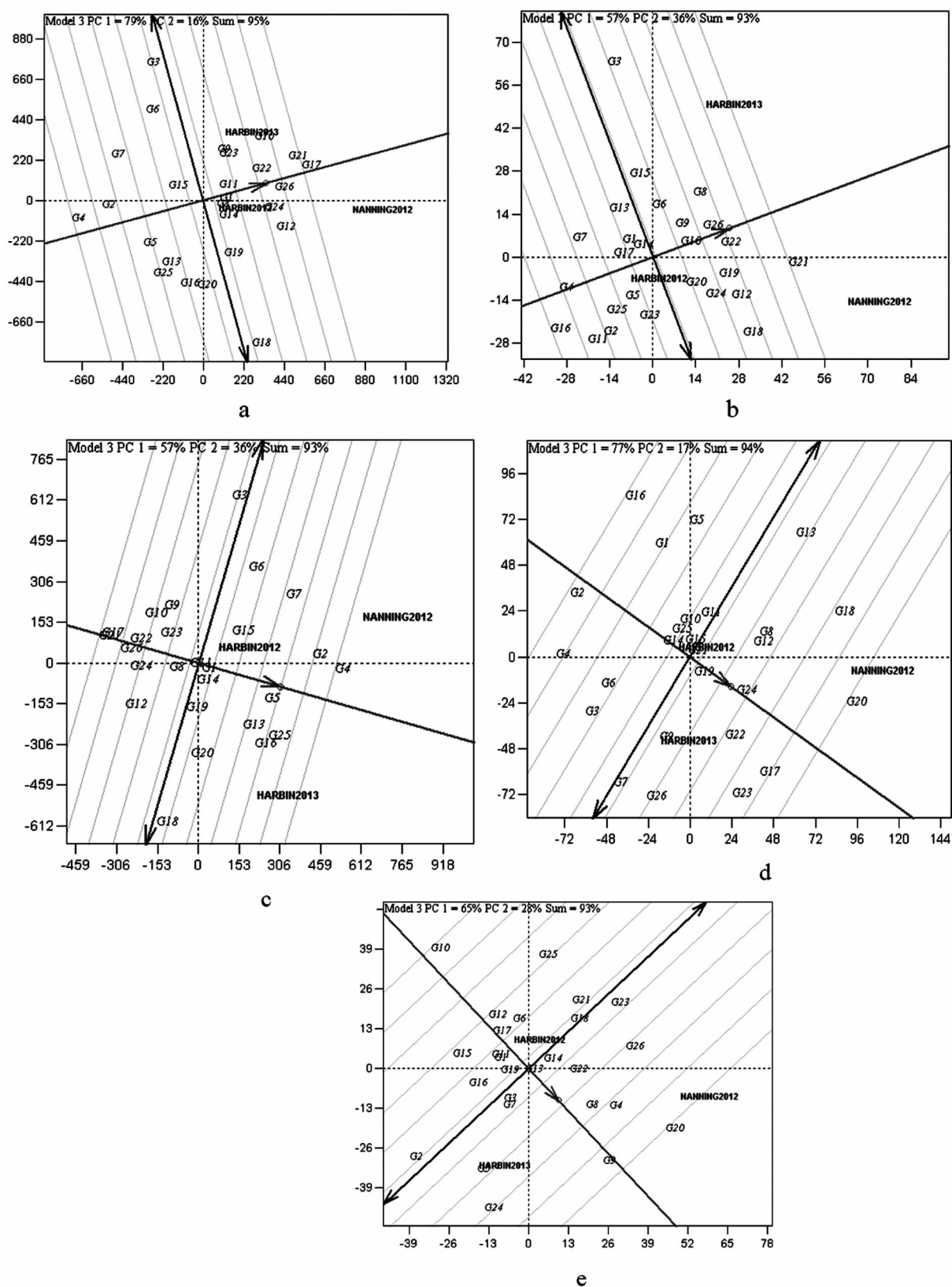
2.1 Genetic parameter analysis

Phenotypic values of FA across three environments were showed in Table 2. The differences among those 26 cultivars were significant across three environments.

Of the five FA, LN was significantly different from different environments.

2.2 Mean performance and stability of the genotypes across locations

Performance and stability of FA of genotypes were visualized graphically through GGE biplot (Fig. 1), which could indicate through average environment coordination(AEC) method. The result showed that twenty-six tested soybean cultivars performed so differently in five FA contents, some of them were excellent germplasm in three years two sites experiment. As showed in Fig. 1, G17, G21, G4, G20 and G20 were the best performing genotypes for PA, ST, OL, LI and LN content, on the other hand, G4, G16, G18, G4 and G2 were the poorest in these five fatty acids, respectively.



a. Palmitic acid; b. Stearic acid; c. Oleic acid; d. Linoleic acid; e. Linolenic acid.

AEC abscissa (delegated by the line with single arrow head) marker average environment and points towards higher mean values, which average PC1 and PC2 scores over all environments. The perpendicular lines to the AEC passing through the biplot origin were referred to as AEC ordinate (delegated by the line with double-arrowed lines).

Fig. 1 Perform of twenty-six cultivar cultivars for five fatty acids

Table 2 Statistical analysis of fatty acid of twenty-six cultivars at different environments

Locations	Fatty acid	Means	SD	CV/%	Range
Harbin 2012	Palmitic acid	12.31	1.19	10.57	8.70-18.21
	Stearic acid	3.09	0.92	19.97	1.29-7.30
	Oleic acid	25.37	3.21	23.20	8.88-30.01
	Linoleic acid	55.7	3.01	4.89	47.08-62.48
	Linolenic acid	8.11	1.5	19.56	4.40-13.02
Harbin 2013	Palmitic	13.60	1.38	14.87	10.34-17.77
	Stearic acid	2.80	0.56	20.00	1.76-5.89
	Oleic acid	24.48	5.01	24.01	15.88-48.00
	Linoleic acid	52.24	4.04	9.22	32.15-61.40
	Linolenic acid	8.08	1.08	15.77	3.63-11.99
Nanning 2012	Palmitic	11.88	1.27	10.10	10.32-17.00
	Stearic acid	3.50	0.56	16.00	2.20-5.36
	Oleic acid	34.61	7.79	22.30	19.57-61.91
	Linoleic acid	47.86	4.04	10.11	27.95-59.40
	Linolenic acid	4.20	0.97	10.00	3.67-11.31

2.3 Environment evaluation

The angles between different environments were acute (Fig. 2), which are indicative of closer relationship among the environments. It showed that the three location were highly correlated (Fig. 2). On the other hand, discriminating ability of the tested environments were also analyzed with projection of the environments to the average environment axis (AEA, Fig. 3). Thus Nanning in 2012 was closest to the average environment followed by Harbin in 2013 and Harbin in 2012.

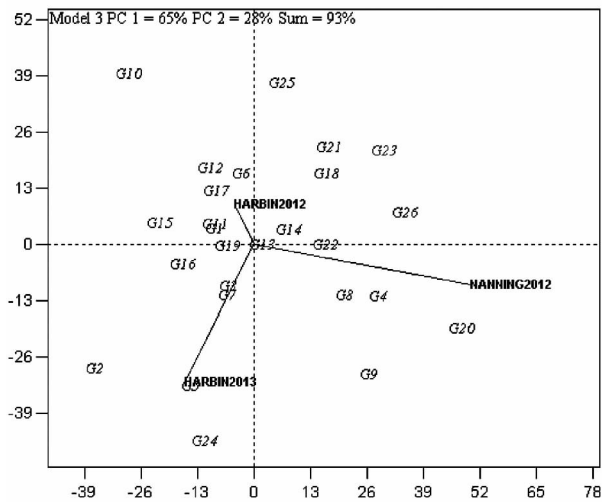


Fig. 2 Analysis of relatedness among different environments

2.4 Ideal genotype analysis

Fig. 4 showed the ranking of the genotypes for these five FA content in terms of ‘ideal genotype’. An ‘ideal genotype’ is high performer with high stability of the five FA content across three tested environments. From our study it may be stated that G9 and G20 were close to ideal genotypes.

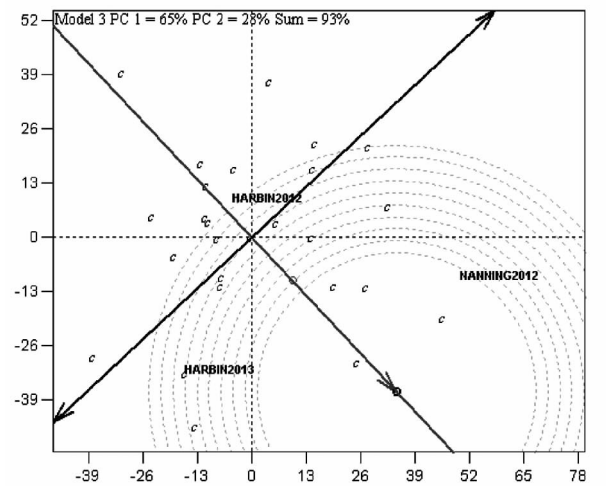
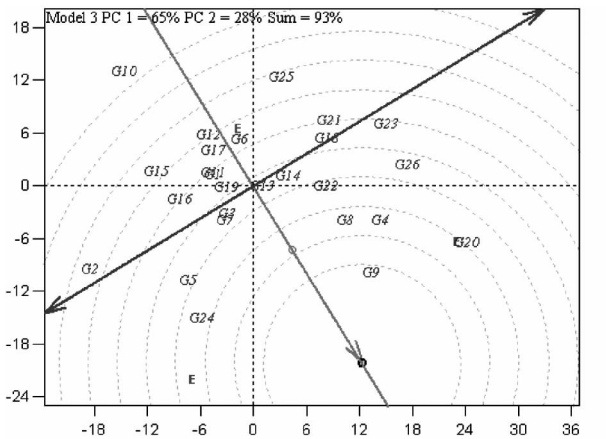


Fig. 3 Ranking of environment based on discriminating ability and representativeness



The small circle on average environment coordinate, AEC

Fig. 4 Ranking of genotypes relative to an ideal genotype

2.5 ‘Which-won-where’ and mega-environment identification

The performances of five different FA content on each environment were evaluated. With the environment linked to Harbin in 2012, Harbin in 2013 and

Nanning in 2012 as the corner environment, other four FA (PA, SI, OL and LI) fell in the sector in which Nanning in 2012 had the strongest discriminating ability for those four FA, respectively (Fig. 5). Harbin in 2013 had the strongest discriminating ability for LN.

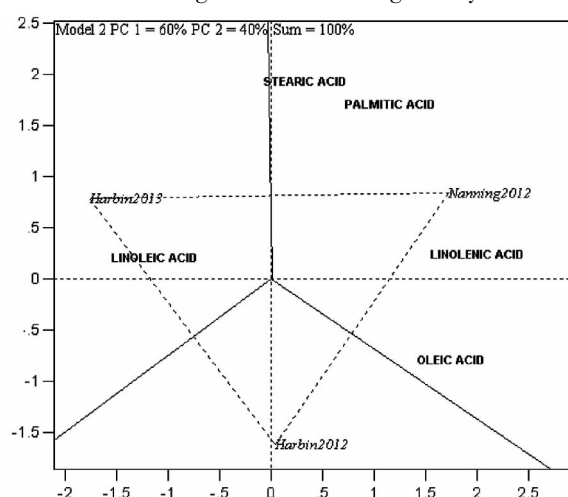


Fig. 5 Five fatty acid perform of twenty-six cultivars in different environments

3 Discussion

GGE biplot could effectively detect the interaction pattern graphically besides identifying ‘which won-where’ and delineation of mega-environments among the testing locations^[14]. FA perform stability of twenty-six cultivars was evaluated through this analysis, the result showed that five genotype respectively were the strongest genotype for five different fatty. Of them, G17, G21, G4, G20 and G20 were the best performing genotypes, respectively. Relationship between tested environments could be explored through cosine of the angle between their vectors, which was the line connecting its marker to the origin of the GGE biplot. Thus, our study clearly indicated that all tested locations were closely related and Harbin in 2013 were close to the average environment.

GE interaction significantly effect perform stability of FA of twenty-six cultivars. GGE biplot could graphical presentation of GE interaction; thus, GGE biplot could define ideal genotype through having greatest vector length of five FA genotype with zero GE as located at the center of the concentric circles. Genotypes G9 and

G20 located closer to the ‘ideal genotype’ were more desirable than others. The result of the present study indicated that most genotypes varied depending on the tested environment.

Reference

- [1] Wilson R F, Burton J W, Brim C A. Progress in the selection for altered fatty acid composition in soybeans [J]. Crop Science, 1981, 21:788-791.
- [2] Yaklich R W, Vinyard B T. Estimating soybean seed protein and oil concentration before harvest [J]. Journal of American Oil Chemistry, 2004, 81:189-194.
- [3] Rose D. Effects of dietary fatty acids on breast and prostate cancer: Evidence from *in vitro* experiments and animal studies [J]. Journal of American Clint Nutrition 1997, 66:1513s-1522s.
- [4] Demaison L, Moreau D. Dietary n-3 polyunsaturated fatty acids and coronary heart disease-related mortality: a possible mechanism of action [J]. Cell Molecular Life, 2002, 59(3):463-477.
- [5] Lauritzen L, Hansen H S, Jorgensen M H. The essentiality of long-chain n-3 fatty acids in relation to development and function of the brain and retina [J]. Programmer Lipid Research 2001, 40(1-2):1-94.
- [6] Yan W, Kang M S, Ma B L, et al. GGE biplot vs. AMMI analysis of genotype-by-environment data [J]. Crop Science, 2007, 47:643-653.
- [7] Yan W, Hunt L A. Biplot analysis of diallel data [J]. Crop Science, 2002, 42:21-30.
- [8] Samonte S O P B, Wilson L T, McClung A M, et al. Targeting cultivars onto rice growing environments using AMMI and SREG GGE biplot analysis [J]. Crop Science, 2005, 45:2414-2424.
- [9] Roozeboom K L, Schapugh T, Tuinstra M R, et al. Testing wheat in variable environments: genotype, environment, interaction effects, and grouping test locations [J]. Crop Science, 2008, 48:317-330.
- [10] Putto W, Patanothai A, Jogloy S, et al. Determination of mega-environments for peanut breeding using the CSM-CROPGRO-peanut model [J]. Crop Science, 2008, 48:973-982.
- [11] Yan W, Fregeau-Reid J, Pageau D, et al. Identifying essential test location for oat breeding in Eastern Canada [J]. Crop Science, 2010, 50:504-515.
- [12] Rao P S, Reddy P S, Ratore A. Application GGE biplot and AMMI model to evaluate sweet sorghum (*Sorghum bicolor*) hybrids for genotype 9 environment interaction and seasonal adaptation [J]. Indian Journal of Agronomic Science, 2010, 81:438-444.
- [13] Xie D, Han Y, Zeng Y, et al. SSR- and SNP-related QTL underlying linolenic acid and other fatty acid contents in soybean seeds across multiple environments [J]. Molecular Breeding, 2012, 30:169-179.
- [14] Yan W, Kang M S. GGE biplot analysis: a graphical tool for breeders, geneticists, and agronomists [M]. CRC Press, 2003:42-45.