

Use of structured antedependence models to estimate genotype by environment interaction

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The objective of this research was to compare structured antedependence models (SAD) to random regression models (or reaction norm models) (RRM) in their ability to estimate genotype by environment interaction. In RRM, random effects for a trait are estimated as a regression on the environments and the (co)variances are modelled by a covariance function. In SAD, random effects for a trait are estimated as a function of the same trait in different environments and the (co)variances are modelled by so-called innovation variances and antedependence parameters. One of the major differences between the models is that the SAD allows the genetic correlations between a trait in different environment to be less than unity in situations where the genetic variance is constant across environments, whilst RRM implicitly model the change in covariances and variances simultaneously. Thus, SAD might be more flexible in estimating genetic correlations between a trait in different environments. Initial results from a simulation study indicate that genetic correlations between a trait expressed in different environments tend to be overestimated when using RRM and underestimated when using SAD.