

Scientists tap trees' evolutionary databanks to discover environment adaptation strategies

December 23 2014



Amy Brunner

After decades of extrapolating about gene function in trees based on gene function in a tiny, less complex plant, a team of scientists has sequenced whole genomes—determined the DNA sequence of all the genes—from 544 unrelated trees of the same species.

"Basically, most of our knowledge of what [genes](#) are important for environmental adaptation of trees has been educated guessing built on studies in the model plant, Arabidopsis, which is a member of the mustard family" said Amy Brunner, associate professor of molecular genetics in Virginia Tech's College of Natural Resources and Environment.

To determine the impact of environment on growth, cuttings from trees in many wild populations were grown in research plots in four distinct environments from California to British Columbia.

Brunner is co-author of an article in the Aug. 24 issue of *Nature Genetics* about the study, which identified gene sequences from *Populus trichocarpa*, commonly known as black cottonwood. One goal is to understand how trees adapt to different climates and to use that information to advance tree breeding for different environments.

"Our approach is particularly powerful because we are mining standing [natural variation](#) resulting from tens of thousands of years of evolution and selection," said Stephen DiFazio, associate professor of biology at West Virginia University, in a U.S. Department of Energy news release. The study was led by DiFazio and Gerald Tuskan of the Oak Ridge National Laboratory and the U.S. Department of Energy's Joint Genome Institute.

"With this approach there is no need to have a preconceived notion of what genes are important," Brunner said. "Instead, existing natural variation in physical traits can be associated with genetic variation in all the genes in a tree. This work advances the first step—the need to know which genetic variations are important to adaptation. Then you have to know why that variation is important."

"The challenge is that we have identified all these genes but don't yet

have a good idea of their function," Brunner continued.

She said her research, to understand specific genes' regulatory networks, can be a bridge between genome-wide studies of the ways trees in different environments adapt and the understanding of the role of specific genes in a process.

A notable exception is that this study identified two related genes in [trees](#) that Brunner and others had previously characterized from *Populus*. The FT1 gene was known to regulate the transition to flowering and FT2 is important for controlling fall growth cessation and bud set.

"The population genomics data not only supported that [genetic variation](#) in FT2 is associated with variation in time of fall bud set, but added an interesting twist in that it indicated an additional function for FT1 in release of winter dormancy," said Brunner.

"Trees must time entry and exit from winter dormancy appropriately for their climate to maximize growth but avoid damage by fall and spring frosts, so it is very interesting that these two genes may have a crucial role in the timing of both dormancy transitions," she said.

Brunner, who is based in the Department of Forest Resources and Environmental Conservation and is affiliated with the Fralin Life Science Institute, contributed her knowledge of genetic mechanisms, development processes, and function of genes to the study.

"The collaboration of scientists with computational skills, others with population genetics and large-scale genomics knowledge, and those with in-depth understanding of gene function and interaction from the molecular to the whole-tree level is a major step forward," she said. "We need to do more in the actual tree system rather than relying solely on extrapolating from model herbaceous plants."

More information: "Population genomics of *Populus trichocarpa* identifies signatures of selection and adaptive trait associations." *Nature Genetics* 46, 1089–1096 (2014) [DOI: 10.1038/ng.3075](https://doi.org/10.1038/ng.3075)

Provided by Virginia Tech

Citation: Scientists tap trees' evolutionary databanks to discover environment adaptation strategies (2014, December 23) retrieved 25 April 2024 from <https://phys.org/news/2014-12-scientists-trees-evolutionary-databanks-environment.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.