Association and Quantitative Genetics of Wood Properties in Loblolly Pine

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One of the main approaches for improving the efficiency and sustainability of wood production is the genetic improvement of select forest tree species. In the case of loblolly and slash pines in the southeastern USA, genetic improvement is still in its infancy with breeding programs just entering their 4th selection cycle and being directed at improving stem form, growth, and disease resistance but not wood properties per se. Advances in high throughput wood property phenotyping and SNP genotyping now enable the dissection of the genetic architecture and association of specific alleles with these traits that could not only permit but also accelerate the breeding for wood properties tailored to specific end uses. Towards this goal of accelerating the breeding for improved wood properties in loblolly pine, we have phenotyped juvenile corewood anatomical (density), chemical (carbohydrate, lignin content) and physical (stiffness) properties in a large clonally propagated genetic test to better understand the genetic architecture of these traits and to discover the alleles and genes controlling these properties via association genetics. As expected wood anatomical, chemical, and physical properties are inherited as polygenic traits with the greatest level of genetic control being observed for stiffness and the least for chemical composition. For the association genetic analyses, a new Bayesian approach with a novel missing data imputation method was developed that permits the simultaneous testing of large numbers of SNPs with phenotypes. These analyses have identified significant associations between wood properties and the 2182 informative SNP genotypes available for this structured population.

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