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GENETIC EVALUATION OF SWEDISH SCOTS PINE BREEDING PROGRAM

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Genetic evaluation of the Swedish Scots Pine breeding program uses a multivariate BLUP (Best Linear Unbiased Prediction) approach which integrates all available data by using inter-site type, inter-trait and inter-age correlations. This avoids biases in predicted values due to artificial or natural selection (mortality) on correlated traits. A database of genetic parameters is used to model correlations separately from the BLUP evaluation. The strong provenance cline in northern Sweden is accounted for by dividing sites on latitude and site harshness, and defining provenances based on country, latitude and selection history. Provenance and provenance-progeny trial survival and height data are included to overcome the narrow provenance representation in routine progeny trials. The growth traits (survival, health, height and diameter) have different additive correlations on the harsh and mild sites and inter-latitude correlations have an auto-regressive decay pattern. Estimation of variance components for survival data on the liability scale remains a challenge. Spatial analysis and data adjustment is used to deal with high within site environmental heterogeneity and to pseudo-normalise the data. High between-site variance and heritability heterogeneity is accounted for by standardising the data by the additive genetic variance for each trait in each trial, and allowing a separate error variance. Correlations between four growth and six form and branching traits, and Lambeth model age:age correlations allow integration of all data. The largest runs predict genetic values for 124 traits for 535,000 genotypes from 41 provenances. The results show reasonable congruence with externally developed transfer functions. Selections for different site types are derived from appropriate provenances and trials from appropriate regions and these show increased gain compared to historic selections from univariate analysis of groups of trials.