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The influence of error variance variation on analysis of genotype stability in multi-environment trials

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ABSTRACT

Multi-environment trials are often analyzed to assess the yield stability of genotypes. Different approaches to stability analysis can be cast into a unifying mixed modeling framework. The choice of the class of candidate mixed models and the estimates of the model parameter have direct implications for the stability measure. The heterogeneity of residual error variances across environments generally exists in multi-environment trials. The objectives of this study were to investigate the impact of the analytical procedure with different considerations about error variances when assessing yield stability of genotypes. A series of 16 multi-environment trials from a corn-breeding program in the north of China were simultaneously analyzed from 2005 to 2008 using a randomized complete block design at each environment; the analysis used five most common stability models with homogeneous residual error variances, as well as their heterogeneous residual error variance versions to take into account that different environments may have different levels of precision. The results showed that whether the error variance differences across environments were accounted for in the analysis procedure did not affect the choice of appropriate models for stability analysis, but considerably influenced the estimates of model parameters (percentage difference of the parameter estimates between models with heterogeneous and homogeneous residual error variances varied from −122.4% to 65.7% depended on genotypes and trials), and hence influenced the stability ranking of some genotypes. The models with heterogeneous residual error variances fitted the trial data better and gave (with 2.1–8.4% reduction) smaller standard errors of model parameter estimates than their homogeneous residual error variance versions, which suggests that the model with heterogeneous residual error variances constitutes a good alternative analysis for genotype stability in multi-environment trials.

1. Introduction

When assessing the relative performance of various genotypes or cultivars, stability of their yield performances is an important attribute to consider (Ramana et al., 2011). Different methods and approaches for stability analysis have been researched with constantly growing number (Piepho and van Eeuwijk, 2002). In the analysis history, stability can be ascertained using various stability statistics (Lin et al., 1986; Westcott, 1986; Becker and Leon, 1988; Kang and Gauch, 1996; Piepho, 1998a; Piepho and van Eeuwijk, 2002). Traditional measures of stability include environmental variance (Lin et al., 1986), coefficient of variation (Francis and Kannenberg, 1978) and Shukla's stability variance (Shukla, 1972). Modified stability analysis as suggested by Hildebrand (1984) used the regression approach of Finlay and Wilkinson (1963) and Eberhart and Russell (1966) to assess the stability of treatments or genotypes over a wide range of environmental conditions. An alternative approach to the regression analysis is the additive main effects and multiplicative interaction (AMMI) model (Kempton, 1984; Zobel et al., 1988; Gauch, 1992). The AMMI model was originally proposed as a fixed effects model. Assuming environments (or genotypes) as random, the genotype–environment interaction can be analyzed in a mixed-model framework with a factor-analytic covariance structure to model the multiplicative terms (Piepho, 1997, 1998a,b). Denis et al. (1997) and Piepho (1999) pointed out that most of the common stability measures may be embedded in a mixed-model framework, where environments are a random factor and genotypes are fixed. The estimated variance components of an appropriate mixed model serve as measures of stability. A major advantage of mixed model approach with restricted maximum likelihood (REML) estimation is its applicability for unbalanced data. An other salient feature of the mixed model approach is that it is not

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only possible to consider the correlation (or variance-covariance) structure of genotype–environment interaction but also to model residual error variance heterogeneity between the trials conducted in different environments with different levels of precision and eventually to model spatial variation of error terms (Frensham et al., 1997; Piepho, 1999; Smith et al., 2001, 2005; Ramana et al., 2011).

Piepho (1999) showed how mixed model analyses of unbalanced data for the most common stability measures are readily available through the variance structures fitted using SAS procedure MIXED. Piepho and van Eeuwijk (2002) demonstrated with a realistic example the choice of an appropriate model and the interpretation of variance components as measures of stability. It is emphasized that usefulness of any measure of stability depends crucially on how well the underlying model approximates the real data (Piepho, 1998a), which means that the choice of the class of candidate mixed models and the estimate of the variance component have direct implications for stability measure.

Multi-environment trials play an important role in evaluating genotypes at many stages of plant-breeding programs, as well as when recommending varieties for plant production. In these trials, it is quite common that the variances of genotype–environment interaction vary due to performance difference of genotypes across environments (Piepho, 1999; Piepho and van Eeuwijk, 2002; Hu and Spilke, 2011) and that the variances of residual errors vary across environments due to differences in natural conditions (e.g. soil and weather, etc.), as well as experimental operations across different environments (Casanoves et al., 2005; Hu et al., 2013).

There are already several studies on the impact of the heterogeneity of error variances on the point estimate and statistical hypothesis testing of genotype effects (Casanoves et al., 2005; Hu and Spilke, 2011; Hu et al., 2013) and numerous studies on yield stability analysis (Kempton, 1984; Frensham et al., 1997; Parsad et al., 2009; Piepho, 1999; Virk et al., 2009; Smith et al., 2001, 2005; Ramana et al., 2011) for multi-environment trials or on-farm trials. Some of these studies also accounted for the heterogeneity of genotype variances, the heterogeneity of residual error variances or both of them. But most of these contained no worked example or just a small data set for demonstration.

The objective of this contribution was to investigate the direct implications of heterogeneity of residual error variances for stability analysis of genotypes based on diverse data sets from realistic multi-environment trials and hence to convince the practitioner of using the appropriate mixed model or/and appropriate procedure for stability analysis, where the variance heterogeneity of both genotype–environment interaction effects and residual error effects would be simultaneously accounted for. The analysis contains three consecutive steps: (1) fitting the most common stability models to each data set using REML under two different considerations about residual error variances. One assumed homogeneous residual error variances and the second assumed heterogeneous residual error variances; (2) ranking the models in goodness-of-fit and comparing the goodness-of-fit as well as the ranking of the models between the two considerations; and (3) comparing estimates of model parameters and ranking order of genotype stability between the two considerations based on the selected stability models.

2. Materials and methods

2.1. Data

The data sets used in this study came from multi-environment trials in a corn breeding program in northern China conducted from 2005 to 2008. There were 4 trial groups in these regions for different production types during each year, i.e. the genotypes were not the same under different trial groups and years. Therefore, in total there were 16 (4 years × 4 groups) independent data sets. Some 15–17 genotypes were tested at 22–23 environments each year. All trials in each environment were laid out as a randomized complete block design (RCBD) with three replicates. All trial plots were 12 m^2, and yield data were expressed in kilograms of corn per plot. In 2006 and 2008, some genotypes' yield data were not available in some of the test environments, and hence data sets for these trials were unbalanced. For details of the data set structure, see Hu et al. (2013).

2.2. Analysis models

We conducted a combined analysis within each data set using the following multi-environment trial model:

$$y_{ijk} = \mu + b_{jk} + \alpha_i + \beta_j + (\alpha\beta)_{ij} + e_{ijk}, \quad (1)$$

where y_{ijk} ($i = 1, \ldots, I$; $j = 1, \ldots, J$; $k = 1, \ldots, K$) is the yield of genotype i, in environment j, block k; μ is the overall mean; b_{jk} is the effect of block k within environment j; α_i is the main effect of genotype i; β_j is the main effect of environment j; $(\alpha\beta)_{ij}$ is the effect of the interaction of genotype i with environment j and e_{ijk} is the random residual error associated with observation y_{ijk}.

The effect α_i was considered as fixed. The block effect b_{jk} was considered as random with constant variance. The effects β_j and $(\alpha\beta)_{ij}$ were treated as random and their variance covariance could take various forms depended on model assumptions. For example, in model of analysis of variance (ANOVA), it is usually assumed that β_j and $(\alpha\beta)_{ij}$ are independent and normally distributed with constant variances σ^2_β and $\sigma^2_{\alpha\beta}$, respectively, which implies that the variances of all genotypes are equal, i.e. the stability of genotypes across environments is the same, and that covariance, i.e. the correlations of each pair genotypes, are also equal. This corresponds to the CS (compound symmetry) variance covariance structure in mixed models.

As stability variance model, the Shukla's (1972) stability variance model, the Finlay–Wilkinson (1963) regression model, the Eberhart–Russell (1966) model were used in present research. These models correspond to the mixed model with variance covariance structures of UN(1), FA1(1) and FA(1), respectively, and for facilitating later reference the three stability variance models will be referred to as UN(1), FA1(1) and FA(1) models in present contribution, respectively. Additionally, the AMMI model (Gauch, 1988), as discussed by Piepho (1997, 1998a, b), was also used. Depending on the number of multiplicative terms, the AMMI has various forms. For simplicity we used the AMMI with one multiplicative term as the model on which to base stability analysis. The unstructured environmental variance covariance model (usually abbreviated as UN model) is not used in present study due to frequent occurrence of convergence problem in our data fitting and that the multiplicative models FA(1) and AMMI are useful approximation of the UN models (Piepho and van Eeuwijk, 2002). All these stability models, including CS structures, are based on Eq. (1) and differ only in the variance covariance structure for β_j and $(\alpha\beta)_{ij}$. Specifically, variances differ, i.e., variability (stability) of yields across environments depends on the genotype. Details about these models and their implication for stability measures are reported in Piepho (1999) and Hu and Spilke (2011).

The variance covariance of residual error e_{ijk} could also take various forms according to the principle of the mixed model. We used two typical forms here. The first form corresponded to the traditional method, which assumes that homogeneous residual error variance σ^2 under environments exist, i.e. $e_{ijk} \sim N(0, \sigma^2)$. The second form permitted heterogeneous residual error variances across environments, i.e. $e_{ijk} \sim N(0, \sigma^2_j)$ and $\sigma^2_1, \sigma^2_j, \ldots, \sigma^2_J$ were not all the same.