SMarTForests

Newsletter

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Contents:

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From the Lab to the Forest: Social Perception Survey on Marker-Assisted Selection

The emblematic forests of Canada constitute 39% of its land base, representing 10% of the world's forests and 30% of the world's boreal forests (Government of Canada, 2013). With an $18.7 billion forest industry, Canada is the leading exporter of softwood lumber, newsprint, and wood pulp (Government of Canada, 2013; Rank, 2013).

Although now stable, the forest sector saw a significant decline in GDP between 2005 and 2009. This was a result of the U.S. housing crisis, the global economic recession of 2009, and a decreased demand for graphic paper. Moreover, Canadian forests have experienced a number of environmental challenges, including changes in average temperature, wildfires, droughts, pests, and disease (Rank, 2013). In British Columbia, the pine beetle epidemic devastated 18.3 million hectares of pine forests, just over half of its pine inventory (Government of Canada, 2013; Rank, 2013). With changes in climate expected to continue, the incidence of environmental challenges is projected to increase (Rank, 2013).

To address past and present challenges and to ensure a strong future for the forest industry, the federal government has committed to transforming this sector through innovation, environmental performance, and expanded market opportunities (Government of Canada, 2013). Porth *et al.* (in press) reported that over $123 million dollars has already been invested in forest genomic research over the last decade. Included in that research is the SMarTForests project, sponsored by Genome Canada, Genome Quebec and Genome BC. The project, currently underway, has five main objectives:

- Deliver a draft sequence assembly of the white spruce genome and integrate spruce genome resources with Swedish researchers' Norway spruce genome project;
- Identify, validate, and demonstrate the value of genetic markers and biomarkers for insect resistance, growth, and wood quality;
- Develop marker systems for spruce tree breeding programs;
- Determine the economic conditions and assess the potential for genomic tools in forestry decision-making;
- Conduct business development activities to facilitate technology transfer.

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 combines the strengths of the two previous projects, building on their extensive background knowledge and experiences. Our mission is to break new ground in spruce genome sequencing and strongly represent Canada 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.

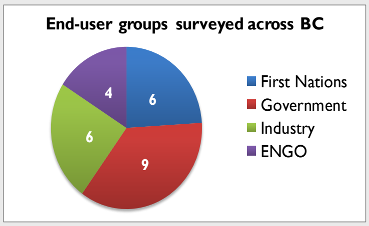
The GE^{3}LS component of the project, which focuses on genomics and its related ethical, environmental, economic, legal and social aspects, is aligned with the last two points. Among its goals is to survey the challenges, real or perceived, by potential end-users of genetic marker systems.

The inclusion of a social science perspective to our SMarTForests project is imperative. Firstly, genomic breeding technologies are relatively new, hence without precedent for implementation in tree breeding practices in Canada. Secondly, there is limited knowledge around policy and the legislative framework; and finally, benefits may not be equally shared by all stakeholders. By addressing these issues through an end-user research study, we bridge the gap between wet-lab research and practical tools used in the field. The research study starts by surveying the perceptions of potential end-users regarding the implementation of a forest-related genomic technology (marker-assisted selection), and determining if this perception is dependent on the context of implementation.

Marker-assisted selection (MAS) is an innovative, biotechnological tool that flags desired traits on the genome. Through an indirect selection process, traits of interest are selected based on the genetic marker(s) linked to them, rather than the trait itself measured on individual trees. MAS can be used to efficiently select the traits that are typically difficult, expensive, and time-intensive to measure, that demonstrate poor heritability, and that are expressed late in development (Brumlop & Finckh, 2011). This tool could potentially be extremely useful to tree breeders because it allows genotypic characteristics to be identified at the seedling stages, as opposed to traditional tree breeding methods which require a tree to reach maturity (approximately 30 years for white spruce) for those same said traits to be identified (Brumlop & Finckh, 2011; Forest Practices Branch, 2008; Yanchuk, 2002). Unlike genetic modification, MAS does not transfer, manipulate, or alter the DNA of the individual in any way (Vogel & Van Aken, 2009). It simply reads genetic markers to identify naturally-occurring genetic variations so that individuals with the best potential to meet production goals and sustainability objectives can be selected.

For this research study, we surveyed potential end-users across BC. All individuals invited to participate in the survey had a demonstrated knowledge and link to silvicultural practices in BC. We developed qualitative, semi-structured, open-ended individual interviews, supplemented with a quantitative questionnaire designed on a Likert scale. As we anticipated that participants would be unfamiliar with this new technology, we commenced each interview by showing the participant a brief, non-directive 10-minute video that described MAS. This video was taken from a segment that was originally aired on Télé-Québec in 2008 on a scientific program called ‘Le Code Chastenay.’

Upon completing 25 interviews and reaching data saturation, we subsequently categorized our findings into four groups by end-user type (First Nations, government, industry, and environmental non-governmental organizations [ENGOs]) (Samure & Given, 2008). Interestingly, preliminary analyses have shown that potential end-user groups identified similar benefits; however, the four groups differed in their concerns.



Participants identified the benefits of MAS to be:

- Selection of desired traits,
- An additional tool for tree breeders,
- A time-saving tool .

The ENGO participants also identified that MAS could be used to reduce pressure to intact forests by increasing volume within a stand and subsequently decreasing harvesting in other areas that were previously needed to achieve the same volume. Industry, government and First Nation participants indicated that this tool could be used towards climate change adaptation, through identifying genes related to pest and disease resistance and various abiotic stresses.

Conversely, some of the perceived concerns identified by government were that MAS is an expensive tool to develop and implement, while limited funds are allocated to breeders to develop the skills and resources to use this technology. Government participants shared a concern over what traits could be missed, and if that could lead to future susceptibility in an unpredicted way. Furthermore, it could be challenging to gain public support if the public confuses this technology with genetic engineering.

Industry participants likewise addressed concerns around public perception, stating that the public typically associates biotechnology with genetically modified organisms (GMOs), and that it would be challenging to educate them otherwise. Participants also expressed concern over the difficulty in predicting which traits will be desired 50 years from now.

Neglecting other forest values, a loss of diversity, and a tool designed primarily for industry were all concerns identified by First Nations and ENGOs. First Nations participants also stated that it would be necessary to educate their community on the tool to ensure support, and that trials needed to be done first. Some participants further expressed a concern that this tool may pave the way towards monocultures, and that policies and regulations need to be developed around the use of this tool.

Although these preliminary findings indicate that each user-group expressed varying concerns around the future use of MAS in BC forests, their perceptions on the technology could be improved if a few key concerns were addressed. By performing trials, developing a complementary policy framework, and creating further opportunities for open-discussions among end-users, perception by stakeholders and First Nations surrounding MAS could be ameliorated. Moreover, the best way to strengthen support for a new biotechnology is through education. Educating end-users and the public may serve to be a significant hurdle - yet pivotal component - to the future implementation of MAS in BC.

References:

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- Yanchuk, A. D. (2002). The role and implications of biotechnology in forestry. *Food and Agriculture Organization of the United Nations, Unasylva*(30), 18–22.

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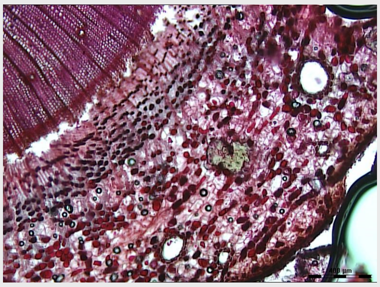
Data Release:

White Spruce (*Picea glauca*) PG29 genome 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). In addition to the NCBI portal, we have also provided a separate portal for the first draft assembly [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. The current white spruce genome assembly data release aims to support research and development in the scientific community according to the principles outlined in the Toronto workshop on pre-publication sharing of genomic data. [**/Portals/0/1st%20assembly%20release%20notice.pdf**]

To cite this resource, please use the following article:

Birol, I., A. Raymond, S.D. Jackman, S. Pleasance, R. Coope, G.A. Taylor, M.M. Saint Yuen, C.I. Keeling, D. Brand, B.P. Vandervalk, H. Kirk, P. Pandoh, R.A. Moore, Y. Zhao, A.J. Mungall, B. Jaquish, A. Yanchuk, C. Ritland, B. Boyle, J. Bousquet, K. Ritland, J. MacKay, J. Bohlmann & S.J.M. Jones. 2013. Shotgun sequencing and assembly of the 20 Gb white spruce (*Picea glauca*) genome. *Bioinformatics*. http://dx.doi.org/10.1093/bioinformatics/btt178.

White Spruce (*Picea glauca*) Short Read Archive (SRA) of PG29 RNA

RNA sequences from PG29 various tissues, short sequence reads (http://www.ncbi.nlm.nih.gov/bioproject/210511). This data was generated using Illumina HiSeq techonology.

White Spruce (*Picea glauca*) Short Read Archive (SRA) of WS7711 seed tissues

mRNA sequencing from white spruce seed tissues (megagametophytes and embryos), short sequence reads (http://www.ncbi.nlm.nih.gov/bioproject/245361). Data generated using Illumina HiSeq techonology. Verta & *al.*, 2014; doi: http://dx.doi.org/10.1101/007153.

White Spruce (*Picea glauca*) PG29 2nd draft assembly

A second draft assembly of *Picea glauca* (PG29) has been deposited into National Centre for Biotechnology Information (NCBI). The data was generated using Illumina HiSeq technology. The sample catalogue is **Bioproject PRJNA83435**, Accession AL-WZ0000000000. The data can also be found at the FTP site hosted by BCGSC (ftp://ftp.bcgsc.ca/public/Picea_Glauca/).

White Spruce (*Picea glauca*) WS77111 1st draft assembly

The SMarTForests project has released a first assembly of a second white spruce (WS77111) through the National Center for biotechnology information (http://www.ncbi.nlm.nih.gov/bioproject/242552).

SNP data. 13,461 *Picea glauca* SNPs described in Pavy 2013 (PMID: 23351128)

SNPs described in Pavy 2013 (PMID: 23351128) have been deposited and accepted into the Single Nucleotide Polymorphism Database of NCBI (http://www.ncbi.nlm.nih.gov/projects/SNP/). SNP detection methods and genotyping results are described in publication (list).

High-confidence in silico SNP atlas containing 212,765 SNPs

SNPs were detected on full length sequences (FLICs) using Varscan software. Next-generation sequences were aligned on the white spruce gene catalogue (GCAT) using Mosaik software. SNPs with minor allele frequency MAF < 0.01 were automatically discarded. Genotyping, using part of a custom iSelect Infinium, was used to assess the validity of 5,938 of the predicted SNPs. In the end, criteria to develop the atlas were established as: non-singletons, depth ≥ 10 and VarScan p-value < 0.10. The overall validation rate reached 92.1% with these criteria.

Short version: SNPs were detected on full length sequences (FLICs) using Varscan software. Next-generation sequences were aligned on the white spruce gene catalogue (GCAT) using Mosaik software. Genotyping, using part of a custom iSelect Infinium, was used to assess the validity of 5,938 of the predicted SNPs. The overall validation rate was 92.1%.

Arborea Spruce 32K expression array

Microarray for expression profiling, GEO platform GPL15033. Publicly available.

Evaluation of differential expression in the vascular transcriptome among *Picea* species

Expression profiling experiment, GEO accession GSE35922, published in Raherison *et al.*, 2012. Publicly available.

Interspecies *Pinaceae* comparison experiment

Expression profiling experiment, GEO accession GSE35847, published in Raherison *et al.*, 2012. Publicly available.

PiceaGenExpress database of expression profiles

Expression profiling experiment, GEO accession GSE35624, published in Raherison *et al.*, 2012. Publicly available.

Direct measurement of heritable gene expression within single individuals from wild populations

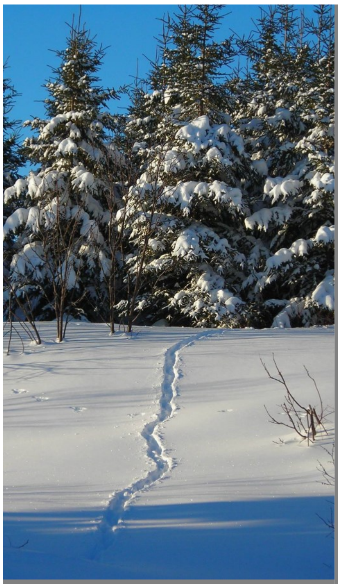
Expression profiling experiment, GEO accession GSE35337, published in Verta *et al.*, 2012. Publicly available.

Transcript profiling of early and late wood in four conifer species

Expression profiling experiment, GEO accession GSE51884, submitted for publication. Awaiting publication for public release.

Transcript profiling of seven tissues in *Picea glauca*

Expression profiling experiment, GEO accession GSE60277, submitted for publication. Awaiting publication for public release.



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News and past events

- **2nd Conifer Genome Summit**
  The 2nd Conifer Genome Summit convened at Forêt Montmorency near Québec City (Canada) on 16-18 June 2014 to facilitate updates on advanced approaches in conifer genome sequencing, assembly and annotation, as well as updates on the interpretation and practical tree breeding applications of the information gleaned from conifer genomes.
  This year's Summit also highlighted a range of studies revealing biological insights into such processes as stress responses, insect and pathogen resistance mechanisms, adaptation to climate, wood formation, and regulatory control, in addition to research linking phenotype to genotype. It brought together 60 participants from Canada, New-Zealand, Norway, Spain, Sweden, Italy, USA and UK.

- E-lectures via Canadian Forest Institute (http://cif-ifc.org/site/electure) presented in November 2013:
  November 13, 2013: "Introduction to Forest Genetics and Genomics, and application of genomic selection to wood quality," by **John MacKay** and **Jean Bousquet** with contributions from **Jean Beaulieu**.
  November 20, 2013: "Genomics of insect resistance in spruce and breeding applications," by **Jörg Bohlmann** and **Alvin Yanchuk**.
  November 27, 2013: "Is the application of genomics to growing trees competitive and acceptable?" by **Nancy Gélinas** and **Gary Bull**.

- Tree Genomics Symposium. June 9th 2014 held at Forest Sciences Centre, University of British Columbia. Participants from 4 of Genome Canada Large Scale Applied Tree projects (SMarTForests, AdapTree, TAIGA, POPCAN)

New articles (for a complete list, please go to www.smartforests.ca)

◊ Beaulieu & *al.*, 2014 Heredity
◊ Doerksen & *al.,* 2014 Tree Genetics and Genomes
◊ Roach & *al.*, 2014 Journal of Biological Chemistry
◊ Duval & *al.,* 2014 Journal of Experimental Botany
◊ Stival & *al.*, 2014 BMC Plant Biology

Upcoming events

Workshop: 3rd Annual Conifer Genome Summit (2015)

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