

ADAPTATION OF WESTERN GULF LOBLOLLY PINE TO A CHANGING ENVIRONMENT

A McIntire-Stennis supported project



TEXAS A&M
UNIVERSITY

Southern forests dominated by pines contain one third of the forest carbon in the contiguous U.S. Among the southern pines, loblolly pine is the most common, providing great economical and ecological value. In the face of changing climate, the development and deployment of improved genetics will play important roles in pine adaptation, resilience and sustainability. Populations in the western part of the loblolly range are likely to be severely affected in the future. The long-term goal for this project is to develop knowledge and methods that will allow us to breed loblolly pines adapted to a changing environment, primarily through selection for high water-use efficiency while at the same time, improving growth. To reach this goal, we are working to identify molecular markers and bio-markers to identify families with both high water-use efficiency and growth rates and to develop a better understanding of fundamental traits related to tree water use.



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



Western Gulf Forest Tree Improvement Program (WGFTIP).

Accelerate Breeding

WGFTIP members provide access to germplasm, data and test plantations while this project provides tools and scientific discoveries.

IMPACT

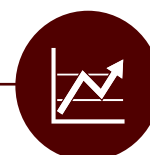
We are contributing to the use of molecular markers in loblolly pine breeding, focusing on improving adaptation and growth in the western part of the range where climate change is expected to be pronounced.



2.8 million single nucleotide polymorphisms (SNPs), have been identified.



Molecular markers associated with phenotypic traits including growth, adaptation and cellular phenotypes have been identified using the 2.8 million SNPs.



New markers A new project will identify molecular and biomarkers useful for breeding for improved water-use efficiency, drought resistance and growth.