

A comparison of analysis methods for late-stage variety evaluation trials

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The primary aim of crop variety evaluation programs is to reliably predict the performance of potential new varieties relative to existing commercial varieties. This is achieved through multi-environment trials (METs), that is, series of field trials conducted across a range of geographic trial locations and possibly over several years. Usually, a program of METs is established to take varieties through from the initial selection of potential breeding lines (often called early generation variety evaluation trials) to eventual commercial release and recommendation to farmers (late-stage variety evaluation trials). This paper is concerned with METs in the latter stages of this process, although many of our results will also apply to early generation trials.

The Australian and UK late-stage variety testing systems were used as the basis of this study. In both cases, a series of trials is set up annually to test a relatively small number (≤ 100) of candidate varieties, which usually contains a set of standard or control varieties, highly-performing established varieties and emerging varieties identified from earlier trials. The set of trials within (and across) years is designed to provide a range of growing conditions, and the term environments is used to describe the set of trial conditions. The aim of the statistical analysis is to use an appropriate model to provide reliable predictions of variety performance across target environments.

The focus in this paper is on the use of linear mixed models which can be implemented as one-stage or two-stage analyses [1]. In a one-stage analysis individual plot data from all trials is combined in a single analysis. In a two-stage analysis variety means are first obtained from the separate analysis of individual trials (stage I), and are then combined in an overall mixed model analysis (stage II). The stage II analysis may be unweighted or weighted to reflect the relative precision of variety means from each trial. In each case, a linear mixed model may be constructed to describe the structure of the data, and this model is usually fitted using REML estimation.

Two sets of trials from Australia and the UK are used to provide realistic scenarios for a simulation study to evaluate the different methods of analysis. This study showed that a one-stage approach gave the most accurate predictions of variety performance overall or within each environment, across a range of models, as measured by mean squared error of prediction or realised genetic gain. A weighted two-stage approach performed adequately for both overall variety predictions and variety predictions within environments. A two-stage unweighted approach performed poorly both for overall variety predictions and for variety predictions at individual environments. The performance of the two-stage methods was related to the change in heritability between the methods.

References

- [1] Smith A, Cullis B & Thompson R. (2005) The analysis of crop cultivar breeding and evaluation trials: an overview of current mixed model approaches. *Journal of Agricultural Science* 143:449-462.