

GENETIC ANALYSIS OF REGIONAL MULTI-ENVIRONMENT TRIALS
OF *PINUS TAEDA* REVEALS FAMILY LEVEL PATTERNS OF
GEOTYPE-BY-ENVIRONMENT INTERACTION

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Loblolly pine (*Pinus taeda* L.) is the predominant plantation timber species in the southeast United States, covering more than 80m hectares of plantation forests from east Texas to southern Virginia. This range encompasses a wide array of environmental conditions, such as a gradient of minimum winter temperatures, climatological differences between coastal and continental regions, and a large variety of different soil types. For this reason, growers of loblolly pine have environmental adaptability as one of their primary concerns when choosing genotypes to deploy in their production area. In order to understand the genetic potential of loblolly pine genotypes in breeding programs, genetic tests are conducted in multiple environments representing, as accurately as possible, the range of potential environments in which they will be deployed. In this report, genetic analysis was conducted on a multi-environment trial dataset with 324 half-sib families planted in five test series across thirty-eight locations ranging from southeast Mississippi to northeastern North Carolina. These test locations span a range of latitude from 35.5N to 29.7N, and a range of mean minimum winter temperatures from to -11.5C to -5.1C. Each series represented a group of tests established with the same genetic entries, but tests in different series were highly unbalanced. Out of $(329 \times 38)=12502$ possible genotype-by-environment combinations, 2640 were present in the data. To account for this imbalance, a hierarchical analytical approach was undertaken. Single test series were analyzed independently using factor analytic mixed models in order to estimate genetic correlations and variance components, followed by a combined analysis in which the parameters estimated from the first step were held fixed. In the combined analysis, the type B genetic correlation between test sites in different series was fixed at a global value estimated as the average of the among-site correlations from the first step. Traits measured included tree height, volume, and stem form. The average type B genetic correlation for height, volume, and stem form were 0.73, 0.64, and 0.78 respectively, indicating GxE was more important for volume than for height or stem form. In the combined analysis, the inclusion of a nested parent-by-site mean minimum temperature interaction effect significantly improved model fit. These results contribute to a more granular understanding of the magnitude of genotype-by-environment interaction in loblolly pine, as well as the relationship between geographic origin and genotype performance over a wide environmental range.