

UNDERSTANDING GENOTYPE-BY-ENVIRONMENT INTERACTION ON LOBLOLLY PINE CLONAL TRIALS

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The success of genetic improvement program is to provide genotypes with guaranteed superior performance in terms of productivity and or quality across environmental conditions. To achieve this goal it is necessary to have a good understanding of the phenotype, which is a result of the combination between genotype's performance and environmental. The present study evaluates a series of six loblolly pine (*Pinus taeda* L.) clonal trials established on the southeast U.S. that were measured for total stem volume and survival. The main objective of this study is to explore GxE interaction for this clonal population by fitting a range of linear mixed models. The dataset came from a series of genetic trials established by the FBRC from the University of Florida (CCLONES). This study contains 61 full-sib loblolly pine families planted in single-tree plots as an incomplete block design with eight full replicates assigned to a silvicultural treatment (operational or intensive management). The variables evaluated were total stem volume and survival.

Initially, a single-site analysis was fitted for each of the two silvicultural treatments, the objective was to evaluate if there are statistical differences among treatments, in terms of genetic control of the traits of interest. Also one- and two-stage analyses were performed to obtain the information required for an MET analysis, in both cases, the silvicultural treatment effects were ignored. For the two-stage MET analysis several models of lesser complexity were fitted. The first stage consists on performing single-site analyses where all the design features of each trial are considered. For the second stage, the predicted means are used as response to fit a simpler weighted linear mixed model of the following form based on the implicit model.

The results of this study indicate that it is expected to obtain very similar rankings for genotypes selected under the two silvicultural levels evaluated (operational and intensive) in this trial series. The results of the explicit model analysis provided with an interesting Type B genetic correlations of 0.627 and 0.566 for VOL and SURV, respectively. For the implicit model, the results for VOL show values ranging from 0.412 to 0.802 (average of 0.568).

The one- and two-stage analyses provided very similar correlations, rankings and breeding values; however, the two-stage analysis resulted in increment in the genetic correlations. This increment ranged from 0.62% to 36.91% (average increment of 14.46%). Factor analytic analysis is appropriate when there are a large number of trials with high genotype-by-environment interaction. Biplots analysis summarized the genotype-by-environment successfully and confirmed the positive correlation between all the environments for volume found earlier.

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