Update on statistical methods for NVT

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ABSTRACT

The accuracy of variety predictions from the analysis of multi-environment trial (MET) data depends not only on the amount of data but also on the goodness of fit of the statistical model to that data. The model traditionally used for the annual analyses of National Variety Trials (NVT) data is a variance component model (see Smith et al. 2001a). Such models are parsimonious, with only a small number of variance parameters to be estimated, but do not fit the data well. We know from experience in analysing plant breeding METs that the goodness of fit of factor analytic (FA) models (as first proposed in Smith et al, 2001b) is usually excellent. We therefore propose to use FA models for NVT data in order to extract the maximum amount of useful information for both grower and breeder decisions. FA models cannot be applied to NVT data in the same way as for plant breeding data (i.e. at the variety by trial level) due to computational issues associated with the large numbers of trials involved and the potential poor variety concurrence between some pairs of trials. Thus a new approach is required and is currently under development. In this paper we demonstrate some of the concepts using NVT data from canola trials sown in 2010. This includes the application of the tools developed by Cullis et al (2010) to assist with the investigation of variety by trial interaction.

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