

Modeling of genotype-to-phenotype relations using multi-environment trial data

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Classical use of multi-environment trial data aimed at global (across environments) and local (environment specific) prediction of variety performance, with an emphasis on yield related traits. The class of mixed models proved a convenient vehicle for such predictions. Developments in molecular biology have led to the production of large numbers of genomic traits that are measured on the same genotypes on which traditionally a limited set of agronomic traits was measured. Furthermore, on the genotypes also more sophisticated physiological traits are measured. This extensive genomic and physiological information on the genotypes is matched by more detailed description of the environmental conditions. The supplementary information on genotypes and environments allows more profound biological questions to be asked with regards to the genetic and environmental structures and processes underlying yield and development. To answer such biological questions, mixed models still are useful. In our presentation, we will show for a mixed model framework how multiple traits can be modeled across multiple environments, incorporating genetic, genomic, physiological and environmental information. We will touch on issues related to modeling of genotype by environment interaction, QTL by environment interaction, genetical genomics, QTL mapping, association mapping and genotype-to-phenotype modeling.