Forest and Wildlife Research Center interim director Bob Karr, right, and Daniel Peterson examine small pine trees in the College of Forest Resources' Biotechnology/Genetics Lab.

Marco Nicovich

MSU RESEARCH *Unravels Pine Tree Mysteries*

Loblolly pine is the primary source of pulpwood for the entire U.S. paper industry and the most economically important crop of any kind in the Southeast.

Despite its economic importance, little is known about the genome of loblolly pine. The term genome refers to the DNA that defines an organism, including its genes and the DNA sequences containing 'blueprints' for all the heritable characteristics of the organism. In short, the genome is what makes a human a human, a cat a cat and a pine tree a pine tree.

Mississippi State University recently received a $1.6 million, three-year grant from the National Science Foundation to use state-of-the-art molecular biology techniques, robotics and powerful computational methods to research the pine genome.

Daniel Peterson, an assistant professor of molecular biology in the Department of Plant and Soil Sciences, leads the research group. The grant includes $1 million earmarked for research in Peterson's lab, the Mississippi Genome Exploration Laboratory (MGEL), and is one of the largest NSF grants ever awarded to MSU's College of Agriculture and Life Sciences.

The work on the project is being conducted through the Mississippi Agricultural and Forestry Experiment Station.

Peterson said characterizing the pine genome will not be an easy task because the vast majority of its makeup is highly repetitive 'junk DNA.' In fact, only about 2 percent of the pine genome contains genes.

"Additionally, the genome of pine is seven times larger than

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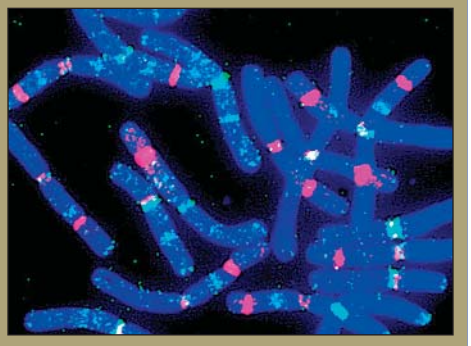

that of the human genome," Peterson said. "While both pine trees and humans have about 20,000 to 50,000 genes, pines have a lot more repetitive DNA. It will take a lot more >sifting' to get the pine genes out of the pine genome."

Peterson is especially qualified to tackle the monstrous pine genome. In 2002, while doing postdoctoral research at the University of Georgia, he was lead inventor of Cot-Based Cloning and Sequencing, a technique that allows scientists to efficiently separate genes from repetitive sequences. CBCS is being used in the research for the new NSF-funded project at MSU.

In addition to Peterson, other members of the research team include Dana Nelson and M. Nurul Islam-Faridi of the U.S. Forest Service's Southern Institute of Forest Genetics in Harrison County, and Doreen Main and Jeffrey Tompkins with the Clemson University Genomics Institute.

College of Forest Resources interim dean Bob Karr said the project is significant for Mississippi and other states with large forest industries. The university administration strongly supports this effort as MSU researchers take leadership roles in the pine genome research.

"The pine genome project is an important first step in the basic science necessary to apply some of the new technology in genetics to forest research," he said. "This will be a foundation other scientists can build on for the improvement of our forests."

Additional information about the pine genome project is available at the MGEL Web site: **http://www.msstate.edu/research/mgel.**