

**Exploiting all your knowledge and information for breeding value prediction –
experience in Norway Spruce and Scots Pine.**

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Tree breeding programs are run over many years and much data is collected and knowledge derived from that information during that time. The sheer amount of data and knowledge presents such a problem in management and processing that rarely is all of it integrated when we come to genetic evaluation. To effectively exploit the hard work of many years you need both an intellectual and software framework to allow integration of both the data and the knowledge. Multivariate genetic models and the use of bio-economic models provide such an intellectual framework to allow the prediction of both breeding (BVs) and total genetic values (TGVs) (both generically referred to as genetic values-GVs) to guide breeding and deployment activities. The TREEPLAN® system, its supporting database (DATAPLAN®) and allied tools provide the software framework for the analysis to take place and the results used. Ongoing projects for the prediction of breeding values for Skogforsk's Scots Pine and Norway Spruce breeding programs provide case studies on how integration can be done.

Bio-economic models allow you to weight harvest age traits according to their economic importance. Models to weight different traits economically for the Skogforsk analyses have only so far been used to weight different seed orchard indices for pine according to the different proportions of site types likely to be present in the deployment zones for the orchards. Otherwise subjective trait weighting has been used. Harvest age trait GVs can be predicted from measured trait GVs once estimates are available of the genetic variance of the harvest age traits, and their correlations with earlier measured traits. Realised gain trials can also be used to help with such estimates. Stand volume has been predicted for Skogforsk from tree health and size GVs for site types spread across 11 latitude and site harshness classes for pine, as well as up to 6 other form and wood quality traits for each species from early age measurements. Genetic values of measured traits can also be predicted using these same genetic correlations and appropriate models for the data in each of the trials in which the data has been collected. The largest evaluation to date has analysed to 62 traits simultaneously on over 100,000 genotypes, although more genotypes have been analysed in other species with fewer traits. Databases of genetic parameters (correlations and heritabilities) compiled for each species have allowed construction of inter-trait, -latitude, -site type, and -age models of genetic correlations to allow the multivariate GV prediction. These models are still under discussion and development as more correlation estimates are compiled. Within site analyses have routinely used spatially augmented comprehensive design models to best account for within site variation. Final models for each site have used the modelled genetic correlations and heritability limits from the genetic parameter database to estimate all other significant fixed effects, variances and correlations for use in the combined model, as well as to eliminate data that does not fit the population genetic parameters. The estimated additive genetic variance for each trait in each trial is used to standardise the data and, by allowing a separate error variance for each trait on each site, weight the data by its heritability. A comprehensive probabilistic pedigree has allowed use of all families of the trial species in each trial, including bulks of various sorts, as well as the normal single pair, polymix and open pollinated families. Clonally propagated genotypes of Norway Spruce have also been successfully integrated into the BV prediction. The BVs have been partially validated and used for grafting for future seed orchard establishment across both species.

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*Genecar meeting - Next Generation in Tree Breeding
Örenäs Slott, Sweden
15 September 2009*

The project will enable integration of most of the knowledge and data in the species under study as it is processed. Integrated analysis however requires a substantial commitment in resources to ensure that all of the data and meta-data is gathered, validated and analysed in a consistent way. Once a critical mass of information is compiled and processed, routine breeding value evaluation can proceed smoothly, rapidly and incrementally as new data is collected and processed. Major revision of the systems are only needed as the knowledge of the genetic architecture improves or new trait types are collected, requiring period revisions of the definitions of the measured and harvest age traits for which to predict genetic values. Integration of all data and GVs into a single database however also facilitates the easy implementation of management decisions, as well as the development of further tools to exploit the value in the comprehensive analyses that are carried out. Modules for selection, mating and seed orchard design are currently under development and have been tested in a variety of situations.

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