Mixed-Model Analysis of Genotype-Environment Interactions. (C01-yang162358-Oral)

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Abstract:

Variation of genotype-environment interactions can be divided to determine whether or not the interactions involve change in genotype or cultivar ranks across environments. However, no sound statistical tests are available for such determination. In addition, the conventional multivariate analysis of variance estimates of genetic parameters have a number of undesirable properties such as non-positive definite estimates of genetic variance -covariance matrices (leading to negative heritability and out-of-bound estimates of genetic correlation) and large sampling variability. In this talk, we will exploit the power and flexibility of the mixed-model analysis to develop sound statistical tests for crossover vs. non-crossover interactions and to constrain genetic variances and covariances within acceptable ranges. The focus of our presentation will be on identifying some commonly used covariance structures for characterizing and testing different causes of genotype-environment interactions. Examples will be given to illustrate the use of the SAS MIXED procedure for the mixed-model analysis.

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Presentation Information:

Presentation Date: Thursday, November 14, 2002 Presentation Time: 8:30 am

Keywords:

Genotype-environment interactions, Restricted maximum likelihood, Mixed models, Covariance structure