

RESEARCH

K University of Kentucky

Department of Forestry and Natural Resources

WHITE OAK GENETICS AND GENOMICS RESEARCH PROGRAM

PRINCIPAL INVESTIGATORS: Dana Nelson, Co-Director, Forest Health Research and Education Center (FHREC), USDA Forest Service, Southern Research Station; Bert Abbott (FHREC) and Seth DeBolt, University of Kentucky, Department of Horticulture and Director, Beam Institute for Kentucky Spirits

CO-INVESTIGATORS: Laura Dewald (UK), Shenghua Fan (UK), Tatyana Zhebentyayeva (Penn State University), Meg Staton (University of Tennessee), Mark Coggeshall (USDA Forest Service, Northern Research Station), Scott Merkle (University of Georgia), Jeff Stringer (UK)

STUDENT: Rachel Thunder, Masters of Science (UK)

PROJECT GOAL: Sustaining and improving white oak through integrated research in genetics, genomics and biotechnology.

PROJECT DESCRIPTION: Sustaining white oak resources is critical to the forest products and distilling industries, responsible for generating billions of dollars to local economies, throughout the region. However, sustainability of white oak dominated forests is



challenged by demand pressures and numerous ecological and environmental threats like exotic insects and diseases. Our research team will direct genetics research to understand the genetic variability of white oak and its relationship to whole-tree and wood characteristics important to white oak dependent industries and conservation efforts. The team is also providing biotechnological solutions for removing bottlenecks to rapid selection and breeding of improved white oaks. Within the framework of this program we are determining the genome sequences (DNA and RNA) of white oak that will be the foundational repository of gene information to be used for identifying genes and manipulation of traits. The project is also characterizing white oak germplasm and developing molecular markers to be used to improve traits and assist in breeding improved trees, including development of Rapid Cycle Breeding (RCB) that uses biotechnological approaches to introduce genes producing flowers at an early age shortening the traditional breeding cycle.

PROGRESS: White oak DNA and RNA are in the pipeline for sequencing and final analysis of genetic variation associated with white oak management is scheduled to be completed in 2020. White oak transformation technology is in the development for Rapid Cycle Breeding of white oak.

NEEDS:

- Short-term includes support for technicians, graduate students, post-doctoral researchers and their project costs.
- $\bullet \ Long-term needs include faculty level positions in tree genetics/genomics, tree physiology, bioinformatics.$

FUNDING AND RESOURCES:

- Grants/Cooperatives/Contracts through UK: \$1.265 million
- USDA Forest Service, Southern Research Station and UK: \$250,000