

Genomics in forest genetic resource management

Genomics is the science of sequencing the nucleotides that make up the DNA molecule and the genetic code it contains. Sequencing technologies and analytical methods have advanced dramatically over the last decade due to massive investments in genomics in Canada and other parts of the world. Genomics includes both sequencing and mapping entire genomes and fine-scale genetic mapping to find genes that influence an organism's specific functions.

Knowing the sequence of genes in an organism and understanding the functions of the genes are very different areas of investigation. With tens of thousands of genes producing proteins for highly complex biological functions, unraveling the contribution of any single gene or set of genes is difficult. Large investments in tree genomics have advanced knowledge a great deal, but there remains much to learn about gene function and what genes influence the complex development pathways for growth or other traits. Explaining the phenotype by knowing the genotype is still only possible for a handful of simple traits.

In BC, Genome Canada and GenomeBC have supported genomics research primarily on interior spruce (*Picea glauca* x *P. engelmannii* hybrid complex^a), Sitka spruce^b, and poplar^c. These investigations have applied sequencing and bioinformatic assembly technologies to both sequence the genomes and to search for genes that influence key functions such as growth rate, pest resistance, or wood properties. More recently, the Genome-Canada supported AdapTree^d project is applying genomic methods to examine natural patterns of adaptation. Knowledge from this work will inform the development of climate-based seed transfer standards.

At the present time, genomic applications to breeding in some agricultural crops are common and forestry applications are emerging. These include the use of many genetic markers to select for economic traits in trees, guiding seed transfer, and pest identification. In BC, genomics is not yet used for the selection of trees for traits of economic significance. However, with the fast pace of this research, genomics is likely to have a role in BC tree breeding programs in the near future. It is a tool that tree breeders must evaluate relative to the cost of other options. For example, using tree measurements from traditional progeny field trials allows breeders to obtain genetic gains for traits like growth rate. The application of genomic selection can shorten the time for selection of better trees, potentially increasing genetic gain per year across a breeding cycle. However, these potential gains must be evaluated with an understanding of the uncertainty of the technology, the cost, and other potential methods.

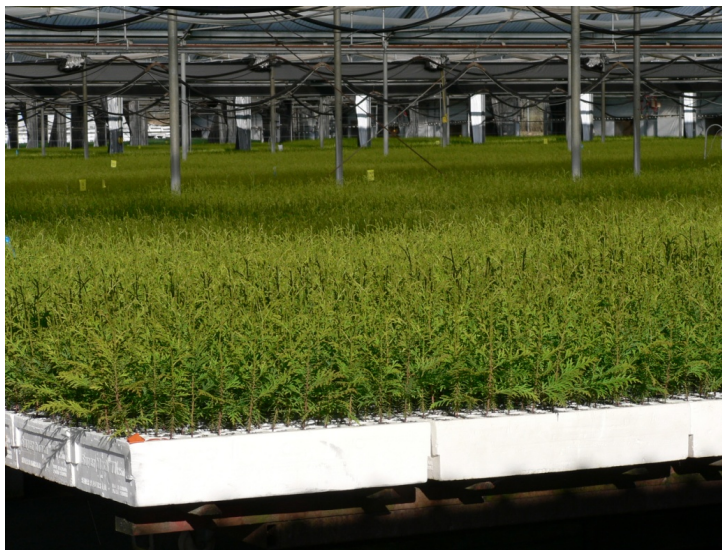


Photo: Western redcedar seedlings at Western Forest Products nursery. Genomic selection may offer a solution to the problem of selecting trees at a young age for mature traits such as wood extractive content and rot resistance. (*J. Woods*)

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^b Treenomix – project leaders Dr. Jörg Bohlmann (UBC) and Dr. Kermit Ritland (UBC)

^c PopCan - project leaders Dr. Carl Douglas (UBC) and Dr. Shawn Mansfield (UBC)

^d AdapTree - project leaders Dr. Sally Aitken (UBC) and Dr. Andreas Hamann (U. Alberta)

It is not our expectation that genomics will displace long-term field testing. Genomics will, however, become one of the tools available to help breeders select trees for seed orchards.

Genomics will likely be most useful for traits that are difficult to evaluate at a young age, such as terpenoid extractive content in redcedar, a key trait for rot resistance in lumber. Resistance to some pests, such as mountain pine beetle, is also difficult or impossible to evaluate in a young tree as only larger trees are attacked. For traits of this type, genomics may be the only practical method that can be applied to select desirable trees within a practical time frame. It is also useful for understanding genetic diversity patterns and management impacts.

While the hurdles preventing full application of genomics in BC remain significant, it is likely that these will continue to drop and more opportunities will arise in the near future.

Author: Jack Woods. This article originally appeared in the FGC Annual Report 2012/13.