

An International Consortium in Conifer Genomics. Why, How, Who and What?

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Conifers have among the largest known genomes. At 20 to 30 Gigabases, their genomes are 7 to 10 times larger than the human genome. Their genome structure and the cause of this very large genome size are poorly understood. Sequenced genome sequences are completely lacking for conifer trees and the entire group of gymnosperms.

Next-generation sequencing technologies represent an opportunity that could revolutionize our ability to sequence the large uncharacterized conifer genomes in the very short term. Seizing this opportunity could lead to new and innovative approaches that would profoundly transform conifer genetics.

We are proposing to form an international consortium to help pave the way to whole genome sequencing in multiple conifer genomes. One of the first goals of the consortium will be to produce and disseminate genome sequences of a few major conifers. It will also aim to create knowledge, resources, methods and know-how that will greatly facilitate genome sequencing in multiple species and genotypes so that basic and applied outcomes of whole genome analysis can become widespread.

The purpose of the presentation is to review the basic premises for forming a consortium, and discuss a proposal in preparation for Genome Canada's International Consortium Initiative program. The aim is to engage participants in the development a long term strategic vision and in the definition of an integrated research plan.

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