Study of Genotype x Environmental Interaction Effects -Using SAS MACROs for AMMI and Tai's Stability models-

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Abstract

This paper discusses the applications of AMMI and Tai's stability methods, which are used to analyze the genotype x environmental interaction (GEI) effects when both genotype and environment are considered fixed. Stability statistics, AMMI, and Tai's stability plots are obtained by using SAS MACROs and user-friendly SAS MACRO-CALL windows. Previously published winter rapeseed yield data (Shafii et al. 1998) is used for validating the SAS MACROs developed. To select the high yielding and relatively more reliable genotypes, an informative 3-d plot is used, which is based on the Tai's alpha, the slope from the regression of genotype means of GEI component on environmental index; and lambda, the deviation from the linear response in terms of error variance and the mean response. The different impacts of taking the year effect as a fixed or random effect in the AMMI and Tai's analyses are also discussed here.

Keywords: Genotype x environmental interaction (GEI), AMMI, Tai's stability, SAS MACRO, SAS MACRO-CALL, alpha, lambda, mean yield.

Introduction

Genotype x environmental interaction (GEI), differential genotype responses in different environments, has a significant impact in multi environmental trials. Selection of genotypes for high and low yielding environments could be severely limited in the presence of GEI. Therefore it is necessary to assess the environmental sensitivity of genotypes in terms of higher yields and stability.

In Tai's (1971) stability analysis, the interaction term is partitioned into two components. They are the linear response to environmental effects, which is measured by a statistic α, and the deviation from the linear response, which is measured by another statistic λ (Tai 1971). A perfectly stable variety has (α, λ) = (-1,1) and a variety with average stability has (α, λ) = (0,1). Tai's analysis provides a method of obtaining the prediction interval for α = 0 and a confidence interval for λ values, so that genotypes can be distributed graphically in different stability regions of the Tai's plot.

The Additive Main Effects and Multiplicative Interaction (AMMI) model is a hybrid model and incorporates both the additive and multiplicative components of the two-way data structure (Shafii, et al. 1992 & 1998). The AMMI biplot analysis is considered to be an effective tool to diagnose the GE interaction patterns. In AMMI, first, the additive portion is separated from interaction by ANOVA. Then the Principal Components Analysis (PCA), which provides a multiplicative model (Gabriel 1971; Zobel, et al. 1988), is applied to analyze the interaction effect from the additive ANOVA model. The Biplot display of PCA scores plotted against each other provides visual inspection and interpretation of the GEI components. Integrating biplot display and genotypic stability statistics enables genotypes to be grouped based on similarity of performance across diverse environments.

SAS program statements for performing Tai's stability analysis were published previously (Fernandez, 1991). Shafii et al. (1998) also presented the SAS program statements to perform the AMMI analysis. However, as the SAS program-based approach is not user-friendly, a good knowledge in SAS programming is essential to modify these published codes and to perform these GEI analyses. Therefore, one of the objectives of this study is to develop user-friendly SAS applications to perform Tai's and AMMI stability analyses by developing SAS MACROs and SAS MACRO-CALL windows.

SAS MACRO

SAS MACRO programs are developed for Tai's and AMMI methods. The relevant MACRO-CALL files for these two MACROs are developed. The MACRO-CALL windows are made simple by allowing the agronomists and horticulturists to input their data set name and the relevant variables, to run the Tai's and the AMMI analyses. An example of a user friendly MACRO-CALL window is shown in Figure 1. The end-users can download the MACRO-CALL files via the internet by visiting Fernandez's (1999) homepage at http://www.ag.unr.edu/gf. During the SAS session, the MACRO-CALL file automatically accesses in one run the SAS MACROs and provide the required exploratory graphs, stability estimates, and stability plots.

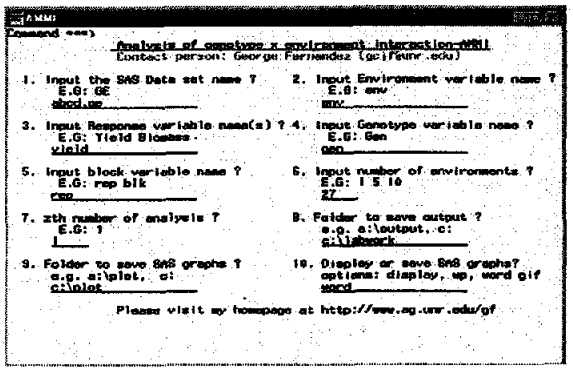


Figure 1

Results and Discussion

To validate the two SAS MACROs, we used the published winter rapeseed variety yield data that consist of yield for 6 genotypes grown in 14 sites for three years with 4 replicates per trial. In the original analysis, 14 sites and 3 years with different combinations were treated as 27 fixed environments. Two AMMI analysis biplots (Figures 2a and 2b) and the Tai's stability plot (Fig. 2c) that were obtained by running SAS MACROs of AMMI and Tai's analyses, are similar to the published figures (Shafi, et al. 1998). By using these MACROs, agriculturists can obtain the AMMI biplots and Tai's stability plots to evaluate genotypes more efficiently without writing SAS program codes.

An additional 3-d plot of response mean by Tai's stability estimates (alpha, lambda) (Fig. 2d) is produced by running the SAS MACRO of Tai's stability analysis.

It can be argued that mere alpha and lambda statistics derived from the GEI component values are not sufficient to select the best high yielding stable genotype, but the mean yield values also should be considered while making the decision. This 3-d plot is useful to visually evaluate the yield potential and stability estimates of the genotypes.

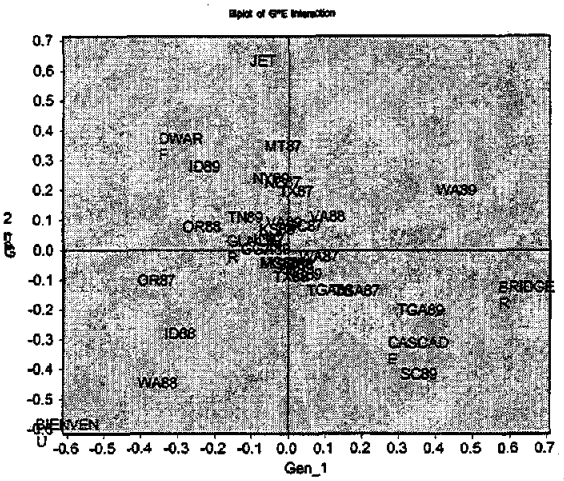


Figure 2a

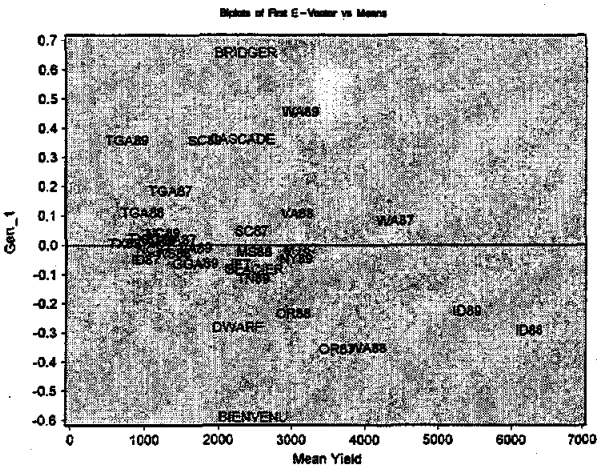


Figure 2b

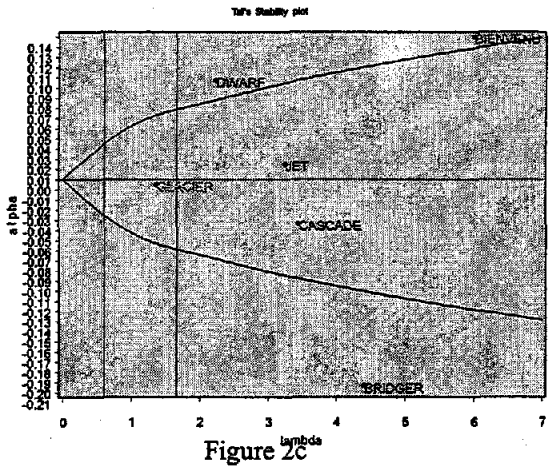


Figure 2c

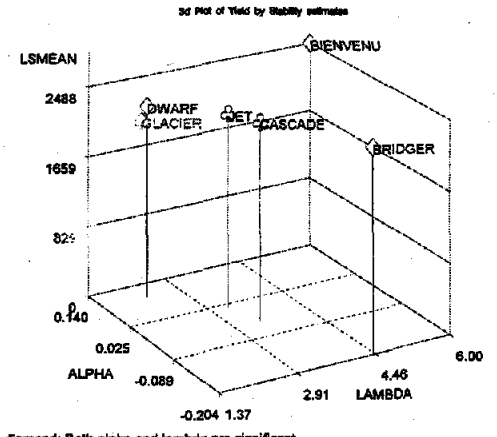


Figure 2d

The graphical analyses indicate that Glacier is the most stable variety and Jet and Cascade come next in order. The other three varieties Bienvenu, Dwarf and Bridger, are classified as highly unstable genotypes as their alpha and lambda values are significant even though their mean yields are high. Although the Bienvenu variety has produced the highest yield, based on stability statistics, this genotype is named as a highly sensitive and unstable genotype.

It is arguable that the year should be treated not as a fixed effect as in Shafii et al.'s (1998) GEI analysis but rather as a random variable, because as we cannot assure how the climate could change from year to year. However, in the AMMI and Tai's analyses, environmental effect is considered as fixed and an option of including a random factor in the GEI analyses is not available. Therefore, two more variations of these analyses (analyses 2 and 3) are presented: 1) consider locations as environment (fixed) and year effect (random) is treated as additional replicates (total number of replicates 12 : 3 year x 4 replicates); and 2) consider locations as environment (fixed) and year effect (random) is treated as the only replicate (total number of replicates 3 : 3 year). Since the replicates (blocks) were not significant in the original analysis, the mean of 4 replicates are now used as the response in the present analysis.

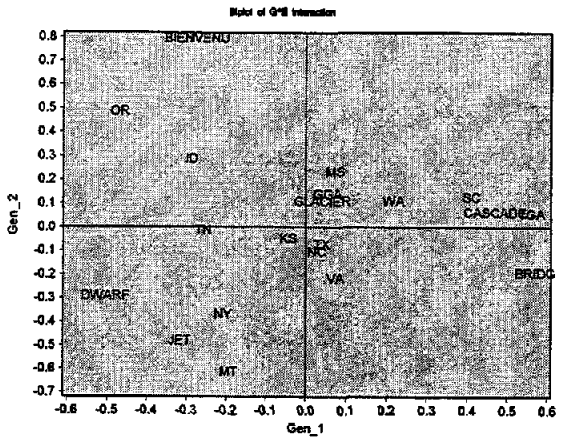


Figure 3a

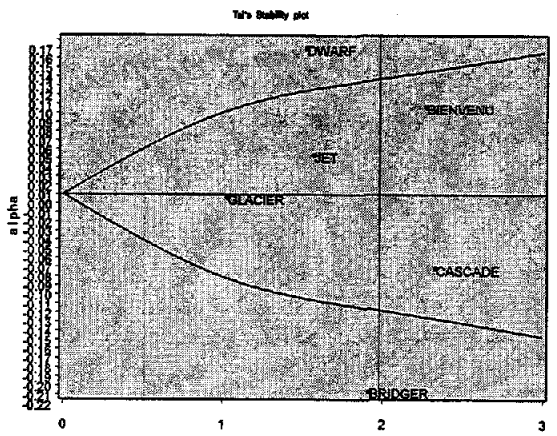


Figure 3c

Figures 3a, 3b, 3c and 3d are obtained for the same winter rapeseed data where locations are treated as fixed environments and year effects are treated as additional replicates. Figures 4a, 4b, 4c and 4d are also obtained when the locations are taken as fixed environments; three years are treated as replicates; and the mean yield of four replications is treated as the response.

Although the AMMI biplots are the same for analysis 2 and 3, the Tai's stability plot and the 3-d plots differ from each other in those cases.

AMMI biplots provide a visual discrimination of genotypes in relation to the environment, and treating year as a random effect has changed the inter-relationship between genotype and environment in the biplots (Figures 2 a&b and 3 a&b). Reducing the number of replications from 12 (Analysis 2: 3year x 4 replication) to 3 replications (Analysis3: 3 years) didn't affect the biplots (Figures 3 a&b and 4 a&b). Since confidence level estimates are not performed in the AMMI analysis, changing the number of replicates does not alter the biplot display in analysis 2 and analysis 3.

Tai's stability analysis estimates, alpha and lambda, are sensitive to changing the year effect as random, as well as changing the number of replicates. The range of the

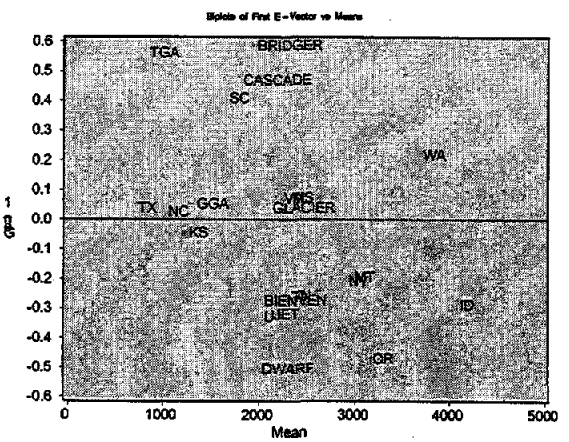
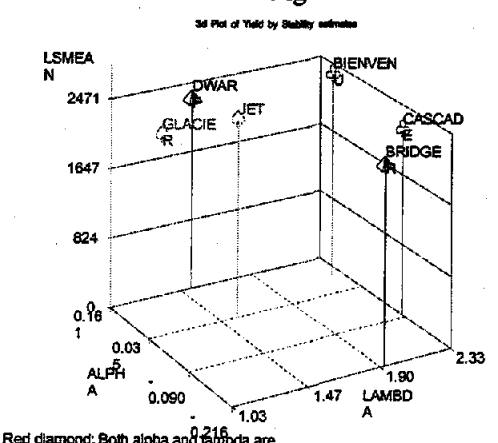


Figure 3b



Red diamond: Both alpha and lambda are
Yellow pyramid: Only alpha is
Blue heart: Only lambda is
Green cube: Both alpha and lambda are not
significant

Figure 3d

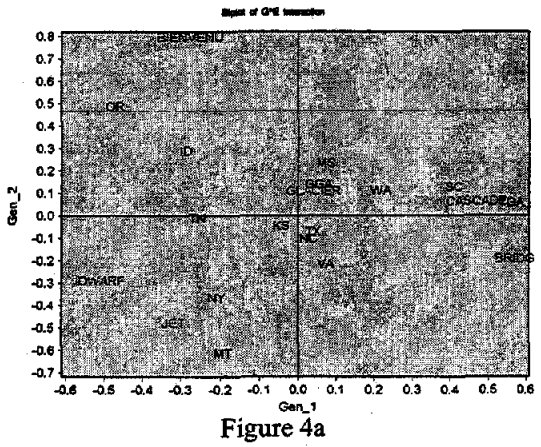


Figure 4a

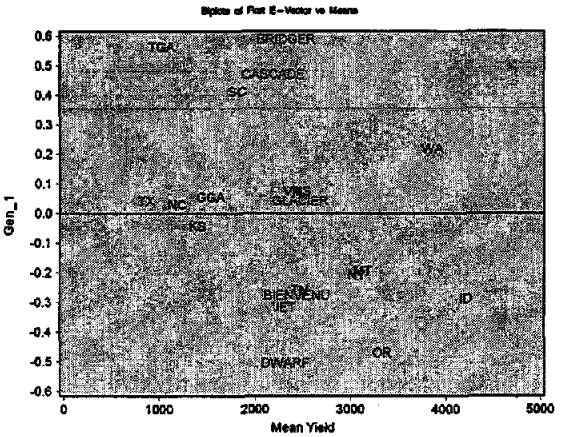


Figure 4b

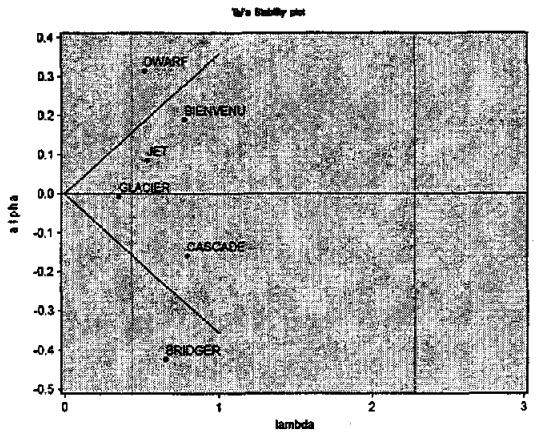


Figure 4c

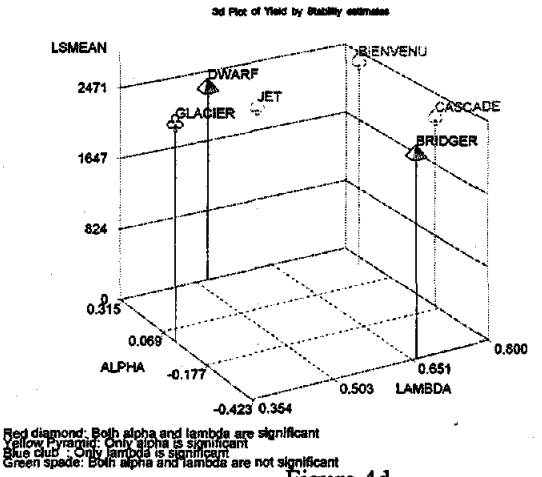


Figure 4d

lambda estimates decreased to 3 (Figures 3 c &d) from 7 in Figures 2c and 2d. The significance of alpha and lambda is also altered significantly by changing the analysis. The high yielding genotype Bienvenu was identified as very sensitive and unstable in the original analysis (Figures 2 c&d) . However, in analysis 3, based on Tai's stability estimates, the same Bienvenu was classified as a stable genotype (Figures 4 c&d).

Therefore, the same data is giving different conclusions when environmental variables and the replicates are changed. Future studies are underway to include random effects (year) in the Tai's stability models.

Exploratory analysis of GEI data

First, the environments are classified as Low (Environment mean < Q1, First quartile), Medium (Environment mean = Q1-Q3) and High (Environment mean > Q3) yielding. Then the genotypes are classified as High (H), Medium (M) and Low (L) yielding under each of the three environments based on the following criteria:
High (H) If Genotype mean > (High environment mean + LSD value).
Medium (M) If Genotype mean = (Medium Environment mean +/- LSD value).
Low (L) If Genotype mean < (Low environment mean - LSD value).

Thus, according to the levels of average yield obtained in each environment, the genotypes are categorized again as MMM, MMH, etc. as shown in Figure 5. For instance, MMM indicates that the particular genotype gives medium levels of yield in all three environments. A new SAS MACRO, EXPLORGE, produces the genotype groupings represented in Figure 5.

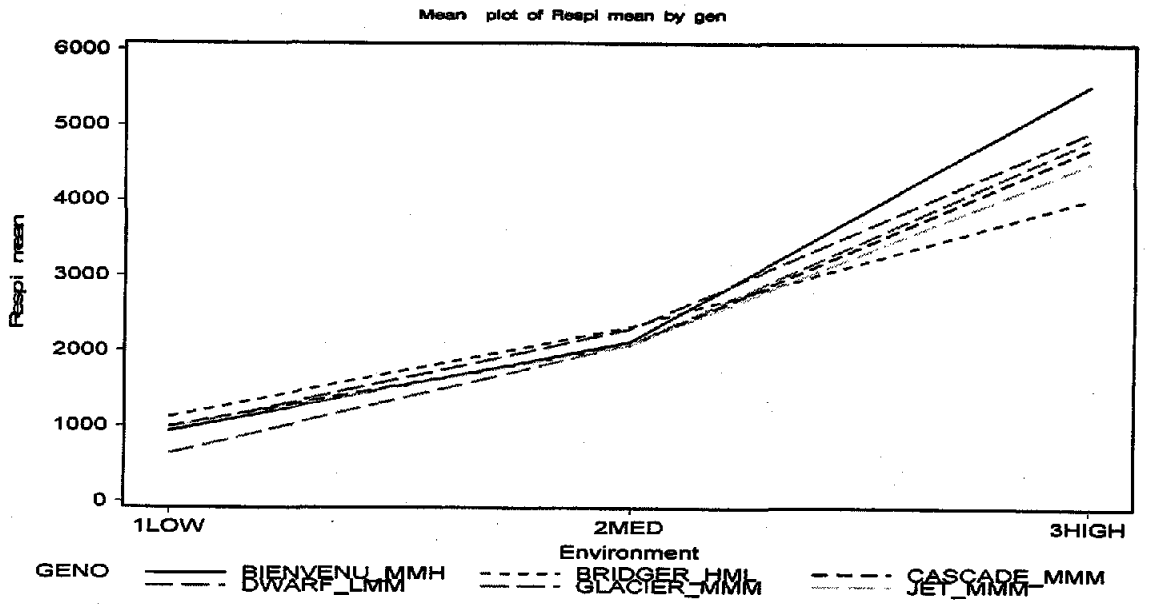


Figure 5

According to this exploratory analysis, Glacier, Cascade and Jet are classified as average stable genotypes (Figure 5). Bienvenu is falling into the category of MMH where it is giving a medium yield at low and moderate environments and a higher yield at the favorable environment. Therefore, according to the plot shown in Figure 5, it can be seen that the variety Bienvenu is the most desirable and high yielding genotype.

This result contradicts the conclusions made in AMMI and Tai's stability analyses. Therefore, the question is whether all environmentally sensitive genotypes are undesirable. Additional research is required in GEI.

Summary

SAS MACRO programs are developed for Tai's, AMMI and ExplorGE models, and the researchers could use these user-friendly MACROs directly from the internet, by following the instructions given in the following homepage: (http://www.ag.unr.edu/gf) Fernandez (1999). The data used by Shafii et al.'s study is analyzed here and different answers for treating location-years and location as environment are obtained. Treating the years as random effects and the ways to incorporate them in the GEI analysis are left for future studies.

The 3-d plot of yield by stability estimates is more informative to plant breeders wishing to select higher yielding stable genotypes.

The exploratory mean yield plot shown in Figure 5 gives a clear picture of the yield trends of different genotypes under three environments, but the results contradict with AMMI and the Tai's stability analyses. Therefore, we are investigating another study where the yield data is simulated artificially for all possible environmental combinations. In addition, those trends are analyzed and compared with the AMMI and Tai's stability plots.

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