

# EXPERIENCES OF GENETIC EVALUATION

**Genetic analysis with parameter estimation (using REML) precedes the breeding value computation (BLUP). The genetic model is usually the simplest possible estimation of additive components and their correlations.**

**The basic tools** currently available include ASReml for genetic parameter estimation from mixed-model analysis and TREEPLAN® for breeding value prediction using information from multiple generations, multiple sites, and multiple traits. We have to consider intensified efforts to optimise the analyses, including evaluation of all kinds of special/unusual genetic trials (e.g., trials where seedlings and clones with common parents are mixed).

“*Post-hoc*” blocking and/or spatial analysis with ASReml will be carried out to reduce environmental variation as much as possible and increase heritability. Generally, all data, including non-normal, continuous and categorical data types, are analysed without transformations, since the methods used are sufficiently robust against violations of distribution assumptions.

In older genetic tests where competition among trees becomes significant, there is a need for a “correction for competition”. New models should be tested as they become available and possibilities to compare single-tree and multi-tree plots should be utilised whenever available. Development of competition models is currently a focus area for tree improvement research and Skogforsk contributes actively.

Alternative Bayesian methods for genetic analysis are known and under continuous development, but as yet they demand too much computer power for practical use. If, in the future, marker data can contribute to genetic-merit estimates, Bayesian methods are likely to be introduced.

**Assessment and selection criteria.** We focus on assessment traits that are efficient, i.e., inexpensive to measure and highly correlated with one or more objective traits. Common wood production measures such as height, diameter and density correlate to a varying extent with volume/biomass/



growth per unit area, while quality measures such as straightness/forks/branch angle have additional impact on tree quality and the economic yield of the forest.

**Economic weights** traits and matching selection criteria is critical to achieving an economic impact from breeding. Considering the rotation length of Swedish forests and the uncertainty regarding the potential areas for use of wood raw material in the future, we have to focus primarily on economic weights for the most incontrovertible objective traits of general importance, as presented in a previous section. There is an urgent need to conclude on the economic weights.

**TREEPLAN.** From 2009, the TREEPLAN® project entered a phase when its tools entered practical use for breeding value estimation. The combined analysis of very large numbers of trees and trials has implications for the allocation of material to genetic trials, both as regards to geographic trial location as well as genetic content in order to improve connectedness among populations as described in next section.

**Databases** The TREEPLAN® project has an integrated database system where all measurements and trial information from the genetic tests are stored, together with the pedigree data including all genotypes from founder trees and onwards. It is not as detailed as is the Skogforsk breeding database (Fritid), with the exception of pedigree information and measured data, but has a better structure for its purpose. Fritid is the indispensable source when information has to be searched for updating the TREEPLAN® database; they complement each other.

**Breeding value reports.** The form and format for breeding value reporting will be prepared according to new requirements, among other things depending on whether TREEPLAN® will evolve as the standard breeding value generator. Report generation should be (semi-)automatic and perhaps published on the web in order to be easily accessible to forest managers.

**Data acquisition and use.** The genetic evaluation of field trials is dependent of an adequate measurement and recording of tree data, including their validation and preparation, pedigree preparation, etc. The whole chain from measurements to TREEPLAN® run needs skilful co-operators, for:

- Organisation and performance of trial measurements
- Validation and preparation of recorded data
- Completion of pedigree information, etc. (Fritid)
- Carrying out genetic analysis with the new measurement data
- Uploading pedigree, measurement and other data into the TREEPLAN® database
- Model construction and parameter updates for TREEPLAN®
- TREEPLAN® runs and breeding value prediction
- Result presentation.

Relevant competency and co-operation is essential for all involved in planning, data collection, analyses, etc. All must be aware of a common responsibility to avoid misunderstandings with regards to naming conventions, classifications, and so on.



Review of  
the Swedish  
tree breeding  
programme



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REVIEW OF THE SWEDISH  
TREE BREEDING  
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