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## **Bridging Comparative, Population and Functional Genomics to Identify and Experimentally Validate Novel Regulatory Regions and Genes for Crop Improvement**

<b>Status</b>	Approved
<b>Competition</b>	Applied Genomics in Bioproducts or Crops
<b>Sector</b>	Agriculture - Crops
<b>Genome Centre</b>	Genome Quebec
<b>Project Leader</b>	Thomas Bureau, McGill University

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### **Project Description**

Genomic methods, pioneered in studies of simple, single-celled organisms, are being applied with great success to important crop plants. Genomics provides a way to examine and analyze all of the genes (i.e., the genome) that define the crop with a view to enhance yield and productivity, while reducing production costs.

In recent years it has become clear that the genome is more than the sum of genes that code for cellular proteins. Indeed, the regions (“non-coding DNA”) between the protein-coding genes are important for regulating their activity. Studies in plants, humans and other animals now suggest that many of these non-coding DNA regions may have profound significance, harbouring the very elements that regulate genes or provide novel functionality. Our goal is to use genomics as a means to identify, characterize and validate non-coding DNA regions that have a direct role in determining characteristics that are important for Canadian crops.

We have chosen to concentrate on a plant called Arabidopsis for two reasons. First, more is known about the genetics and genomics of this plant than any other in the world. Second Arabidopsis is a close relative of several crops important to the Canadian economy (e.g., canola). Thus, through the comparison of Arabidopsis with other plants, we can identify important non-coding DNA regions, including those relevant for Canadian crops.

We will approach this by determining the whole-genome sequence of several close relatives of Arabidopsis and canola, using this information for within species and between species comparative studies. Non-coding DNA regions will be identified by computer-based predictions and will be validated by experiments that use population genetics and genomic methods. Important findings will be protected for further exploitation.

We anticipate that our project will identify non-coding DNA regions that will have proven potential for crop improvement. We will also generate valuable data, expertise and trained personnel that will provide the basis for future crop-improvement applications.