

HIGH RESOLUTION X-RAY MICRO COMPUTED TOMOGRAPHY FOR GENETIC ANALYSIS OF WOOD TRAITS

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Wood density is commonly measured in wood cores with a 2 dimensional x-ray scanning densitometer. An alternative is x-ray computed tomography (CT), which provides a higher resolution method that creates an image of wood which can be used to measure wood, annual growth ring, earlywood and latewood density, as well as cell wall thickness and lumen area. We have developed analytical methods to use x-ray CT to enhance our understanding of wood density, tracheid diameter and lumen area. In the winter of 2011-2012, three 2-mm diameter micro-cores per tree were collected from 5600 trees from 6 repetitions of the intensively managed treatments from the Nassau Co., FL; Cuthbert, GA and Palatka, FL sites of the CCLONES loblolly pine (*Pinus taeda L.*) clonal study. Using the freeware Image-J software, density profiles were generated from each image and later this data was processed based on the predicted value of density generated using a linear model where the gray-value of each pixel is strongly correlated with density ($R^2 = 0.99$). Using this technique, and a SAS program, we quantify density for each growth year and earlywood and latewood within each annual growth, latewood percentage, and tracheid radial dimensions. Using a quantitative genetic analysis approach we computed heritabilities and Type B genetic correlations for these traits. Heritabilities for density were in the range of 0.35 with SE of 0.05. Type B genetic correlations for density were found to be significantly high with low standard errors. Latewood percentages were low to moderate depending on the year and cell dimensions were also low. A secondary R code was developed to detect false rings and correct the transition point between earlywood and latewood and re-estimate means, heritabilities and Type B correlations. The result of this correction was very significant since some genetic estimates were actually improved.