



## Ecogenomics: From Laboratory to Landscape

What do white spruce, spruce budworm and white pine blister rust have in common? All three are the subject of forest ecogenomics research under way at the Canadian Forest Service.

Ecogenomics is a new discipline that studies the structure and function of a genome – the complete set of genes making up an organism – to gain insight into the relationship between an organism and its environment. Ecogenomics tools can be used to monitor and predict how changes in the environment, the landscape and the climate will affect populations and ecosystems.

### One gene at a time

Researchers in the field of ecogenomics begin by characterizing the genome of a particular tree, insect or pathogen species. This can be more or less time-consuming depending on the size of the genome (see table).

Tools can then be developed to test the organism's responses to changes in its environment. By investigating these interactions in a number of individuals, it is possible to identify, for example, populations or species that are vulnerable to environmental change.

### Trees: victims of their longevity?

The adaptation of trees to new environmental conditions depends primarily on the genetic diversity present in existing populations since trees cannot "escape" from adverse changes in their environment. Knowledge acquired about the molecular mechanisms involved in tree adaptation and stress responses is used in breeding programs.

For example, ecogenomics research is used in marker-assisted selection, a socially acceptable approach.

Current models for predicting the impacts of climate change on forest productivity consider all trees as being equal and therefore as exhibiting uniform responses to changes in environmental conditions. Thanks to ecogenomics, however, researchers can assess genomic variability in trees and incorporate this information into the models. This allows tree populations to be mapped in relation to a specific agent of change.

### Genome size

	Number of megabases*
White spruce	Between 10,000 and 20,000
Human	3,000
Poplar	520
Spruce budworm	450
White pine blister rust	About 100

\* Rather than compare genomes based on the number of genes they comprise, geneticists prefer to use the number of nitrogenous bases. The genome consists of a set of genes composed of DNA, which itself contains nitrogenous bases. 1 megabase = 100 million bases



White spruce trees growing under homogeneous environmental conditions but showing differences in growth at the same age.  
Photo: A. Bertrand (Agriculture and Agri-Food Canada)

## Tree defence responses: identifying the enemy

Trees can come under attack from a variety of pests. Ecogenomics approaches can be used to study the molecular defence mechanisms that are induced in trees in response to attacks by specific pests. The information that is acquired can lead to the identification of new avenues for increasing tree resistance as well as to a better understanding of how a biological control method influences the physiological status of a tree.

In light of the globalization of trade and the ever-greater volumes of wood being transported, ecogenomics can provide diagnostic tools that use DNA fingerprinting to identify insect and pathogen species. Some of the pests currently under investigation are the emerald ash borer, sudden oak death, scleroderis canker and poplar canker.



## At the heart of the tree: fibre

Why are there diameter and height differences among trees in a given plantation? The answer to this question can be found by identifying the genes responsible for growth. Ecogenomics researchers can also identify genetic traits related to wood quality and select trees with the desired wood properties.

## Exploiting winter survival genes

Spruce budworm outbreaks cause major losses of timber. Researchers at the Canadian Forest Service and Université Laval are working to crack the genetic code of this insect species through DNA sequencing. They are focusing on genes that can be exploited in order to develop pest control tools, such as the genes involved in winter survival.



## Tracking trees at the molecular level

CFS researchers have developed molecular tools and models to assess the short- and long-term effects that hybrid trees with exotic components (poplars, for example) have on the genetic diversity of native species. They can monitor gene flow from hybrid poplar plantations to native trees, and thus provide useful information for companies seeking to obtain or maintain ecocertification for their products.

## Ecogenomics: a long-term perspective

Because trees live a long time, the results of gene expression cannot be observed for a number of years. Therefore, it is essential to continue forest ecogenomics studies over the long term in order to increase the competitiveness of the Canadian forest sector.

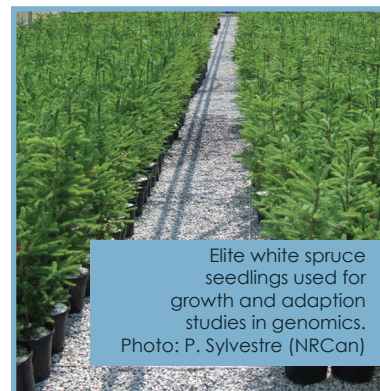
## Useful links

Arborea:  
<http://www.arborea.ulaval.ca/>

The DNA barcode: a unique identifier for pathogenic forest fungi:  
<http://cfs.nrcan.gc.ca/pubwarehouse/pdfs/31314.pdf>

Impact of exotic poplars on natural stands:  
<http://cfs.nrcan.gc.ca/publications?id=31064>

Using genomics to enhance forests:  
<http://www.nrcan.gc.ca/com/elements/issues/51/genom-eng.php>



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