

Canada

http://www.Arabidopsis.org/info/2010_projects/Canada.jsp

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In March of 2006, 57 laboratory groups known to be conducting research with *Arabidopsis* were polled by Email for contributions to the MASC report. Of these, approximately 30 responded and their contributions are summarized in this report. The past two years have witnessed a period of rapid turnover and new hires among University Faculty in Canada – in part due to the retirement of those Faculty hired in the late 1960's and early 70's. As a result, a number of new and exciting young scientists have joined the plant science research cadre, including a significant number of *Arabidopsis* researchers.

Reports

- François Belzile- l'Université Laval (fbelzile@rsvs.ulaval.ca)
The Belzile lab studies *Arabidopsis* DNA mismatch repair (MMR) in regards to both microsatellite instability and homoeologous recombination.
- Thomas Berleth – University of Toronto (thomas.berleth@utoronto.ca)
The Berleth lab developed approximately 4,000 indirect enhancer trap lines, together with ~ 70,000 indirect activation tags (among them ~30,000 conditional activation tags) for use in the study of very early vascular genes. In addition, they are conducting a study to map QTLs defining *Arabidopsis* fibre properties.
- Malcolm Campbell – University of Toronto (campbell@botany.utoronto.ca)
The Campbell lab investigates (1) the perception of sugars, amino acids and water, and how this affects the allocation of resources to key facets of metabolism and development, (2) comparative genomic analyses with the model woody perennial genus *Populus*.
- Jin-Gui Chen – University of British Columbia (jingui@interchange.ubc.ca)
The Chen lab investigates signal transduction networks using both forward- and reverse-genetic, molecular and cellular biological, and biochemical approaches.
- William Crosby – University of Windsor (bcrosby@uwindsor.ca)
The Crosby lab investigates the role of E3 ubiquitin ligase (E3) complexes in the regulation of patterning and development in *Arabidopsis*.
- Raju Datla – NRC Plant Biotechnology Institute (raju.datla@nrc-cnrc.gc.ca)
The Datla lab investigates gene expression dynamics during embryo development, currently focusing on genes in *Arabidopsis* as well as the closely related *Brassica napus*.
- Michael Deyholos – University of Alberta (deyholos@ualberta.ca)
The Deyholos lab applies genetic analysis and functional genomics of *Arabidopsis* to two areas of research: vascular development, and abiotic stress responses.
- Sonia Gazzarrini – University of Toronto, Scarborough, (gazzarrini@utsc.utoronto.ca)
The Gazzarrini group uses functional genomic, molecular and chemical genetic approaches to study the molecular mechanisms that regulate early developmental phase transitions and plant resistance to abiotic stresses in *Arabidopsis*.
- Vojislava Grbic – University of Western Ontario (vgrbic@uwo.ca)
The Grbic lab investigates the diversification of plant forms by studying a set of late-flowering *Arabidopsis* accessions with naturally occurring variant morphology.
- George Haughn – University of British Columbia (haughn@interchange.ubc.ca)
The Haughn laboratory studies regulation of plant morphogenesis and seed coat differentiation in *Arabidopsis* and oversees the Canadian reverse genetic TILLING facility, CAN-TILL (<http://www.botany.ubc.ca/can-till/>).
- Shelley Hepworth – Carleton University (shelley_hepworth@carleton.ca)

The Hepworth lab focuses on determining how positional information is translated into morphological asymmetry, an important aspect of developmental patterning in plants.

- Robert Hill – University of Manitoba (Rob_Hill@umanitoba.ca)
The focus of the research in the Hill laboratory is on ABA receptors and their mechanism of interaction with other signaling components.
- Kenton Ko – Queens University (kok@biology.queensu.ca)
The Ko lab uses *Arabidopsis* as a model for studying the relationship between plastid protein delivery, adaptation, and organelle biogenesis.
- Igor Kovalchuk – University of Lethbridge (igor.kovalchuk@uleth.ca)
The Kovalchuk lab uses *Arabidopsis* to study genetic and epigenetic aspects of plant genome stability and plant stress response.
- Ljerka Kunst – University of British Columbia (kunst@interchange.ubc.ca)
The Kunst laboratory studies lipid metabolic pathways in higher plants, focusing on two specific areas of lipid metabolism: cuticular wax biosynthesis and secretion.
- Xin Li – University of British Columbia (xinli@interchange.ubc.ca)
The Li group is studying R-protein signaling pathways that play central roles in recognizing pathogens and initiating downstream defense cascades.
- Jaideep Mathur – University of Guelph (jmathur@uoguelph.ca)
The Mathur lab studies sub-cellular dynamics and organelle interactions in order to understand the early responses of plants to various abiotic / biotic stimuli.
- Doug Muench – University of Calgary (dmuench@ucalgary.ca)
Research in the Muench laboratory is aimed at understanding the role of the plant cytoskeleton, specifically microtubules, in subcellular mRNA localization, protein sorting, and low temperature stress signaling.
- Roger Lew – York University, Toronto (planters@yorku.ca)
The Lew lab is interested in the electrical properties of *Arabidopsis* root hairs. Current studies involve ion transport in cellular expansion and plant cell stress response.
- Nicholas Provart – University of Toronto (nicholas.provart@utoronto.ca)
The Provart lab oversees the Botany Array Resource (see Functional Tools at the end of this section.) In addition, the wider *Arabidopsis* research group at the University of Toronto has generated 10,000 DEX inducible random insertion lines which will be deposited to the stock center in the future.
- Przemyslaw Prusinkiewicz – University of Calgary (pwp@cpsc.ucalgary.ca)
The Prusinkiewicz group focuses on simulation modeling of *Arabidopsis*, including the multiple roles of auxin in plant morphogenesis, general methods of modeling plants across multiple scales of organization, and further development of simulation software.
- Sharon Regan – Queens University (regans@biology.queensu.ca)
The Regan lab investigates the role of ethylene in regulating developmental processes such as seed dormancy, flowering time, trichome development, and secondary growth.
- Dan Riggs – University of Toronto at Scarborough (riggs@utsc.utoronto.ca)
Research in the Riggs laboratory focuses on two distinct but interrelated processes: factors which affect plant architecture and factors that regulate chromatin condensation.
- Owen Roland – Carleton University (owen_roland@carleton.ca)
The Roland lab studies the synthesis of cuticular waxes and their deposition onto plant surfaces via map-based cloning and reverse genetic and biochemical approaches.
- Kevin Rozwadowski – Agriculture and Agri-Food Canada, Saskatoon (rozwadowskik@agr.gc.ca)
The Rozwadowski group is interested in DNA double-strand break repair in vegetative and meiotic cells. The lab uses *Arabidopsis* as a model to characterize the details of the repair process and evaluate plant responses to genotoxic stress.
- Lacey Samuels – University of British Columbia (lsamuels@interchange.ubc.ca)
The Samuels lab is conducting a multi-disciplinary research project to study the plant cuticle. The project involves characterizing biosynthetic mutants (Kunst Lab), studying wax export and the cell structure of these mutants (Samuels Lab) and analyzing the chemical composition and biosynthetic pathways of cuticular lipids (Jetter Lab).
- Dana Schroeder – University of Manitoba (schroed3@cc.umanitoba.ca)
The Schroeder group works on the regulation of light signaling and DNA repair by DET1, DDB1A, and DDB2 in *Arabidopsis*.
- Elizabeth Schultz – University of Lethbridge (schultz@uleth.ca)
The Schultz lab studies the regulation of leaf vein pattern and its relation to leaf shape.

- Geoffrey Wasteneys- University of British Columbia in Vancouver (geoffwas@interchange.ubc.ca) His laboratory uses *Arabidopsis thaliana* as a model system to understand how microtubule function is regulated in eukaryotic cells.
- Randall Weselake – University of Alberta (randall.weselake@afhe.ualberta.ca)
The Weselake group is (1) assessing the functionality (in this case the ability to impart tolerance to abiotic stress) of a number of oilseed rape genes using *Arabidopsis*, and (2) researching novel methods for modifying the fatty acid composition of seed oils.
- Tamara Western – McGill University (tamara.western@mcgill.ca)
The Western lab uses a combination of forward genetics screens for mutants affected in mucilage production and reverse genetics identification of knockouts in genes predicted to act in cell wall synthesis and modification.
- Stephen Wright – York University (stephenw@yorku.ca)
The Wright lab is interested in (1) understanding the forces driving gene and genome evolution in the genus *Arabidopsis*, (2) testing for the accumulation and increased activity of transposable elements in the allopolyploid genome of *Arabidopsis suecica*, and (3) sequencing of the genomes of *Arabidopsis lyrata* and *Capsella rubella*.
- Jitao Zou – NRC Plant Biotechnology Institute (jitao.zou@nrc-cnrc.gc.ca)
The Zou lab is primarily interested in lipid and carbon metabolism. They study enzymatic components of the lipid metabolic network and are also interested in exploring natural variation in wild type accessions to dissect regulatory components of seed oil deposition.

Arabidopsis genomics tools and resources:

- Canadian reverse genetic TILLING facility, CAN-TILL (<http://www.botany.ubc.ca/can-till/>).
- Botany Array Resource (<http://bbc.botany.utoronto.ca>): Contains more than 1000 gene expression data sets consisting of more than 24.6 million data points. Tools available for the exploration of these data include: [1] an Expression Browser for performing electronic Northern blots [2] a new Fluorescent Protein Browser tool, which paints gene expression information from the Gene Expression Map of *Arabidopsis* Development onto a diagrammatic representation of the developmental series used, [3] Expression Angler, to identify genes that are co-expressed with gene of interest in a specified data set, and [4] Promoter for the identification of potential *cis*-regulatory elements in the promoter of a given gene, or in the promoters of a set of co-regulated genes. Additional tools include a database of genome-wide predicted CAPS markers across 96 accessions, based on sequence data from Magnus Nordborg and colleagues (2005, PLoS Biol. 3:e196).