# Growing better poplars for biofuels

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Victor Busov tends the baby poplars whose genetics he is studying.

(Phys.org)—It took mankind millennia of painstaking trial and error to breed hardier, healthier food crops.

"We can't wait that long to develop better crops for biofuels," says Victor Busov, a plant geneticist at Michigan Technological University's School of Forest Resources and Environmental Science. "We need to move faster to meet the needs of tomorrow, and the only way we can do that is through knowledge."

So Busov is using some 21st century tools—the genome of the poplar tree and snippets of DNA known as activation tags—to identify the genes that make plants grow faster or change their chemical or physical properties.

He recently received a $1.1 million grant from the US Departments of Energy and Agriculture to analyze the genetic traits that affect the quality and yield of woody biomass from Populus, a species that includes poplar trees like aspens and cottonwoods.  Michigan Tech will work with the Oak Ridge National Laboratory (ORNL) and the National Renewable Energy Laboratory (NREL) on the 3-year study.

Busov is growing 5,000 independent lines of poplars in controlled laboratory conditions at Michigan Tech. Into each of these lines, the scientist has inserted activation tags in different positions in the poplar genome. The insertion of the tags leads to activation of the gene closest to them—thus their name, activation tags.

The major goal of this project is to find the genes whose activation changes woody biomass growth and/or properties. So the Michigan Tech team—with the help of NREL, a lab that has developed specialized pyrolysis mass spectrometry technology—will study the growth and wood properties of each individual line relative to ones without the tag.

They aim to identify lines in which activation of genes leads to beneficial changes in wood growth and properties. Since the researchers know the DNA sequence of the tags and have the full poplar genome sequence, they can use simple techniques to go back and identify the activated genes that are causing the beneficial changes. Busov anticipates identifying 160 or more tagged genes that could affect the speed of growth of the tree or the quantity and quality of the wood.

At the same time, ORNL will sequence 1,100 wild-growing poplar trees

in the Pacific Northwest. ORNL will correlate the genetic changes that Busov identifies to genetic changes in the trees grown in the wild. The team is hoping to find DNA changes in native genes that can confer similar properties to those identified in the activation tagging lines. This should enable them to develop DNA markers that can help poplar and other tree breeders to select for beneficial growth and wood properties more accurately and faster.

"Once you know which DNA sequences are causing the various changes, breeders can use that information to breed trees for exactly the qualities they want," the researcher explains.

"Breeders need simple, fast and inexpensive technology that they can use to help them to change the characteristics of the varieties they select for biofuel," he adds. That technology is exactly what Busov and his colleagues hope will emerge from their genetics research on poplars.

"This work would not have been possible without the investment the Department of Energy made to sequence the entire poplar genome," Busov adds. There are approximately 480 million base pairs—the building blocks of DNA—in the poplar genome.  It would have been a Herculean task to tag and identify that many genes without knowing the genome sequence.

Provided by Michigan Technological University