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Discovering the genetics of wood leads to quality improvement

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Wood is the most abundant form of biomass on earth and is also the leading industrial raw material. Americans are dependent upon wood for home construction, other building materials, furniture, and paper products.

Forest tree breeders are working to improve wood characteristics in pine, although progress is slow because very little is known about the underlying genes that produce wood.

With support from USDA's National Research Initiative (NRI), researchers at the Institute of Forest Genetics (IFG) at the University of California at Davis are using genomic sciences to identify the genes that produce wood.

They are also seeking to develop technologies that will enable pine breeders to make rapid improvements in the quality of wood.

RESEARCHERS BEGAN GENETIC MAPPING FOR WOOD PROPERTY TRAITS IN LOBLOLLY PINE ALMOST 10 YEARS AGO. THEY CONSTRUCTED THE FIRST GENETIC MAP FOR LOBLOLLY PINE TO IDENTIFY QUANTITATIVE TRAIT LOCI (QTL) FOR WOOD DENSITY.



WOOD PROPERTIES

The physical properties of wood, such as density and the angle of microfibrils in the cell wall, are major determinants of the strength of solid wood products. Chemical wood properties, such as the amount and type of lignin and cellulose, are important in pulping and the production of paper.

Wood property traits are generally under moderate to strong genetic control.

This NRI-funded research program has led to a significant advancement in the understanding of which genes produce wood in pine.

Genetic improvement through breeding has already been accomplished. Wood property traits are all assumed to be under the control of many genes.

Breeders use quantitative genetic models for the selection and testing of superior genotypes. However, knowledge of the exact genes controlling wood property traits is lacking.

The IFG began genetic mapping for wood property traits in loblolly pine almost 10 years ago. The researchers constructed the first genetic map for loblolly pine using restriction fragment length polymorphism (RFLP) markers. They then used this map to identify quantitative trait loci (QTL) for wood density.

The results of this work enabled the researchers to determine the locations in the loblolly pine genome for wood property traits and to estimate the effects of individual QTLs on individual wood property traits.

Subsequently, they have mapped QTLs for other important wood property traits such as microfibril angle, percent late-wood, and wood chemistry components.

COOPERATIVE PROJECT

With funding help from the National Science Foundation, researchers at North Carolina State University initiated a loblolly pine gene-sequencing project. Their

goal is to identify most, if not all, of the genes that are expressed during wood development.

The IFG lab is mapping genes from this database onto its genetic maps where wood property QTLs have already been found. This mapping will lead to identifying the genes most likely controlling the wood property traits of interest to breeders. This action is known as candidate gene mapping.

The researchers have already observed several examples where QTLs and candidate genes map to similar locations. Two promising associations include: (1) S-adenosyl methionine synthetase and (2) phenylalanine ammonia-lyase (both genes in the lignin biosynthesis pathway) with QTLs for wood specific gravity on loblolly pine chromosomes 3 and 6, respectively.

IMPACT

This NRI-funded research program has led to a significant advancement in the understanding of which genes produce wood in pine.

Future goals of this program are to learn how such genes work together to make better wood and to survey large populations of loblolly pine to find the very best variants of these genes that can be incorporated into existing breeding programs.



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