



EXECUTIVE SUMMARY

The SMarTForests project delivered fundamental new knowledge, innovative tools and practical applications to enhance conifer breeding in partnership with end users and stakeholders. The project firmly established Canada as an international leader in conifer genomics. With its focus on spruces as the most widely planted trees in Canada, the project targeted economically and ecologically important traits of 1) enhanced insect resistance and 2) improved wood quality and growth to maximize value recovery and yields from planted spruce forests, with the overall goal to increase forest sustainability under conditions of current and changing climates. Using innovative genome sequencing methods and novel bioinformatics tools, the SMarTForests project produced some of the very first and most advanced conifer genome assemblies. The project's research on functional and structural genomics, improved marker systems for breeding applications, along with new economic models and improved understanding of stakeholder perception positioned Canada as a leader for implementing genomics informed marker systems in advanced spruce breeding programs over the next five years.

The **Genome Sequencing** program of the SMarTForests project produced one of the first published conifer genome assemblies. In addition to representing an international landmark achievement, we established that high quality drafts of conifer genomes could be obtained entirely based on assembly of short read sequences. The project's innovative bioinformatics approaches resulted in advanced draft genome assemblies of two white spruce genotypes from advanced spruce breeding programs from end users in both western and eastern Canada. Assembling the extremely large (~20 Gbp) and heterozygous spruce genomes was mastered as a computational tour-de-force with major in-house bioinformatics developments and processing of enormous amount of sequence data (~4.8B reads, ~1Tbp per genome).

The SMarTForests project developed **Genomic Selection (GS)** methods as **Tree Breeding Tools** to provide accurate prediction of breeding values. Their usefulness was shown for traits including structural wood quality traits and growth in both white spruce and black spruce. Major progress was also made for insect resistance in interior spruce. These accomplishments represent a breakthrough in applied forest genomics and represent the most tangible opportunity for short term implementation of Marker Assisted Selection (MAS). Application of GS is predicted to shorten the breeding cycle of spruces for mature traits to a third (from 28 to 9 years) compared to the length of time when using traditional phenotypic selection. Accelerated breeding may translate into reaching economic benefits faster and enhances the ability of the forest sector to adapt faster to changing markets and environments.

The SMarTForests project also developed a suite of **Genetic Markers** and **Functionally Informed Biomarkers** for traits of economic and ecological importance identified by end users in Canadian spruce breeding programs. Based on biological, genomic and functional characterization of spruce defense system and tree resistance against stem feeding (weevils) and foliage feeding (spruce budworm), we developed biomarker tools for assessment of insect resistance. We also advanced detailed understanding of the genetic architecture of wood properties, growth and phenology through association studies, gene expression profiling, gene and QTL mapping, and functional assays. We



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identified genes putatively under selection for adaptation to climate in white spruce as markers for conservation of adaptive genetic resources.

The SMarTForests project also developed and released novel **Conifer Genomics Resources**, including the first spruce genome assemblies defining an international landmark in conifer genomics, along with diverse and comprehensive transcriptome assemblies, gene and genome annotations, and identifications of gene functions. Notably, SMartForests has been the only large scale conifer genomics project with a track record of successfully identifying definitive new gene functions in metabolic systems of key traits. Resources and information are publically available at NCBI (NCBI BioProject PRJNA83435 and PRJNA242552), the conifer specific web portal ConGenIE (<http://www.congenie.org>), and the project's peer reviewed publications. The project also identified and released large datasets of more than 0.5 million high quality SNPs in different spruce species and gene expression datasets through NCBI databases.

The SMarTForests' **GE³LS Research** developed decision support tools and economic models to assess the impacts of genomics in the context of spruce breeding applications in Canada. This led to a better understanding of genomics integration into mainstream forest economic decision making at different spatial scales, from the forest stand level to the regional, provincial and national levels. Tools developed by the GE³LS team are being adopted by the Canadian Forest Service/Natural Resources Canada (i.e. government) and found interest from Forest Product Innovations (representing forest industry stakeholders). Surveys of end users and stakeholders perceptions in three major wood producing provincial jurisdictions revealed different levels of support or concerns from industry and government groups, ENGOs (Environmental Non-Government Organizations), and First Nations regarding the implementation of MAS. This information is critical to guide future activities.

The anticipated **Socio-Economic Benefits for Canada** resulting from the SMarTForests project include substantial positive impacts on the Net Present Value (NPV) of forest production at the stand level. The impacts of Genomic Selection (GS) were estimated based on demonstrated potential to significantly shorten the breeding cycle and accelerate the associated gains for major economic traits. Considering an intensive silviculture scenario with a tree harvest age of 40 years, the NPV could be increased by 40% to reach \$10,800 per hectare. The project's GE³LS research also identified challenges and opportunities along the pathway to deployment of genomics tools. This information will be guiding future steps for short-term implementation. Continuous translation of genomics into applications over the longer term will be based on the greatly advanced knowledge and skills developed in SMarTForests.

The SMarTForests project's **Research Translation** and **Technology Transfer** activities were based on:

- 1) Direct participation of end users from the private and public sector in the project's activities to ensure that marker tools and technologies were tailored to the end users practical needs
- 2) Recommendations from the project's Technology Transfer Advisory Committee (TTAC) including partnering with FP-Innovations



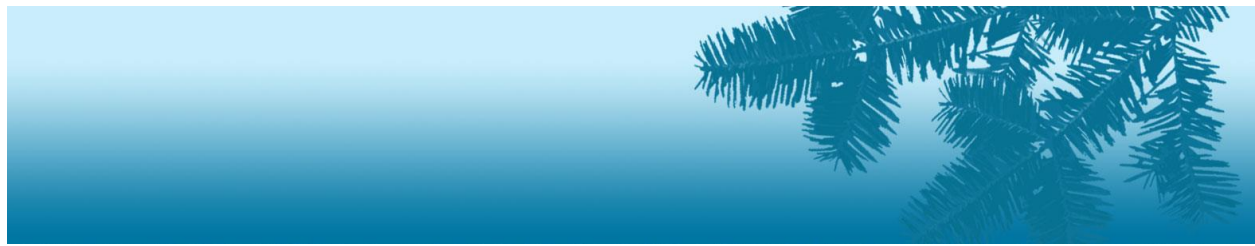
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3) Spin-off projects to accelerate the implementation and broaden the scope of MAS, including the FastTRAC project (Fast Tests for Rating and Amelioration of Conifers) (GAPP project, funded by Genome Canada) and CeDAR project (Western red cedar multi-trait genomic selection) (UPP project, funded by Genome BC)

4) Transfer of economic models to the Canadian Forest Service's Economic Branch in support of public policy development and

5) Diverse outreach activities to inform a broad end user community, including a series of e-lectures on genomics for the forestry sector, each with an audience of over 600 attendees. As a result, markers, tools and methods developed by the SMarTForests project are now being advanced and implemented by end users' organizations.

Overall, the **SMarTForests project cemented Canada's international leadership in fundamental and applied conifer genomics**. Beyond practical applications, the project's scientific leadership is documented with 67 publications in high impact journals, over 125 presentations, as well as 29 awards and distinctions received by members of the SMarTForests project team.



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