## ADDITIVE GENETIC COVARIANCE FUNCTION FOR HEIGHT IN PINUS TAEDA

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Abstract:--Prediction of time trends in additive genetic (co)variances are valuable for estimation of gain over time and for choosing the optimum age of selection. A covariance function, which gives covariance of a trait at any two ages as a function of the ages, is predicted for height in Pinus taeda using data from six progeny tests of P. taeda planted in Eastern Highlands of Zimbabwe assessed at 1.5, 7.5, 9.5, 12.5, 13.5 and 22.5 years. The progeny tests involved factorial matings among 21 female x 7 male phenotypically superior parents selected from plantations in Zimbabwe and South Africa.

The additive genetic covariance matrix of tree heights at the six ages was estimated using individual tree model DFREML. Covariance functions were directly fitted to the covariance matrix using orthogonal polynomials with symmetric coefficients (Kirkpatrick et al. 1990). Full and reduced fits were used to estimate the most appropriate covariance function. A full fit, in which the number of orthogonal polynomials equal the number of ages estimates the coefficient matrix in such a way that the corresponding covariance function exactly reproduces the estimated (co)variances at the ages that were measured. These estimates, however, include the sampling errors. A reduced fit, in which the number of polynomials are less than the number of ages produces a smoothed estimate consistent with the sampling errors. When a reduced fit is used, the program requires the error covariance matrix. The error covariance matrix was estimated by the program after providing it with the phenotypic covariance matrix and assuming that a standard balanced half-sib breeding design with 7 male and 21 female parents, and 20053 residual degrees of freedom. The Lambeth model (Lambeth 1980) was used to estimate the phenotypic covariance matrix because phenotypic covariances between many of the ages at which the assessments were made were not possible to calculate. The justification of using the Lambeth model is that our data was consistent with the model and the model was derived from a larger sample size.

The best fit was a reduced fit (cubic polynomial). Although discrepancies between the observed values and those predicted by the covariance function were significant, the discrepancies were small. The first eigenvalue showed that the first eigenfunction accounted for 99% of the additive genetic variation indicating that there was substantial genetic variation for improvement of height growth at all ages. This also indicates that improvement at one age would result in improvement at all ages. In contrast, the small amount of genetic variation associated with all the other eigenvalues implies that selection to alter the shape of the growth curve will make very little or no progress.

## LITERATURE CITED

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