



CANOLA GENOMICS NEWSLETTER

Issue 1, August 2003



GenomePrairie

Welcome

Welcome to the first issue of Canola Genomics Newsletter. The aim of this newsletter is to inform you about the Genome Prairie project, "Enhancing Canola through Genomics." The information will describe the scientific project, present the project contributors and give updates on the scientific progress. Furthermore, we would like this newsletter to be open to other genomic projects involving canola and related species. We therefore welcome contributions from researchers with similar interests.

Table of contents

	<i>Page</i>
Welcome note.....	1
A note from the President.....	1
Project summary.....	2
Seed Development.....	3
Seed Composition.....	3
History of the development of canola.....	4
First group meeting.....	5
Meet the project scientists.....	6
Coming seminars and conferences...	8
More information.....	8

A note from the President of Genome Prairie:

“Welcome and congratulations from Genome Prairie”

On behalf of Genome Prairie and its Board, I am very pleased to provide a note of encouragement and congratulations to the researchers involved in the Enhancing Canola through Genomics project. This project represents an impressive effort to understand from a genomics perspective the pathways that govern seed development and that regulate the accumulation of reservoirs and metabolites. This is clearly a major opportunity for this agronomically important crop to which Canadian researchers have already contributed so much, and progress in this respect will eventually help to improve the quality and productivity of this domesticated plant. The project reflects a remarkable collaborative effort among leading researchers in the National Research Council Plant Biotechnology Institute and the Agriculture and Agri-Food Canada laboratories in Saskatoon, under the guidance of Dr. Wilf Keller and the Project Steering Committee and Dr. Faouzi Bekkaoui, the Project Manager. We are pleased to see progress accelerating on many fronts and furthermore that the project is beginning to attract international attention, which will be enhanced by Canada’s first Plant Genomics Workshop scheduled for August in Saskatoon.

This project and its researchers are beginning to establish themselves as national leaders in what we hope is an emerging consortium of agricultural and forestry genomics researchers. The potential for scientific and economic benefits to Canada through these projects is enormous, and we look forward to your success.

President & CEO
Genome Prairie

Project summary

The “enhancing canola through genomics” project will develop and employ genomics, tools in the study of the genes that control seed development and composition in Brassica oilseed crops.

Agriculture and food processing is the third largest industrial sector in Canada and generates more than \$100 billion in annual economic activity. The economic viability of agricultural production is the focus of the proposed initiative. The research will target seed development and seed composition with the long-term aim of developing crop varieties with improved quality that will help to sustain commodity prices or will provide access to new value-added and niche markets. This value-added principle was already employed over thirty years ago in the development of canola in Canada. Removing erucic acid from rapeseed produced a healthy, edible oil with a much improved market position and the removal of anti-nutritional compounds from the meal converted a green manure into a valuable constituent of animal feed.

Canola has a very low level of saturated fats compared to other vegetable oils. It is now desirable to reduce the saturates even lower from 7% currently, ideally to 3%, and raise mono-unsaturates to levels found in olive oil. Ideally poly-unsaturates will also be slightly reduced (from 8% to approximately 4%). This will increase the shelf life of the oil. It is also desirable to produce more oil per acre in order to open up new bulk markets.

Canola meal is not currently as digestible as soybean meal. Canola protein could be improved through the application of genomic technologies and could eventually enter into the human food market.

Given the nutritional and economic importance of canola, as well as changes in the world market for vegetable oils, canola is an important target for genomic research. Genomics is revolutionizing the speed with which biological information can be accumulated through the use of large-scale, semi-automated molecular and informatics technologies. Canola is in an ideal position to apply genomics resources and information developed in the closely related model plant, Arabidopsis.

Genome Canada will contribute \$3.75 million to the project. In addition the National Research Council (NRC) and Agriculture and Agri-Food Canada (AAFC) are contributing \$5.25 million in funding to produce a large scale project with approximately \$9 million of support.

Researchers from NRC-PBI and AAFC will collaborate to achieve various objectives aimed at understanding seed development and composition. We expect that the new knowledge will reinforce Canada’s strong position in crop genomics and will permit the application of new discoveries to agricultural production and industries in Canada.

Wilf Keller (Plant Biotechnology Institute, NRC) and Derek Lydiate (Saskatoon Research Centre, AAFC)

Seed Development, Raju Datla, NRC-PBI, Saskatoon

Seed is the harvested part of most established crop species. In canola, the seed accounts for about 15 to 35 per cent of the total dry matter produced. Crop value is determined by key characteristics such as the size and number of seeds, the rate of seed growth, the chemical composition of the seeds (the identity and amounts of oils, carbohydrates, etc.) and the efficiency and speed of germination of crops after sowing. Developmental processes play critical roles in defining these important functions. However, there are substantial gaps in our understanding of the many interdependent biochemical and molecular processes that control development in plants, including crop species such as canola.

The seed phase of the plant life cycle commences with fertilization, followed by embryogenesis, maturation, dehydration, imbibition and terminates with germination. Despite significant advances in recent years (especially from *Arabidopsis* embryogenesis research), there are many knowledge gaps remaining in our understanding of embryogenesis and seed development. For example, little is known of the pattern elaboration processes of the mid- to late-stages of embryo development that contribute to determining the embryo/seed size.

This project entails conducting a global survey of gene expression patterns, and their implications to seed development, from early embryo development to the initiation of germination in canola and related species. This effort will build upon the information base available in *Arabidopsis thaliana*, including the complete sequence of its genome (Arabidopsis Genome Initiative, 2000). This project will also address the correlation of transcript, protein and metabolite profiles with an emphasis on understanding the regulation of seed development. Initially a baseline dataset will be collected for seed development in canola. This will be used to make informative comparisons with development in other *Brassica* species.

Seed Composition, Dwayne Hegedus, AAFC, Saskatoon

Seeds accumulate three major storage reserves. These are proteins, complex carbohydrates and triacylglycerols (oil). In oilseed crops, such as canola and sunflower, the oil is currently the most valuable component of the harvested seed. However, gains in oil content through conventional breeding have been slow and increasingly difficult to attain and new approaches are required. Modifications to lipid biosynthesis that create oil profiles tailored to specific food or industrial uses will produce new crops from an established agronomic platform. At present, canola seed protein is treated as a by-product of the oil extraction process and is marketed mainly as a livestock feed supplement. However, there are limits on the amount of canola meal that can be used in feed formulations due to its relatively poor digestibility. Improvements in storage protein structure and the reduction of cell wall components will improve the digestibility and increase the value of canola meal. The seed can also provide a platform for molecular farming applications by accumulating valuable proteins.

Canola seeds also accumulate an extensive array of secondary metabolites. Some of these compounds are of value but are present at sub-optimal levels due low metabolic rates or the conversion of the desired production into less valuable derivatives. Examples of such compounds include antioxidants and vitamins such as tocopherols (vitamin E), ubiquinone and carotenoids (vitamin A). Other secondary metabolites are undesirable in animal feeds. (*Continued page 5*)

Brief history of the development of canola

The “canola” name was registered in Canada in 1970. Canola refers to *Brassica* varieties that have 5% or less erucic acid and 3 mg per gram or less of glucosinolates in the seed products. Prior to 1970, the name “rapeseed” was commonly used and is still used for varieties used in industrial oil production and also in certain countries. The “canola” name is now used for three *Brassica* species: *B. napus* also known as “Argentine variety”, *B. rapa* also known as “Polish variety” and *B. juncea* or mustard.

Rapeseed was essentially a weed in Canada at the beginning of the 20th century. From 1920 to 1950, rapeseed oil was used as a lubricant in steam engines of ships. In 1943, 1300 hectares of rapeseed were sown and 1000 tonnes of seeds harvested (2). The oil was considered not edible due to high levels of erucic acid. Because rapeseed was well adapted to cold climates of the prairies and because Canada was a net importer of edible oils, rapeseed presented an opportunity for producing edible oil (1).

After World War II, Canadian researchers started improving the quality of the oil for food and feed use. The improvement targeted the reduction of erucic acid and glucosinolates that were not desirable for human and animal consumption. Erucic acid, a long chain C: 22 fatty acid is present at 20% or more in rapeseed oil and is considered poisonous when consumed in high quantities. Glucosinolates produces a sharp taste in the meal and are not desirable in animal feed.

Canadian scientists, in particular from Agriculture Canada, the National Research Council and the University of Manitoba were able to develop new varieties of *Brassica* thanks to new oil testing methods and to intensive breeding programs.

Canola is now a major crop in Canada with a five-year average of 11 million acres harvested each year. Canola is ranked third after wheat and barley in terms of acres seeded in Canada. Canola has an economic impact of \$2.5 billion in Canada per year. This impact consists of a farm gate value of \$1 billion, with value-added activities, such as processing, accounting for the rest. Rapeseed with high levels of erucic acid continue to be grown on a contract basis but the oil is used for industrial purposes and cannot be purchased in food stores.

Genomics provide a new potential for further improvement of this crop. The "Enhancing Canola through Genomics" project will attempt to gain a greater understanding of the genes involved in seed development and seed composition with the aim of improving or developing novel canola varieties with, for example, enhanced oil composition or vitamin content. Another example of an improvement would be to reduce other anti-nutritional compounds in the meal.



1- The National Research Council. 1992. From Rapeseed to Canola. The Billion Dollar Story. NRC publication Ottawa, Canada.

2- Saskatchewan Canola Development Commission, http://www.scdc.sk.ca/html/scdc_fs.html

First group meeting

The investigators of the “Enhancing Canola” project met on June 26, 2003. The scientists presented a summary of their objectives followed by a discussion. It is expected that there will be regular scientific meetings involving all scientists who will present their research progress.



Standing from left to right: Derek Lydiate³, Jas Singh², Martin Reaney³, Ed Tsang⁵, Neil Westcott³, Adrian Cutler⁵, Jitao Zou⁵, Wilf Keller⁵, Raju Datla⁵, Andrew Ross⁵, Andrew Sharpe³, Faouzi Bekkaoui⁴

Sitting from left to right: Sue Abrams⁵, Don Palmer⁴, Gijs van Rooijen⁴, Fawzy Georges⁵, Abdelali Hannoufa³

Other project investigators not in the photograph: Yuhai Cui¹, Alison Ferrie⁵, Dwayne Hegedus³, Joan Krochko⁵, Chris Lewis³, Chad Matsalla³, Isobel Parkin³, Larry Pelcher⁵, Jacek Nowak⁵, Kevin Rozwadowski³, Gopalan Selvaraj⁵, David Taylor⁵ and Albana Zeko⁵. 1. AAFC, London. 2. AAFC, Ottawa. 3. AAFC, Saskatoon. 4. Genome Prairie. 5. NRC-PBI Saskatoon.

Seed Composition (continued from page 3)

For example, seed phosphate is stored as phytate and the phosphate in phytate is inaccessible to animal absorption. This is wasteful because animal feeds need to be supplemented with accessible phosphate and environmental phosphate pollution occurs following the breakdown of phytate released in animal waste. Another secondary metabolite, sinapine, has a bitter flavour that has been linked to poor palatability for livestock and fish.

We are employing functional genomics and proteomics methods to identify the genes that control the potential to improve seed composition. The knowledge gained will be used to develop seeds with compositions tailored to specific applications and hence of increased value.

Presentation of the project scientists

Dr. David Taylor

Dr. David Taylor's objective within the "Enhancing Canola through Genomics" project is to study genes involved in lipid biosynthesis using *Arabidopsis* mutants. Dr. Taylor works at the National Research Council, Plant Biotechnology Institute in the area of Lipid Biochemistry and Seed Oil Biotechnology. Other areas of interest include the isolation and characterization of genes encoding strategic lipid-modifying proteins (e.g. acyltransferases) and proteins regulating carbon flux for seed oil modification through transgenic expression; fatty acid elongation and the incorporation of very long-chain fatty acids (e.g. erucic acid) into seed storage lipids in Brassicaceae and other oilseeds; modification of canola, *B. juncea*, flax and other oilseeds of value-added acyl composition (e.g. reduced saturated or polyunsaturated fatty acids) and oil content.



Dr. David Taylor obtained his PhD in 1987 at Carlton University in Ottawa. He is a coauthor of more than 80 lipid-related publications in refereed journals, book chapters and conference proceedings. He is co-inventor on five patents related to seed oil modification. In 2000, Dr. Taylor received an NRC corporate outstanding achievement award, and in 2002, her Majesty the Queen's Golden Jubilee medal. Since 1993, he has been principal applicant or co-investigator on externally funded research programs with a total value of \$10 million. Dr. Taylor is an Adjunct Professor in the department of Plant Sciences, University of Saskatchewan.

Recent Scientific publications From Dr. David Taylor's group.

Marillia EF, Micallef BJ, Micallef M, Weninger A, Pedersen KK, Zou J and Taylor DC. 2003. Biochemical and physiological studies of *Arabidopsis thaliana* transgenic lines with repressed expression of the mitochondrial pyruvate dehydrogenase kinase. *J Exp Bot.* 54:259-70

Yao K, Bacchetto RG, Lockheart KM, Friesen LJ, Potts DA, Covello PS and Taylor DC. 2003. Expression of Arabidopsis ADSI Gene in *Brassica juncea* Results in Decreased Level of total Saturated Fatty Acids. *Journal of Plant Biotechnology* (In Press)

Qi Q, Huang YF, Cutler AJ, Abrams SR and Taylor DC. 2003. Molecular and biochemical characterization of an aminoalcoholphosphotransferase (AAPT1) from *Brassica napus*: effects of low temperature and abscisic acid treatments on AAPT expression in Arabidopsis plants and effects of over-expression of BnAAPT1 in transgenic *Arabidopsis*. *Planta.* 217:547-558.

Qi Q, Huang Y, Cutler AJ, Abrams SR and Taylor DC. 2003. Cloning and characterization of a *B. napus* CPTase and its functional expression in *A. thaliana*. *Planta* (In Press).

Presentation of the project scientists (continued)

Dr. Dwayne Hegedus

Dr. Hegedus's objective within the "Enhancing Canola through Genomics" project is to examine genetic and biophysical factors affecting the accumulation of seed storage proteins. Dr. Hegedus leads the Molecular Plant Protection group within the Molecular Genetics Section at the Agriculture & Agri-Food Canada Research Centre in Saskatoon. His other research interests include genomic approaches for the study of plant defences, insect and pathogen genomics and proteomics, insect digestive biochemistry and the development of molecular tools for plant transformation and transgene containment.



Dr. Hegedus received his PhD in 1995 from the University of Saskatchewan in the areas of fungal molecular biology and insect immunity. This was followed by an NSERC Post-doctoral Fellowship at the University of British Columbia where he worked to develop genetic mechanisms for insect control as well as a commercial system for the production of complex proteins in insect cells. He is a coauthor of more than 40 publications in refereed journals, book chapters and conference proceedings and is a co-inventor on four patents related to insect cell protein expression and plant transgenic technologies. Since 1997, he has been principal applicant or co-investigator on externally funded research programs with a total value of \$5 million. Dr. Hegedus is also an Adjunct Professor in the department of Applied Microbiology and Food Science at the University of Saskatchewan.

Recent Scientific Publications from the Hegedus Group.

Sarauer BL., Gillott C and Hegedus DD 2003. Characterization of an intestinal mucin from the peritrophic matrix of the diamondback moth, *Plutella xylostella*. *Insect Mol. Biol.* 12: 333-343.

Chamankhah M, Braun L, Visal-Shah S, O'Grady M, Shi X, Hemmingsen SM, Alting-Mees M and Hegedus DD 2003. *Mamestra configurata* Serpin-1 homologues: Implications for a regulatory role for serpins in molting. *Insect Biochem. Mol. Biol.* 33: 355-369.

Li R, Rimmer R, Yu M, Sharpe AG, Séguin-Swartz G, Lydiate D and Hegedus DD 2003. Two polygalacturonase inhibitory protein genes are differentially expressed in response to biotic and abiotic stresses in *Brassica napus*. *Planta* 217: 299-308.

Hegedus DD, O'Grady M, Chamankhah M, Baldwin D, Gleddie S, Braun L. and Erlandson M 2002. Changes in cysteine protease activity and localization during midgut metamorphosis in the crucifer root maggot (*Delia radicum*). *Insect Biochem. Mol. Biol.* 32: 1585-1596.

Coming seminars, conferences and courses

First Canadian Plant Genomics Workshop, Saskatoon, Aug. 23 –26, 2003,
<http://www.extension.usask.ca/plantgenomics/program.html>

National Genomics and Proteomics Symposium, Toronto, Sep. 25-26, 2003,
<http://www.genomecanada.ca/symposium/>

The Applied Computational Genomics Course, Toronto, Nov. 29 – Dec. 7, 2003,
<http://www.gcbioinformatics.ca/>

More information...

More information on the institutions involved in the "Enhancing Canola through Genomics" project is available using the following Internet links:

AAFC-Saskatoon: <http://www.agr.gc.ca/science/saskatoon>

AAFC-London: <http://www.agr.gc.ca/science/london>

AAFC-Ottawa: <http://www.agr.gc.ca/science/ecorc>

Genome Prairie-Calgary: <http://www.genomeprairie.ca>

NRC/PBI-Saskatoon: <http://pbi-ibp.nrc-cnrc.gc.ca/en/pbi.htm>

An electronic form of this newsletter and other information about the project are available at <http://www.genomeprairie.ca/canola/index.htm>

If you have comments about this newsletter or would like to contribute with a relevant article, please send your comments and contributions to:

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