



SMarTForests

Newsletter

Edition 1

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SMarTForests overview

The forest products industry contributes \$20 to \$30 billion per year to Canada's gross domestic product (GDP) but its economic prosperity is dwindling. Changing environments, pressure to conserve forest lands, and demands for sustainable forest management call for new approaches to extract value and obtain benefits from Canada's forests. Genomic sciences can accelerate the development of novel tools and information that will help forest managers adapt to these changes. The SMarTForests project will develop tools to enhance forest health and productivity and increase the value recovered from forest plantations.

In Canada, spruce trees are a prime target to generate both environmental and economic benefits from genomics. They account for 58% of the 650 million tree seedlings planted each year, covering 2,164 km² of reforested land annually. The SMarTForests project will leverage the power of genomics to develop diagnostic markers based on DNA, metabolites and proteins to advance breeding in Canada's major spruce species. Marker systems are aimed at identifying trees and seedlings with improved growth, wood properties, and insect resistance. They will be used in an approach called Marker Aided Selection (MAS). Estimates are that MAS could increase annual wood yield by 1.5 million cubic meters per year over the long term if applied to only 20% of Canada's white spruce plantations. This gain translates into a potential GDP increase of \$300 million. Methods like MAS can help to concentrate wood production on a smaller land area and allow for more forest land to be set aside for conservation.

The SMarTForests project brings together genome scientists, forest geneticists, tree biologists and end-users from two research teams: Arborea, led by the Université Laval, and Treenomix, at the University of British Columbia. These groups have joined forces so that applied spruce genomics research in Canada is highly integrated and efficient. The newly formed team is in a strong position to break new ground in conifer genome sequencing and represent Canada in international initiatives. The active participation of forestry end-users from tree breeding programs is helping to focus MAS development on practical needs and maximizes existing resources. Integrated impact analyses (GE³LS research) deliver an unprecedented understanding of the economic, socioeconomic and legal issues of implementing MAS for forestry in Canada.



Our research activities involve:

- GE³LS = Genomics and society
- Sequencing the white spruce genome
- Developing tree breeding tools for growth and wood quality
- Identifying biomarkers and genetic markers for insect resistance





Mission and Project Goals

The SMarTForests project builds on a decade of research discoveries in spruce genomics by previous projects: Arborea (Université Laval; Natural Resources Canada; University of Alberta) and Treenomix (University of British Columbia). The new team combines the strengths of the two previous projects, building on their extensive background knowledge and experience. Our mission is to break new ground in spruce genome sequencing and represent Canada as an important force in international conifer genome initiatives, and to achieve efficient translation of results toward end-users from across Canada.

The SMarTForests project has three major goals:

1. Develop marker systems to aid in MAS.
2. Sequence the white spruce genome.
3. Analyze impacts of forest genome on economics and society.

Principal Investigators

John MacKay, Project Leader, Professor and Associate Dean, Faculty of Forestry, Geography and Geomatics, Université Laval. E-mail : john.mackay@sbf.ulaval.ca.

Dr. John MacKay's research interests span three areas: transcriptome sequencing and profiling, functional genomics of wood formation and secondary metabolism, and quantitative genetics of wood. His research program is aimed at enhancing our understanding of fundamental tree biology and developing applications in forest genetics such as genetic markers for tree breeding and conservation. As co-leader of the SMarTForests project, John co-coordinates the project as a whole. He is also involved in genome sequencing and analysis, and contributes to marker development for wood and growth traits in white and black spruces (i.e. eastern Canadian spruces).

Jörg Bohlmann, Project Leader, Professor and Distinguished University Scholar, Michael Smith Laboratories and Departments of Forest Sciences and Botany, University of British Columbia. E-mail : bohlmann@mssl.ubc.ca.

Dr. Jörg Bohlmann has established an internationally recognized research program in forest health genomics, biochemistry of plant secondary metabolism, and bio-products. His research covers conifer defences against insects and pathogens, terpenoid biosynthesis, and genome analysis of conifers, mountain pine beetle, and bark beetle associated fungi. As co-leader of the SMarTForests Project, Jörg co-coordinates the project as a whole, as well as collaboration with the BC Ministry of Forests, and interactions with the Norway spruce genome project. He also leads the research on insect resistance and is involved in white spruce genome sequencing and analysis.



Jean Beaulieu, Regional Coordinator and Research Scientist, Canadian Wood Fibre Centre (CWFC). E-mail : jean.beaulieu@NRCan.gc.ca

Dr. Jean Beaulieu specializes in population and quantitative genetics and forest genomics. In the area of population genetics, Jean deals mostly with conifer phylogeography and the identification of genes for natural selection. In quantitative genetics, he works on genetic variation and control of wood characteristics in spruce, and on the development of clonal forestry. In forest genomics, as member of the SMarTForests team, he specializes in the development of marker-assisted selection for wood characteristics in black and white spruces using candidate gene markers and in genomic selection.

Jean Bousquet, Professor, Department of Wood and Forest Sciences, Université Laval.

E-mail : jean.bousquet@sbf.ulaval.ca

Dr. Jean Bousquet's research is centered around understanding patterns of genetic diversity and their evolutionary implications. In the SMarTForests project, Jean coordinates marker development for wood and growth in white and black spruces in eastern Canadian spruces by using association genetics and genomic prediction, and participates in the mapping and analysis of structural variation of the spruce genome. He is working on the development of SNP inventories for various genome scan applications as part of this research. He is also involved in estimating molecular phylogenies of tree genera and studying their paleo-biogeographical implications, in particular the effects of Pleistocene glaciations and Holocene climate changes on the geographical structure of conifers.

Gary Bull, Professor, Department of Forest Resources Management, University of British Columbia.

E-mail : gary.bull@ubc.ca.

Dr. Gary Bull's research interests, linked to genomics, span three areas: integration of genetic gain into spatial models; economics of genetic gains; and the assessment of policy impacts of genomics. Gary's research program focuses on using various spatial (landscape, regional, provincial, national and international) economic models to develop scenarios for policymakers. Gary is also involved in a range of research activities that focus on the human impacts of natural

resource economic decisions and the economics of ecosystem services from the forest. In the SMarTForests project, he co-leads the GE³LS activities in the area of economic analysis, policy analysis and institutional analysis related to the use of genomics in forestry.

Janice Cooke, Associate Professor, Department of Biological Sciences, University of Alberta.

E-mail : janice.cooke@ualberta.ca.

Dr. Janice Cooke's research focuses on understanding how forest trees respond to environmental cues and how these responses affect growth and productivity. Janice has a particular interest in the adaptive traits that enable temperate forest trees to withstand the harsh conditions of winter. In the SMarTForests project, Janice's lab team participates in marker development for wood and growth traits in white spruce. It's research is aimed at the discovery and functional characterization of genes that exert genetic control over time of bud formation, with the goal of developing genetic markers for use in tree improvement and conservation programs.

Nancy Gélinas, Professor, Department of Wood and Forest Sciences, Université Laval.

E-mail : nancy.gelinas@sbf.ulaval.ca.

Dr. Nancy Gélinas' research interests cover a range of socio-economic forest management issues, such as partnership management, economic assessment of ecological services and economic analysis. Nancy's current projects focus on three key areas: developing an understanding of the wood value chain, from forest management to wood products; demonstrating the economic importance of forest genomics; and relating forest communities with agroforestry practices, forest management and resources conservation in a REDD context. In the SMarTForests project, she coordinates the GE³LS activities which cover economic analysis, policy analysis and institutional analysis related to the use of genomics in forestry.

Nathalie Isabel, Researcher, Canadian Forest Service, Natural Resources Canada. E-mail : Nathalie.Isabel@NRCan.gc.ca

Dr. Nathalie Isabel's research program centres on the development of methods and strategies (QTL and association mapping, genome scan), and tools for a marker-assisted selection (MAS) system in conifers. It also focuses on the acquisition of empirical data for natural and artificial hybrid zones combined with modelling approaches to support regulatory systems. In the SMarTForests project, Nathalie participates in marker development for wood and growth traits in eastern Canadian spruces. Her research contributes to marker development for adaptive traits (i.e. timing of budset, frost tolerance) by identifying gene regions underlying these key functional traits using different genomic approaches.

Steven Jones, Associate Director and Head Bioinformatics, Canada's Michael Smith Genome Sciences Centre, BC Cancer Agency, Professor, Medical Genetics, University of British Columbia. E-mail : sjones@bcgsc.ca.

Dr. Steven Jones' major research focuses in the computational analysis of DNA sequences from human cancers. Steven has applied next generation DNA sequencing technology to detect mutations arising in both patient samples and in cancer cell lines in various cancer types and under the influence of different therapeutics. Further significant contributions have been in the field of establishing bioinformatics training within Canada. In the SMarTForests project, he is spear heading the bioinformatics of the white spruce genome assembly.

Kermit Ritland, Professor, Department of Forest Sciences, University of British Columbia. E-mail : kermit.ritland@ubc.ca.

Dr. Kermit Ritland's research has traditionally involved population and conservation genetics of a diverse range of organisms, from Kermode Bears to western red cedar to white pine weevil. In genomics, his research focuses on expression quantitative trait locus (QTL) mapping as a way of inferring networks of genes and particularly those deeply nested ("master regulatory gene"), and hence of most importance for candidate genes for tree improvement. Kermit is also interested in evolutionary comparisons of ESTs and genome sequences to gauge features unique to conifers. In the SMarTForests project, he is involved with insect resistance marker development, and genome sequencing and analysis through comparison of the white spruce, loblolly pine and Norway spruce genomes.

Armand Séguin, Researcher, Canadian Forest Service, Natural Resources Canada. E-mail : armand.seguin@NRCan.gc.ca.

Dr. Séguin's research program is focused on molecular mechanisms of stress responses in trees, genetic engineering and potential impacts of transgenic trees on the environment. Studies conducted in his lab have helped to advance knowledge in tree genomics and acquire scientific expertise in the field of regulation of genetically modified trees in Canada. In the SMarTForests project, Dr. Séguin is involved with knowledge development relating to conifer defense systems, and contributes to the development of biomarkers for insect resistance in spruce. He also represents the Canadian Forest Service as a government end-user organization.

Alvin Yanchuk, Senior Scientist, Forest Genetics, British Columbia Ministry of Forests, Lands and Natural Resources Operations. E-mail : Alvin.Yanchuk@gov.bc.ca.

Dr. Yanchuk's main research areas have been in tree breeding theory and application, and conservation of forest genetics resources. More recently, he has been focusing on developing strategies and approaches toward breeding for pest and disease resistance, deployment strategies of improved germplasm under various climate change scenarios, and the integration of genomic tools into applied breeding. In the SMarTForests project, Alvin is involved in the development of molecular markers linked to various pest resistance traits in spruce in B.C.

Meet us on the Web!
www.smartforests.ca

TO CONTACT US:

PROJECT MANAGERS

Sophie Laviolette

Université Laval
1030 avenue de la Médecine
Bureau 2153
Québec, QC Canada
G1V 0A6
Phone: 418.656.2408
Fax: 418.656.7176
E-mail:
sophie.laviolette@sbf.ulaval.ca

Carol Ritland

Dept. of Forest Sciences
University of British Columbia
#3611-2424 Main Mall
Vancouver, BC Canada
V6T 1Z4
Phone: 604.822.3908
Fax: 604.822.2114
E-mail:
critland@mail.ubc.ca

News and events

First draft assembly!

The SMarTForests Project has released a first assembly of the white spruce genome (*Picea glauca*) through the National Center for Biotechnology Information (NCBI : [Bioproject PRJNA83435](https://www.ncbi.nlm.nih.gov/BioProject/PRJNA83435), [Accession ALWZ0000000000](https://www.ncbi.nlm.nih.gov/nuclink/ALWZ0000000000)) and a FTP site [ftp://ftp.bcgsc.ca/public/Picea_Glauca/].

This initial assembly of the white spruce genome sequence of an individual diploid tree was based on shotgun sequencing using a high performance sequencing platform (HiSeq2000). We will continue to produce improved sequence resources and to up-date the white spruce genome assembly. We are also working on large-scale analyses of this genome sequence for a timely scientific publication. See www.smartforests.ca for more details.

New articles (for a complete list, please visit our website)

- ◆ Namroud M.-C., Bousquet J., Doerksen T., and Beaulieu J. 2012. Scanning SNPs from a large set of expressed genes to assess the impact of artificial selection on the undomesticated genetic diversity of white spruce. *Evolutionary Applications* 5:641-656. doi: 10.1111/j.1752-4571.2012.00242.x.
- ◆ Mackay J., Dean J., Plomion C., Peterson D.G., Canovas F., Pavy N., Ingvarsson P., Savolainen O., Fluch S., Vinceti B., Abarca D., Diaz-Sala C., and Cervera M-T. 2012. Towards decoding the conifer giga-genome. *Plant Molecular Biology*. doi: 10.1007/s11103-012-9961-7.
- ◆ Buschiazzi E., Ritland C., Bohlmann J. and Ritland K. 2012. Slow but not low: genomics comparisons reveals slower evolutionary rate and higher dN/dS in conifers compared to angiosperms. *BMC Evolutionary Biology*, 12:8. doi:10.1186/1471-2148-12-8.
- ◆ Bohlmann J. 2012. Pine terpenoid defences in the mountain pine beetle epidemic and in other conifer pest interactions: Specialized enemies are eating holes into a diverse, dynamic and durable defence system. *Tree Physiology*, invited commentary 32 (8): 943-945. doi: 10.1093/treephys/tps065.
- ◆ Cooke J.E.K., Eriksson M.E. and Junttila O. 2012. The dynamic nature of bud dormancy in trees; environmental control and molecular mechanisms. *Plant Cell and Environment*, invited review. doi: 10.1111/j.1365-3040.2012.02552.x

The SMarTForests project is featured in the article "Canadian Trends in Genomics: From research to innovation." *Biotechnology Focus*, July/August 2012, page 20-21.

Upcoming events

Workshop: Fall 2013 (Date and place to be determined)

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