COMPARISON OF SEVERAL STATISTICAL METHODS FOR THE SPATIAL ANALYSIS OF EARLY GENERATION VARIETY TRIALS

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In the early stages of a breeding program, the plant breeder makes many crosses and develops many genotypes to evaluate, but there is often little seed available for each new genotype. Even if there is sufficient seed for more than one field plot, it is more important to sample several environments than to replicate plots at only one of the possible environments, and so unreplicated trials are typically used at this stage. It is important to evaluate new genotypes against well-established controls (check, standard or reference varieties) for which there is plenty of seed. Because of the number of genotypes included and large land area requirements, replicated control variety plots are usually distributed over the trial area as a method of local control, and the yields of the control variety are used as a yardstick against which to assess the yield of each test plot. They provide a benchmark for the test lines, allow an estimate of the experimental error, and enable adjustment of the test genotype effects for spatial variation in the field.

We have compared several statistical methods for the spatial analysis of early generation variety trials using internal historical data from our maize field trials database. The traits analysed were yield and moisture content for grain and silage maize. The analysed trials didn't follow any particular spatial design; we have simply selected the trials from the database that were sufficiently large to justify spatial analysis and that had enough replications of several control varieties. The trials analysed spanned several years and covered different geographic regions; several hundreds trials were analysed for each year, and individual trials comprised at least hundred test entries.

The statistical methods used were: 1) simple one-factor (variety) ANOVA that was used as the baseline model; 2) ANCOVA with plot coordinates, their squares and product as covariates; 3) spatially correlated errors (first-order autoregressive model with two-dimensional spatial structure in both directions); 4) generalized additive models with spline or loess smoothing functions of plot coordinates. All models also included variety as (fixed) factor. The computations were carried out using R and ASReml. We have used the Average Standard Error of the Mean as the criteria to compare the efficiency of different methods.

Although in most cases all the methods presented advantage over the simplistic ANOVA model, there was no clear winner. More sophisticated methods (3 & 4) generally performed better than the relatively simple ANCOVA model. However, they presented a serious problem: in numerous cases the convergence was not reached, which is a major drawback for their use in routine analysis of field trials. Fine tuning of smoothing parameters helped to practically do away with the convergence problem for the generalized additive models, while no satisfactory solution was found for the autoregressive model, which, when convergence is reached, presents the best overall results. We were thus not able to find a method that would be universally applicable; to perform the optimal analysis of unreplicated early generation variety trials, either a human intervention is needed, or one must use the software flexible enough to try several methods and select the one that is best adapted to each particular situation.