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Keynote Lecture

Massively multivariate genetic value prediction in tree breeding – experience from a variety of species

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Massively multivariate prediction of genetic values using Best Linear Unbiased Prediction (MM-BLUP) and the additive (or numerator) relationship matrix (NRM) offers the optimal way of predicting breeding values in large multigenerational breeding programs. It can use all historic data and deal with different measurement traits, different ages of measurement, and different site types (genotype by environment interaction). The NRM allows prediction of breeding values for provenances, parents and offspring, regardless of generation and location, to maximise gain. The framework can deal with cloning, non-additive genetic variation, and phenotypic and genomic data.

There are many challenges in MM-BLUP. A comprehensive data management system is needed for the data itself, metadata, trial designs, pedigree and genetic parameters. An efficient mixed model solver is required to allow all of the data to be used. Recovery of data and pedigree from previous decades can be problematic, as can its quality. Bias in the breeding values due to missing selection data can be overcome for known pedigrees and selection intensities by creating binary selection traits that are correlated with the traits under selection. Data needs to be standardised to deal with variance heterogeneity across trials, based on high quality within site and trait analyses. Data needs to be put into classes of traits, ages and site types to reduce the number of equations that need to be solved and the number of genetic parameters to be estimated. While estimation of additive correlations between traits and ages is relatively straightforward, identification of site types can be problematic if differences in provenance performance or other historic program subdivisions mean that there is poor linkage between sites with different environmental parameters. Non-additive genetic parameter estimates can be difficult to obtain due to limited historic crossing programs and shallow pedigrees. Hybrid breeding programs further complicate this issue.