

RANDOMIZATION-DERIVED MIXED MODELS FOR ANALYZING SERIES OF VARIETY TRIALS

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Processes of evaluation of crop varieties for inclusion in a recommended list are based on data from series of field experiments conducted at a number of locations (sites) and possibly over several years. Such series of variety trials are called multi-environment variety trials (METs). There exist an immense literature on transforming MET data into information useful for breeders and crop evaluators. It reflects different approaches to the statistical analysis of such data. Going back to the origins, it may be interesting to recall the approach of Yates and Cochran (1938, Section 2) who indicated that although “it is usually impossible to secure a set of sites selected entirely at random”, it is advisable to proceed in such a way that the experimental fields actually used in the trials could be considered as “representative” for “all fields which are to be covered by the subsequent recommendations”. This approach has been adopted by organizers of variety trials in many countries. Hence, when modelling the analysis of MET data, a mixed model is usually adopted (see the overview by Denis, Piepho, and van Eeuwijk, 1997; Smith, Cullis, and Thompson, 2005). In deriving a mixed model for such analysis various assumptions related to METs are usually made. They have to take into account that in these trials (a) “the varieties are individuals with distinct identities” and (b) one is faced with “the multiplicity of ways in which varietal responses may vary” (see Patterson and Silvey, 1980, Sections 1 and 5.2).

In the paper to be presented, a mixed model derived from randomization procedures applied at various stages of designing a series of variety trials is considered. So, it depends on the designs chosen for individual trials and on the selection of sites for the trials. Assumptions concerning the varietal responses to different environments play also important role in the derivation of a model. As to the experimental designs, attention is confined to the so-called generalized lattice designs, very much advocated for variety trials (see Patterson and Silvey, 1980, Section 4.2).

References

Denis, J.-B., Piepho, H.-P., and van Eeuwijk, F. A. (1997). Modelling expectation and variance for genotype by environment data. *Heredity* **79**, 162-171.

Patterson, H. D. and Silvey, V. (1980). Statutory and recommended list trials of crop varieties in the United Kingdom (with discussion). *Journal of the Royal Statistical Society, Series A* **143**, 219-252.

Smith, A. B., Cullis, B. R., and 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.

Yates, F. and Cochran, W. G. (1938). The analysis of groups of experiments. *Journal of Agricultural Science* **28**, 556-580.