

NEWS RELEASE

Media Contact: Tracey Peake, News Services, 919/515-6142 or
tracey_peake@ncsu.edu

Dec. 14, 2006

Researchers to Study Genomes of Chestnuts, Oaks and Beeches for Clues to Disease Resistance

FOR IMMEDIATE RELEASE

A team of researchers led by scientists at North Carolina State University has been awarded a four-year, \$2.7 million grant from the Plant Genome Program of the National Science Foundation to study the genomes of trees in the *Fagaceae* family, which includes the hardwood species of beech, chestnut and oak.

Dr. Ron Sederoff, professor of forestry and environmental resources in the College of Natural Resources, and a team of colleagues from NC State, The American Chestnut Foundation, Clemson University, Pennsylvania State University, State University of New York, the USDA Forest Service in Gulfport, Miss., and the Connecticut Agricultural Experiment Station will conduct the research.

The American chestnut, a widespread and highly valued tree species of the Appalachian forests, was destroyed during the first half of the 20th century by Chestnut Blight in what has been called the greatest ecological disaster in U.S. history.

Foresters have tried to breed resistance to Chestnut Blight by crossing resistant Asian chestnut species – specifically the Chinese chestnut – with the American species. Sederoff says the research team aims to create an integrated genetic and physical map of Chinese chestnut to pinpoint areas within the tree's genome that determine resistance to Chestnut Blight disease.

Breeding programs – aimed at producing American chestnut trees with resistance to the disease – would be greatly advanced by genomic information that could precisely identify the specific genes involved in disease resistance.

“Looking for the specific genes that have to do with blight resistance is like looking for a needle in a haystack,” Sederoff says. “Creating genetic and physical maps is basically a way to turn a large haystack into a small one, to help us find answers more quickly.”

The genetic and physical mapping studies are an important first step toward the sequencing of the chestnut tree's genome, which would greatly accelerate breeding and support conservation for all beeches, oaks and chestnuts, and their relatives in the *Fagaceae* family.

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