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Arborea: Functional Genomics of Regulation in Forest Trees

Status	Past
Competition	II
Sector	Forestry
Genome Centre	Genome Quebec
Project Leader	John MacKay

Project Description

Canada's forests make up about 10% of the world's total and occupy nearly 35% of our land mass. They are a huge renewable resource, contributing over \$80 billion dollars annually in wood, paper and energy products, and almost 400,000 jobs to our economy. Canada is in intense competition for forest products with other countries in warmer climates. It will be a great advantage to Canada if we can speed up the development of new tree crops that grow faster and yield more wood. So far, this has been done by traditional plant-breeding methods, which are very slow; it takes decades for results to appear. We aim to speed up the process by using genomic research.

We set up some of the basic tools that will allow us and others worldwide to carry out genetic research on spruce and poplar trees. This will lead to a deep understanding of many aspects of tree growth that will be important for genetic improvements such as wood formation and defense against pests and other environmental stress.

We obtained the DNA sequence for nearly 70,000 genetic markers called expressed sequence tags in spruce and poplar. We created close to 2,000 special mutant versions of poplar trees, which are stored for future research. We use a method called DNA microarraying that will enable us to study which poplar and spruce genes are important for many aspects of growth and development. Through international collaborations, we put in place a large database of poplar and spruce genomic information. We make these three experimental tools available to plant researchers all over the world.

Fast Facts

<i>Highlighted outcome:</i>	The development of genomic methods and tools to enhance genetic selection and breeding of softwood forest trees
<i>Number of research personnel employed by the project:</i>	34
<i>Number of peer reviewed publications published:</i>	19 + 1 book chapter
<i>Number of patents in process or obtained:</i>	1
<i>Resources generated:</i>	Gene sequences, cloned gene collections, DNA micro-arrays, cDNAs sequences and clones from spruce and poplar, transgenic cell lines. Two databases (SpruceDB and ForestTreeDB) are publicly available.
<i>Co-funders:</i>	Génome Québec, Canadian Forest Service