GenomePrairie **2003 - 2004**

About the artist – Dr. Morley D. Hollenberg

Educated from an early age both in the arts and sciences, Morley began calligraphy-based brushwork in 1985. His free-form calligraphic images are based on the intrinsic energy and visual motifs that can be observed in nature at the macroscopic and microscopic levels. The abstract brushwork forming the images arises from the movement and composition present in traditional Asian calligraphy. Our cover image is clearly based on the helical structure of DNA and shows the association in red of histone binding proteins. This kind of image also evokes the vibrant metaphor of a whirlwind of activity, reflecting our state over the past year.

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GenomePrairie

Chair and President's Report

This has been a great year for Genome Prairie, with the addition of two new Human Health Genomics projects from the last Genome Canada competition to our already existing projects in agriculture, bioinformatics, technology development and GE3LS, and demonstrating clearly the breadth and depth of expertise in the Prairie region.

These new projects, plus our role in the Bovine Genome Project (shared with Genome BC), brings a total of nine large scale projects under the Genome Prairie umbrella, valued at over $100 Million and supporting world class genomic research in the Prairies. This is a tremendous accomplishment, especially when one realizes that we have quintupled the effort in genomic research in the Prairies in less than three years. It is this kind of commitment that is needed if Canada is going to benefit from investing resources in genomics. In today's environment anything less than world class is not good enough.

Genome Prairie will continue to look for ways in which we can add value to the Prairie research community by establishing linkages not only among the scientific communities but also with industry. This is critical if Canada is going to capitalize on commercializing our discoveries and supporting the Federal Agenda on Innovation.

There is never a dull moment in today's fast moving world of science. Thus, our work is cut out for us to be even more aggressive in the pursuit of strategic projects that will have the support of the many stakeholders that are critical to the economic success of the research and its discoveries.

There are always challenges and one that continues to plague Genome Prairie is matching funds, especially for the corporate office. This continues to be a significant issue for operating Genome Prairie and is of major concern for the Board if we are to give stability to the genomic research community in the Prairies. This is one area that the stakeholders must support to get their unfair share of future Genome Canada funds and to support the excellent research community we have established.

We intend to set even higher goals for Genome Prairie as it enters into the next phase of Genome Canada funding. We look forward to the opportunity to provide our scientists and partners the best chance to be successful in future funding opportunities.

Dr. Pete Desai
Chair, Board of Directors

Dr. Randal Johnston
President and CEO

Communications Report

Effective communications are vital to Genome Prairie as we continue to align our goals with the strategies of Genome Canada and the other Genome Centres. Cultivating our key objectives by providing our youth, the general public and the media with opportunities to gain knowledge and understanding of genomics has been our major goal over the past year. Financial constraints have been significant but even so, we have achieved considerable success and met or exceeded expectations.

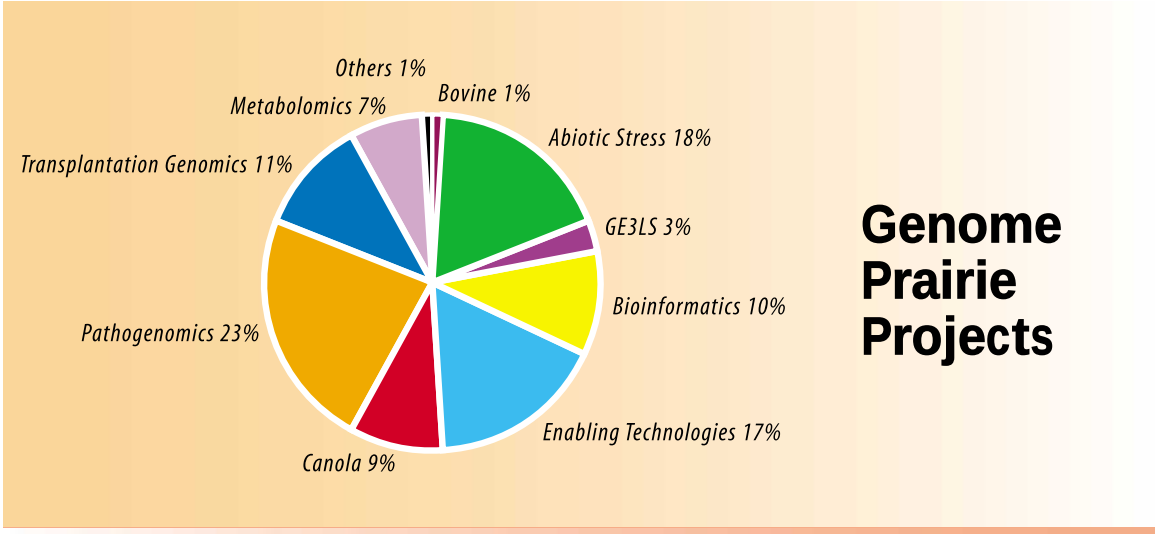
Most significantly, Genome Prairie is one of five regional presenters for the GEEE! In Genome, an innovative and interactive introduction to the world of genomics, as it makes its way across Canada. Starting in January 2004, the exhibit was opened at the Saskatchewan Science Centre in Regina where over 15,500 visitors experienced this entertaining and educational exhibit. Winnipeg hosts the exhibit from April to June when it moves on to its final destination in the Prairie region where the Provincial Museum of Nature in Edmonton will host this national public education project from July through to October. A total of seven public discussion forums will be scheduled throughout the Prairie region from January to October. Accompanying the GEEE! In Genome Program are suitcase exhibits focused at reaching smaller cities and venues. Due to the large number of remote areas within the Prairie Provinces, the suitcase exhibit has been extremely popular among teachers and students alike. We have had two and at times four suitcases circulating throughout the Prairie Provinces since January and will continue to do so until the end of this year to meet the demand.

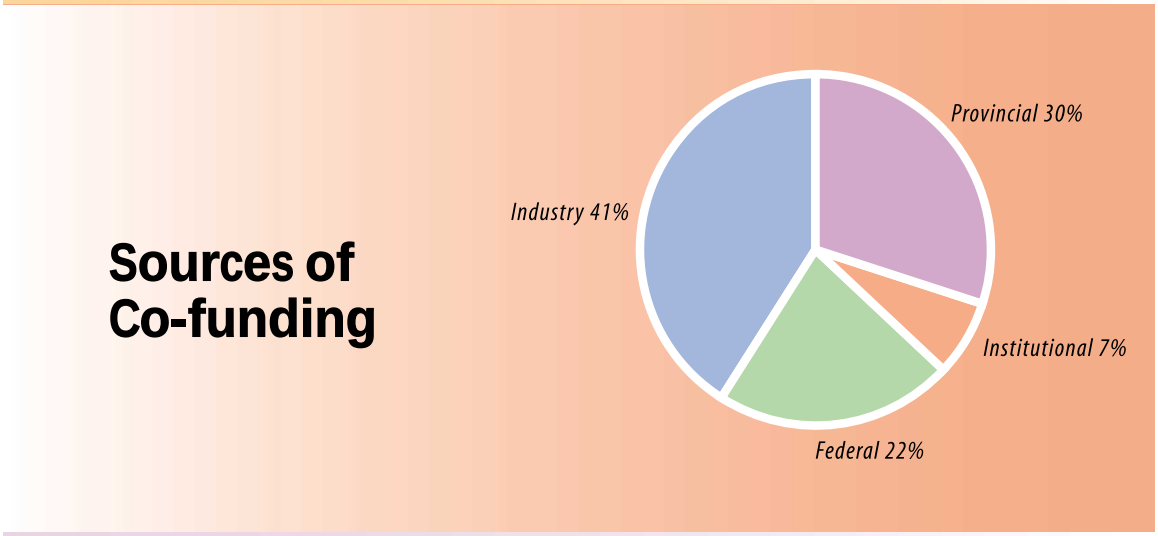
As co-sponsors of the Regional Youth Science Fairs throughout Alberta, Saskatchewan and Manitoba at the elementary, junior and senior levels, we observe every year the increase in projects submitted and the high level of science our students are learning today.

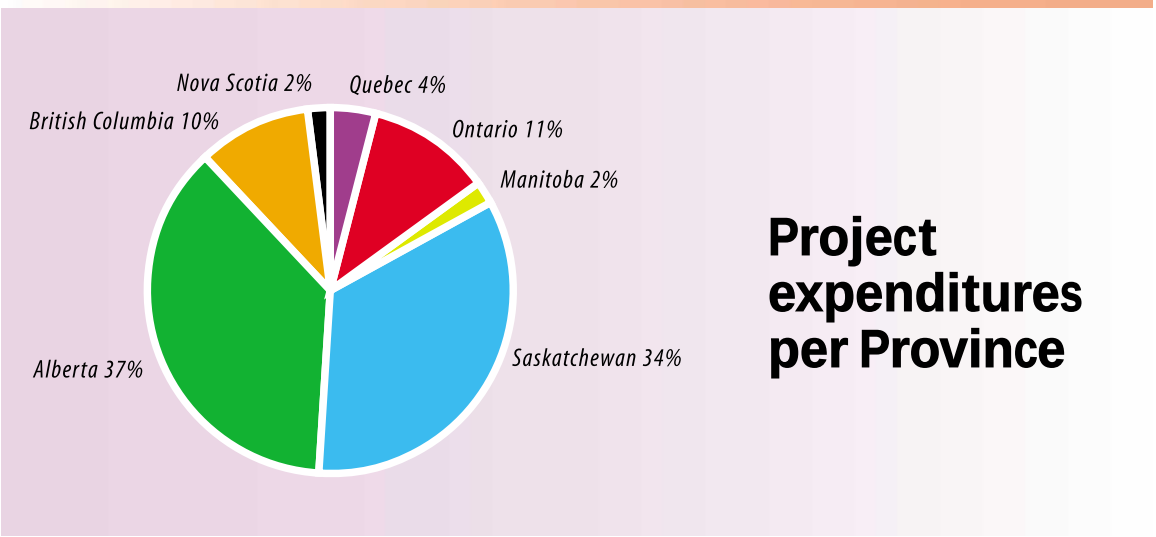
Another national competition that Genome Prairie sponsors at the regional level is Aventis Challenge. This program introduces students to the world of biotechnology by carrying out research projects of their own design. The student teams work with a mentor in their community who provides expert advice and access to equipment and supplies. This competition drives students to broaden their horizons and challenge their intellect.

Genome Prairie is reaping the results of our strong involvement within the community and private sectors and our investment in the various programs and sponsorships. Our commitment to the science of genomics and its various disciplines will enhance our ability to be versatile and flexible as opportunities continue to grow. Working together with the private sector, the provincial governments and our industrial partners allows us to be a key player as we continue to communicate in the disciplines of genomics, proteomics, bioinformatics, health and ethical arenas.

Donna Coad
Communications Officer







Graphical representation of the relative size of the Genome Prairie projects (top), sources of co-funding (middle), and Project expenditures per province

Chief Scientific Officer's Report

The past year has been very exciting and productive for Genome Prairie. Importantly, our two Competition I projects entitled "Functional Genomics of Abiotic Stress" and "GE3LS (Genomics: Ethics, Environment, Economics, Law and Society)" both passed a very rigorous Genome Canada coordinated scientific mid-term review undertaken by an Independent International Scientific Peer Review Panel. Our four Competition II projects will undergo a similar review during the course of this coming year. In addition, we are extremely pleased with the addition of two new Human Health genomics projects plus our role in the Bovine Genome Project.

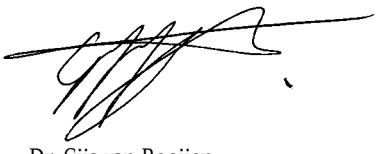
Over the past year we have seen tremendous productivity from our research teams, and it is interesting to note that a high proportion of our researchers have received international and international awards and have participated in international committees and projects. This once again highlights the quality of the research and the international recognition it has received. In addition, we are especially pleased with the interactions among the individual Genome Prairie research teams. For instance:

- Our GE3LS team recently completed a workshop on Plant Made Pharmaceuticals that involved key researchers from our Canola project.
- Our Bioinformatics Platform has now served 14 Genome Canada projects, including Genome Prairie projects.
- Our Canola project organized a very successful microarray workshop targeted to Canola, Abiotic Stress and Pathogenomics researchers. This workshop attracted over 100 participants from Saskatoon alone.

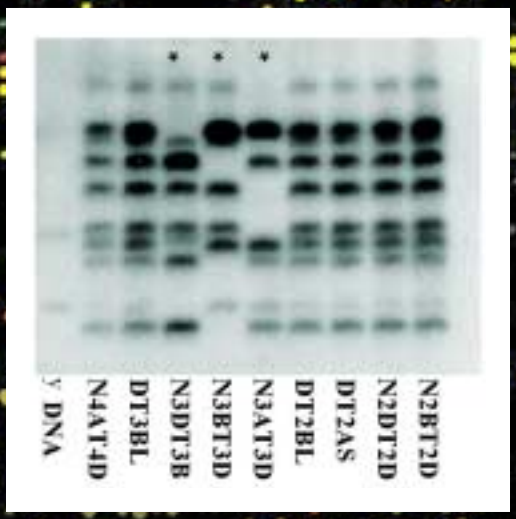
Our Program Managers have been and will continue to be vital to the success of our projects. They are located on-site with each project, rather than in our corporate office. This was necessitated because of our vast geographical distribution and has turned out to be very beneficial for both Genome Prairie and the projects. Being on-site provides the accountability we need and allows the Program Manager to optimally support the Project Leader in all research responsibilities related to the Project, including human resources, coordination of the management meetings, managing the relationship with institutions involved in the project, etc.

Finally, I would like to recognize the extremely valuable contributions the Genome Prairie Scientific Advisory Committee (SAC) has made to Genome Prairie and its Projects. During the past year our SAC has provided wonderful guidance to our Projects in the preparation of the mid-term review documentation and the follow-up that was required. Furthermore it has assisted us and our Prairie researchers in making the proposals for the Applied Health Genomics and Proteomics Competition in Human Health even more competitive.

In summary, Genome Prairie and its projects have accomplished a lot this past year. We are looking forward to next year where we expect to do even better….



Dr. Gijs van Rooijen
Chief Scientific Officer



A microarray showing gene expression data for phosphate stressed canola roots.

(inset) **Genomic hybridization patterns for a stress-induced gene in wheat**

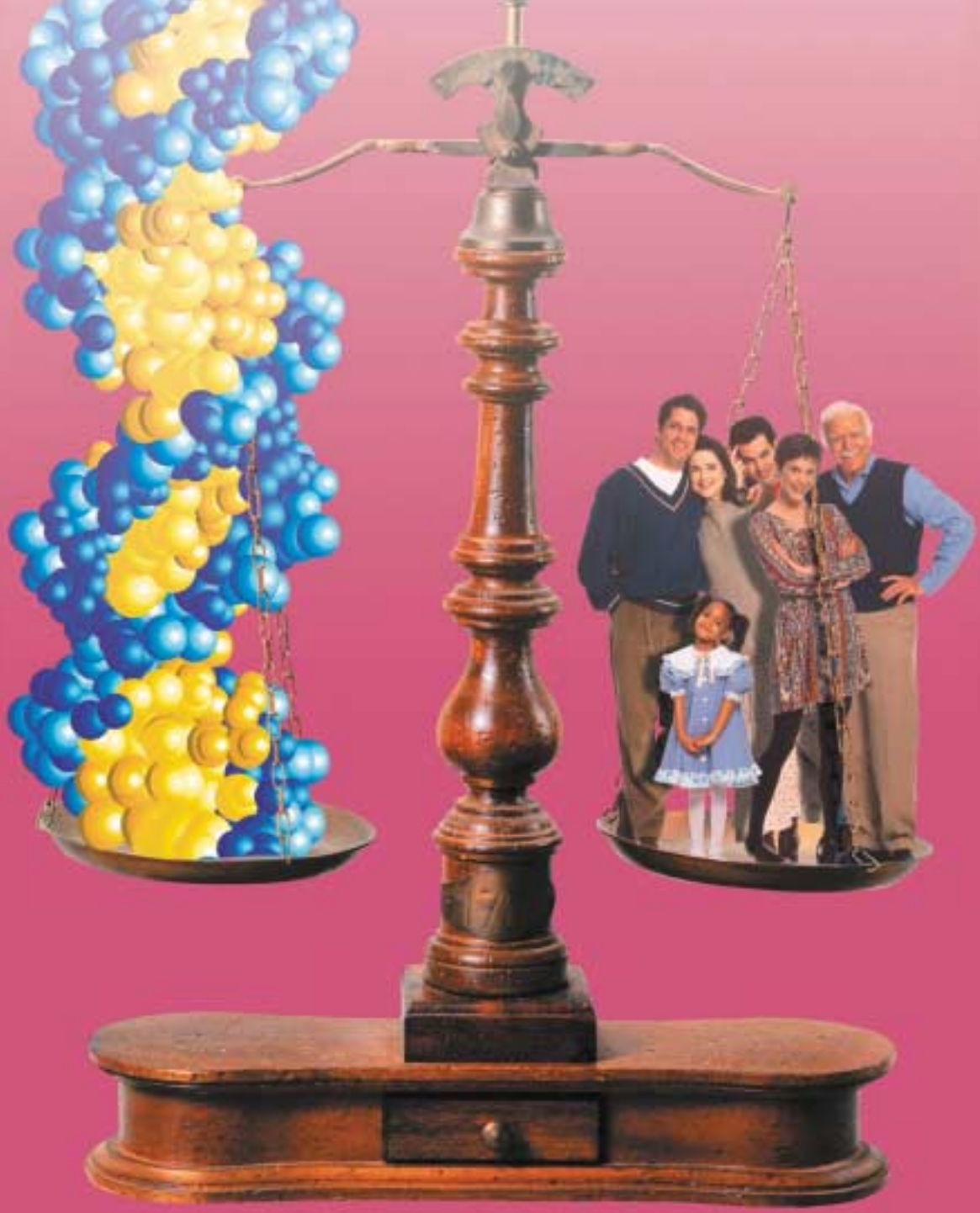
Functional Genomics of Abiotic Stress (FGAS)

The FGAS project is exploiting a range of genomics and proteomics technologies to study how plants respond to various abiotic (environmental) stresses at the gene level, particularly cold, but also heat, drought and nutrient stress. Two crops of importance to Canada, wheat and canola, along with the model plant Arabidopsis thaliana, are being used as experimental systems.

The FGAS team has made significant progress to meeting the goals of the project. These include the implementation of an array of tools including field genetic resources, protein analytical technologies, DNA sequence databases and microarrays that will empower the next project phase concerned with the elucidation of biological mechanisms governing stress adaptation in crops. We have sequenced over 100,000 ESTs in support of the wheat cold-acclimation research and are in the process of mining this data set for lead-candidate genes of possible importance to the regulation of cold tolerance in temperate cereals. Proteomics analyses are being used for identification of lead-candidate gene products whose expression correlates with cold acclimation in both Brassica and Wheat plant systems. FGAS has also implemented an effective informatics infrastructure that permits the secure organization, analysis and exchange of data within and between the 2 project themes (Wheat and Brassica).

The FGAS project has established collaborations with organizations such as the US-based NSF-sponsored '2010' program and USDA research network, as well as the researchers at the Australian Center for Plant Functional Genomics, to participate in global efforts in the elucidation of gene function(s) associated with crop stress adaptation. We have also taken a lead role in the formation of international consortia involving Australia, the USA and the UK, for purposes of jointly developing genomics resources for Wheat and Brassica crops.

We are now entering a knowledge application phase with international strategic opportunities in the area of crop genomics of direct relevance and socio-economic benefit to Canada. Knowledge gained from this project has the potential to improve the tolerance of all plants to environmental stresses, to lengthen their growing season and to improve the quality of crops of importance to Canada.



Genome Prairie's GE^{3}Ls project is investigating the optimal balance between societal needs and genomic opportunities.

The Genome Prairie GE³LS Program

The GE³LS (Genomics: Ethics, Environment, Economics, Law and Society) program of Genome Canada supports research that analyzes a variety of societal issues associated with genomics research. The Genome Prairie component of GE³LS focuses on the opportunities and challenges of the commercialization process (from basic R&D to designing and testing new products through to market diffusion).

The goal of our project is to analyze how research networks form and develop, how policy regarding new innovations is created and adapted, how intellectual property management impacts commercialization, how discoveries are portrayed in the media, and how the public and other stakeholders perceive and involve themselves in innovation processes. Team members come from a variety of academic disciplines including economics, communications, law, sociology, ethics, and management.

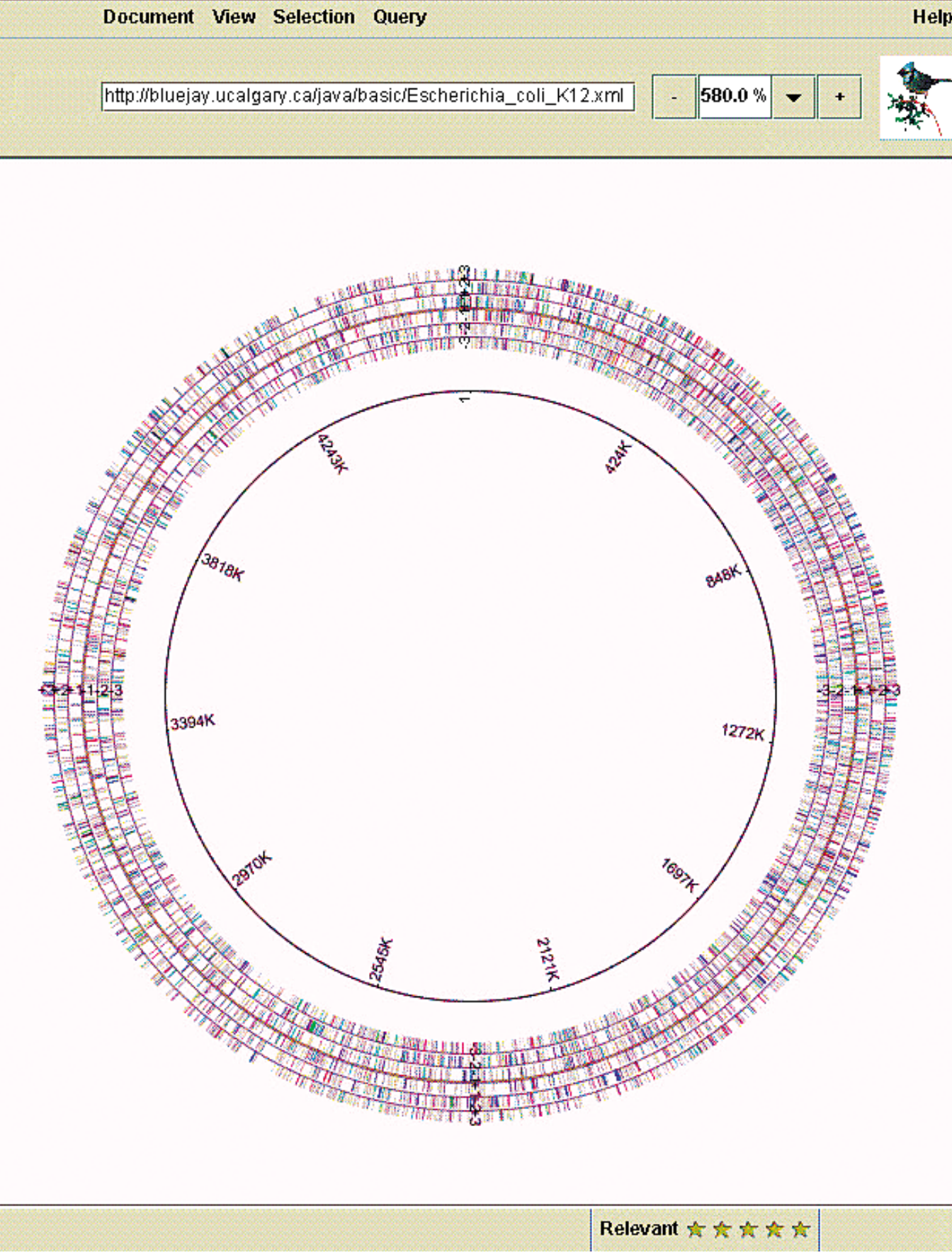
Highlights of our last year include the following:
Social and Economic Implications of Plant Molecular Farming (PMF): This project is our most recent initiative and is examining the use of genetically modified plants to produce pharmaceuticals and industrial products. We are conducting national focus groups to examine public perceptions of this innovation and as well have been documenting the policy consultation process in the U.S. and Canada.

Agricultural Genomics Awards: Four one-year $25,000 awards were created for researchers examining GE³LS aspects of agricultural genomics. Topics include consumer perceptions of canola oil and GM wheat in Japan, producer perceptions of abiotic stress traits in Saskatchewan and a comparison of agricultural policies in Brazil and Canada.

"IP Rights and Living Matter: Issues and Assumptions": A workshop was held in January 2004 on IP management and examined topics such as Benefit-Sharing and Global Equity, Farmers' Rights and Patented Seeds, Traditional Knowledge, and The Place of Public Research and Technology Transfer.

Canadian Consultation Project: Genome Prairie GE³LS has teamed up with the other Genome Canada sponsored GE³LS projects to study public consultations on genomics issues and will characterize each in terms of recruitment, goals, type of event, form of data collection, analysis and results.

Building Networks: Building on the GE³LS project experience, investigators on our research team have become part of a Network of Centres of Excellence (NCE) on Advanced Food Materials and are also working closely with the National Institute on Nanotechnology and the National Research Council to look at ethical, social and legal issues related to nanotechnology. With its solid research base and an evolving network of collaborators, the Genome Prairie GE³LS team will continue to expand its role, both nationally and internationally, in identifying and analyzing the myriad social, organizational and policy questions that are raised by genomics.



Bioinformatics software can be used to display and annotate genomic data, such as the E.coli chromosome shown here.

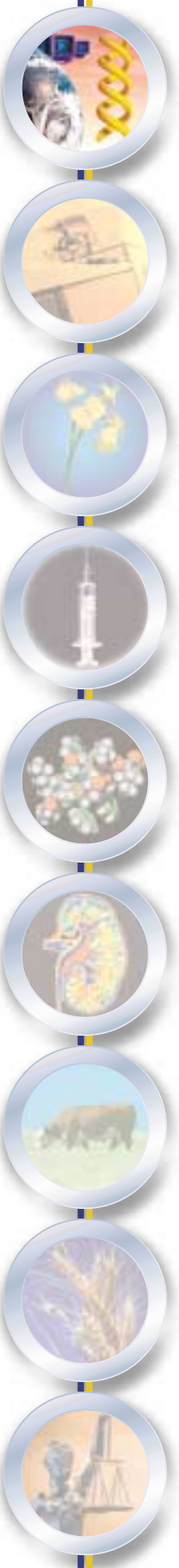
An Integrated And Distributed Bioinformatics Platform For Genome Canada

The overall goal of the Platform is to provide a coherent and powerful bioinformatics infrastructure for use by all Genome Canada-funded and other laboratories. The efforts of the Genome Canada investment are complementary to regional bioinformatics initiatives and components of other projects funded by Genome Canada. The Platform goal requires physical and intellectual developments that together provide genomics researchers with access to diverse infrastructure in a wide-area network, thereby addressing four important aspects of bioinformatics: (1) Science: bioinformatics tools for data integration and visualization, standardization of data formats and data analysis strategies, and distribution of analysis tasks over local- and wide-area networks are in development; (2) Bioinformatics Support Facility: provides assistance and custom programming to Genome Canada-funded projects and those unable to establish a bioinformatics support function intrinsic to their project due to shortage of qualified personnel or lack of funding; (3) Hardware Platform: through the Canadian Bioinformatics Resource network and acquisition of TimeLogic boards and a GeneMatcher, a powerful hardware platform is established, capable of handling the largest analysis needs for Genome Canada and other projects; (4) Bioinformatics Training for Genome Canada Scientists: a dedicated training series called "The Applied Computational Genomics Course" has been developed to enable Genome Canada- and other-funded scientists to rapidly become "bioinformatics power users", with special attention given to Platform services.

The Platform has been successful in achieving its goals, including more than 60 presentations and publications related to Platform research, over 20 students involved in Platform work, media events leading to coverage in over 60 newspaper and journal articles as well as numerous radio and television shows, 34 people trained through Platform workshops, and over a dozen Genome-Canada funded projects served by various Platform services.

Over 30 collaborations exist between the science components of the Platform, and both national and international groups. International outreach of the Platform has led to further initiatives such as interest of German Genome Research efforts in collaborations with Genome Canada. The Bioinformatics Support Facility has responded to over 170 requests, creating almost 80 custom programs in the process. Their biweekly newsletter helps to build a strong bioinformatics community in Canada. A powerful network of dedicated hardware addresses the need of Canadian and other scientists for access to a large-capacity bioinformatics computational infrastructure. Some machines (TimeLogic and GeneMatcher 2) provided by the Platform are unique in Canada.

The Platform is poised to expand and provide a high-quality bioinformatics environment to Canadians and others. Unparalleled software and hardware access and support, highly qualified experts, focus on achieving milestones, and cutting-edge methodology development work together within this Platform to make it internationally competitive.



This project is developing new generations of instruments for accurate, high-throughput characterization of biological molecules.

Development of Enabling Technologies

The development of novel bio-analytical instrumentation from research concept to mature commercial product is a process that generates jobs, spurs new economic activity, and significantly speeds basic and applied research on human health. To create innovative tools for proteomics research, the Enabling Technologies (ET) Project links research groups from the University of Alberta, the University of Manitoba, Queen's University, Laval University, and the University of Victoria with scientists at two Canadian instrumentation companies. MDS Sciex, the Project's major corporate partner, is a world leader in the development and commercialization of mass spectrometers - instruments capable of analyzing the mass of molecules with great precision. Edmonton-based startup Advanced Integrated Micro-Systems (AIMS) develops micro-fluidic devices for pre-analysis sample preparation - a current bottleneck for many proteomics approaches. Through its powerful integration of academic research expertise, industrial know-how and commercialization experience, the ET Project focuses the research activities of over fifty scientists on four critical areas of proteomics technology development: micro-fluidics, nano-fluidic technologies, linear ion trap instruments & high-performance time-of-flight mass spectrometers.

The Project's research team has made significant strides in each of the four focus areas over the past twelve months. Advances in ion optics, vacuum and ion detectors, and in MALDI ion sources, are leading to improved time-of-flight instrumentation and ionization techniques. Assembly and testing of a system coupling chromatographic separation of proteins to ultra-fast tryptic digestion, promises to boost speed, minimize sample handling, maximize protein digestion and provide the full benefits of top-down and bottom-up proteomics. Mass resolution of 25,000 on bread-board TOF systems has been demonstrated; MALDI imaging approaching a resolution of 1 micron has been shown; major advances in LC/MALDI have occurred; orthogonal MALDI on a linear ion trap has been demonstrated; a highly efficient nanoflow electro-spray tip has been developed; and a chip-based two dimensional CE separation has been fabricated and tested. Exciting operational developments have also been realized in the past year. The Genome BC-University of Victoria Proteomics Centre was added to the ET Project's existing beta-testing sites for prototype and application development. Numerous scientific collaborations amongst internal and external teams have been established, in addition to strengthened co-operative relationships with national and international proteomics organizations.

The capabilities provided by these research tools will advance studies in how cells function and hopefully lead to more effective therapeutics in a reduced time frame. The ET Project seeks to communicate the potential societal benefit of these technologies by providing forums for education in the value of proteomic research. Through the Project's public website, in public-outreach activities, and through the ET Spectrum newsletter, we seek to demonstrate the scientific importance and economic impact of the ET Project's goals for the Canadian biotechnology community and for Canada as a whole.

The image shows a high resolution light micrograph of a developing plant embryo.

Enhancing Canola Through Genomics (ECTG)

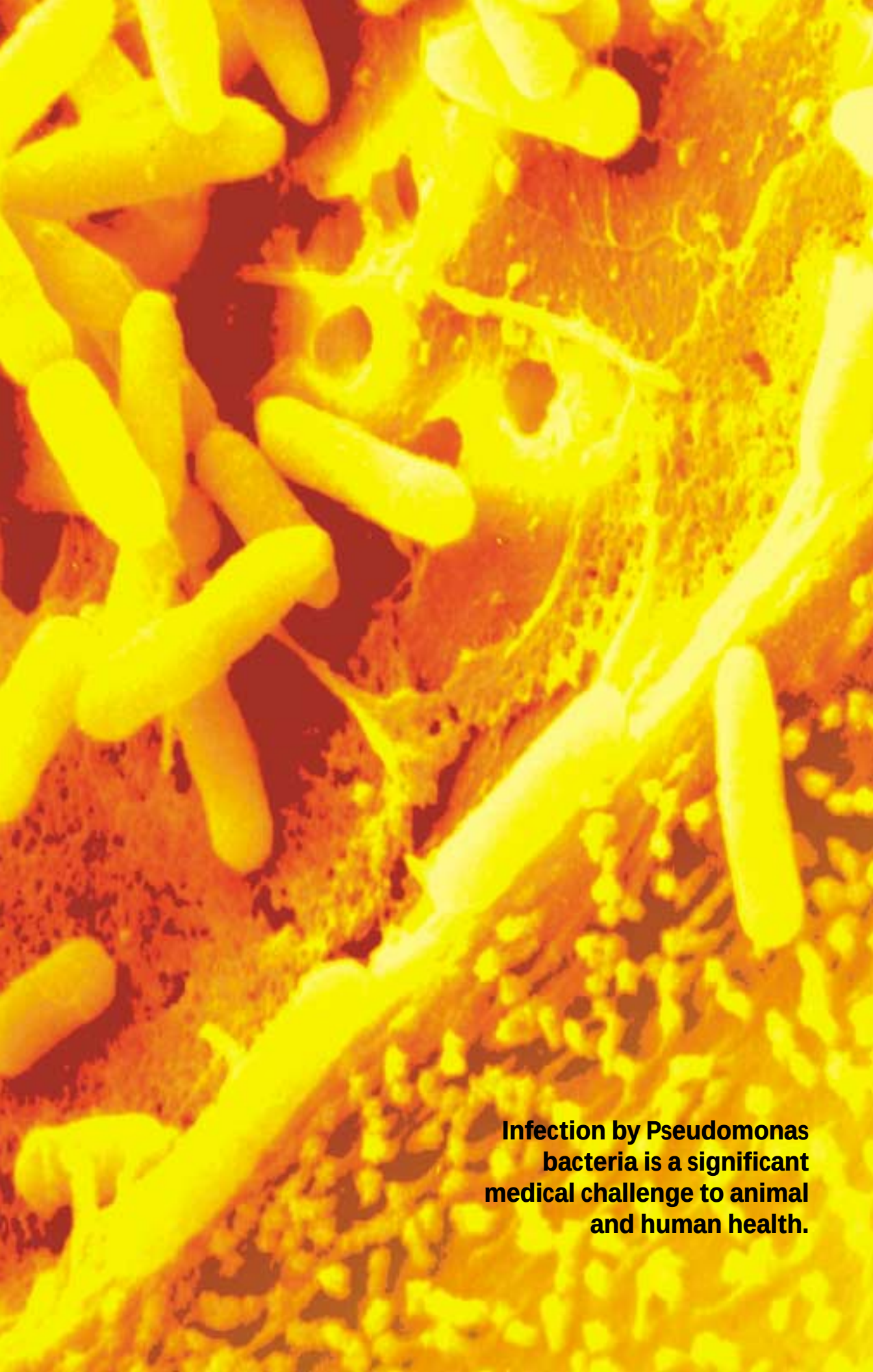
The goal of the ECTG project is to develop and employ genomic tools for the study of seed development and composition in Brassica oilseed crops. During 2003-04, progress was made in research activities related to seed development and composition and also in areas of collaborations, communications and outreach, thanks to the joint efforts of 67 scientists from Agriculture and Agri-Food Canada and from the National Research Council, 41 of whom are funded by the project.

In the seed development activity, a total of 27 cDNA libraries representing different stages of embryo/seed development have been constructed. More than 40,000 ESTs from these libraries were sequenced. Approximately 10,000 unique genes were identified and used for the preparation of a Brassica DNA microarray, an important genomic tool that will be used to improve our understanding of seed development. Preliminary analysis of the EST sequences identified genes that likely play an important role in seed development. These genes are now being studied in more detail.

With regards to seed composition, 17 cruciferin expressed genes were identified and their transcript abundance determined. Strategies are being tested to tailor seeds that produce proteins of greater economic or functional importance. Arabidopsis mutant lines with reduced levels of phytate, sinapine and lignin were identified. The genes controlling these anti-nutrients are being studied for use in Brassica seeds to reduce the level of anti-nutrients and thereby improve the quality and marketability of canola meal.

Thirteen papers related to our project objectives were published in peer-reviewed journals. The project held its first scientific meeting in November 2003 to review the project progress. Several networking meetings were organized to enhance the interaction among the plant genomics projects and to develop joint infrastructure and to share resources. A project website was developed and a project newsletter was published and widely disseminated to inform other scientists and the public at large about our project.

We expect that the Enhancing Canola though Genomics project will reach its peak productive period in years two and three leading to additional original scientific publications and very likely to new intellectual property. This knowledge will reinforce Canada's strong position in crop genomics and will permit the application of new discoveries to enhance Canada crop based industries.



Infection by Pseudomonas bacteria is a significant medical challenge to animal and human health.

The Functional Pathogenomics of Mucosal Immunity (FPMI)

The FPMI program is utilizing genomics and bioinformatics to provide new information about the processes of disease and innate immunity to microbial pathogens. The FPMI research team combines the internationally recognized livestock research expertise of the Vaccine and Infectious Disease Organization (VIDO), the Research and Development capacity of Inimex Pharmaceuticals Inc., and a network of world-class genomics, bioinformatics, microbiology and immunology research experts at the University of British Columbia and Simon Fraser University. The primary strengths of the FPMI research project include the ability to study pathogens of humans and large animals that represent significant infectious disease problems, the modulation of innate immunity by cationic host defence peptides, and the potential for cross-species comparative genomic studies of immunity using bioinformatics.

FPMI research will increase the understanding of how the mucosal surfaces of hosts respond to the presence of infectious agents and to the adjuvants, immunomodulators and vaccines designed to combat these agents. This will enable the rational development of new and effective strategies for improving human health, animal productivity and the economic viability of the livestock industry through enhanced animal welfare and food safety.

Major technical achievements of this project include the optimization of cell and animal model infection systems required for the program, the establishment of functional facilities and the establishment of a high-end bioinformatics operation with an internal web site as a clearing house for ideas and data. The major scientific progress of FPMI stems from common sets of experiments using bovine, chicken and human DNA microarrays using novel bioinformatics tools for microarray data processing (ArrayPipe) and gene discovery (ProbeLynx and Orthologee). These experiments have helped us determine the interaction of bacterial pathogens with immunomodulating compounds including Toll-like Receptor (TLR) agonists and cationic host defence peptides, which can function independent of the TLR, on host cells from humans and several animal species. The microarray results, which have been validated by quantitative real-time polymerase chain reaction (PCR), have revealed patterns of host cell gene expression that may be involved in protection against bacterial infection. Further biological studies will investigate the biology underlying the immune responses described above, which will enable FPMI to develop novel strategies and innovative therapies for infectious diseases in animals and humans.

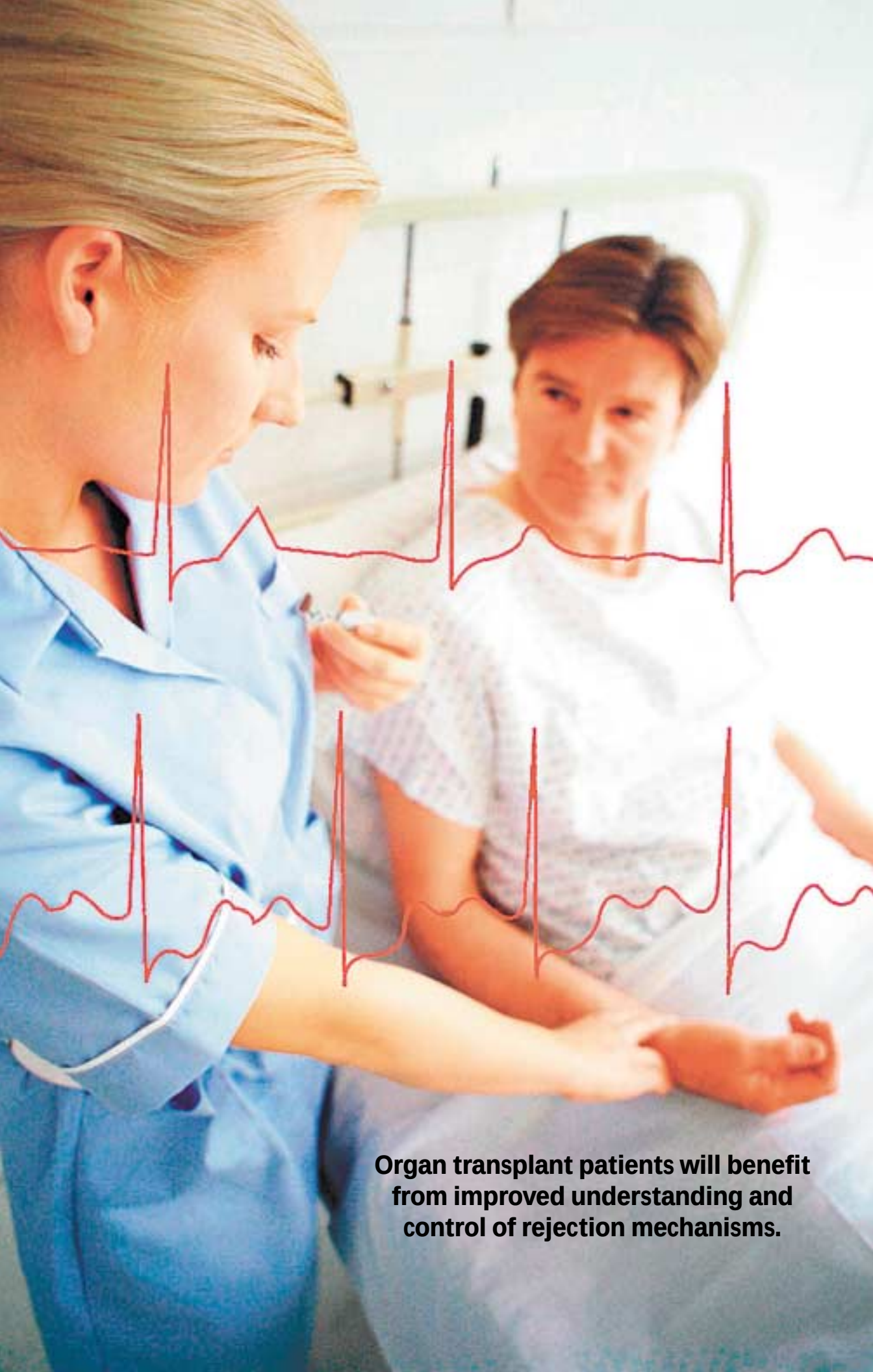
Researchers will characterize small molecule metabolites in body fluids to aid the diagnosis of disease.

Building the metabolomic toolbox: enabling rapid disease diagnosis through metabolic profiling

The metabolome (like the genome or proteome) can be described as the complete complement of small molecule chemicals (metabolites) found in or produced by an organism. Metabolomics, or metabolic profiling, is an emerging branch of genetic research that uses metabolites as very sensitive reporters to: a) detect tiny changes or mutations that happen to genes or proteins, b) monitor and/or measure the larger-scale physiological changes that occur in response to subtle changes in the environment, and c) assist in the improved monitoring of adverse drug reactions (so-called drug allergies). Physicians and scientists around the world are now beginning to realize that metabolic profiling could have a significant impact on the diagnosis, prediction, prevention and monitoring of many genetic, infectious and environmental diseases.

This proposal builds on a number of unique Canadian research strengths and technologies in metabolic profiling to create: 1) comprehensive metabolite databases, and 2) new medical tools (a toolbox of instruments and software) to facilitate the rapid and inexpensive profiling of metabolites for disease diagnosis and management. Specifically, using a combination of analytical methods that includes mass spectrometry (MS), chromatography, and nuclear magnetic resonance (NMR) spectroscopy, we intend to be the first group in the world to "complete" the human metabolome. This large-scale and integrated effort will involve the identification and quantification of many known and hundreds of unknown metabolites in both human tissues and fluids. Building on this effort, and the very valuable data it will provide, we will partner with one of the world's leading metabolomics companies (Chenomx Inc.) to design, prototype and produce both hardware and software to facilitate the creation of a new kind of clinical diagnostic instrument which is expected to be commercializable within 3 years. These databases and instruments will allow literally hundreds of normally expensive and time-consuming medical tests to be performed in just a few minutes thereby shortening diagnosis times by a factor of 100, and reduce testing costs by a factor of 1000 or more.

This proposal brings together researchers from several Canadian universities, hospitals, research institutes and industries to create instruments, technologies and methodologies that will have a significant, positive impact on Canadian healthcare and health management within the next five years.



Organ transplant patients will benefit from improved understanding and control of rejection mechanisms.

Diagnostic Applications of Microarrays in Organ Transplantation

Despite the success of organ transplantation, patient management and drug development are limited by lack of accurate measurements of disease processes either in the graft or in the host blood. The current standard for diagnosis of rejection of kidney transplants is through pathology grading of biopsies, according to the Banff classification system. This has many limitations, leading to inappropriate and inaccurate diagnosis treatment, increased side effects from immunosuppressive drugs, and therapeutic failures. Transcriptome based measurements have the potential to provide new tests for screening (on blood) and definitive diagnosis (on biopsy) for use as routine diagnostic systems in organ transplantation and as endpoints for clinical trials.

Our project combines the research and clinical programs in transplantation at the University of Alberta and the Edmonton regional health care program (Capital Health). Other collaborators consist of clinical and basic researchers from the University of Winnipeg, the University of Minnesota, the University of Alabama, the University of Iowa, the Mayo Clinic, Hennepin County Medical Centre, and Stanford University.

Phase I of our project is designed to develop diagnostic criteria for T cell mediated rejection (TMR), antibody mediated rejection (ABMR), and other injury patterns of rejection using Affymetrix microarray technology. We will perform microarray analysis of human kidney transplants and mouse kidney transplants that are undergoing rejection and other transplant stresses. The human biopsies will represent the spectrum of pathology, and will include clinical course data, permitting correlation of the clinical data and Banff analyses of TCMR, ABMR, and other pathologies, with microarray patterns. In the parallel mouse program, the models recreate Banff lesions of human pathology, permitting us to assign lesions to immunologic mechanisms in knockout mice. We will also look at effects of drugs, injury, and age on the transcriptome, all of which are important components of transplant dysfunction.

In Phase 2 of our project, we will test biopsies and blood screening, in patients from select Canadian and American centers that are currently forming a research consortium for studies in clinical renal transplantation. Related to this, we will use the data to create candidate systems for evaluating clinical trials (microarray endpoints for clinical trials) with the ultimate goal of FDA approval.

This project aims to significantly increase our understanding of immunology and disease mechanisms in general, including organ responses to age and injury. The new diagnostic tools described above will be the basis for transplant diagnosis in biopsies, and provide a greatly needed blood test for screening to detect patient instability. The results can be used as endpoints for clinical trials, and can be readily adapted to other organs and for islet transplants.

Sequencing the bovine genome will provide data to help improve cattle health and productivity.

Bovine Genome Sequencing

With the completion of the human genome sequence, the opportunities available for acceleration of genomics research activities in cattle have increased dramatically. This is even more valid now that the sequencing of the bovine genome has begun. One shortage that has been identified recently is a lack of adequate numbers of cDNA sequences for cattle, known as expressed sequence tags (ESTs), which represent the coding regions of the cattle genome (or genes). Full-length cDNA sequences, which contain the entire protein coding sequence of genes, are important in uniquely defining transcribed genes and assigning function to those genes. As a result of the present effort, it will be possible to determine the fine structure of transcripts by providing details as to the position and structure of genes within the bovine genome sequence.

The aim of this project is to produce a number of cDNA libraries from bovine tissues that are suitable for full-length cDNA sequencing, while at the same time addressing a number of issues important to the cattle industries in Canada and worldwide. The cDNA libraries will be fed into a cDNA sequencing pipeline, established at the Genome Sciences Centre (GSC) in Vancouver. The sequencing project undertaken at the GSC represents Canada's contribution to the international bovine genome sequencing project and will produce up to 600,000 EST reads and up to 412,500 full-length cDNA reads representing approximately 10,000 full-length cDNAs from tissues of importance to beef production. The data bank generated will provide an inventory of genes and gene variants in cattle as well as details about the tissue specificity of these variants. Overall this will enable researchers to strengthen linkages between genotype and phenotype and therefore make stronger inferences with respect to structure/function relationships across species. The ESTs generated will provide the basis for functional genomics studies through the manufacture of specific cattle microarrays to determine gene expression patterns and infer the function of genes with no previously known function as well as contribute to the identification of key genes relevant to cattle. These genes include those related to traits of interest to animal health, immune response to disease challenges and product quality. In this regard, the effort in Alberta will help establish a web-based interface to a relational database of all EST and full-length sequences, together with information on sequence similarity, tissue specificity and gene ontology.

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Edmonton, Alberta

Alberta Heritage Foundation for Medical Research
Edmonton, Alberta

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Calgary, Alberta

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Edmonton, Alberta

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ANNUAL GENERAL MEETING

June 13th, 2003 —Saskatoon, Saskatchewan

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