Reduction of GE Interaction through Classification Technique in Sugarcane Yield Trial

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Abstract

Genotypic response of sugarcane was studied using data from a multilocational yield trial conducted by the Department of Agriculture, Ministry of Agriculture and Cooperatives, Thailand. The data were cane yield, commercial cane sugar (CCS), and sugar yield of four common lines, viz. 3-2-023L, CN1, F140, and UT1, grown in 15 locations. The genotype x environment combinations were grouped by Pattern (PAT) analyses. This technique resulted in the environmental grouping in which Spearman rank correlation was high among environments in each group, except in CCS data of group III. Thus PAT can be employed to reduce the effect of reversal GE interaction.

1. Introduction

Multilocation testing under several environments is an important step in a crop improvement program. Elite breeding lines are normally tested in many locations for many years before the best one can be released to farmers. A large number of data sets are available after a series of experiments. The plant breeder then analyzes the data using combined analysis of variance provided that the experiments have the same error variance. Sum of squares of environments, genotypes, and genotype x environment (GE) interaction are seperated. If GE interaction is not significant, one can use the average performance of genotypes across the environments for selecting good genotypes. However, in the case of significant GE interaction, the interaction can be classified into two types, i.e. change-in-rate (Figure 1A), and reversal (Figure 1B) interaction. In the first type, the best genotype can be identified from the average performance as in the case of no GE interaction. In the reversal type, however, one cannot select a good genotype from its average performance. A careful data analysis is needed to explain and help interpret the GE interaction. There are many procedures to analyze the interaction such

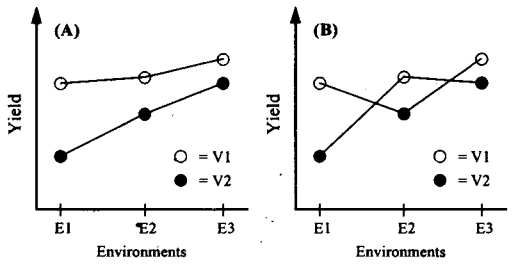

Figure 1. Two types of GE interaction in variety V1 and V2; (A) change-in-rate interaction, and (B) reversal interaction between E1 with E2 and E2 with E3 environments.

as the analysis of variance, linear regression, multivariate analysis, Additive Main effects and the Multiplicative Interaction (AMMI), etc. [1,2,3,4,5]. The analysis of variance is an additive model that can describe effectively only the main effects. The linear regression has some deficiencies such as confounding between interaction and main effects, and the non-linear response of genotypes to environments. AMMI model incorporates both additive and multiplicative components in the model, using analysis of variance to analyze the main effect of genotypes and environments, while using the principal component analysis to dissect GE interaction into principal component axes [3,6,7,8,9].

The pattern analysis is also an analytical method to explain the interaction [10,11]. This method elucidates a complex structure of the data set. Initially, pattern analysis was used as a classification method in the field of ecology and numerical taxonomy. For some crops, Abou-El-Fittouh *et al.* (1969) reported that they used pattern analysis to classify locations in cotton variety testing in the US cotton belt. In grazing experiments, classification and ordination procedures was achieved using classical statistical analyses. [12].

The objective of this study was to examine the efficiency of pattern (PAT) analysis in reducing reversal GE interaction.

2. Material and Methods

In this study, the data sets were obtained from yield trial experiments conducted during 1984-1988 by the Department of Agriculture, Ministry of Agriculture and Cooperatives, Thailand. The experimental design used was randomized complete block with four replications. Each plot comprised 10 rows of 13 by 10 m, with 1.3 m row width and 0.5 m between cutting stems. The tested sites included 15 locations in eight provinces. They were Ban Bung (BBG) and Nong Yai (NYI) in Chonburi, Muang District (RAY) in Rayong, Muang District (CNT) in Chainat, Bang Rachan (BRJ) in Singburi, Si Samrong (SSR) in Sukhothai, Bo Phloi (BOP), Phanom Thuan (PNT) and Tha Muang (TAM) in Kanchanaburi, Samchuk (SAM), Lao Kwan (LWN), Doem Bang Nangbuat (DBN), Song Phi Nong (SPN) and U-thong in Suphanburi, and Tha Yang (TAY) in Phetchaburi. Data from four common clones, viz. 3-2-023L, CN1, F140 and UT1, were compiled from each location. Three traits, viz. cane yield (t/ha), commercial cane sugar (CCS), and sugar yield (t/ha), were recorded. CCS is obtained from the relationship $(\frac{3}{2}\text{pol} - \frac{1}{2}\text{brix})$. While pol and brix are percentages of sucrose and total soluble solid in cane juice.

The linear regression (REG) technique [8] was used to explore linear performance of sugarcane clones grown across the locations. The location standardized data sets were used for pattern analysis, which grouped homogeneous environments together to reduce the effect of the reversal GE interaction. A hierarchical agglomerative clustering procedure with the incremental sum of squares method was combined as the fusion strategy, while standardized squared euclidean distance was used for dissimilarity measurement. The analyses were performed using statistical pakages SAS version 6.03 and SPSS run in a PC.

3. Results and Discussion

Partitioning of sum of squares (SS) by linear regression and ordination in each trait are given in Table 1. The percentages of sum of squares attributable to environments for cane yield, CCS, and sugar yield were 74.9%, 72.0%, and 80.7%, respectively. This was a large portion compared to genotype SS and genotype

x environment (GE) interaction SS. The GE interaction SS showed more effect than genotype SS, and accounted for 12.9%, 19.0%, and 15.0% in the variation of the three traits, respectively. By REG technique, the deviation from regression SS showed a large portion of GE interaction SS, therefore, this method was not effective in explaining the interaction.

Fifteen locations were grouped into 4 different environmental groups by PAT technique (Table 2). Dendrogram in Figure 2 showed different fusion level in each environmental group. Figure 3 A, C, and E displayed overall environmental complex in each clone, whereas grouping reduced the complexity (Figure 3 B, D, and F). Each environmental group had a unique genotypic ranking, however, almost all locations in each group showed similar genotypic ranking.

For cane yield, environmental group I, II, and III consisted of 3, 7, and 4 locations with the correlation coefficients of 0.73, 0.94 and 1.00, respectively (Table 2). The average cane yield of environmental group I, II, III, and IV were 86.86, 80.03, 64.61, and 52.98 ton/ha, respectively. Environmental group I and II comprised 10 superior locations whereas group III and IV comprised five inferior locations. Clone 3-2-023L gave the highest cane yield in group III and IV (72.76 and 54.88 ton/ha), but gave low yield in group I and II (74.95 and 75.41 ton/ha). Thus clone 3-2-023L adapted better than the other three clones in poor environments. CN1 showed the highest cane yield (99.96 ton/ha) which appeared to adapt well in environmental group I. While UT1 was a good clone for group II, giving cane yield of 94.66 ton/ha. Both clones should be recommended for planting in good environments. The above results indicated that grouping of environments can reduce the reversal interaction.

High CCS value was identified in CN1 in group II, III, IV, and F140 in group I. For all groups, correlation coefficient among environments in each group, except group III, showed significance at 1 % level of probability. Each clone produced the highest sugar yield in different environmental groups. CN1, 3-2-023 L, UT1 and F140 had sugar yields of 9.88, 10.76, 12.18 and 9.26 ton/ha in group I, II, III and IV, respectively. All environmental groups showed significant correlation coefficient among environments in each group. The average sugar yield of group I, II, III and IV were 8.83, 9.91, 10.74 and 8.61 ton/ha, respectively. Figure 4 displayed spatial arrangement of 15 locations in two dimensions of PCA1 and PCA2 which were analysed by PAT technique. Thus this technique can be used to reduce the reversal GE interaction through grouping homogeneous environments together.

4. Conclusion

PAT technique can be used to reduce the reversal GE interaction. Each sugarcane clone seemed to adapt to certain group of environments. Thus the sugarcane breeder should group the known homogeneous environments before conducting yield trials in a representative planting area in order to minimize such interaction.

Table 1. Analyses of variance showing mean squares and percentage of sum of squares (in parentheses) for cane yield, CCS, and sugar yield of four sugarcane clones grown in 15 locations.

Source of Variation	df	Mean Squares		
		Cane yield	CCS	Sugar yield
Linear regression				
Environments (Env.)	14	1257.23 (74.9%)	8.51 (72.0%)	25.16 (80.7%)
Clones	3	957.41 (12.2%)	4.96 (9.0%)	6.37 (4.4%)
Clones x Env.	42	72.31 (12.9%)	0.75 (19.0%)	1.56 (15.0%)
Het. due to reg.	3	213.01 (21.0%)	0.35 (3.4%)	4.32 (19.9%)
Dev. from reg.	39	61.49 (79.0%)	0.78 (96.6%)	1.34 (80.1%)
Ordination				
PCA1	16	2.94 (60.0%)	1.35 (48.0%)	1.25 (44.5%)
PCA2	14	0.76 (23.7%)	1.15 (35.8%)	1.18 (36.7%)
Residuals	30	0.24 (16.3%)	0.24 (16.2%)	0.28 (18.8%)

Table 2. Means of environmental groups and genotypic ranking (in parentheses) of each trait of four sugarcane clones grown in 15 locations. Spearman rank correlation was calculated from all possible genotypic ranking among environments in each group.

Trait	Env.	Clones				Env.	No. of	r [1/]
	groups	3-2-023L	CN1	F140	UT1	mean	env.	
Cane yield	I	74.95 (4)	99.96 (1)	80.03 (3)	92.49 (2)	86.86	3	0.73 **
(ton/ha)	II	75.41 (3)	79.47 (2)	70.57 (4)	94.66 (1)	80.03	7	0.94 **
	III	72.76 (1)	63.73 (3)	50.75 (4)	71.20 (2)	64.61	4	1.00 **
	IV	54.88 (1)	48.88 (4)	54.50 (2)	53.69 (3)	52.98	1	***
	Mean	69.50	73.01	63.96	78.01			
CCS value	I	12.73 (2)	11.97 (4)	14.35 (1)	12.44 (3)	12.87	7	0.94 **
	II	13.12 (4)	14.27 (1)	13.45 (3)	13.71 (2)	13.64	2	1.00 **
	III	12.69 (4)	14.56 (1)	14.57 (2)	13.58 (3)	13.85	2	0.80 [ns]
	IV	12.83 (3)	13.58 (1)	12.96 (2)	11.71 (4)	12.77	4	0.88 **
	Mean	12.84	13.60	13.83	12.86			
Sugar yield	I	8.94 (2)	9.88 (1)	8.31 (3)	8.19 (4)	8.83	1	***
(ton/ha)	II	10.76 (1)	10.43 (2)	8.24 (4)	10.22 (3)	9.91	5	1.00 **
	III	9.02 (4)	11.21 (2)	10.55 (3)	12.18 (1)	10.74	7	0.94 **
	IV	8.51 (3)	7.80 (4)	9.26 (1)	8.86 (2)	8.61	2	1.00 **
	Mean	9.31	9.83	9.09	9.86			

[1/] [ns] Non-significant at $P \leq 0.05$, ** Singinficant at $P \leq 0.01$

*** there is only one environment in the group

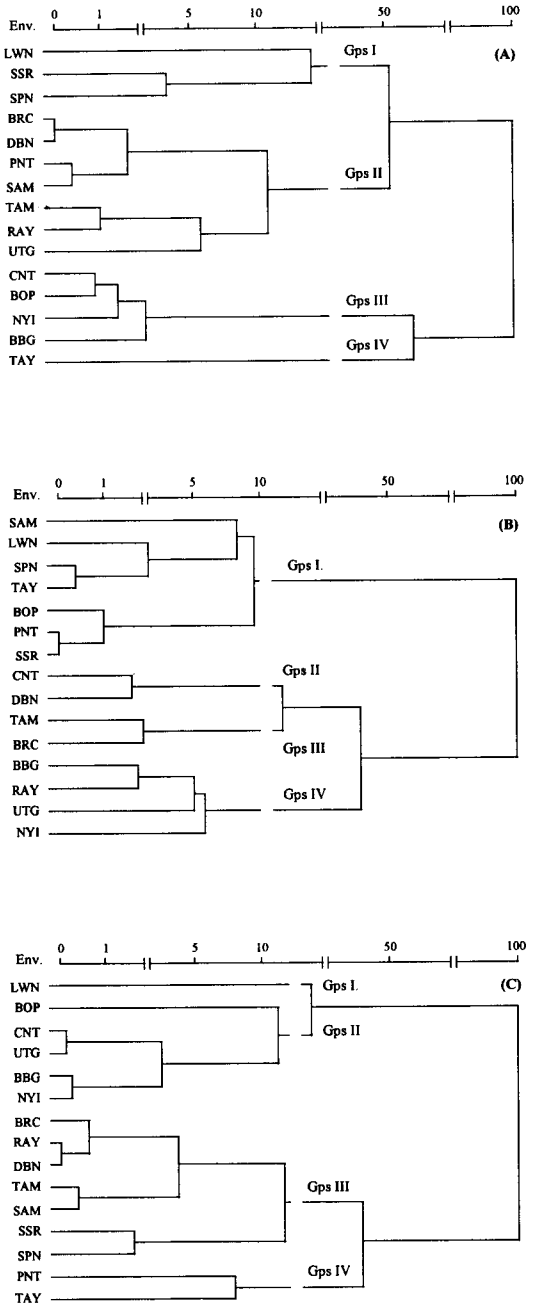

Figure 2. Dendrograms showing four environmental groups from 15 locations clustered based on three characters; (A) cane yield, (B) CCS value, (C) sugar yield.

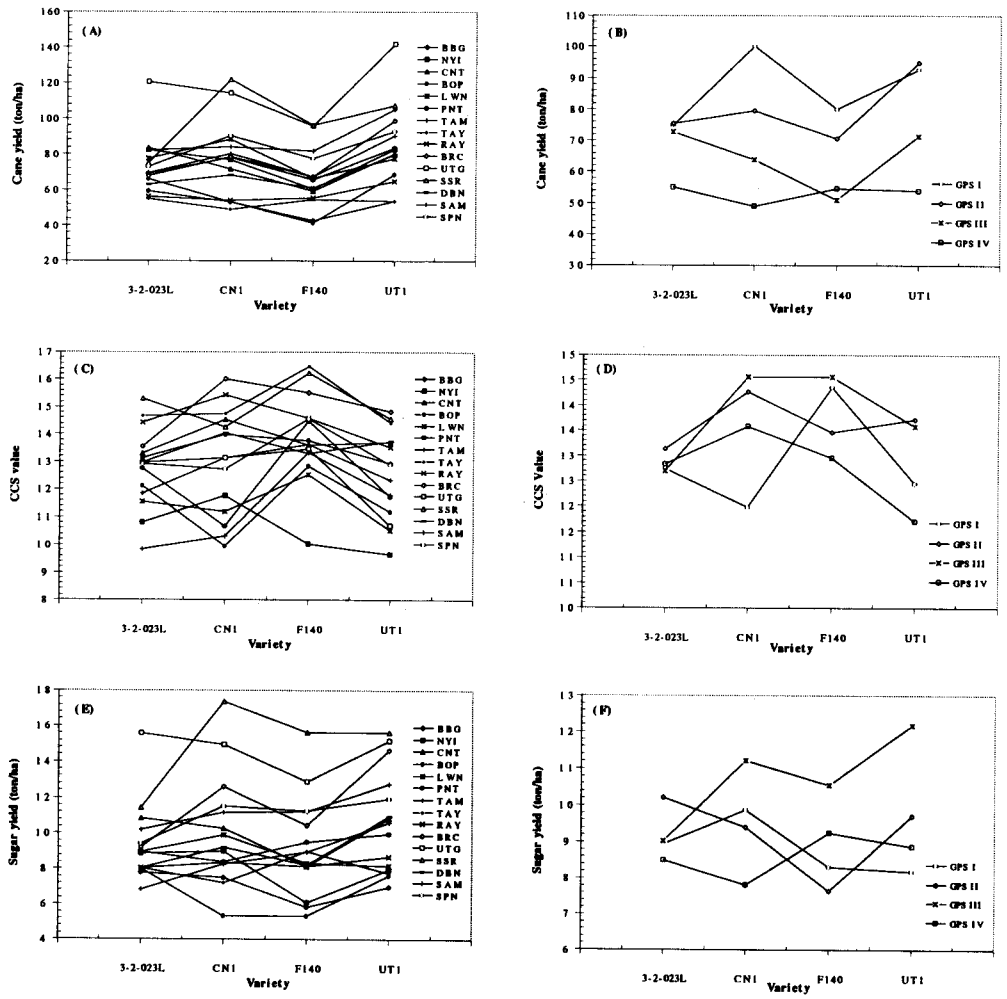

Figure 3. Performance of four sugarcane clones grown in 15 environments (left) compared with the performance in four environmental groups (right); (A) and (B) cane yield, (C) and (D) CCS value, (E) and (F) sugar yield.

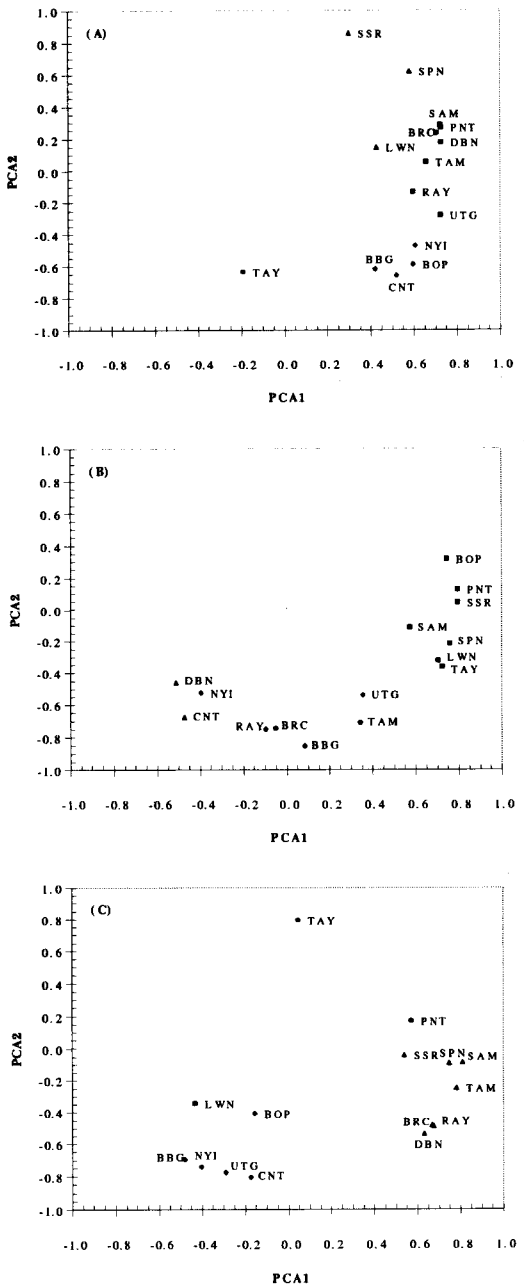

Figure 4. Spatial arragement of 15 locations in two dimensions obtained by ordination procedure; (A) cane yield, (B) CCS value, (C) sugar yield. Each environmental group is represented by different symbols.

5. References

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