SMarTForests
Newsletter

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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 to 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 km^2 of reforested land per year. 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 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 Arborea and Treenomix. These groups have joined forces so that applied spruce genomics research in Canada are highly integrated and efficient. This team is in a strong position to break new ground in conifer genome sequencing and represents 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 the power of existing resources. Integrated impact analyses (GE[3]LS research) delivers an unprecedented understanding of the economic, socioeconomic and legal issues of implementing MAS for forestry in Canada.

Our research activities are:

- GE[3]LS = Genomics and society
- Sequencing White Spruce genome
- Tree breeding tools for growth and wood quality
- 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) and Treenomix, (University of British Columbia). The new team is a strong combination of the two projects, building on the extensive background knowledge and experiences. Our mission is, first, to break new ground in spruce genome sequencing and strongly represent Canada in international conifer genome initiatives, and second, 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. MacKay's research interests span three areas: transcriptome sequencing and profiling, functional genomics of wood formation and secondary metabolism, and quantitative genetics of wood. Dr. MacKay's 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, Dr. Mac-Kay co-coordinates all project activities. Dr. MacKay is also involved in genome sequencing and analysis, and contributes to marker development for wood and growth traits in white and black spruce.

Jörg Bohlmann, Co-Project Leader Professor and Distinguished University Scholar , Michael Smith Laboratories/ Departments of Forest Sciences and Botany, University of British Columbia, E-mail : bohlmann@msl.ubc.ca.
Dr. Bohlmann has established an internationally recognized research program in forest health genomics, biochemistry of plant secondary metabolism, and bio-products. Dr. Bohlmann's 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, Dr. Bohlmann co-coordinates all project activities, collaboration with the BC Ministry of Forests, and interactions with the Norway spruce genome project. Dr. Bohlmann 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 Fiber Centre in Quebec City (CWFC), E-mail : beaulieu@exchange.cfl.forestry.ca.
Dr. Beaulieu specializes in population and quantitative genetics and forest genomics. In the field of population genetics, Dr. Beaulieu deals mostly with conifer phylogeography and the identification of genes for natural selection. In quantitative genetics, Dr. Beaulieu works on genetic variation and control of wood characteristics in spruce and on the development of clonal forestry. In forest genomics, as member of SMarTForests's team, Dr. Beaulieu specializes in the development of marker-assisted selection using candidate gene markers and in genomic selection for wood characteristics in spruces.

Jean Bousquet, Professor, Department of Wood and Forest Sciences, Université Laval
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Dr. Bousquet's research centers around the comprehension of genetic diversity and its' evolutionary implications. As part of SMarTForests project, Dr. Bousquet is participating in the mapping and analysis of structural variation of the spruce genome, and coordinating association genetics and genomic prediction relating to eastern Canadian spruces. In conjunction, the development of SNP inventories for various genome scan applications is part of this research. Dr. Bousquet 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. Inclusive to the research is the pursuit for selection signatures at the landscape and range-wide levels in relation to climate adaptation.

Gary Bull, Professor, Department of Forest Resources Management, University of British Columbia,
E-mail: gary.bull@ubc.ca.
Dr. Bull's research interest, linked to genomics, spans three areas: integration of genetic gain into spatial models, economics of genetic gains and the assessment of policy impacts of genomics. Dr. Bull's research program focuses on using various spatial (landscape, regional, provincial, national and international) economic models to develop scenarios for policymakers. Dr. Bull 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 GE^{3}LS activities in the area of economic analysis, policy analysis and institutional analysis related to the use of genomics in forestry.

Janice Cooke, Professor, Department of Biological Sciences, University of Alberta, E-mail : janice.cooke@ualberta.ca.
Dr. Cooke's research focuses on understanding how forest trees respond to environmental cues, and how these responses affect growth and productivity. Dr. Cooke has a particular interest in the adaptive traits that enable temperate forest trees to withstand the harsh conditions of winter. As part of the SMarTForests project, Dr. Cooke's lab. team is collaborating with Dr. Nathalie Isabel's team to discover and functionally characterize 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. Gélinas' research interests cover a range of issues relating to the socio-economic aspects of forest management, such as partnership management, economic assessment of ecological services and economic analysis. Dr. Gélinas' current projects focus on an understanding of the wood value chain, from forest management to wood products, on demonstrating the economic importance of forest genomics, and on forest communities; their relation with agroforestry practices, forest management and resources conservation in a REDD context. In the SMarTForests project, Dr. Gélinas coordinates the GE^{3}LS 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 : nisabel@cfl.forestry.ca.
Dr. Isabel's research program focuses on (1) the development of methods and strategies (QTL and association mapping, genome scan) and tools for a marker-assisted selection (MAS) system in conifers and (2) the acquisition of empirical data for natural and artificial hybrid zones combined with modelling approaches to support regulatory systems. As part of the SMarTForests project, she 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, E-mail : sjones@bcgsc.ca.
Dr. Jones major research focuses in the computational analysis of DNA sequence from human cancers. Dr. Jones 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 helping to establish bioinformatics training within Canada . In the SMarTForests project, Dr. Jones is spear heading the bioinformatics of the white spruce genome assembly.

Kermit Ritland, Professor, Department of Forest Sciences, University of British Columbia, E-mail : kemit.ritland@ubc.ca.
Dr. Ritland's research has traditionally involved population and conservation genetics of any organism with DNA in it, from Kermode Bears to western red cedar to white pine weevil. In genomics, Dr. Ritland is focussed in expression quantitative trait locus (QTL) mapping as a way of inferring networks of genes and particular those deeply nested ("master regulatory gene"), and hence of most importance for candidate genes for tree improvement. Dr. Ritland is also interested in evolutionary comparisons of ESTs and genome sequences to gauge features unique to conifers. In the SmarTForests project, Dr. Ritland is involved with marker development and 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 centres on current understanding of the molecular mechanisms of stress responses in trees, tree genetic engineering and the potential impacts of transgenic trees on the environment. The studies conducted in Dr. Séguin's lab has helped to advance knowledge in tree genomics and supported scientific expertise in the field of regulation of genetically modified trees in Canada. As part of the SMarTForests project, Dr. Séguin is involved with knowledge development relating to conifer defense systems, and contributes to the development of biomarkers. insect resistance in spruce. He also represents the Canadian Forest Service as government end-user organizations.

Alvin Yanchuk, Senior Scientist, Forest Genetics, British Columbia Ministry of Forests, Lands and Natural Resources Operations, E-mail : Alvin.Yanchuk@gov.bc.ca.
His main research areas of interest have been in tree breeding theory and application, and genetic conservation of forest genetics resources. More recently he has been focusing on developing strategies and approaches for 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. As a co-investigator in the SMartForests project, he is involved in the sub-activity looking for molecular markers linked to various pest resistance traits in spruce in B.C.

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News and events

First draft assembly

The SMarTForests Project has released a first assembly of the white spruce genome (*Picea glauca*) through National Center for biotechnology Information (NCBI : Bioproject PRJNA83435, Accession ALWZ0000000000).

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 the 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 go to 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

Mackay J., Dean J., Plomion C., Peterson D.G., Canovas F., Pavy N., Ingvarsson P., Savolainen O., Fluch S., Vinceti B., Abarca D., Díaz-Sala C., and Cervera M-T. 2012. Towards decoding the conifer mega-genome. *Plant Mol. Biol.* doi.org/10.1007/s11103-012-9961-7.

Buschiazzo 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.

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

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

Upcoming events

Course: Genomics 101 (November 5 and 6, at UBC)

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

Special thanks to our sponsers