ABSTRACT

Forest genetic evaluation (EGF) involves analyzing data from progeny tests using mixed linear models to calculate “best linear unbiased predictors” (BLUP) of tree breeding values. As BLUP depends on the values of the (co)variance matrices for the assumed model, the specification of the dispersion parameters should take into account the positive spatial correlation due to the environmental heterogeneity, and the negative correlation caused by competition among individuals. An additional issue relates to the fact missing data affect the distribution of the maximum likelihood estimates of genetic parameters. In the current thesis, Bayesian methods via Gibbs sampling (GS) and Full Conjugate Gibbs (FCG) were used to estimate the additive genetic and environmental (co)variance components for different individual tree mixed models. The first of these models involved multiple traits and missing records, and the dispersion parameters were estimated by FCG. Within this model, different specifications of the genetic means of hybrid pines using the parametrization of W. G. Hill were compared by means of the Bayesian Deviance
Information Criterion (DIC). Expressions for the additive variance of a trait affected by genetic effects of competition were obtained for a second model, which was later fitted to data of pines.

Direct and competition additive genetic variances and their covariance were estimated using GS for the first time in EGF. Finally, the mixed model for penalized splines by means of a covariance structure and the tensor product of B-splines was expanded to two dimensions, to account for continuous spatial variation. The fit of the model to data from *E. globulus* produced a reduction in error variance and an increase in additive variance, heritability and accuracy of predicted breeding values.

**Key words:** missing records, additive and direct competition effects, spatial trend, individual tree mixed model, tensor product of B-splines, Bayesian estimation, Gibbs sampling, Full Conjugate Gibbs.