ENHANCED DETECTION OF GENETIC EFFECTS FROM FORESTRY FIELD TESTS USING SPATIAL ANALYSIS

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Abstract. The precision of forest genetic field tests is limited by heterogeneous environmental variation within blocks caused by gradients in moisture, nutrients, or other factors that vary over a scale smaller than plot size. This nonrandom variation reduces heritability and obscures genetic differences. Here, we use spatial analysis to remove environmental trends from field data and increased the statistical power to detect genetic effects. We applied a random field model to height data that was defined by position (row and column) in a field test. This model described broad environmental trends for a whole (10 x 10) tree family block plot. Residuals from the random field model contain "detrended" phenotypic information (systematic environmental variation removed) and decrease the intensity of autocorrelation between neighboring individuals.

A field test established in Lumberton, North Carolina, with the objective to detect average effects QTLs for shoot elongation in loblolly pine was used as an example. Five 100-tree rectangular family plots in blocks 4, 5, 6, 8 and 9 were evaluated for second year height increment. From the overall data (500 trees), a subsample of individuals was taken to obtain RAPD marker information from megagametophytes.

Results show that the random field method is efficient in removing fixed environmental trends in the data which due to their intensity usually mask real genetic differences. Considering the data from forest genetics field experiments within a spatial framework is more natural and can refine statistical analysis and improve the reliability of the inferences drawn from it. Taking into account spatial relationships lowers both environmental and phenotypic variances and increases heritability.

Keywords. Data analysis, spatial statistics, spatial autocorrelation, QTL, heritability.