

## Jason Holliday receives \$2.5 million NSF grant to research poplar genome



IMAGE: ACCORDING TO JASON HOLLIDAY (PICTURED), POPLARS ARE ESPECIALLY WELL SUITED TO THIS TYPE OF RESEARCH, ENABLING SCIENTISTS TO GROW GENETIC DUPLICATES OF THE EXACT SAME TREE.

The revolution in genome sequencing has radically changed the field of forestry, allowing researchers to understand how the genome influences specific traits of economic and ecological importance.

Now, a \$2.5 million grant from the National Science Foundation will help Associate Professor Jason Holliday of the College of Natural Resources and Environment research the genomic architecture of poplars, fast-growing trees that are a crucial source of forest products.

The field of forest tree genetics has a long -- and slow -- history. To determine how a trait like height or diameter is manifested through generations of interbred trees, researchers would have to wait until the trees produce seeds, which can take a decade or more. Improvements in genome sequencing have accelerated that research: instead of waiting years for a generation of trees to mature, researchers can now sequence the genetic code of trees and use the results to better understand the interplay between a tree's genetics, its growth, and the interaction between these factors and the environment.

"The revolution in genome sequencing has made it possible to drill down into the relationship between genetic variation and variation in traits of economic significance. This allows us to select on the genetics themselves for traits like height, diameter, or adaptability to the environment in which we wish to grow the trees. This has real potential to accelerate tree breeding programs," said Holliday, a faculty member in the Department of Forest Resources and Environmental Conservation and an affiliate of the Fralin Life Sciences Institute.

Holliday's research focuses on the natural hybrids of two western North American poplars: black cottonwood and balsam poplar. Poplar hybrids are capable of growing as much as 8 feet in a single year and are an important resource in forest product and bioenergy plantations. Holliday's research will seek to understand how variation in both hybrid genomes and environmental conditions impact desirable traits.

"We're trying to understand how the genomes of the parent trees come together to produce offspring that are more productive but also well adapted to a particular growing site," Holliday explained. "We'll be sequencing the genomes and using a variety of ecological modeling approaches to understand how different parts of the genome contribute to adaptation across different environments."

Holliday's team will be sampling across the natural hybrid zones in western North America, from Oregon to Alaska. They will also be taking samples on an east-to-west grid in an effort to capture the genomic "history" of hybridization that has occurred over thousands of years.

To conduct this research, Holliday is partnering with Assistant Professor Stephen Keller of the University of Vermont, Associate Professor Matthew Fitzpatrick of the University of Maryland Center for Environmental Science, and Assistant Professor Jill Hamilton of North Dakota State University.

"One of the things you want to do in this kind of study is to grow trees in lots of different environments, so you can separate how the environment influences the traits versus the traits that are hardwired in the genome," Holliday said. "Poplars are especially suited to this type of work because it's very easy to make rooted cuttings, which allows us to grow genetic duplicates of the exact same tree."

"In this project, we'll have big gardens of hundreds of trees in Vermont, Virginia, and North Dakota," he continued. "These trees will have the same genetics in all environments, so we can tease apart the extent to which genetics and environment influence growth and adaptability outcomes."

To further diversify the environments captured in the study, Holliday's group has teamed up with ArbNet, an international community of arboretums, to create 20 "mini gardens" of poplar hybrids across North America. Partner arboretums will grow replicates of the same poplar trees, allowing researchers to test their responses to different environments.

To aid in data collection and encourage STEM education to students, Jill Hamilton of North Dakota State University will work with a postdoctoral fellow to develop a middle school curriculum that will include hands-on collection and synthesis of data at these growing sites.

The project aims to provide the most comprehensive picture to date of the genomics of hybrid poplar trees, allowing researchers to examine the ways that genomics influence a tree's capacity to adapt to a range of environmental factors.

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