Estimation of Genetic Parameters and Breeding Values Using ABLUP And HBLUP in *Pinus taeda* L. Piedmont Rooted Cutting Trials

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Multi-environmental trials are the standard for estimation of genetic parameters and breeding values in pine tree improvement programs. Traditionally, analysis of multi-environmental trials has been performed using pedigree information to estimate relationships between individuals for ABLUP analysis. However, growing accessibility to genomic tools for pine species has made the implementation of genomic based analysis methods such as HBLUP more commonplace. In this study, five trials located across the Piedmont region of the southern United States were analyzed at age six using pedigree based ABLUP and genomic based HBLUP to estimate genetic parameters and breeding values in a population of clonally propagated *Pinus taeda*. Analysis of the growth traits height, diameter at breast height, and volume showed individual tree heritabilites ranging from 0.18-0.25 using ABLUP to 0.22-0.34 using HBLUP. Type B genetic correlations for each trait were high, between 0.89-0.92, indicating minimal genotype by environment interaction. Breeding value accuracies were high for both analysis methods, between 0.87-0.95. Utilization of HBLUP, increased the mean breeding value accuracy values across all traits for genotyped, ungenotyped, and parental breeding values compared to ABLUP. These results indicate that while clonal progeny testing alone can generate breeding value estimates with high accuracies, incorporating genomic relationships through a blended relationship matrix using HBLUP further improves breeding value accuracies while increasing heritability estimates for growth traits.