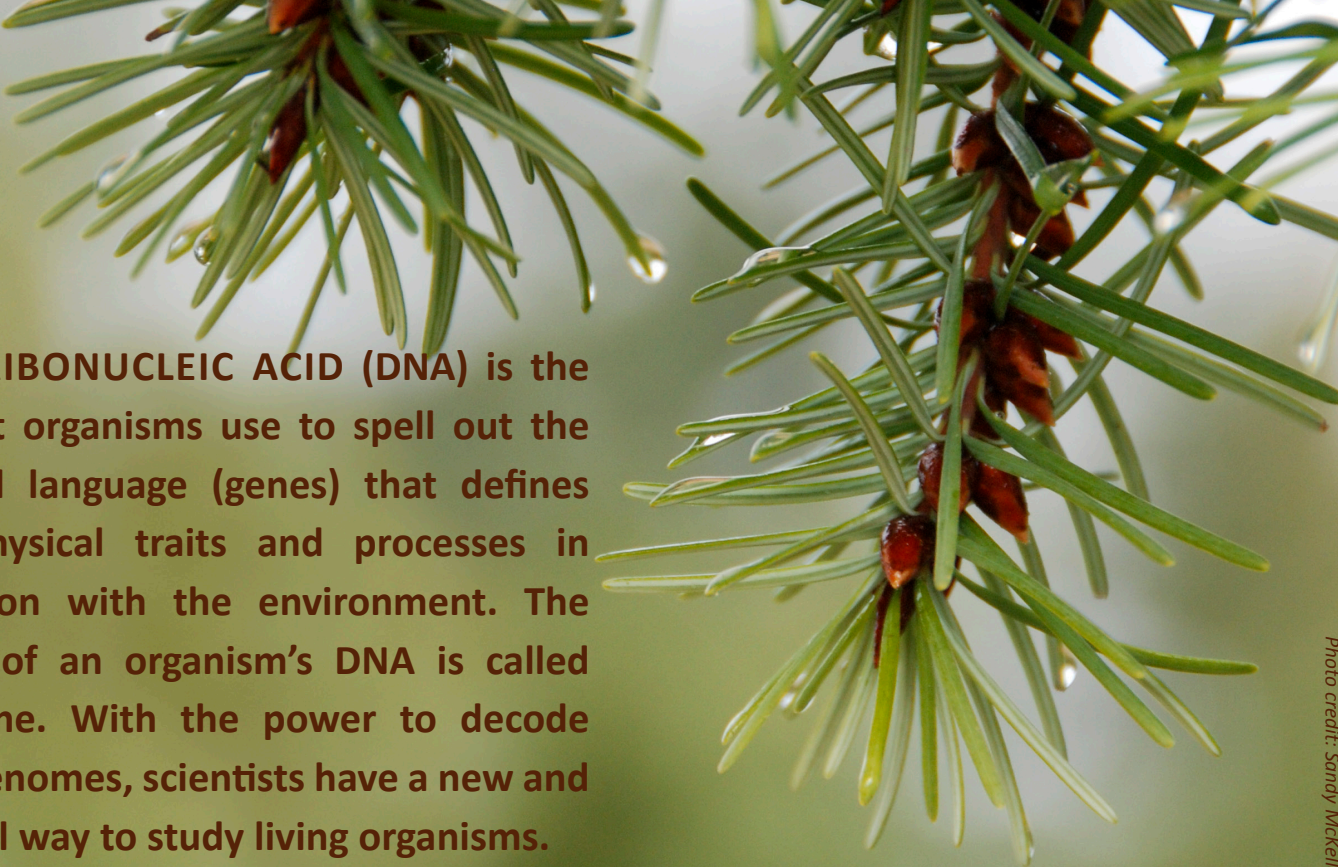


RESEARCH HIGHLIGHT

The Pacific Forestry Centre

January 2022

USING GENOMICS TO PROTECT FORESTS AGAINST PATHOGENS AND ADAPT TO CLIMATE CHANGE



DEOXYRIBONUCLEIC ACID (DNA) is the alphabet organisms use to spell out the chemical language (genes) that defines their physical traits and processes in interaction with the environment. The full set of an organism's DNA is called a genome. With the power to decode entire genomes, scientists have a new and powerful way to study living organisms.

Canadian forests are threatened by pathogens and ecosystem-changes driven by climate change. At the same time, accelerated international trade has provided a conduit for invasive (non-native) pests. To help protect the forested land base from these threats, research scientists at Natural Resources Canada, in the Pacific Forestry Centre (PFC) in Victoria, are contributing to a unique field of research called genomics.

Exploring the magic of genomics are NRCan research

scientists Nicolas Feau (a forest pathologist and mycologist) and Gwylim Blackburn (who specializes in the ecology and evolution of invasive insects). Blackburn, who says we're in a genomic revolution right now, enthused, "the last ten years have been an incredible period – thanks to advancements in genetic data collection, computing capacity and statistical tools - it's like being at a carnival with all the ride tickets you could ever want. And having candy floss too!"



Nicolas Feau

Nicolas Feau is using population genetics and genomics to develop tools to detect and prevent pest outbreaks while assisting trees to adapt to changing climate. This involves understanding the interaction between tree pathogens and their hosts. By identifying the physical expression of genes that are involved in an interaction, Feau can find genomic markers that help tree breeders identify potentially resistant trees in the natural population. The ability to do this saves considerable time. Under conventional practices, tree breeders would have to select and rear resistant specimens then test them before they could be sure, a process that would take years. Feau's focus is not only understanding the interaction between host and pathogen, but to ensure that while breeding for resistance, selected trees are also resilient in the long term in the context of climate change.

Dothistroma needle blight and Swiss needle cast, two important diseases of lodgepole pine and Douglas-fir, are predicted to have an increased impact as our climate warms. "What's interesting," explained Feau, "is that neither of these are exotic pathogens, they are native to our forests. But in the

past 40 to 50 years, changes in climate and forest practices have impacted the interaction between the pathogens and their hosts, causing more epidemics".

Feau is part of a multidisciplinary team of scientists and academics who are working on breeding programs for adaptive trees and making sure they are planted in the right place for the future. As a member of the CoAdapTree collaborative project, Feau is working on tools to protect lodgepole pine and Douglas-fir from these pathogens.

With rapidly changing climate, local seed for reforestation may not be the best choice when replanting after harvest. Using climate models, assisted migration means planting a forest today with

seedlings adapted to a future climate. But, how do we know how the pathogens are going to respond? The CoAdapTree Project aims to develop genomic tools and strategies for improved tree breeding, not only for warmer or drier climate conditions but also for resistance to pathogens.

But, according to Feau, "genomics is of no use in the absence of the ecological context to which it applies. Our research has shown how a formerly endemic pathogen suddenly became a big problem, simply because the climate conditions changed". In this regard, Genomic tools won't replace other silvicultural tools such as ecological surveys and planning, rather, they will enhance current land management practices.

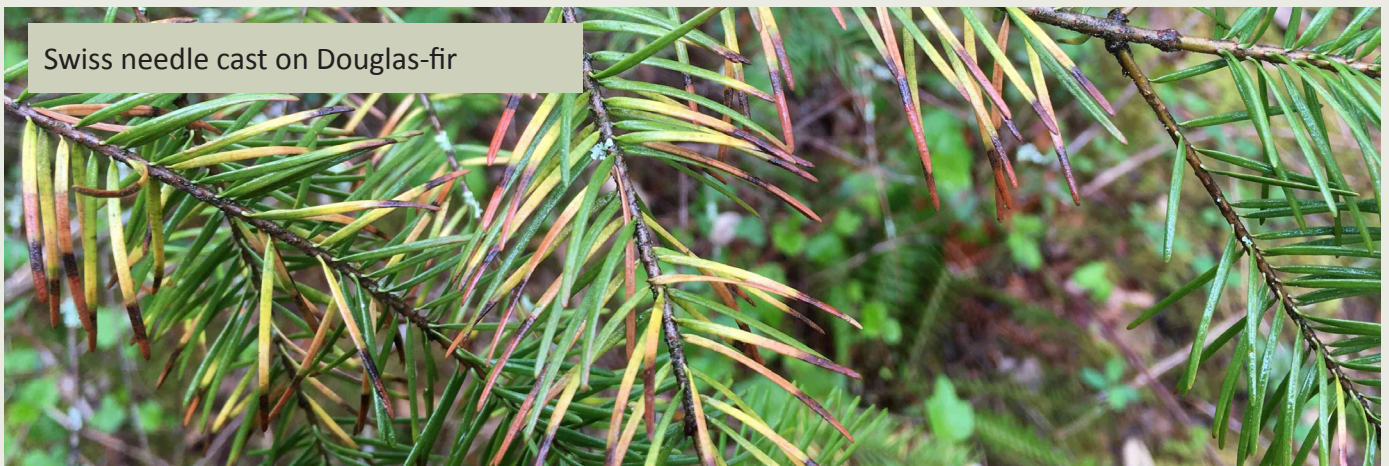


Photo credit: NRCan

Gwylim Blackburn

Gwylim Blackburn is a key contributor in BioSAFE (Biosurveillance of Alien Forest Enemies), another collaborative program protecting Canadian forests. The goal is to improve the detection and surveillance of forest invasive species by developing genomic biosurveillance tools that will: allow rapid and accurate identification of insects and pathogens; determine their origin, provide an assessment of the risk they pose; and provide the end users with a decision-support system to guide their management and mitigation actions.

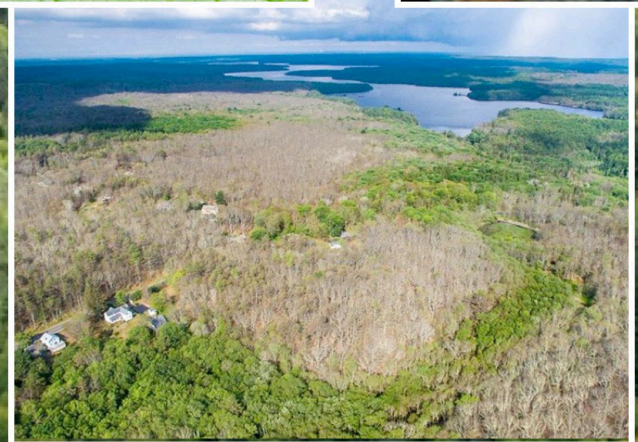
Determining the invasive nature of the Asian Gypsy moth (AGM) (*Lymantria dispar asiatica*) is Blackburn's specialized area of research. He is using the science of genomics to document the functional abilities of the AGM to invade North America, with a focus on flight genetics and capacity to spread. To do this, he analyzes genomic signatures to reveal markers that will identify these traits. "I make use of whole genome data to profile AGM in terms of their flight ability", he explained. Flight is a major component of the ability of AGM to disperse, and how far they can travel has huge implications to someone managing an invasion.



Managing Asian gypsy moth invasion risk



Lymantria dispar asiatica,
Asian gypsy moth



Lymantria dispar moths around the world vary drastically in their ability to fly. AGM can disperse tens of kilometers, while Lymantria dispar dispar, European form, show relatively limited dispersal capacity. “This is because the females in some sub-lineages can’t fly, and even if the males can, a flightless female limits migration,” Blackburn explains. As such, if an egg mass is detected on an incoming ship at port, it is of great interest in North America to sample those eggs and profile them for flight ability. “What I’m trying to do, in very simple terms, is find out if there’s a way we can take that egg mass and in a few hours or days genetically profile it for the flight ability of the adults that will emerge”.

The expansion of genetics into full genome mapping—going from a limited number of markers to millions of markers—creates the potential to not only track insect and pathogen invasions but to see the adaptive-potential of the pathogen in a changing climate. Ultimately predicting how and where new outbreaks could occur – increasing our ability to protect Canada’s forests and natural landscapes.

Resources:

- **Genomics helps Canada’s forests adapt to the future**
www.nrcan.gc.ca/genomics-helps-canadas-forests-adapt-future/22931
- **Responding to invasive and alien forest pest**
www.nrcan.gc.ca/our-natural-resources/forests/wildland-fires-insects-disturbances/forest-pest-management/responding-invasive-and-alien-forest-pests/13411
- **NRCan Climate Change: Impacts on forests**
www.nrcan.gc.ca/climate-change/impacts-adaptations/climate-change-impacts-forests/impacts/13095
- **bio SAFE**
www.biosafegenomics.com
- **The CoAdapTree Project**
<https://coadaptree.forestry.ubc.ca>

Photo credit: Sandy McKellar

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www.nrcan.gc.ca/science-data/research-centres-labs/forestry-research-centres/pacific-forestry-centre/13489