

GENE EVOLUTION AND ADAPTATION IN PINE TREES

A McIntire-Stennis supported project



TEXAS A&M
UNIVERSITY

Forest ecosystems and tree plantations are experiencing increasing levels of abiotic and biotic stress including changes in climate regimes and novel invasive pests and pathogens. Understanding the genetic diversity of keystone forest species and widely planted trees is critical to long-term goals pertaining both the stewardship of forest ecosystems and the maintenance of sustainable productivity in commercial forests. Genomic resources can substantially accelerate the assessments of genetic diversity and the discovery of genetic variants involved in key forest tree traits. This research program aims at developing and analyzing genomic resources in loblolly pine, the most planted forest tree in Southeastern United States, and other conifers to assist genetic-based tree improvement efforts and to identify drought-tolerance varieties. A second goal of this research is to facilitate the development of high-quality genomic resources in pine trees using laser-capture microscopy and DNA sequencing of single chromosomes.



About McIntire-Stennis

The McIntire-Stennis program, a unique federal-state partnership, cultivates and delivers forestry and natural resource innovations for a better future. By advancing research and education that increases the understanding of emerging challenges and fosters the development of relevant solutions, the McIntire-Stennis program has ensured healthy resilient forests and communities and an exceptional natural resources workforce since 1962.



COLLABORATION



This program included collaborations with the U. S. Forest Service Southern Research Station, the Texas A&M Forest Service, the Western Gulf Forest Tree Improvement Program, and researches at Texas A&M University and eight other Universities.

Decoding the Douglas-fir genome
Development of the most comprehensive catalog of genes involved in drought tolerance in loblolly pine.

IMPACT

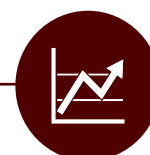
This program enhanced the understanding of the genetic basis of drought tolerance in loblolly pine and informed on the genetic changes involved in adaptation in conifers.



\$968,570
leveraged funding for additional projects.



2,372 drought-related genes
These markers will assist breeding program in loblolly pine.



High-quality genome
First single chromosome sequencing experiments in conifers.