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Poplar mechanics

The poplar tree is helping a UVic biologist understand how trees defend themselves against attack

by Shannon McCallum

Most of us wouldn't know a poplar tree even if we bumped into one. Yet it turns out this tree may be a key ally in our ongoing battle to reduce pest outbreaks in B.C. forests and to help offset global warming.

According to Dr. Peter Constabel, a researcher in UVic's centre for forest biology, the recent sequencing of the genome of the poplar tree by an international consortium is a breakthrough that will reverberate in the tree biology community for years to come.

A genome is an organism's complete set of DNA, the double-helix molecule that carries all the genetic instructions for an organism to develop and function. Genome sequencing allows researchers to identify all of an organism's genes and their relative positions on the DNA molecule.

"Through the sequencing of the poplar genome—which is our first complete DNA sequence of any tree—we now have a general road map for how all trees work," says Constabel. "We'll know essentially every gene it takes to make a tree."

The poplar was chosen for sequencing because it has a compact genome compared to other trees—about 40 times smaller than the pine genome, for example. Also, poplar is extensively studied and is an economically and ecologically important species worldwide.

Constabel is very familiar with poplars because he uses them to study the physiological and biochemical defence mechanisms that trees have evolved to protect themselves from attack by an insect or disease.

DIANA NETHERCOTT

Constabel and a young poplar tree

Specifically, he wants to understand how these defence mechanisms operate and are regulated at the DNA level.

"There are a lot of things that go on when a tree is attacked," he explains. "For example, if an insect chews on a poplar leaf, you have hundreds of genes that suddenly change the way they behave. Also, the tree's genetic response can differ depending on whether it's attacked by an insect or by disease."

Constabel's experience with tree defence mechanisms enabled him—in collaboration with UVic colleague Dr. Ben Koop and post-doctoral researchers Manoela Miranda and Matthew Rise—to make a small but significant contribution to the international poplar genome sequencing project.

"We submitted our unique collection of poplar gene sequences associated with disease resistance," says Constabel. "Locating the genes within the DNA sequence is done by computer, which looks for specific genetic signatures, so our collection was used to compare our known genetic sequences with what was identified by the computer."

The poplar genome was released this fall, yet it's already changing the way Constabel and his team are doing their research.

"It used to take weeks or months to identify genes that are directly involved in defence, such as those that make proteins to interfere with insect digestion," he says. "Now, in a matter of minutes, we can go into the genome database and find perhaps 30 defence genes of this type. We can also locate nearby DNA sequences that regulate the defence genes, which previously were very hard to get at."

The implications of Constabel's research go beyond simple scientific curiosity. "The exciting part is that if we can identify the master switches or key genes that turn on and regulate defence systems in poplars, we can look at an individual tree's genome to see whether it has the right genetic stuff to make it resistant to pests or pathogens," he says. "Then we'll select those trees for future forestry applications.

"Furthermore," he continues, "if we can understand the underlying defence mechanisms in poplars, we can look for similar gene sequences in other species such as cedar, pine and spruce."

This will be welcome news for the B.C. forestry industry, which has lost millions of trees and dollars to the mountain pine beetle epidemic in recent years. But, as Constabel is quick to caution, these potential applications are still far down the road. "Sequencing the poplar genome is a great step forward, but it's really just the beginning. We've still got a lot of work ahead of us."

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The first genome to be sequenced was of a virus in 1980. By 2001 an international team had mapped the three billion bits of genetic code that define the human organism.

The poplar species *Populus trichocarpa*, or black cottonwood, is the first tree and the third plant to have its entire genome sequenced. *Arabidopsis thaliana*, a plant in the mustard family, was sequenced four years ago and has one of the smallest genomes in the plant kingdom, about four times smaller than poplar.

In addition to improving pest and pathogen resistance in trees, research on the poplar genome may one day lead to the development of trees that: grow faster, can sequester more carbon from the atmosphere (and help counteract global warming), and can produce more biomass that can be converted to fuel.

UVic's centre for forest biology carries out basic and applied research with emphasis on forest regeneration and biotechnology. Members of the centre, which include faculty, graduate students and post-doctoral researchers, work closely with government and forest industry researchers. For more information visit **web.uvic.ca/~forbiol**.

This article was written by Shannon McCallum, a student in the faculty of graduate studies, as a participant in the UVic SPARK program (Students Promoting Awareness of Research Knowledge), supported by the vice president academic and provost and the vice president research.