Biology Annual Report • 2005

Department of Biology

McMaster University

McMaster University

Department of Biology
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Annual Report 2005

This report is dedicated to

Herb Pohl

who served as senior demonstrator in the Department of Biology for 25 years.
Herb passed away on July 17, 2006
while on one of his solo canoe trips in northern Ontario

Annual Report Committee

Bhagwati P. Gupta, Ph.D.

Kimberley Dej, Ph.D.

Kathy Greaves

The research activities described here cover the time period of January 2005 through December 2005. The research findings must not be cited or discussed in official forum since some of it is still ongoing and not complete.

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Message from the Chair

We are delighted to present you with the Annual Report for the Department of Biology at McMaster University.

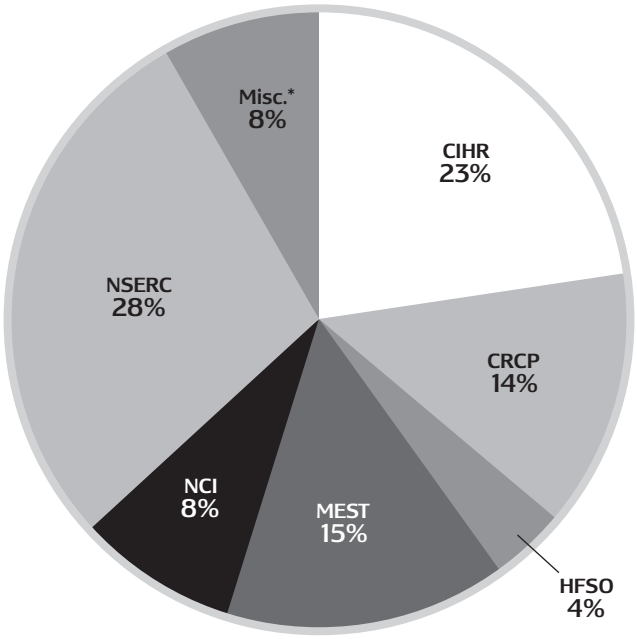
Including Darwin's theory of Evolution there have been many great advances in biological sciences over the past two centuries. We are presently in the midst of an information explosion in the release of complete genome sequences, so much so, that one is challenged to keep abreast or aware of what organisms have been sequenced. These data are impacting all areas of Biology and in many ways demand a greater integration of biological information. At the same time, as a society, we are confronted with the challenges of Global Warming and the rapid loss of natural lands. What an interesting time for biologists!

This report outlines what we do in the Department of Biology. We would appreciate your help in its dissemination and welcome your comments.

Dr. Turlough Finan
Chair, Department of Biology

Highlights

Total budget (2005-06): $4.4 Million



* Aquanet, International Copper Association Ltd., Environment Canada, International Lead Zinc Research Organization Inc., Indian and Northern Affairs Canada, International Nickel Company, National Institutes of Health, Nickel Producers Environmental Research Association, Noranda Inc., National Water Research Institute, Ontario Genomics Institute, Ontario Ministry of Natural Resources, Parks Canada, Teck Cominco Limited, U.S. Department of Defense Breast Research Program

CIHR: Canadian Institutes of Health Research
CRCP: Canada Research Chairs Program
HSFC: Heart and Stroke Foundation of Ontario
MEST: Ministry of Energy, Science and Technology
NCIC: National Cancer Institute of Canada
NSERC: Natural Science and Engineering Research Council
PREA: Premier's Research Excellence Award
Misc: Miscellaneous Sources*

Number of Publications

112 Research papers/articles in peer reviewed International journals
9 Book chapters

Teaching

In 2005-6, we taught 9016 students, of which 3669 were in Level 1 (40.7%) and we taught a total of 50 courses.

Achievements and Awards

FACULTY

Journal Editors

Dr. B. Golding – Associate Editor, Genome
Dr. R. Singh – Associate Editor, Genome
Dr. P. Chow-Fraser – Associate Editor, Journal of Great Lakes Research

Research Grant Panels

Dr. C. Baron (NSERC, Cell Biology)
Dr. R. Cameron (NSF, NSERC)
Dr. A. Campos (NSERC, Genetics and Developmental Biology, member and Chair)
Dr. J. Daniel (US Army DOD, Pathobiology)
Dr. J. Daniel (Cancer Research Society, Cell Signalling)
Dr. J. Daniel (NSERC, Discovery Grants)
Dr. S. Igdoura (NSERC, CIHR)
Dr. R. Jacobs (CIHR, NSERC, Developmental Biology)
Dr. C. Nurse (NSERC, CIHR)
Dr. C. Wood (NSERC, CRC Chair Program, Intn'l Copper Assoc)

Canada Research Chairs

Dr. C. Wood (Tier I, Environment and Health)
Dr. G.B. Golding (Tier I, Environmental Genomics)
Dr. B. Gupta (Tier II, Developmental Biology)
Dr. M. Elliot (Tier II, Microbiology)

University Committees and Appointments

Dr. C. Baron (Member), University Senate
Dr. C. Baron (Member), University Biosafety Committee
Dr. A. Bedard (Member), Graduate Curriculum, Admissions & Study Committee
Dr. A. Campos (Member), Joint Science and Engineering Tenure & Promotions Comm.
Dr. J. Daniel (Member), Human Rights Educator Position Interviewing Committee
Dr. J. Daniel (Member), McMaster Inclusion Steering Committee
Dr. J. Daniel (Member), Faculty Health Science (FHS) Research Council
Dr. S. Dudley (Chair), University Committee for Northern Studies
Dr. B. Golding (Director), Center Environmental Genomics and Biotechnology
Dr. B. Golding (Member), School of Computational Engineering and Sciences
Dr. B. Golding (Member), Mobix Steering Committee

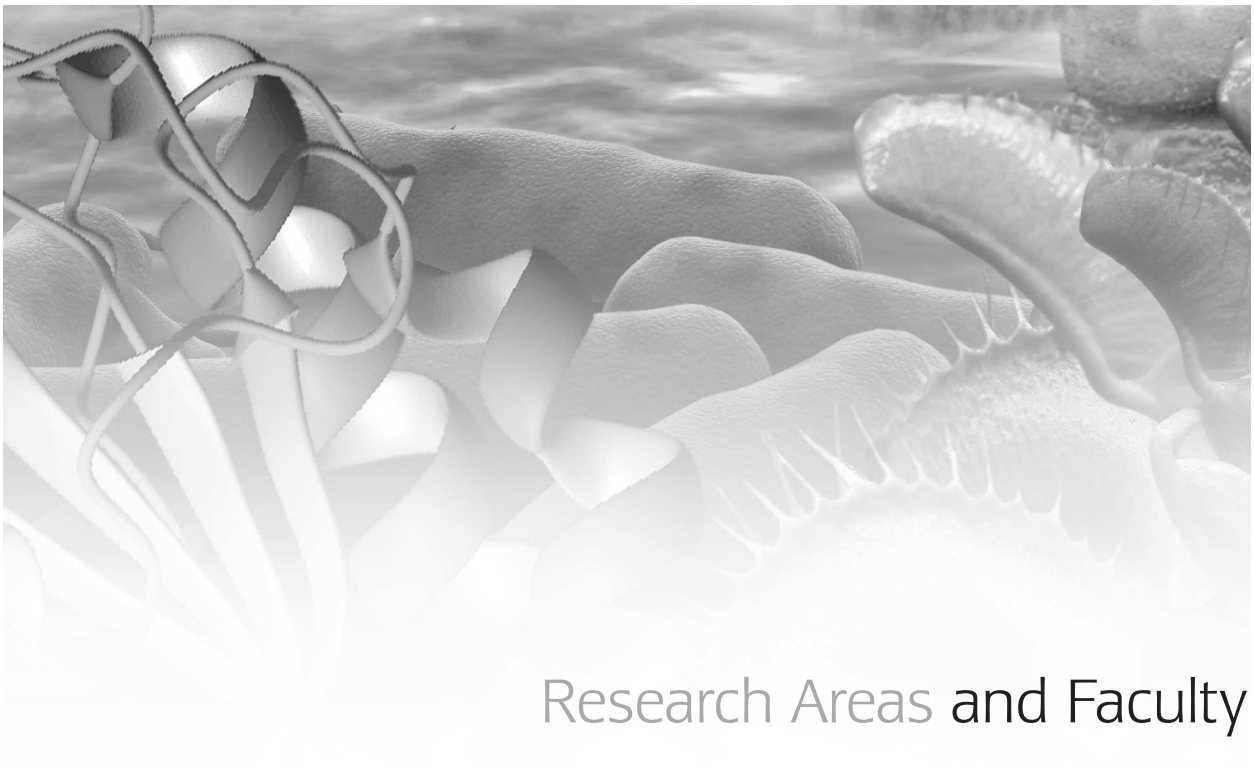
Dr. B. Golding (Member), Origins Institute Steering Committee
Dr. S. Igdoura (Member), The center for Functional Genomics
Dr. J. Quinn (Member), Faculty of Science Joint Health & Safety Committee
Dr. D. Rollo (Member), Animal Research Ethics Board (Presidential Committee)
Dr. R. Singh (Member), Faculty of Humanities, Peace Coordinating Council
Dr. R. Singh (Chair), Gandhi Lectureship
Dr. R. Singh (Chair), Gandhi Peace Festival
Dr. R. Singh (founder), Women's Peace Corp – McMaster/India
Dr. J. Stone (Associate Director), Origins Institute

Dr. J. Stone (Member), Library Committee
Dr. J. Stone (Member), Science Liaison Committee
Dr. E. Weretilnyk (Member), University Faculty Adjudicator, Faculty of Science
Dr. J.P. Xu (Chair), Undergraduate Awards Committee
Dr. J.P. Xu (Member), Senate Graduate Council

Distinguished University Professor Award

Dr. Chris Wood was honored with the "Distinguished University Professor Award" by McMaster University. This lifetime title is given to a full time University member for their truly outstanding contributions in research, scholarship and education and can only be held by only up to eight faculty members at any time.

Dr. Wood, a senior Canada Research Chair in Environment and Health, is one of the world's foremost experts in fish physiology and aquatic toxicology. His research has fundamentally changed our understanding of how fish maintain acid-base balance and regulate internal levels of ions and nitrogen. His research also reveals how acid rain, global warming and metal contaminants affect fish physiology. Dr. Wood's studies of how metal toxicants act in aquatic environments have changed how regulatory agencies set acceptable environmental levels for toxic metals. He is one of the most cited researchers in animal biology, and has trained numerous scientists from Canada and around the world. In 2003 he was elected as a Fellow of the Royal Society of Canada, one of Canada's most prestigious academic accolades.



Research Areas and Faculty

New Appointments

Dr. Marie Elliot

Dr. Elliot joined the Department of Biology in January 2005. Her research focuses on multicellular development and antibiotic production in bacteria, and the role that novel RNA regulators and proteins play in these processes. Dr. Elliot's laboratory applies genetic, biochemical and cell biological methods to understand the regulatory networks that underlie differentiation and antibiotic production. She received her Ph.D. in Microbiology and Biotechnology from the University of Alberta. Before joining McMaster, she was a post-doctoral fellow in Mark Buttner's laboratory at the John Innes Centre (Department of Molecular Microbiology) in the U.K.

Areas of Research Activities*

Bioinformatics and Functional Genomics

Deriving functional information from the data of large scale genome sequencing projects of bacteria and of eucaryotes is one of the biggest challenges of modern biology. The faculty members with interest in this area use state-of-the-art computational, genomics, transcriptomics (DNA chip), metabolomics and systems biology approaches to understand the function(s) of biological systems and of their evolution. Models analyzed in the Biology Department are the agriculturally important bacterium *Sinorhizobium meliloti,* the environmental stress-tolerant plant *Thellungiella salsuginea,* the human pathogen *Brucella suis* and the model bacterium *Escherichia coli.* Student participation in the inter-disciplinary research at the interface of informatics and biology will contribute to applications such as new treatments for bacterial infectious diseases and improved agricultural practice.

Developmental Biology

The combination of molecular genetic technologies with other contemporary tools of biology, such as electrophysiology, electron microscopy, immunochemistry and DNA chip analysis has fueled dramatic advances in both cell and developmental biology. Our laboratories use recombinant genetics, mutagenesis, biochemistry, confocal and electron microscopy, tissue culture, and transgenic organisms to work on models such as the multicellular bacterium *Streptomyces coelicolor,* the nematode *Caenorhabditis elegans,* the fruit fly *Drosophila melanogaster* and mammalian cells. Currently studied research questions encompass gene regulation, cancer biology, neurosystem and reproductive system development and function. Students at all levels are welcome to get involved in this research, which will influence applications in medical therapy, diagnostics and applied biotechnology.

Cell and Molecular Biology

Researchers on the Biology Department carry out basic and applied research in this area using state-of-the-art methods such as tissue culture, RNAi technology, transgenic animals, DNA chip, laser dissection and immunofluorescence technology. The different laboratories study a wide variety of models such as the tissue cell culture, the domestic mouse *Mus musculus,* the nematode *Caenorhabditis elegans,* the plant *Arabidopsis thaliana* and the fruit fly *Drosophila melanogaster.* The research is of immediate relevance to human heath in different areas, such as breast cancer, genetic diseases and disease resistance, DNA repair, neurosystem development and function. Work in the Biology Department gives students at all levels the opportunity to contribute to scientific progress, which may lead to improved treatment of diseases.

Microbiology and Plant Biology

The natural biodiversity of microorganisms surpasses that of all other organisms and their metabolic capabilities, adaptability and interactions with plants and animals shape our planet. Researchers in the Biology Department study a variety of metabolic processes, such as the stress response of *Escherichia coli* and of plants and their seeds, *Arabidopsis thaliana* plant disease resistance, the agriculturally important legume plant symbiotic interaction with *Sinorhizobium meliloti,* human diseases caused by *Brucella suis,* population genetics of human pathogenic fungi and gene transfer from *Agrobacterium tumefaciens* to plants and between antibiotic-resistant bacteria and multicellular development and regulation of antibiotic production in *Streptomyces coelicolor*. Students at all levels are involved in this research, which is highly applicable to industrial and agricultural biotechnology and health research.

Environmental Physiology

Studies on the adaptation of animals to environmental changes, pollutants and stress conditions have high relevance for human health. Researchers in the Biology Department use a variety of modern techniques such as microinjection, patch-clamp analysis, tissue culture, confocal immunofluorescence analysis, transcriptome and proteome analysis to study models such as mice, fish and human cells. The research covers diverse areas such as environmental physiology and aquatic toxicology of aquatic animals, heavy metal metabolism, the effect of hypoxia on ion channel function in the neurosystem, growth hormone action and exercise physiology. Students at all levels can contribute to this research, which is relevant for the protection of human health and of the environment.

*These research areas are not necessarily the same as those recognized by OCGS.

Ecology and Evolution

The analysis of natural biodiversity and of the impact of modern society on ecosystems plays a major role in the conservation of our environment. Research in this area is supported by funding and collaborations with the Georgian Bay Association, Environment Canada and the Ontario Ministry of Natural Resources, the Royal Botanical Gardens and conservation authorities elsewhere, which provide logistical support for field studies. Faculty research interests cover theoretical, evolutionary and applied ecology; the latter has resulted in the development of ecosystem-health indicators for coastal wetlands of the Great Lakes that have been adopted by environmental agencies of both Canada and the United States. Research in the Biology Department on the impact of environmental pollution on human health, and the effect of habitat fragmentation and degradation on loss of biodiversity have garnered a great deal of public interest both locally and internationally, and have attracted top students into our research programs at all levels..

Population and Evolutionary Genomics

Population genetics is the theoretical powerhouse of evolutionary biology. The discipline of population genetics in combination with technical breakthroughs in molecular biology has opened the floodgate of large-scale genomic comparisons between distantly related species that were not possible before. Biology Department members are carrying out population and evolutionary genomic research on a variety of organisms including bacteria, *Drosophila,* fungi, plants, fishes and humans. These studies are meant to shed light on mechanisms of adaptation, host-pathogen interactions and co-evolution, sexual reproduction, sexual selection and speciation. A new area of research in germ cell genomics, using model organisms such as mouse, *Drosophila,* nematode and trout, promises to revolutionize the science of gamete biology and fertilization systems.

Research Faculty

PROFESSOR

Patricia Chow-Fraser
Assessment of anthropogenic impacts on the functional ecology of freshwater ecosystems, in particular, lakes and wetlands of the Great Lakes basin

Turlough M. Finan
Molecular genetic analysis of the N2-fixing bacterium *Sinorhizobium meliloti*

G. Brian Golding
Molecular evolution, genomics, bioinformatics, computational biology

J. Roger Jacobs
Developmental genetics, cancer genetics

Colin A. Nurse
Cellular and molecular mechanisms of O2, and CO2/pH sensing in vertebrates

Michael J. O'Donnell
Ionoregulation and excretion in invertebrates and fish: Cellular mechanisms and control of epithelial transport

Andrew J. Rainbow
Molecular mechanisms for DNA repair in mammalian cells and their role in human disease using viruses as probes

C. David Rollo
Exploration of the regulatory integration of mammalian form and function utilizing transgenic mice as probes

Herbert E. Schellhorn
The regulation of stress genes in Escherichia coli

Rama S. Singh
Population and evolutionary genetics, molecular evolution and speciation

Elizabeth A. Weretilnyk
Plant abiotic stress tolerance; Metabolomics; Environmental genomics; Chemical biology

Christopher M. Wood
Environmental physiology and aquatic toxicology of aquatic animals

ASSOCIATE PROFESSOR

Christian Baron
Pathogenic bacteria, antimicrobial drugs, chemical biology

André Bédard
Characterization of cell proliferation and transformation

Robin Cameron
Elucidation of the signal transduction pathways that lead to, and the processes responsible for, induced resistance responses, including Systemic Acquired Resistance (SAR) and Age-related Resistance (ARR)

Ana R. Campos
Genetic and molecular analysis of visual system development in *Drosophila melanogaster*

Juliet Daniel
Roles of Catenins and Transcription Factors in Normal Cell Growth and Development

Susan A. Dudley
Evolutionary ecology of carbon acquisition traits in plants; natural selection, quantitative genetics, and phenotypic plasticity of adaptations to drought stress and competition

Suleiman Igdoura
Molecular genetics of Tay-Sachs disease and Sialidosis

James S. Quinn
Genetic relatedness, parentage and behavioural ecology of colonial and cooperative-breeding birds and anthropogenic induction of germline mutations in gulls and mice

Jianping Xu
Molecular Ecology and Evolutionary Genetics

ASSISTANT PROFESSOR

Ben Evans
Molecular evolutionary analysis of biodiversity and gene duplication

Marie Elliot
Development in multicellular bacteria; Regulation by small RNAs; Antibiotic production

Bhagwati P. Gupta
Development and evolution of the reproductive system in nematodes

Grant McClelland
Integrative physiology of muscle and animal performance, environmental stress

Jonathan Stone
Computational Biology conducted at multiple heirarchical levels

Xu-Dong Zhu
Functional analysis of DNA repair complexes at human telomeres

Christian Baron

Functional Proteomics, Chemical Biology, Antimicrobial Drugs

Laboratory Personnel

Postdoctoral fellow: Dr. Athanasios Paschos; Ph.D. *students:* Khaled Ahmed Aly, Durga Sivanesan, Qing Yuan; *M.Sc. Students:* Chan (Daphne) Gao, *Undergraduate students:* Mike Chmatil, Fargol Firouzchian; *Research technicians:* Gregory Rekas, Yanixia (Sally) Li

Research Collaborators

Peter Christie (Houston, USA), Turlough Finan (McMaster), Günter Koraimann (Graz, Austria), Alexander Iakounine (Toronto), Graham McGibbon (McMaster), David O'Callaghan (Nîmes, France), Peter Summers (McMaster), Andy Teng (Rochester, USA), Renee Tsolis (Davis, USA), Gabriel Waksman (London, UK), Elisabeth Weretilnyk (McMaster), Patricia Zambryski (Berkeley, USA)

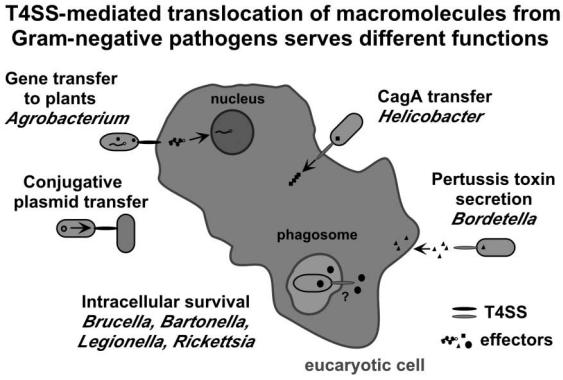
Funding

Canadian Institutes of Health Research (2003–2006), Natural Sciences and Engineering Research Council (2003–2007), Genome Canada (2003–2007)

Research Interests: Functional Proteomics, Chemical Biology, Antimicrobial Drugs

Genome sequencing and proteome analyses have revolutionized our insights into the workings of life. Basic aim of our research is to unravel the molecular mechanisms of bacterial virulence functions and host-pathogen interactions. To this end, we use comparative genomics, functional proteomics, cell biological and structure biological methods. Primary areas of research are **type IV secretion systems** (**T4SSs**) and a subset of highly conserved **proteins of unknown function** (**PUFs**) from alpha-proteobacteria. The methods developed in our laboratory are broadly applicable to other host-pathogen systems and will lead to novel approaches for the rational design and screening of inhibitors. Based on the understanding of the molecular details of protein-protein interactions, we seek to develop innovative antimicrobial treatments to counter the threat of resistant pathogens to human health.

Role of T4SSs in pathogen-host Interactions and the A. tumefaciens model system



T4SSs translocate virulence factors from bacteria to eukaryotic cells and thereby modulate their host's defense response. This strategy is used by many important human and animal pathogens (Baron, 2005, Fig. 1). T4SSs also mediate the spread of broad-host-range plasmids, which carry antibiotic resistance genes between Gram-negative bacteria. The most-advanced model for mechanistic studies is that of gene transfer from *Agrobacterium tumefaciens* to plants. The protein components of the T4SS form a membrane-spanning complex and catalyze the assembly of surface-exposed structures, such as T-pili, and the translocation of effector molecules into recipients. Four groups of proteins are required for T4SS function(s): The translocated **effectors,** the **transporters** (VirB4,

VirB11 and VirD4), the components of the T4SS **core complex** (VirB6, VirB7, VirB8, VirB9 and VirB10), and **surface structures** (VirB2 and VirB5), which may contact host cells. We identified VirB5 as a minor component of the T-pilus and structure-function analysis has revealed its localization in the T-pilus and contribution to host cell recognition (Aly and Baron, submitted). Based on the results of genetic and biochemical studies, we have proposed a mechanism of T-pilus assembly (Yuan *et al.* 2005).

Virulence of the mammalian pathogen Brucella suis

As model of intracellular mammalian pathogens, we study *Brucella* species, which exploit T4SSs for their survival and multiplication. They cause infections in livestock and long-lasting highly debilitating disease in humans. Aided by the T4SS the organism thrives in the otherwise inhospitable environment of macrophages. We use biochemical and cell biological methods to study the *B. suis* T4SS, which contains orthologs of all the eleven VirB proteins of *A. tumefaciens.* Several VirB proteins were purified and the analysis of their interactions yielded insights into their spatial organization in the cell envelope (Höppner *et al.,* 2005, Yuan *et al.* 2005). Analysis of the X-ray structure of *B. suis* VirB8 revealed key features of this T4SS assembly factor (Terradot *et al.,* 2005). We have conducted a structure-function analysis of VirB8 and have unraveled the molecular details of its interaction with VirB5 and other T4SS components (Paschos *et al.,* submitted; Sivanesan *et al.,* submitted). In addition, we have developed an assay of *B. suis* T4SS assembly in a heterologous host, which has greatly advanced our ability to conduct structure-function analyses of VirB protein interactions *in vivo* (Carle *et al.,* 2006).

Functional genomics of alpha-proteobacteria

The group of alpha-proteobacteria comprises several human and animal pathogens and plant symbionts. We anticipate insights into common features of this group of bacteria will identify novel targets for antimicrobials. To this end, we study protein-protein interactions of proteins of unknown function (PUFs), which are conserved among the genera *Agrobacterium, Brucella* and *Sinorhizobium.* Using a variety of methods (purification of TAP-tagged complexes followed by mass spectrometric analysis, metabolome analysis and enzyme assays) we seek to understand PUF protein functions for the bacteria in the context of their host interaction.

André Bédard

Control of Cell proliferation and Transformation

Laboratory Personnel

Graduate students: Jenny Wang, Bart Maslikowski; *Post-doctoral fellow:* Nishi Singh; *Research technician:* Ying Wu, Sam Yan

Research Collaborators

Dr. Ana Regina Campos (Department of Biology, McMaster University)

Funding

Canadian Institutes of Health Research (2005-2009), Natural Science and Engineering Research Council (2005-2010), National Cancer Institute of Canada (with A. Campos) (2004-2007)

Transformation by the v-Src Oncoprotein:

Transformation by the v-Src Oncoprotein: My laboratory is interested in the study of cell proliferation and transformation by the v-Src tyrosine kinase. Through the characterization of genes activated aberrantly in transformed cells, we have identified several transcription factors and signaling pathways targeted by the v-Src oncoprotein. Particular attention is devoted to the study of JunD/AP-1 and NF-κB, two transcription factors providing a survival advantage to v-Src transformed cells. Using a variety of approaches of cellular and molecular biology, we are characterizing the role of v-Src regulated genes, activated by these transcription factors, in cell transformation (funded by the Canadian Institutes of Health Research).

Characterization of the Menin Tumour Suppressor:

Our studies on AP-1 led to the finding that v-Src transformed chicken embryo fibroblasts (CEF) express reduced levels of the Menin tumour suppressor. Menin, the product of the multiple endocrine neoplasia type I gene *(Men1)* has been implicated in several biological processes including the control of gene expression, apoptosis and MAPK signaling pathways. However, the mechanism(s) by which Menin exerts its function of tumour suppressor is unknown. Therefore, we have initiated the study of Menin in the model system *Drosophila melanogaster,* a project done in collaboration with Dr. Ana Campos in the Department of Biology at McMaster University. Using tools unique to *Drosophila,* we have uncovered a role for Menin in the control of the stress response and, in particular, in the expression of heat shock proteins. This work led to the conclusion that Menin is required for the response of *Drosophila* to several stresses including heat shock, hypoxia, hyper-osmolarity and oxidative stress. The relationship between the action of Menin in the stress response and its function of tumour suppressor is the subject of current investigations in the *Drosophila* model system (funded by the National Cancer Institute of Canada).

Characterization of Growth-Arrest Specific (Gas) Gene Expression:

Cells exiting the cell cycle induce the expression of a class of genes known collectively as *growth-arrest specific* or *gas* genes. By in large, the function of this class of genes remains unknown. Our research program on *gas* genes has for objective to elucidate the function of the products of these genes and to characterize the regulatory mechanism of their induction in quiescent cells. While several factors can induce cell quiescence, we are particularly interested in the control of gas genes by contact inhibition. Using the p20K lipocalin gene as a model, we identified C/EBPβ as the central activator of this gene in contact inhibited CEF. We have demonstrated a role for C/EBPβ in the inhibition of CEF proliferation and in the induction of several other gas genes. Other transcriptional activators of gas genes, working cooperatively with C/EBPβ are presently under investigation (funded by the Natural Sciences and Engineering Research Council of Canada).

Mechanisms of cell transformation by v-Src

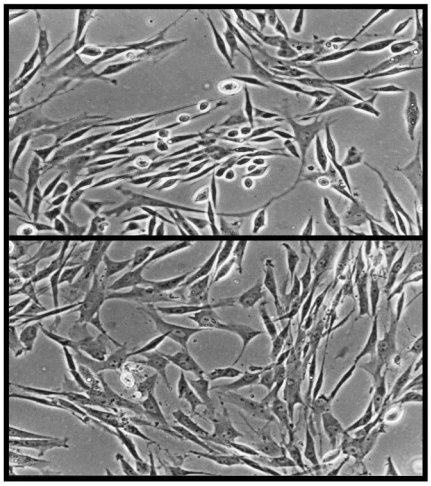


FIGURE: The Menin tumor suppresssor is down-regulated in v-Src-transformed chicken embryo fibroblasts (CEF), which exhibits the elongated and refractile morphology of transformed cells (upper panel). The re-expression of Menin results in the flattening of the cells and a more normal morphology (lower panel).

Robin K. Cameron

Elucidation of the signal transduction pathways that lead to, and the processes responsible for, induced resistance responses, including Systemic Acquired Resistance (SAR) and Age-related Resistance (ARR)

Laboratory Personnel

PhD student: Fadi Al-Daoud; *MSc student:* Jessie Carviel; *undergraduate student:* Cherise Poo, *Post-Doctoral Fellow: Marc Champigny*

Research Collaborators

Pierre Fobert (Plant Biotech Inst., Saskatoon), Nancy Dengler (University of Toronto), Daphne Goring (University of Toronto), Keiko Yoshioka (University of Toronto), Chris Lamb (John Innes Centre, UK)

Funding

Natural Science and Engineering Research Council (2003-2007)

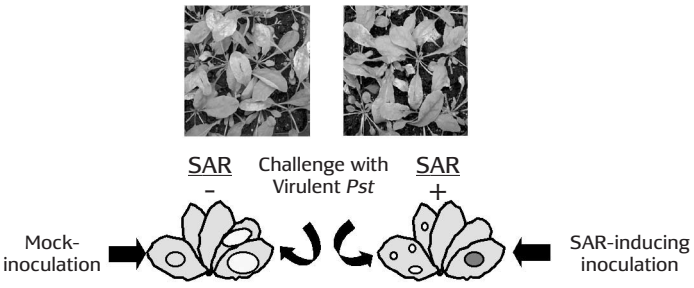
To elucidate and understand the signal transduction pathways that lead to, and the processes responsible for, induced resistance responses in plants to disease, including Systemic Acquired Resistance (SAR) and Age-related Resistance (ARR), using molecular genetics, plant pathology, physiology, biochemistry, genomics and cell biology.

SAR is induced by an initial "immunizing" infection in one part of the plant resulting in broad non-specific resistance throughout the plant to normally virulent pathogens. The outcome of the SAR response is similar to vaccination in mammals except that it protects the plant against many different unrelated pathogens (bacteria, viruses, fungi, nematodes). The accumulation of a set of pathogenesis-related (PR) proteins (anti-microbial) and salicylic acid (SA) has been correlated with SAR in tobacco, cucumber and in *Arabidopsis thaliana*. A long distance signal moves, perhaps via the phloem, from the "immunized" leaf to the rest of the plant where it is perceived and the plant becomes primed or "immune" as indicated by SA accumulation and subsequent PR-1 expression. Upon challenge with a virulent pathogen, the plant responds in a resistant manner, which includes production of a number of anti-microbial PR proteins and compounds. It is thought that different subsets of these are effective against different pathogens, resulting in the broad spectrum of resistance observed during SAR. Little is known about the nature of the long distance SAR signal or how it translocates from the induced leaf via the vasculature to distant leaf cells to produce a primed or "immune" plant. Our studies will contribute to elucidation of long distance signaling during SAR and will form the basis to genetically modify crops to respond to many diseases in a resistant manner.

Over the years we have observed that in some experiments, older Arabidopsis displayed resistance to normally virulent *Pseudomonas syringae pv tomato (Pst)*. This Age-Related Resistance (ARR) has been described in the literature in a number of plant species and in a few cases the resistance observed is correlated with anti-microbial phytoalexin production. Studies in our lab using plant lines which do not accumulate SA (NahG, sid1, sid2) demonstrate that ARR is a distinct defense response from SAR, but is similar to SAR in that SA accumulation is required. Intercellular washing fluids (IWFs) from plants expressing ARR exhibit anti-bacterial activity to Pst . These data suggest that SA may accumulate in intercellular spaces and act as an anti-microbial agent during ARR, rather than as an intracellular signaling molecule as it does in SAR. Our studies (measuring SA levels in IWFs, adding SA destroying enzymes or SA to the intercellular space) suggest that SA must be present in the intercellular space for a functional ARR response, providing support for an anti-microbial/non-signaling role for SA during ARR. Very little is known about the genes required for the ARR response. Therefore, we have also taken a molecular genetic approach to identify genes involved in ARR, using classical and reverse genetics (ARR microarray/T-DNA knock-out lines).

ARR

SAR in Arabidopsis to Pseudomonas syringae pv tomato



A number of interesting genes are up-regulated during ARR and to determine which of these genes are actually required for the response, T-DNA knock-out lines from the SALK collection have been obtained and characterized at the molecular level (reverse genetics). Seven T-DNA mutant lines exhibited a reduced ARR response indicating that these genes are required for ARR (discussing potential for genetic manipulation with Performance Plants Inc, Kingston ON). Moreover, mapping and ultimately cloning of the ARR mutant (iap, important for ARR pathway) identified by classical genetics is ongoing and should provide key insights into ARR signaling. Our studies suggest that IAP encodes a positive regulator acting at the beginning of the ARR pathway. Recent experiments demonstrate that iap mutants don't produce the intercellular anti-microbial activity, providing support for our hypothesis that IAP is a positive regulator that is activated in response to Pst to initiate the ARR signal pathway leading to resistance (anti-microbial activity to Pst) in mature plants.

SAR

Studies in our lab using dir1-1, a SAR-defective mutant, indicate that *dir1-1* can perceive the SAR signal present in petiole exudates (enriched for phloem sap) from wild type SAR-induced plants, but *dir1-1* exudates do not contain this signal indicating that DIR1 is required for long distance signaling during SAR. Protein gel blot analysis demonstrated that DIR1 protein is present in petiole exudates of SAR-induced wild type, but not *dir1-1* or mock-inoculated plants. These results suggest that DIR1, which encodes a putative lipid transfer protein (LTP), may be involved in the production of the SAR mobile signal or in transporting a lipid signal to distant tissues (perhaps via the phloem) to establish SAR. We have successfully immunoprecipitated DIR1/LTP and its lipid from petiole exudates and are in the process of identifying its ligand using GC-MS. We have constructed a number of transgenic Arabidopsis lines to localize DIR1/LTP in healthy plants and track its movement during SAR (DIR1 promoter/reporter gene [GUS], DIR1promoter/DIR1coding sequence fused to the GUS/GFP reporters). Homozygous lines have been obtained and characterized and microscopic studies reveal that DIR1/LTP is expressed in the vasculature (xylem parenchyma and phloem cells) and therefore DIR1/LTP has access to both transportation systems of the plant, for movement to distant tissues upon SAR induction.

Patricia Chow-Fraser

Assessment of anthropogenic impacts on the functional ecology of freshwater ecosystems, in particular, lakes and wetlands of the Great Lakes basin

Laboratory Personnel

Ph.D students: Sheila McNair, Titus Seilheimer, Anhua Wei; *M.Sc. students:* Kristina Kostuk, Mel Croft; *Undergraduate students:* Roxanne Razavi, Maja Cvetkovic, Tim Mahoney, Lindzie OíReilly, Mike Alkema, Ken Mak

Research collaborators

Lake Huron Management Unit, Owen Sound (Ontario Ministry of Natural Resources), Georgian Bay Association (Georgian Bay Foundation), Dr. Nick Eyles (University of Toronto)

Funding

Natural Sciences and Engineering Research Council (2003-2007), Ontario Ministry of Natural Resources, Canada-Ontario Agreement (2004-2006), Environment Canada (2004-2006), Parks Canada (2005-6)

Coastal wetlands are among the most productive ecosystems in the world, comparable to tropical rain forests and coral reefs. Despite their great ecological value, many of the large wetland complexes in settled areas of the Great Lakes basin have been either lost due to draining, dredging or filling, or have been severely degraded because of their sensitivity to altered land uses (agricultural and urban development) and to invasion by exotic species. My research program on wetlands began in 1991 when I became involved in the restoration of Cootes Paradise Marsh. Using a 60-year data record, I showed that reduction in cover of emergent vegetation (from 85% in 1934 to 15% in 1993) was significantly related to increased water levels (Chow-Fraser et al. 1998; Chow-Fraser 2004), and that the disappearance of a diverse community of submergent macrophytes was linked to increased eutrophication and water turbidity (Chow-Fraser et al. 1996; Lougheed et al. 1998; Lougheed and Chow-Fraser 1998; Wei and Chow-Fraser 2005). The disappearance of submergent vegetation affected the zooplankton, benthic invertebrate and ultimately the fish communities (Chow-Fraser et al. 1998).

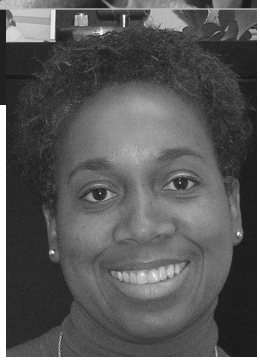
I examined the sources of turbidity in the marsh over a 4-year period and determined that sediment resuspension by wind and wave action, disturbance by a large population of common carp, and excessive growth of algae, as well as sediment input from the watershed were all major contributors (Chow-Fraser 1999). The conceptual ecological models, based on effects-hypothesis diagrams, were used to evaluate the appropriateness of various management and restoration options, including carp exclusion (Chow-Fraser 1998; Lougheed et al. 1998). In 1995-6, we conducted in-situ experiments to determine how different size and biomass of carp affected water turbidity, nutrient levels and the plankton community, and these results were used to predict the impact of carp exclusion (Lougheed et al. 1998). We also conducted experiments in 1999 and 2000 to determine other confounding factors that may slow down restoration efforts, such as internal loading from the historically enriched sediments (Kelton and Chow-Fraser 2004; Kelton and Chow-Fraser, 2005). Through my research, I also initiated a pilot planting program using community volunteers that has become a model for other restoration projects (Chow-Fraser and Lukasik, 1995; Chow-Fraser 1999b). Research results stemming from our work in Cootes Paradise Marsh have provided guidance to wetland managers elsewhere regarding the general feasibility of biomanipulation as a restoration strategy to restore wetlands (Angeler et al. 2003).

The research I conducted to guide the restoration of Cootes Paradise Marsh indicated clearly that polluted runoff associated with altered land in the watershed played a major role in marsh degradation. In 1996, I began a parallel research program that specifically addressed the impact of land use alteration on water and sediment quality in wetlands (Crosbie and Chow-Fraser 1999). In Chow-Fraser and Albert (1999), I highlighted the need to develop ecosystem-level indicators of wetland quality to track changes in habitat quality. In 2000, the Great Lakes Fishery Commission funded a 4-year, bi-national program to develop ecological indicators to assess fish habitat in coastal wetlands of all five Great Lakes, because coastal wetlands provide critical spawning and nursery habitat to the Great Lakes fish community. Products of this research program include the development of indicators of wetland quality based on data collected from over 150 wetlands throughout Canada and the U.S. shoreline of all five Great Lakes. Indicators include macrophyte species richness (Lougheed et al. 2001), zooplankton species (Lougheed and Chow-Fraser 2002), periphyton biomass (McNair and Chow-Fraser 2003), water quality (Chow-Fraser 2005), and fish species (Seilheimer and Chow-Fraser 2006). We are now applying these indices to assess the ecological status of coastal wetlands of Georgian Bay and the North Channel, which are two areas of the Canadian shoreline that are being threatened by recreational development.

We are also creating a Great Lakes GIS database that contains the current and historical distribution of fish, plant and macro-invertebrates, and some associated land-cover information. This database will eventually house all information derived from our sampling program, and we are making it available to managers and other researchers through our WIRE Net website (Wetland Inventory for Research and Education Network; www.wirenet.info). It is also being used to investigate the spatial relationship between fauna/flora and coastal wetlands at the scale of all five Great Lakes. Using historical fish surveys and wetland maps, we have already demonstrated that more than two-thirds of all Great Lakes fishes are spatially associated with coastal wetlands in Lake Ontario (Wei et al. 2004). My long-term research goal is to be able to measure changes in both the quantity and quality of fish habitat in coastal wetlands of the Great Lakes, to relate these changes to natural and human-induced stressors, and to help environmental managers and regulators predict impacts of proposed land uses or restoration efforts on these fish habitats.

Students setting up fykenets to survey the fish community of Cove Island in Fathom Five National Marine Park during July 2005.

Juliet Daniel



Role of Catenins and Transcription Factors in Normal Cell Growth and Development

Laboratory Personnel

Post-doctoral Fellows: Hong Wang; *Ph.D. Student:* Kevin F. Kelly; Nickett S. Donaldson; *M.Sc Students:* Abena A. Otchere; Mai Almardini; *Research Technician:* Monica Graham.

Research Collaborators

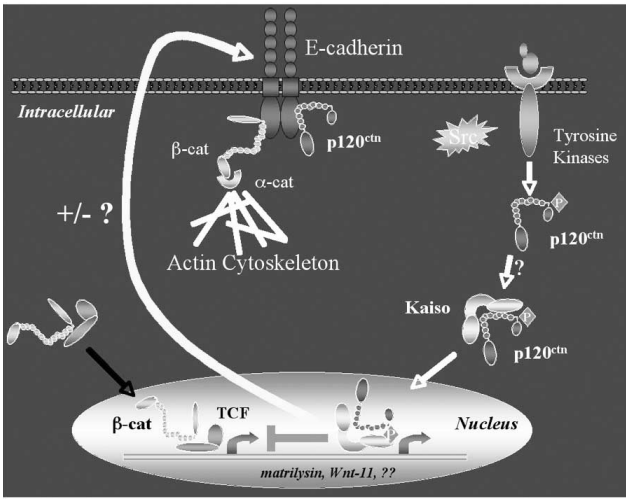
Dr. Pierre McCrea (University of Texas MD Anderson Cancer Center, Texas, USA), Dr. Pierre deFossez (Institut Curie, Paris, France), Dr. Bob Eisenman [a]Fred Hutchinson Cancer Research Center, Washington, USA)

Funding

Canadian Institutes of Health Research (2004-2007), US Army Department of Defense (2002-2005), Premier Research Excellence Award (2001-2006)

Our research program aims to understand the cellular and molecular basis of cadherin-mediated adhesion in normal cell growth, development and tumourigenesis. Currently, we are most interested in the primary epithelial cell-cell adhesion system involving E-cadherin and its cytosolic cofactors, the catenins α- β-, γ- and p120^{ctn}. This adhesion system is perturbed in ~50% of human metastatic tumours, and its malfunction correlates with the metastatic, invasive phenotype. Hence a thorough understanding of the factors that regulate and control cell adhesion and motility would significantly facilitate the development of improved cancer therapies. Recently, in addition to their established roles in cell-cell adhesion, the catenins were found to also play a role in signal transduction via their transcriptional regulation of target genes involved in tumourigenesis. One of the least characterized components of the cadherin-catenin complex is the catenin p120^{ctn} that was first identified as a Src kinase substrate. However our discovery of the BTB/POZ transcription factor Kaiso as a specific binding partner for p120^{ctn} has further strengthened the idea of dual roles for the catenins in cell adhesion and signaling, and has opened new areas of research in the cadherin-catenin field.

Kaiso is a member of the POZ-ZF family of transcription factors with roles in cancer and development. It is the first POZ-ZF transcription factor with dual-specificity DNA-binding and transcriptional repression ability; Kaiso binds and recognizes either a sequence-specific Kaiso binding site, TCCTGCNA or methylated CpG-dinucleotides. Thus far we have identified *matrilysin* and *cyclinD1* as potential Kaiso target genes and more importantly, we found that β-catenin-induced activation of the *matrilysin* promoter was repressed by Kaiso overexpression. Our findings thus implicate Kaiso as an inhibitor of the Wnt signaling pathway and a regulator of genes involved in tumourigenesis (e.g. *matrilysin*).



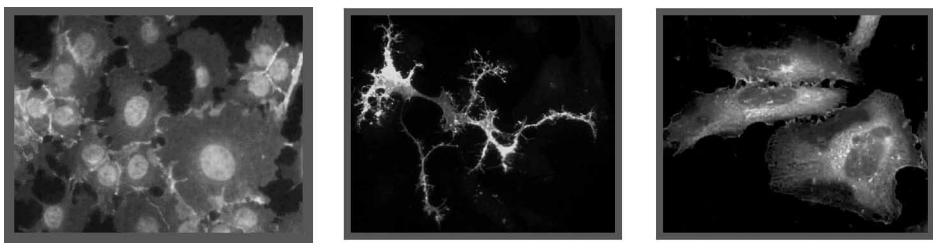
Another ongoing project is to determine what event or signaling molecule triggers the nuclear translocation of p120^{ctn} and its interaction with

Kaiso. Since p120^{ctn} is implicated in cadherin–initiated signaling through the Rho GTPases, it is possible that p120^{ctn} mediates the long-suspected adhesion signal. While this trigger remains unknown, we have discovered that nuclear p120^{ctn} inhibits Kaiso DNA-binding and Kaiso-mediated transcriptional repression. In addition, we recently mapped the Kaiso and p120^{ctn} nuclear localization signals and determined that nuclear localization of p120^{ctn} was required for its inhibitory effect on Kaiso-mediated transcriptional activity.

The third major project in my laboratory involves a yeast two-hybrid screen to identify additional Kaiso-binding partners. Using the Kaiso POZ domain as bait, the proteins identified so far include the cytoskeletal protein Nexilin, and the DNA-binding proteins ZNF131 (a new, minimally characterized POZ-ZF protein) and CTCF (a vertebrate insulator protein and tumour suppressor). We are currently characterizing the interactions between Kaiso and ZNF131, and we are collaborating with Dr. Pierre Defossez (Institut Curie, France) to determine the significance of the Kaiso-CTCF interaction in mammalian chromatin insulation.

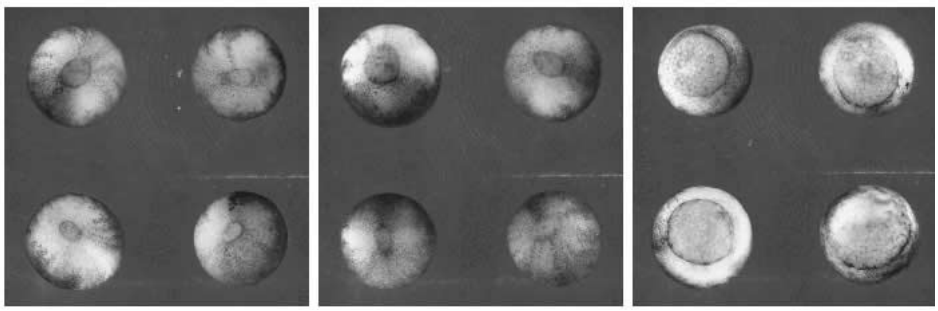
In addition to the above studies that were conducted entirely in my laboratory, I have several ongoing productive collaborations. First, Dr. Pierre McCrea (MD Anderson Cancer Center, Houston, TX) and I are seeking to elucidate the role of *Xenopus* Kaiso in signaling and development. So far we have found that Kaiso misexpression causes ectodermal cell shedding and gastrulation defects in developing *Xenopus* embryos. Second, Dr. Bob Eisenman (Fred Hutchinson Cancer Center, Seattle, WA) and I are investigating the role of the histone deacetylase/mSin3A corepressor complexes in Kaiso-mediated transcriptional repression. We have found that like other BTB/POZ transcription repressors, Kaiso immunocomplexes contain histone deacetylase activity and that Kaiso coprecipitates with the corepressor Sin3A.

Collectively our data allude to p120^{ctn} and Kaiso as key modulators of cell adhesion and motility in development and cancer. We are now strategically poised to unravel the putative adhesion-signaling pathway and elucidate the role of the p120^{ctn}-Kaiso interaction in development and tumourigenesis. Our current experiments are now aimed at (1) elucidating and understanding the molecular mechanism(s) of Kaiso-mediated transcriptional repression, (2) identification and characterization of *bona fide* Kaiso target genes using unbiased ChIP cloning and ChIP-CpG microarray strategies, (3) elucidating the role of Kaiso in canonical and non-canonical Wnt signaling and (4) determining the molecular basis of Kaiso function during normal cell growth, development and disease states. Our data offer exciting promise for the development of therapeutic strategies and animal models for the treatment of malignant tumours.



A B C

FIGURE: (A) p120^{ctn} and Kaiso colocalization. (B) p120^{ctn} overexpressing cells. (C) p120^{ctn} NLS mutant localization.



Uninjected stdMO MOtss

Vegetal views of control (stdMO) and Kaiso-depleted (MOtss) *Xenopus* embryos showing defective blastopore closure.

Susan A. Dudley

Evolution of plant carbon acquisition traits in response to variable environments

Laboratory Personnel

M.Sc. student: Guillermo Murphy; *Undergraduate students:* Clarise Chan, Amanda File, Jake Graham, Tanner Hukezalie

Research collaborators

Lisa Donovan (Department of Botany, University of Georgia)

Funding

Natural Science and Engineering Research Council (2005-2010)

My research program integrates ecology, evolutionary biology, and developmental biology to determine how plants adapt to different environments through their carbon acquisition traits. Though individuals in different environments may differ in phenotype, either because of genetic differentiation or phenotypic plasticity, such differences cannot be assumed to be adaptive. In my research, I study the fitness consequences of phenotypic plasticity and local adaptation. By contrasting natural selection between environments on a suite of interacting traits identified from functional literature, I can better compare the results with the expected costs, benefits, and constraints among these traits.

My research program on the evolution of plant carbon acquisition traits has included studies that integrate the physiological ecology of drought stress with the natural selection on drought stress traits, and genetic differentiation between populations from environments differing in water availability and salinity and other stresses. My predominant focus, however, has been plant adaptation to neighbour densities. I have examined the fitness consequences of phenotypic plasticity to density in the field, conclusively demonstrating that this is adaptive plasticity. I demonstrated genetic differentiation between wood and clearing populations for responses to the light quality cues of density. I have investigated phenotypic plasticity for gas exchange, allocation, and leaf and stem morphology traits in response to R:FR and to high densities. I have contributed to reviews and conceptual syntheses for the evolution of physiological traits and phenotypic plasticity. I developed new approaches and statistics within my papers. I have been first to measure plant responses to both R:FR and root neighbour cues of competitors. Currently, my lab examines plant responses to R:FR and root competitors in soybean. Phenotypic plasticity is as important for plants as behaviour is for animals: it allows plants to defend against herbivores, compete, and forage for mineral nutrients and water. I now ask whether phenotypic plasticity in plants, like animal behaviour, evolves in response to kin selection.

Hamilton's theory of kin selection recognizes that individuals can increase their inclusive fitness through behaviour that increases the fitness of related individuals. However, there have been relatively few plant studies of kin selection in competition, likely because of the belief that plants have limited abilities to interact with one another. It is now known that plants do have a form of social behaviour. Plants sense the presence of other plants, and responses to cues of neighbours are important in competition. Plants have a well-studied aboveground mechanism for sensing neighbours. In the natural environment, the ratio of red to far-red wavelengths of light (R:FR) is only reduced by the presence of chlorophyll in plants. Plants have a photoreceptor, phytochrome that perceives the relative abundance of red and far-red photons. Recent studies have shown that plants have a second, belowground system to sense the presence of neighbours. Recent studies that kept belowground resources constant, while manipulating the presence or absence of root neighbours, demonstrated that plants respond to roots of other plants, often by increasing their allocation to roots. In a collaboration with Lisa Donovan (University of Georgia), we manipulated both root neighbour and R:FR cues independently. We showed that in

Chenopodium album plants responded to root and R:FR cues simultaneously, confirming that plants can sense competitors both above- and belowground. But in contrast to previous studies, we found that in C. album, the belowground cue elicited responses that increased aboveground competitiveness, though only when belowground resources were abundant.

Some very intriguing results have been found in this new field of responses to root neighbours. Effects of root neighbours on root allocation vary from increases, to no effect, to reductions, apparently depending on species. Individual root growth responses depend on the genotype of the neighbour, the species, and whether the neighbouring root is self or non-self, even in genetically identical individuals. For herbaceous plants, neighbours may be trees, interspecific competitors of similar size, unrelated intraspecific competitors, or close kin. Moreover, the densities of neighbours will range greatly. While the R:FR signal strongly conveys information about density, there is the possibility that the root signal may convey specific information about the nature of the competitor. Highly structured monospecific stands create an opportunity for kin selection in plants. If plants have a kin recognition mechanism, the evolution of less selfish competitive responses in such stands becomes possible if not probable.

Marie Elliot

Development in multicellular bacteria; Regulation by small RNAs; Antibiotic production

Laboratory Personnel

Ph.D. Students: David Capstick; *M.Sc. Students:* Henry Haiser, Pan Chen; *Undergraduate Students:* Amanda Cocca, Sandy Shamon

Research collaborators

Dr. Greg Hannon (Cold Spring Harbor Laboratories), Dr. Joanne Willey (Hofstra University), Dr. Justin Nodwell (McMaster University)

Funding

Canadian Institutes of Health Research (2005-2008), Natural Sciences and Engineering Research Council (2005-2010), Canadian Foundation for Innovation (2005), Ontario Innovation Trust (2005), Canada Research Chairs (2005-2010)

The goal of our research is to understand development and regulation in multicellular bacteria, using Streptomyces coelicolor as a model system. The streptomycetes are extremely important to the pharmaceutical industry as they make a large number of 'secondary metabolites' having a profound medical benefit, including anti-cancer agents, immunosuppressants, and the majority of clinically useful antibiotics. They are also unusual in that they have a complex, multicellular life cycle and are capable of differentiating into distinct tissue types. Intriguingly, this differentiation process coincides with the production of secondary metabolites. One aspect of our research is focused on understanding the components necessary for differentiation, and centres on a novel family of proteins, termed the chaplins, that are essential for the transition from one differentiated state to another. We are also interested in the regulatory networks that control differentiation, metabolism, and environmental adaptation in *S. coelicolor*, and are focussing on a newly emerging, and universally important, class of regulators known as the small RNAs.

Aerial development in *S. coelicolor*

The multicellular development of *S. coelicolor* is a complex process, and the transition from vegetative growth to aerial hyphae formation is tightly regulated. Using microarray analysis, we have identified a novel family of hydrophobic proteins, termed the chaplins, that are required for aerial hyphae formation. The eight chaplin proteins are secreted from the cytoplasm, and are all localised to the cell wall. Three of the chaplins (the 'long' chaplins) have a C-terminal extension that is covalently anchored to the peptidoglycan, and we believe that these long chaplins act as nucleation sites for the binding and polymerisation of the other 'short' chaplins. The chaplins are predicted to coat the surface of the aerial hyphae, forming a hydrophobic layer that allows the hyphae to extend into the air, and resist desiccation. Current studies are focussed on (1) understanding the functional specialisation of the eight chaplin proteins, and the nature of their polymerisation; (2) investigating the interaction of the chaplins with other cell-wall components and morphogenetic factors; and (3) elucidating the regulatory network that culminates in the expression of the chaplins.

Regulation by small RNAs

The last five years have seen the small RNAs emerge as important regulators in bacteria, archaea, and eukaroyotes. There is considerable interest in identifying and characterising these sRNAs to provide an understanding of their prevalence, mode of action, and impact on cellular processes, as they are predicted to be a 'missing link' in many

important pathways. We have begun to mine the S. coelicolor genome for sRNAs, and are taking a direct cloning approach to identifying these novel regulators. The long-term aim of this work is to define novel sRNA regulatory networks, and integrate sRNA regulation into known cascades controlling morphogenesis and antibiotic (secondary metabolite) production, thus providing fundamental insights into the biology of these medically and developmentally important bacteria.

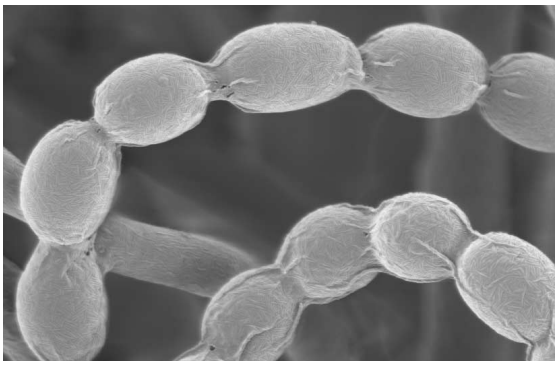


FIGURE 1: Sporulating *S. coelicolor*

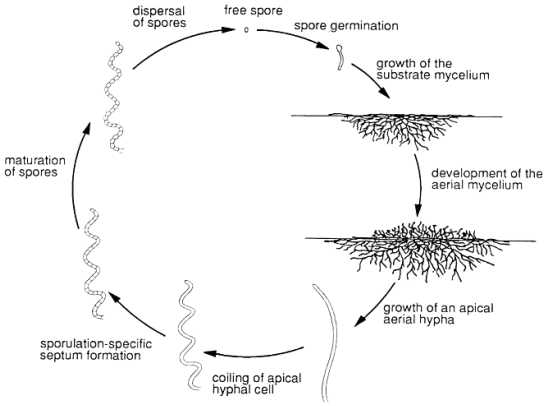


FIGURE 2: Life cycle of *S. coelicolor*

Ben J. Evans

Molecular evolutionary analysis of biodiversity and gene duplication

Laboratory Personnel

Ph.D. students: Frederic Chain, Mohammad Iqbal Setiadi

Research Collaborators

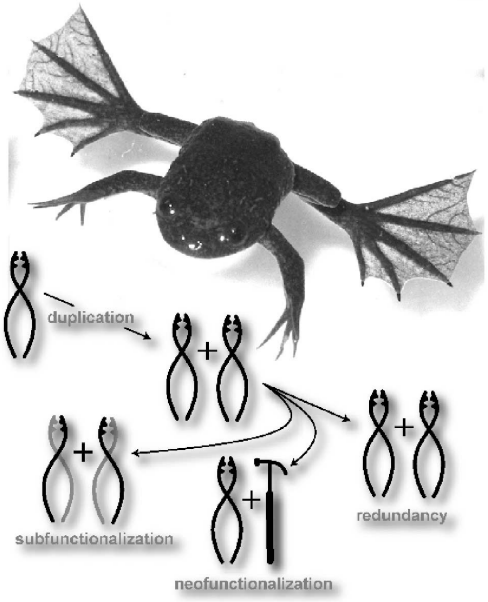
Darcy Kelley (Columbia University), David Cannatella (University of Texas Austin), Don Melnick (Columbia University), Jim McGuire (University of California Berkeley), Rafe Brown (University of Kansas), Richard Tinsley (University of Bristol), Jatna Supriatna (University of Indonesia), Noviar Andayani (University of Indonesia)

Funding

Natural Sciences and Engineering Research Council (2004-2007), Canadian Foundation for Innovation (2005-2008)

In 2005, we completed two studies of molecular evolution of polyploid clawed frogs. One was published in Molecular Biology and Evolution and the other is in press at PLoS Genetics. These studies characterize evolutionary relationships among these species and explore why both copies of a duplicate gene are still expressed millions of years after duplication.

Genome duplication in clawed frogs led to new species such as this dodecaploid, *Xenopus longipes.* Duplicated genes encode protein tools, and their expression can be maintained by mechanisms that enhance, degrade, or do not alter protein function (See figure).



Turlough Finan

Genomic analyses of the soil bacterium *Sinorhizobium meliloti*

Laboratory Personnel

Ph.D Students: Allyson MacLean, Branislava Poduska, *M.Sc. Students:* Laura Smallbone, Andrea Sartor; *Research Associates:* Jiujun Cheng, Alison Cowie, Rahat Zaheer

Research Collaborators

Dr. B. Golding (McMaster University), Dr. C. Baron (McMaster University), Dr. D. Morton (McMaster University), Dr. E. Weretilnky (McMaster University), Dr. J. P. Xu (McMaster University), Dr. B. McCarry (McMaster University), Dr. Philip Poole, University of Reading), Dr. Didier Hérouart (Université de Nice), Dr. Siv Andersson (University of Uppsala), Dr. Barry P. Rosen (Wayne State University)

Funding

Natural Sciences and Engineering Research Council (2001-2005), Genome Canada (2003-2006), ORDCF (2003-2008)

The soil bacterium Sinorhizobium meliloti is best know for its ability to form N2-fixing root nodules on alfalfa. The genome of this bacterium is large and is composed of three replicons – a chromosome and two large plasmids, called megaplasmids pSymA and pSymB. In 1991, we constructed a genetic map for the 1700 kilobase pSymB megaplasmid and ten years later, we were part of the international consortium that determined the DNA sequence of the genome of this organism – all 6,691,694 base pairs. Analysis of this sequence revealed that it contained 6,204 protein coding genes and interestingly the functions of about 2,500 of these genes are unknown. Many of these proteins of unknown function have homologs or similar genes in other organisms. Our major, current, focus is directed to determining the biological roles for these genes of unknown function. In that work, primarily, we are employing a gene fusion - expression approach and have constructed a library of six thousand gene fusions that is presently being analyzed.

A second major project is directed to understanding how replication of the pSymA and pSymB megaplasmids is controlled. In that work we recently discovered a small antisense RNA that appears to play a central role in controlling replication of these plasmids.

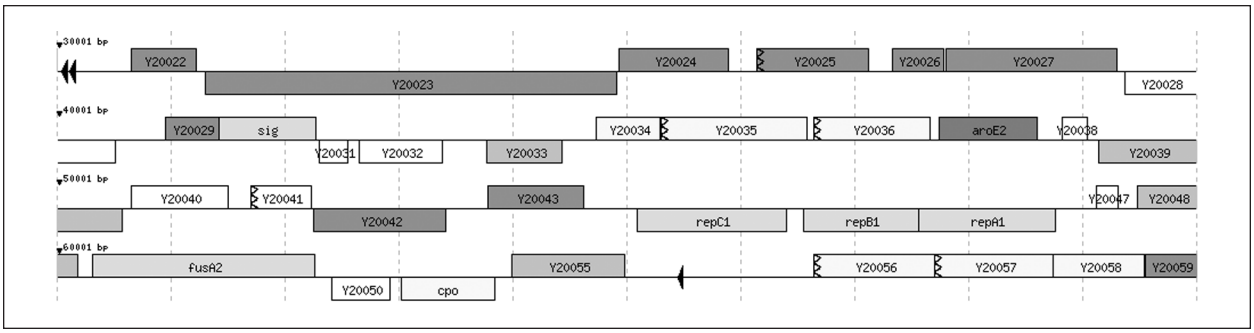
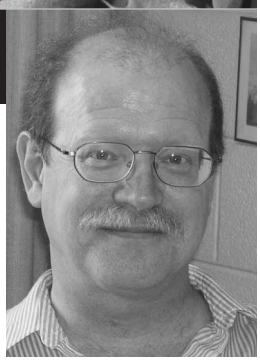


FIGURE: Schematic of a gene region from the *Sinorhizobium meliloti* pSymB megaplasmid including the *repA1, repB1* and *repC1* genes together with several genes of unknown function prefaced by a Y.

Brian Golding

Molecular Evolution, Genomics, Bioinformatics, Computational Biology



Laboratory Personnel

Postdoctoral fellows: Pradeep Reddy, Zaid Abdo; *Graduate students:* Melanie Huntley, Weilong Hao, Melanie Lou; *Research technician:* Ying Fong

Research Collaborators

Darcy Kelley (Columbia University), David Cannatella (University of Texas Austin), Don Melnick (Columbia University), Jim McGuire (University of California Berkeley), Rafe Brown (University of Kansas), Richard Tinsley (University of Bristol), Jatna Supriatna (University of Indonesia), Noviar Andayani (University of Indonesia)

Funding

Natural Sciences and Engineering Research Council (2000-2005), Genome Canada (2003-2007), Canadian Foundation for Innovation (2002), Ontario Innovation Trust (2003-2007), Canada Research Chairs (2002-2009)

Our research interests are in the area of bioinformatics, molecular evolution and DNA sequence analysis. Our research attempts to understand how the processes of evolution act to cause the changes actually observed between molecules, between genes and between genomes. The recent advances in molecular genetics are providing a storm of new data on DNA sequences, on gene structure and higher order genomic structure. However, the implications of these new data are not always clear. This area of scientific inquiry is called bioinformatics and is a relatively new inter-disciplinary field between biology, computer science and mathematics.

We make use of computer based analysis, statistical analysis and mathematical models to answer broad questions about the biology of all organisms. We are presently investigating the following,

- The frequency and properties of genes that have been horizontally transferred between bacterial species. We are developing methods to detect these unusual events and to measure their extent of transfer.
- We are uncovering the determinants of the rates of amino acid replacements as they relate to the three-dimensional structure of proteins. This has involved the development of new statistical methods to measure evolutionary signal across a potentially large phylogenetic history.
- We are determining the properties and determinants of simple repeats within individual proteins. This has included demonstrating that these repeats can form a significant proportion of the genomic protein sequence.
- We are involved in the creation of genomic databases. For example, we are participating in a large scale, multi-university project to determine and archive protist expressed sequence tags. In collaboration with Dr. T. Finan we performed the bioinformatics for a project to sequence the *Sinorhizobium meliloti* 1.7Mbp pExo replicon.

Individual projects change over time but they are united by a consistent, broad interest in the fields of genomics, bioinformatics and molecular evolution.

Bhagwati P. Gupta

Development and evolution of the reproductive system in nematodes

Laboratory Personnel

M.Sc. students: Sujatha Marri, B. Nagagireesh; *Undergraduates:* Cindy Lai, Tram D. Nguyen, Ashwin Venkat; *Technician:* Karen Haines

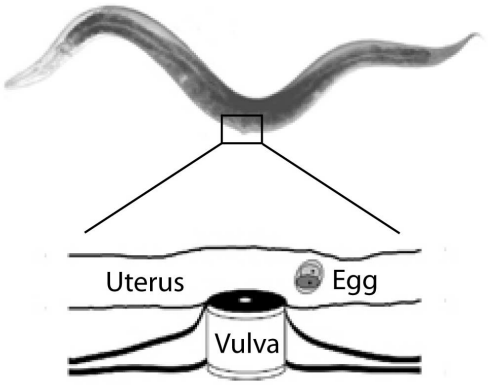
Research Collaborators

Dr. Paul Sternberg (California Institute of Technology), Dr. David Baillie (Simon Fraser University), Dr. Raymond Miller (Washington University School of Medicine)

Funding

Natural Sciences and Engineering Research Council (2004-2009), National Institutes of Health (2005-2007), Canada Research Chairs (2004-2009)

Our laboratory uses soil-nematode, *Caenorhabditis elegans,* to understand how genes function to control cell identity and organ formation in multicellular species. Our system of choice is the hermaphrodite vulva, a tubular organ necessary for mating and laying fertilized eggs. We take classical genetic, molecular, and genomic approaches to study genes and their regulatory networks during vulval tubule morphogenesis.



To understand the mechanism of tissue morphogenesis, we are focusing on the regulation and function of a LIM homeobox (LHX) family of transcription factor LIN-11. LHX genes are present in all metazoans and control diverse morphogenetic events. Targeted deletion and RNA interference (RNAi) of some of the family members in vertebrates (mouse, chick and Xenopus) have been shown to cause severe growth and viability defects. In *C. elegans,* mutations in *lin-11* give rise to an egg-laying defective phenotype due to the defects in the hermaphrodite vulval tubule and vulval-uterine connection. Our work has established that these abnormalities result from the failure in morphogenetic processes such as cell adhesion, polarity and migration. Thus, *lin-11* plays an essential role in vulval tubule morphogenesis. To understand the molecular basis of *lin-11* function, we are focusing on the target genes of *lin-11* and their regulatory network.

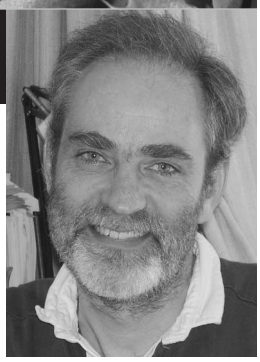
Our comparative studies aim at understanding evolutionary changes in vulval gene networks in *Caenorhabditis* nematodes (such as *C. briggsae, C. remanei,* and *C. spCB5161*) that are closely related to *C. elegans.* Over the past two years, we have carried out multiple genetic screens in *C. briggsae* to isolate vulval mutants. The preliminary analysis has revealed that some of the mutants display unique phenotype not reported for the *C. elegans* vulval mutants. In parallel, we are using bioinformatics tools to compare the genomes of *C. briggsae* (and other *Caenorhabditis* nematodes) with *C. elegans* and analyzing sequences of *C. elegans* orthologs involved in vulval development. These findings are being complemented with specific experiments.

To facilitate the genetic analysis of *C. briggsae* vulual mutants, we are working with other laboratories to develop

resources and tools for comparative studies. One such resource is the genetic linkage map of *C. briggsae* that is being developed in collaboration with Dr. Paul Sternberg (California Institute of Technology), Dr. David Baillie (Simon Fraser University), and Dr. Raymond Miller (University of Washington School of Medicine). A high-resolution linkage map will not only benefit our own research but will also be a valuable resource for the entire nematode research community.

Roger Jacobs

Developmental Genetics, Cancer Genetics



Laboratory Personnel

PhD students: Allison MacMullin, Leena Patel, Katie Moyer, Noor Hossain; *Undergraduate students:* Christine Elder; *Research Technician:* Mihaela Georgescu

Funding

Natural Sciences and Engineering Research Council, Discovery (2002-2005), Canadian Institutes of Health Research (2002-2005), National Cancer Institute of Canada (2003-2006)

Our research program explores the molecular and genetic basis of cell to cell signaling events in developing and mature tissues. We employ *Drosophila* as a model organism, because the rapidity with which we can isolate new mutations, or otherwise modify gene expression. *Drosophila* is a relatively complex organism, wherein the functions of most genes are reflected by conserved (similar in structure) mechanisms in humans. All of our three research streams examine cell to cell signaling that is conserved at the molecular level, but less well understood in humans. Through applying an unbiased genetic approach in *Drosophila,* we can discover new dimensions of signaling events that are impossible or difficult to uncover in mammals.

Function of Veli in polarised signaling

Veli, or vertebrate Lin-7 is a small protein that acts as a scaffolding protein at the apical cell surface. Veli acts to organise into larger complexes, signaling molecules that function as a unit. Typically these molecules include ones that protrude from the cell surface, and are engaged in cell to cell communication. Veli is expressed at the sending and receiving sides of the major cell to cell signaling system in the nervous system, the synapse. We have isolated and characterised the *Drosophila* form of this protein, and used genetic tools to alter its function. We have discovered that it is required to efficient presynaptic signal release, and that altered function reduces output. The synapse attempts to compensate for reduced Veli protein levels by expansion of cell to cell contacts in the synapse (see Figure 1) but nevertheless, impaired veli function results in sluggish behaviour.

Molecular and genetic analysis of the morphogenetic functions of Slit

The formation of complex tissues in the embryo requires the directed movement of cells (migration) or directed growth of cell processes, like the axons of the nervous system. We co-discovered the primary repellent guidance signal for migration in the nervous system, called Slit, in 1999. Today we are examining its function in the assembly of a simpler tissue, to better understand the molecular basis of its activity. We focus on the *Drosophila* heart, whose development mirrors the vertebrate heart up to the point of looping morphogenesis. We have discovered that Slit can act as an attractant in heart cell migration events, and that this function is strongly affected by other cell adhesion signals, in particular from the integrin family (see Figure 2). Currently we are using gene misexpression tools, and timelapse studies of cell movements in living tissue, to see how cells react to the intersecting signals of attraction, repulsion and adhesion.

Genetic dissection of mammalian ErbB2 signaling in *Drosophila*

Nearly a third of human breast cancers involve a change in the regulation or expression of a major cell to cell signaling system, involving ErbB2, a member of the Epidermal Growth Factor Receptor family. ErbB2 signals growth and differentiation signals, and in cancer, unregulated cell growth, by recruiting and activating many intracellular messenger proteins, called second messengers. Clinicians and scientists would like to determine what specific outcomes result from the activation of each second messenger, so that we may identify more specific targets for therapeutic intervention. Scientists looking at the mammalian model have designed altered forms of ErbB2 that can only activate a small set of second messengers at a time. Technically, it is very slow and expensive to determine the effects in living mammalian models of cancer.

Drosophila shares a signaling pathway that is strongly conserved with vertebrate ErbB2. We have discovered that expression of mammalian ErbB2, including the altered forms, can signal through *Drosophila* second messengers. Moreover, we can apply genetic approaches in *Drosophila* to identify which second messengers, or discover new second messengers that are required for specific signaling pathways that radiate from ErbB2. Currently we are focused upon discovering the signal pathways employed by ErbB2 to down-regulate its own outputs.

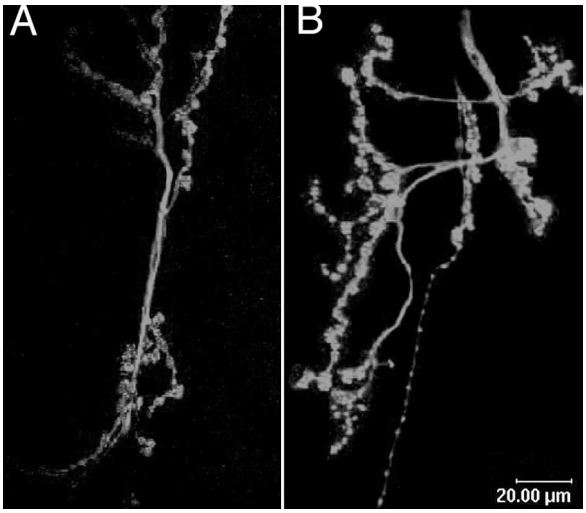


FIGURE 1:
Panel A shows the size and location of synaptic boutons on the muscle of a normal fly. Panel B shows the increased size and number of boutons when Veli levels are reduced.

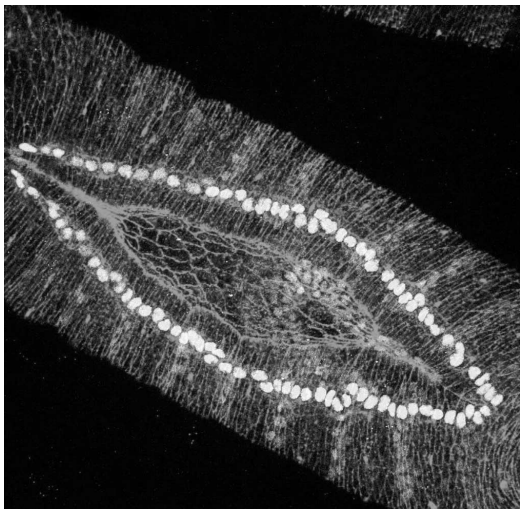
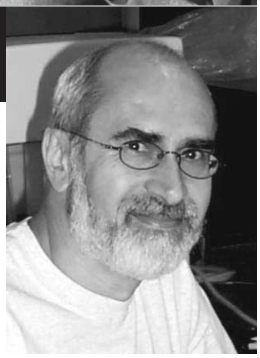


FIGURE 2:
This is a dorsal view of the *Drosophila* embryo, as the heart cells (nuclei marked in green) move from both sides towards the midline, to form a tube. The red label outlines the actin filaments underlying each cell membrane.

Jurek Kolasa



Interactions Between Habitat Structure and Variability and Biodiversity Patterns

Laboratory Personnel

Postdoctoral fellow: Ermias Azeria; *Ph.D students:* April Hayward, Shubha Pandit; *Undergraduate students:* Jennifer Lavery, Ashley Gaw, Marissa Sebastin, Marselina Maciejewski

Research Collaborations

David Jenkins (South Florida Univeristy), Beatrix Beisner (Universite Du Quebec A Montreal), Larry Li (Univ California, Riverside).

Funding

Natural Science and Engineering Research Council (2000-2005)

Our main focus is on organization and function of ecological systems and their biodiveristy in context of heterogeneity, habitat hierarchy, and scale.

One of the conceptual bottlenecks of ecology is posed by the multitude of interacting components and factors such as individuals, populations, habitat patches, abiotic resources, disturbances, and others, affecting or expressed in any single community or ecosystem. I am interested in analytical approaches to such complex ecological systems, with special focus on aquatic habitats and their fauna. Specific areas of research include organization and structure of aquatic communities as a function of spatial and temporal scale and habitat heterogeneity. Much of the field work is being conducted at a site in Jamaica and include experimentation of rock pool communities and coral reef fish. Recently, we have focused on conditions under which species diversity affects stability of whole communities, probability of species extinction, and fluctuations of individual populations. These conditions may include body size structure, system productivity, habitat variability, or interactions among these factors.

Grant McClelland

Integrative physiology of muscle and animal performance, environmental stress

Laboratory Personnel

Ph.D. students: Paul Craig; *M.Sc. students:* Marie-Pierre Schippers, Andrea Morash, Kristina Murphy; *Undergraduates:* Kalindi Dhekney; Lab volunteers: *Julie Kim*

Research Collaborations

Dr. Reuven Dukas (McMaster Psychology); Dr Chris Wood (McMaster Biology); Jim McGeer (Natural Recourses Canada); Jim Staples (University of Western Ontario); Steve Britton and Lauren Koch (University of Michigan).

Funding

Ontario Early Researcher Award (2005-2010), Natural Sciences and Engineering Research Council, Discovery (2004-2008), NSERC CRD Grant & industrial partners (with C. Wood) (2005-2008)

Our lab focused on gaining a better understanding of the cellular, molecular, genetic, environmental and evolutionary determinants of fuel selection with an emphasis on lipid metabolism. In the last year we focused on several major research themes:

Vertebrate muscle metabolic remodeling

This research focuses on muscle plasticity to environmental and energetic stress and how this impacts on whole-animal performance. Using adult zebrafish and trout as model systems we have been investigating an apparent paradox concerning the qualitative changes in mitochondrial biogenesis with chronic increases or decreases in muscle metabolism. We are also examining the regulation of muscle lipid metabolism in response to environmental stress at both the genetic and nongenetic level.

Lifetime performance and muscle physiology

We have also been investigating the relationship between lifetime learning and foraging performance changes in relation to muscle physiology in honeybees. (With R. Dukas)

Toxicogenomics

To examine the relationships between oxygen delivery and fuel metabolism we are using lines of rats selectively bred for high and low aerobic running capacity. This model system is ideal to study the relationship between exercise intensity and fuel kinetics.

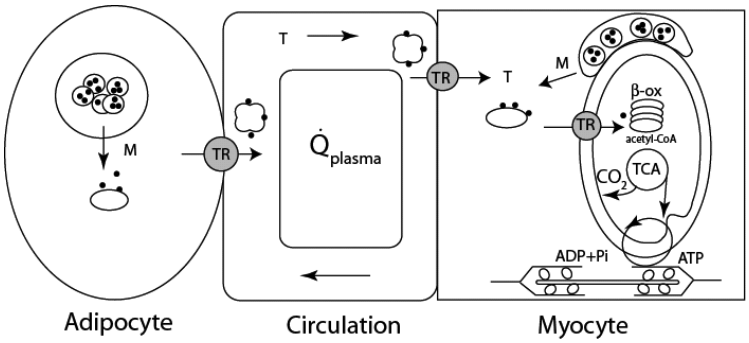
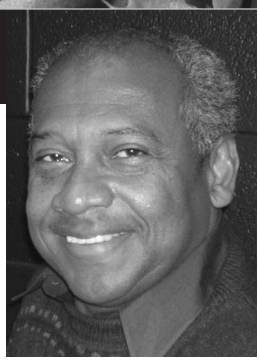


FIGURE:
Transport steps in fat delivery from storage sites to working muscle mitochondria

Colin Nurse



Cellular and molecular mechanisms of O_2, and CO_2/pH sensing in vertebrates

Laboratory Personnel

Ph.D. students: S. Brown, J. Buttigieg; *M.Sc. students:* J. Liu, K. Clarke; *Undergraduate students:* L. Dookhoo, P. Sharma; *Senior technician:* Cathy Vollmer; *Research Associate:* Dr. Min Zhang; *Research Assistant:* M. Lowe

Research Collaborators

Ernest Cutz (Hospital For Sick Kids), Ian Fearon (University of Manchester), Alison Holloway and Ana Campos (McMaster University)

Funding

Canadian Institutes of Health Research (2004-2009 and 2005-2010), Natural Sciences and Engineering Research Council, Discovery (2003-2007), Heart and Stroke Foundation (2001-2006)

Dr. Nurse's laboratory is interested in the cellular and molecular mechanisms by which cells sense changes in oxygen (O_2), CO_2, and pH, and make appropriate physiological responses. For example, we study specialized receptor cells and neurons that respond to low O_2 (hypoxia) by activating a signaling cascade leading to regulation of plasma membrane K+ channels, and release of neurotransmitters (e.g. catecholamines, ATP, nitric oxide). We combine primary cell culture, patch clamp electrophysiology, confocal immunofluorescence, chemiluminescence methods, RT-PCR, and western blotting techniques, with the use of cell lines to characterize key components in the signaling pathway. A major focus has been on characterization of O_2, CO_2, and pH sensing in specialized chemoreceptors of the mammalian carotid body (CIHR funded), in nitric oxide-producing autonomic neurons that regulate carotid body function (CIHR funded), and in chromaffin cells of the neonatal adrenal medulla (HSFO funded). We have also characterized an immortalized O_2 -sensitive cell line from the rat adrenal medulla (MAH cells) to aid studies on the role of the mitochondrial electron transport chain in acute oxygen sensing, and on the regulation of gene expression by chronic hypoxia (HSFO and NSERC funded). Finally, we are exploring cellular/ molecular O_2-sensing mechanisms in vertebrates from a comparative and evolutionary perspective, by focusing on innervated neuroepithelial cells in gills of water-breathers, e.g. zebrafish and Xenopus tadpoles (NSERC funded).

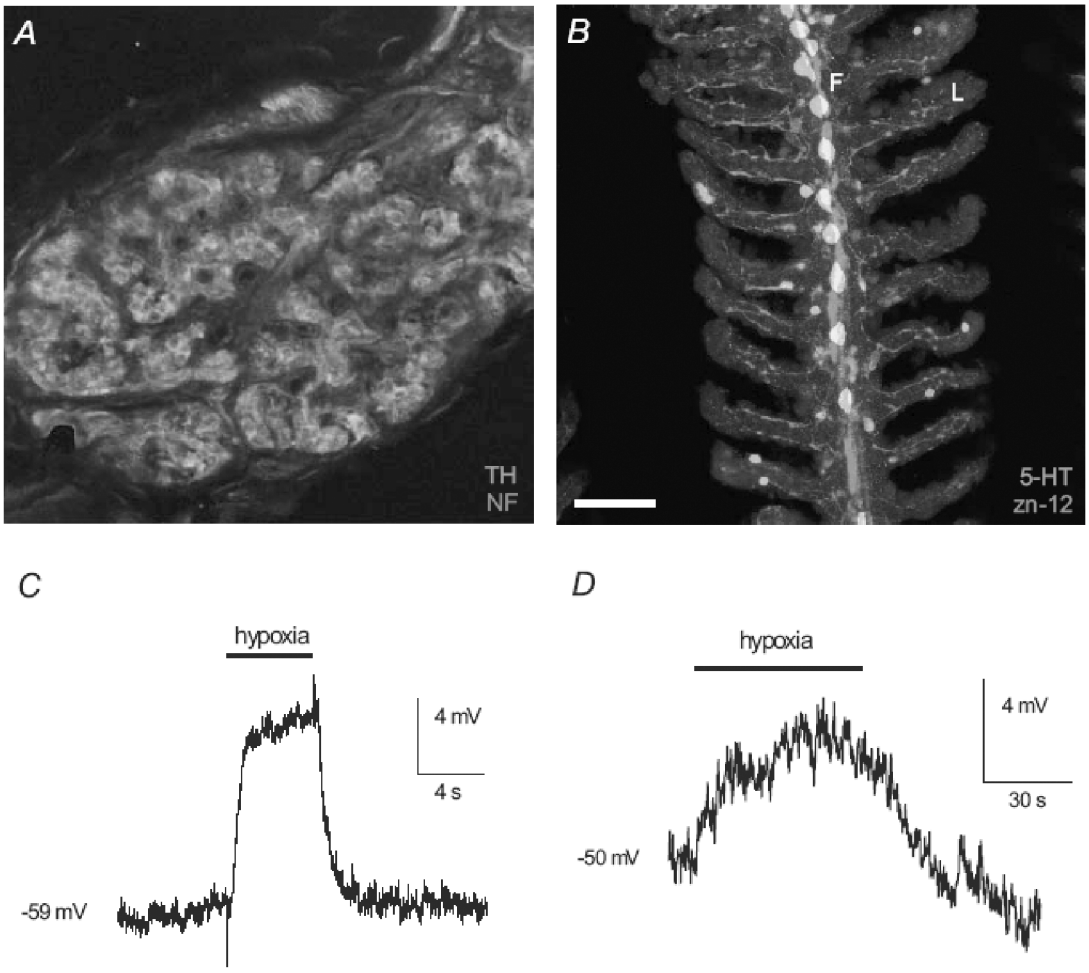
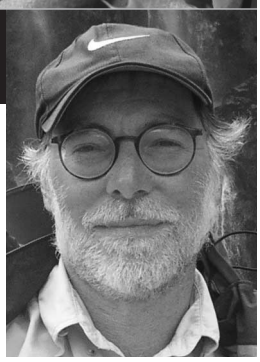


FIGURE: Fluorescence images of O_2 receptors, their innervation, and their physiological response to hypoxia in rat carotid body (A,C) and zebrafish gill (B,D). For colour photo and details see article by Jonz & Nurse *(Physiol. News: 2005).*

Michael J. O'Donnell



Electrophysiological studies of ionoregulation, excretion and toxicology in invertebrates: Cellular mechanisms and control of epithelial transport

Laboratory Personnel

Postdoctoral fellows: Dr. Andrew Donini; *Ph.D. students:* Esau Ruiz-Sanchez; *Undergraduate students:* Samantha Wong, Ivan Kamikovski, Melanie Foley, Dana Strasberg

Funding

Natural Sciences and Engineering Research Council (2005-2010)

The primary goal of my research program is to elucidate the cellular and molecular mechanisms of excretion and ion transport by insect epithelia. A related objective is to explain how such processes are controlled by hormones and intracellular second messengers. My research makes extensive use of electrophysiological methods, including intracellular recording, ion-selective microelectrodes and patch clamping. My students and I must also develop or adapt specialized micro-techniques for measuring pH or ion concentrations inside or adjacent to epithelial cells, or in nanolitre samples of biological fluids. Our studies of physiological mechanisms of ionoregulation and excretion provide insights that we hope will aid development of novel, environmentally-benign insecticides for pest species.

Transport of organic cations and organic anions by insect epithelia

Excretion and ionic and osmotic regulation in insects are accomplished by the Malpighian tubule/hindgut system. The functional kidneys of insects are the Malpighian tubules that transport a wide variety of organic anions and organic cations including metabolites and both natural pesticides (*e.g.* nicotine) and anthropogenic compounds. Recent studies by other groups suggest that organic ion transporters play a role in insecticide resistance.

Current models propose that type I organic cations (<400 Da, monovalent) enter renal cells through an electrodiffusive pathway driven by the inside negative membrane potential, whereas the larger (>500 Da) more hydrophobic OCs of type II may diffuse across the cell membrane. Transport of type I organic cations across the apical membrane may involve OC/H^+ exchange, whereas type II organic cations are substrates of the multi-drug resistant (MDR) gene product p-glycoprotein (P-gp), an ATP-dependent pump. Organic anions enter the cells through several pathways which may involve cotransport with protons or exchange for cellular dicarboxylic acids. Organic anions may cross the apical membrane into the lumen through a voltage-dependent transporter, through exchange for other anions in the lumen, or though a multidrug resistance associated protein (MRP).

Development of novel electrophysiological methods for analysis of organic ion transport

We recently developed two novel electrophysiological techniques to study transport of the prototypical organic cation (OC) tetraethylammonium (TEA). The first technique involves a TEA-selective self-referencing (TEA-SeR) microelectrode which exploits the 10^7-fold higher selectivity of a common ion exchanger for TEA relative to K^+. This non-invasive technique provides excellent spatial and temporal resolution of TEA transport by the Malpighian tubules, ureters and gut of insects, even those as small as the fruit fly *Drosophila.* We also developed TEA-selective microelectrodes to measure TEA concentration in nanoliter droplets of fluid collected from isolated Malpighian tubules set up under paraffin oil in the Ramsay assay. TEA flux (pmol min^{-1}) by individual Malpighian tubules can be calculated as the product of secreted fluid TEA concentration (mmol l^{-1}) and secretion rate (nl min^{-1}). TEA-selective microelectrodes can also measure changes in haemolymph [TEA] after injection of TEA or after insects are fed TEA-enriched diets. We extended strategies developed for TEA measurement to measurement of the organic anion (OA) salicylate, using ion exchanger microelectrodes based on tridodecylmethylammonium. TEA-selective

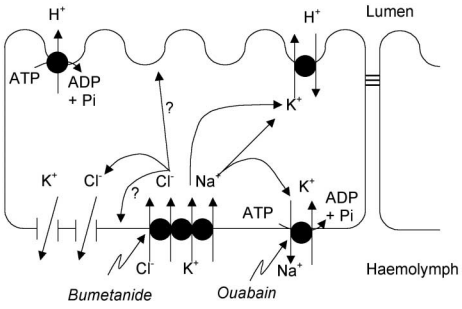
or salicylate-selective microelectrodes provide rapid, safe, and low cost methods for analysis of Malpighian tubule transport of OCs and OAs. Detection limits are actually lower than those achievable using liquid scintillation counting.

Mechanisms of organic cation and organic anion transport in insects

Basolateral uptake of the prototypical organic cation TEA by MTs of *Drosophila* is a saturable process and is dependent on basolateral membrane potential, indicating electrogenic transport. The posterior midgut and the lower region of the MT and ureter also transport TEA, and multiple transporters appear to be involved. Moreover, diuretic factors which stimulate active transport of Na^+, K^+ and Cl^- osmotically obliged water flow also stimulate TEA transport. MTs of insects from 8 species in 6 orders also transport TEA and the p-glycoprotein (P-gp) substrate nicotine at high rates. In conjunction with collaborator C. Donly we initiated the isolation of lepidopteran P-gp cDNAs using degenerate primers based on *Drosophila* P-gp sequences. We used RT-PCR and unique primer sets to determine expression of 4 related MDR genes in Malpighian tubules and other tissues of caterpillars. We have also used confocal microscopy to show that organic anions are transported across the cytoplasm of principal cells both by diffusion and in vesicles, indicating multiple transport mechanisms.

Mechanisms of Na+, K+ and Cl- transport by insect Malpighian tubules

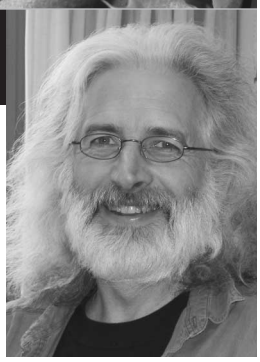
A striking aspect of insect Malpighian tubules is their capacity for varying the Na^+:K^+ ratio in secreted fluid to compensate for variations in dietary Na^+ and K^+ intake. Our model for secretion of K^+-rich fluid by Drosophila MTs proposes that K^+ and Cl^- cross the basolateral membrane through a Na^+-driven Na^+:K^+:2Cl^- cotransporter; most of the Na+ that enters cells is returned through the Na^+/K^+-ATPase (5). Thus, although the main driver for transport is the apical H^+-ATPase, the Na^+/K^+-ATPase plays an important role in fine tuning the secreted fluid cation composition.



Ion transport by anal papillae and Malpighian tubules of larval mosquitoes

Classic work done on fresh water species used whole larvae and radioisotopes to assess kinetic parameters of ion uptake in dilute waters. Little is known of the cellular mechanisms involved and virtually nothing is known of the role of hormones in controlling ion uptake or excretion by the Malpighian tubules, hindgut and anal papillae in the larvae. We used self-referencing ion-selective microelectrodes positioned near the surface of papillae in intact larvae to directly measure fluxes of Na^+, H^+, Cl-, K^+, Ca^{2+} and NH_4^+.

Jim Quinn



Genetic relatedness, parentage and behavioural ecology of colonial and cooperative-breeding birds and anthropogenic induction of germline mutations in gulls and mice

Laboratory Personnel

Gregory Schmaltz, Heather Reider, Megan Barclay, Laura Golding, Stephanie Fairfax, Amit Rahalkar, John Beduhn and Samantha Green.

Research Collaborators

Dr. Mark Hauber (University of Auckland), Dr. Steve Schoech (Memphis University), Dr. Jonathan Wright (Trondheim University)

Funding

Natural Sciences and Engineering Research Council (2005-2010), Great Lakes Clean-up Fund (2005-2007), Premier Research Excellence Award (2001-2006)

Our research has focused in two directions. First, we have been trying to understand the complex social system of a communal plural breeding joint-nesting bird, the smooth-billed ani *(Crotophaga ani).* Progress on that front follows:

We have developed microsatellite markers for smooth-billed anis and a species of future research interest – pukeko *(Porphyrio porphyrio).* In the field we have made significant improvements in techniques and equipment for capturing and video taping anis in Puerto Rico. Recent local studies of colonial nesting waterbirds have allowed the development of techniques for non-destructive sampling and isolation of maternal DNA from the external surface of eggs. This latter method, which appears effective for ani maternal genotyping, will represent an important advance in field studies as it limits the need to sample the mother directly and it increases the statistical power of identifying the father by allowing a focus on specifically paternal alleles.

We have extracted DNA samples from 350 ani adults and 420 chicks from 45 territories over the past 7 years. Many of these have been genotyped with 5 microsatellite loci using ^{33}P labelled primers. Preliminary analyses have revealed that a) both sexes have extra-pair fertilizations and b) young from most groups disperse to join other groups. Most groups (N = 13) examined were unrelated adults (10% of within-group dyads are related) while two groups had many more related dyads (about 30 to 66.7% of within-group dyads related), suggesting that offspring in these two groups had not dispersed.

We developed three general methods for capturing anis (netting nocturnal roosts, trapping adults on territory using lure birds, and radio-controlled nest traps) and field tested a video recording system. We have found that smooth-billed anis while socially monogamous, engage in extra-pair fertilizations and live in groups of mostly unrelated adults. We know that egg tossing and burial represent deliberate behaviours and that nocturnal incubation involves actively repelling potential predators such as rats (both from video evidence).

In 40 communal nests analyzed, we found that 56% of all eggs laid ended up buried or tossed. As a result, the number of eggs incubated per capita significantly decreased with increasing group size. Because of intense competition during egg-laying in anis, we expect females to adjust their laying behavior to advantage their offspring. Results suggest that females do so in different ways. First, we found that as female group size increases, females lay more eggs per capita. Second, we found that females deposit more testosterone and corticosterone in late-laid eggs Vs early laid eggs. Because of burial and tossing, eggs laid later are more likely to hatch. Females therefore seem to

adjust testosterone concentrations in eggs depending on the probability of a given egg to hatch. Since increased testosterone levels in eggs have been found to positively affect chick begging abilities, growth, and survival, we hypothesize that these maternal hormonal depositions may lead to the production of a more competitive chick. We are currently investigating how these different maternal effects influence offspring and adult fitness during sibling-sibling competition.

Novel field methods for pukeko studies have already been worked out. We have established three microsatellite markers that will facilitate rapid genotyping of eggs and adults in some pukeko groups. I have established an important collaborative relationship with Dr. Mark Hauber at University of Auckland that will facilitate field studies of pukeko north of Auckland, New Zealand.

In another area of research we followed up on our previous findings that germ-line tandem repeat DNA mutations are induced by human produced pollution. We recently demonstrated that air pollution can induce mutations and that the particulate component is responsible (Figure 1). This work was accomplished through experimental exposure of lab mice in to air pollution in "mouse hotels" located downwind of Hamilton's industrial core compared with those housed 35 km north on a non-polluted reference site. This work has led to prominent and important publications in *PNAS* and *Science* showing that germ-line tandem repeat DNA mutations in gulls and mice are related to particulate air pollution associated with heavy industry and diesel exhaust. I hope that demonstrations such as these will lead to reductions in pollution-inducing urban sprawl and a tightening of restrictions on the release by industry and traffic of particulate air pollution that has already been implicated in deadly cardiac and respiratory disorders.

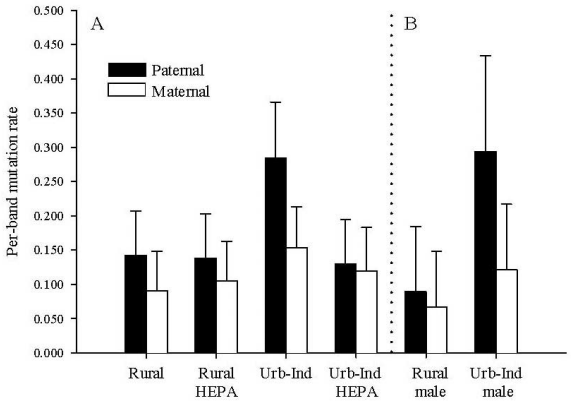
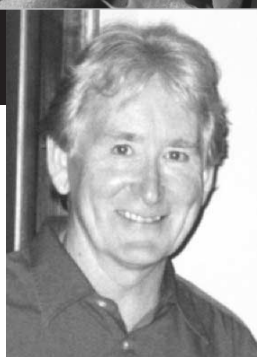


FIGURE: (A) The paternal and maternal per-band mutation rates (+ 95% CI) measured in the offspring of sentinel mice exposed in situ to ambient or HEPA-filtered ambient air at the urban-industrial (Urb-Ind) and rural field sites. Mutation rates are for ESTR single loci Ms6-hm and Hm-2 pooled, and are based on analysis of 94 to 114 offspring (177 to 220 bands) in 17 to 20 pedigrees from each treatment group. (B) Mutation rates resulting from mating males exposed to ambient air at the rural and Urb-Ind sites to unexposed females. Mutation rates are for Ms6-hm and Hm-2 pooled from 8 pedigrees (45 to 48 offspring, 79 to 91 bands).

Andrew J. Rainbow



Molecular mechanisms for DNA repair in mammalian cells and their role in human disease using viruses as probes

Laboratory Personnel

Research Assistant: Natalie Zacal; *Post-Doctoral Fellow:* Photini Pitsikas; *Graduate students:* Robert Cowan, Shaqil Kassam, Adrian Rybak, Diana Dregoesc, Alicia O'Neill, Prachi Sharma, Shari Yasin and Derrik Leach

Research Collaborators

Dr. Gurmit Singh (Department of Pathology and Molecular Medicine, McMaster University.), Dr. Regen Drouin (Department of Pediatrics, University of Sherbrooke, Quebec), Dr. Girish Shah (CHUL Research Centre and Faculty of Medicine, Laval University, Quebec), Dr. Xu-Dong Zhu (Department of Biology, McMaster University)

Funding

National Cancer Institute of Canada (2005-2010), Ontario Cancer Research Network (2005-2008)

Our research objective is to understand the role of DNA damage and DNA repair in the induction of human cancer as well as to improve protocols for radiation therapy, photodynamic therapy and chemotherapy of cancer. Knowledge concerning DNA repair comes from comparative studies of cell strains from normal individuals as well as from patients suffering from a number of human genetic diseases including xeroderma pigmentosum (XP), Cockayne syndrome, Bloom's syndrome, Fanconi's Anemia and ataxia telangiectasia. Cells from most patients with these diseases are hypersensitive to certain cytotoxic agents, show some deficiency in DNA repair and have a predisposition to cancer. For example, the majority of XP patients are deficient in the first step of nucleotide excision repair (NER) of DNA and the incidence of sunlight-induced skin cancer in these patients' approaches 100%. Efficient DNA repair thus plays a major protective role from cancers resulting from exposure to the sun.

Our research uses cell culture, recombinant DNA techniques and viruses as probes and expression vectors to examine DNA damage induced by ionizing radiation, ultraviolet light, cisplatin and other cytotoxic agents and the repair of this damage in several different mammalian cell types. DNA damage and DNA repair play an important role in the response of tumour cells to radiation therapy and chemotherapy. In our research we are also examining the response to DNA damaging and other cytotoxic agents of tumor cell lines with an altered response to radiation, chemotherapeutic agents and/or photodynamic therapy (PDT) treatment. The information we gain from these studies is expected to lead to new approaches which reduce the detrimental effects of DNA damaging agents in the environment and help in the management of individuals at high risk for carcinogen induced malignancy. Such knowledge will also be used to improve protocols for radiation therapy, chemotherapy and photo chemotherapy of cancer.

In recent years a major finding of our laboratory is that pre-treatment of normal human cells with low exposure to UVC light or heat shock enhances the repair of UVC-induced DNA damage, indicating an inducible NER response in human cells (Rainbow et al., 2005, Eds. Drouin et al., Comprehensive Series in Photosciences. Elsevier Science, pp. 181-204). NER has two sub-pathways: transcription coupled repair (TCR) that preferentially repairs lesions in the transcribed strand of active genes and global genomic repair (GGR) that repairs the non-transcribed transcribed strand of active genes and inactive regions of the genome. In recent work we show that the inducible NER response is transient in normal human fibroblasts and that both the TCR and GGR sub pathways are inducible by pretreatment with low UVC exposure (Pitsikas et al., J. Photochem. Photobiol. B: Biology, 81, 89-97; Liu and Rainbow 2005, Bioscience Reports, 24, 559-576). UVA alone, as well as several photosensitizing agents

plus visible light, can produce oxidative DNA damage which results in damage to single DNA bases that are repaired by base excision repair (BER). We are currently extending our studies to examine the genes required for BER and to determine if BER, like NER, can be induced in cells.

One of our approaches to examine the mechanisms of PDT is by inducing and selecting PDT-resistant cell variants and determining alterations in gene expression that lead to resistance. We have generated several photosensitizer specific PDT resistant cell variants of HT29 human colon adenocarcinoma cells and recently reported several alterations in mitochondrial and apoptosis regulating gene expression in these cells (Shen et al., 2005, Photochem. Photobiol. 81, 306-313). Although these alterations increase the resistance of HT29 cells to PDT they result in increased sensitivity to the anti-cancer drug cisplatin (Zacal et al., 2005, Biochem. Biophys. Res. Commun., 331, 648-657).

Cisplatin is a very useful drug in the treatment of many types of cancer. The cytotoxicity of cisplatin is thought to result from the local DNA distortion caused when cisplatin binds to genomic DNA. This damage induces apoptosis through signaling pathways that are not well understood. In a recent report we show that a deficiency in the TCR pathway of NER results in amplified and prolonged activation of the Jun N-terminal kinase (JNK) following treatment of cells with cisplatin, due to persistent damage in active genes. Further, it is this amplified and prolonged JNK activation that correlates with cisplatin-induced cell death (Bulmer et al., 2005, Cancer Chem. Pharm., 56, 189-198).

Adenovirus (Ad) vectors are a very efficient method for delivering foreign genes into mammalian cells and show great promise for gene therapy of cancer. The cytomegalovirus (CMV) immediate-early (IE) promoter is one of the most commonly used promoters in eukaryotic expression vectors and several reports have proposed the use of Ad gene delivery in combination with radiation therapy and chemotherapy. We show that expression of a CMV-driven reporter gene is enhanced following treatment of several human tumor cell lines with DNA damaging agents including UV, cisplatin and N-acetoxy-acetylaminofluorine (Zacal et al., 2005, Biochem. Biophys. Res. Commun,, 332, 441-449). This finding has important implications for combined chemotherapy and gene therapy using CMV-driven expression vectors.

C. David Rollo

Regulatory Intregration: From evolutionary ecology to gene transcription

Laboratory Personnel

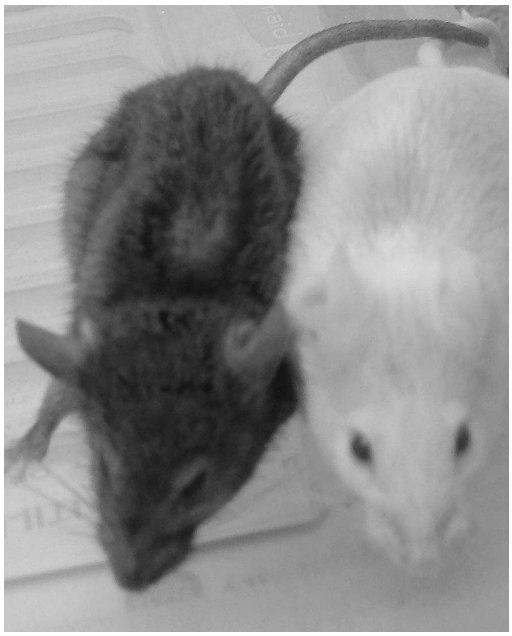
M.Sc. Students: Vadim Aksenov; *Undergraduate Students:* Heather Soannes, Elaine Keung, Arti Kumar, Erin Langs, Judith Ancheta.

Research Collaborators

NIH (United States) Longevity Consortium; Jiankang Liu, UC Berkeley; Henry Szechtman, Boris Sakic, Dept of Psychiatry and Behavioural Neurosciences; Douglas Boreham, Carmel Mothersill, Jennifer Lemon, Medical Physics and Applied Radiation Sciences; Jack Rosenfeld, Department of Pathology and Molecular Medicine; Biomarker Pharmaceuticals, California

Funding

Natural Sciences and Engineering Research Council

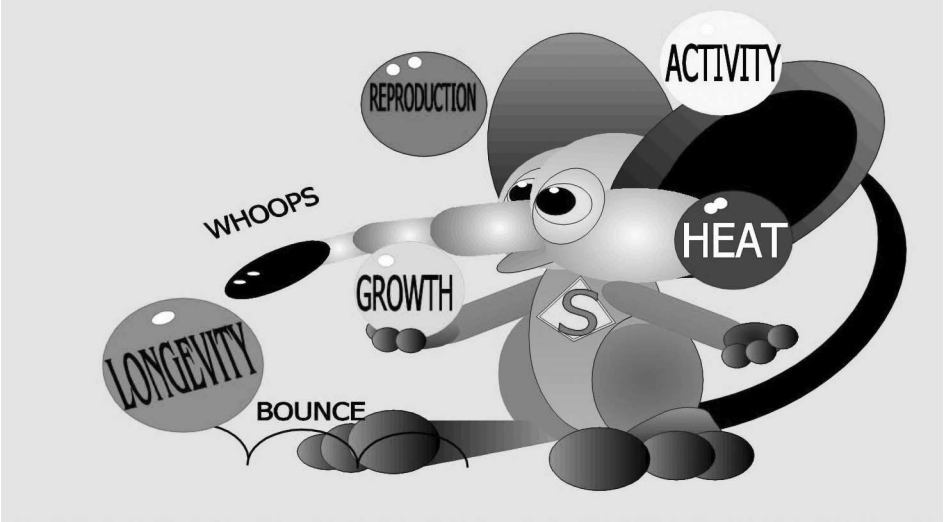


The research programme evaluates tradeoffs among system-level organismal functions (Evolutionary Ecology), how the adaptive allocation program is coordinated (Evo-Devo and Integrative Physiology) and how decisions are transmitted via cellular transduction signalling to tissue-specific functions and gene regulation (Cell and Molecular Biology). Models include various transgenic and mutant mice. Size and growth rate most strongly determine other attributes of form and function so transgenic growth hormone mice (TGM) are ideal subjects. What are the impacts (tradeoffs) among other functions for a mouse that grows to double mature sizes at twice normal rates?

At the forefront of current interest is the fact that TGM express accelerated aging (Gerontology) associated with elevated free radical processes. This makes them excellent models for studying both aging and radiation biology. TGM have enhanced youthful learning, but subsequent drastic deterioration of cognition and brain (Psychology). They sleep excessively, a feature we found was ameliorated by energy supplements.

We developed a theory of regulatory organization suggesting that anabolic and catabolic functions are temporally separated between sleeping (GH axis) and waking (stress hormone axis). TGM expressed greatly increased growth efficiency that involves diversion of energy from thermogenesis and locomotion. Alterations in mitochondrial metabolism are suggested. My meta-analysis (n = 796) of intra-specific longevity demonstrated that longevity declined with increasing size in both mice and rats. We designed an "anti-aging" dietary supplement that significantly increased longevity of TGM and normal mice. Based on evidence that sleep synergizes memory we tested TGM and showed that they learn a complex maze at double normal rates when young but these abilities rapidly decline with age.

Remarkably, the supplement completely preserved youthfully enhanced cognition. TGM have larger youthful brains but their cognitive decline traces to loss of > 50% of their brain cells (similar to Alzheimer's). The supplement completely prevented loss of brain cells. We are currently examining major mechanisms associated with aging and associated pathologies (insulin resistance, free radical, antioxidants, inflammation, mitochondrial functioning, membrane integrity, NADPH oxidases, cancer and stem cells).



Herb Schellhorn

The regulation of stress genes in Escherichia coli

Laboratory Personnel

M.Sc. Students: Sarah Chiang, Tao Dong, Daniel Gyewu, Mirella Younes, Thuraya Shaban; *Undergraduate students:* Alvin Choi, Andrew Hughes, Ali Ibrihami Daniel Li, Susan Sullivan

Funding

Canadian Institutes of Health Research (2005-2008), Natural Sciences and Engineering Research Council (2005-2010)

My laboratory examines how bacteria adapt to suboptimal growth conditions by turning on expression of specific sets of genes. Recent advances in genome sequence information, bacterial chromosome modification and gene expression detection technology permit new approaches in out ongoing studies. Using microarray and gene fusion technology, we have demonstrated that many (~250) genes are controlled by RpoS, a primary regulator of adaptive genes in *Escherichia coli,* a bacterium that has long served as a model for regulation and metabolism. Because RpoS is a conserved regulator (found in many bacteria) and has been implicated in human, animal and plant disease processes, understanding the signals that activate this regulator will further our understanding of bacterium/host interaction. A second project in my laboratory, as described below, examines the role of vitamin C metabolism in mammals.

RpoS-regulated genes and RpoS regulation in Escherichia coli

Sarah Chiang, Alvin Choi, Daniel Gyewu, Ali Ibrihami, Mirella Younes

We have recently reported the culmination of an extended project in my lab to identify members of the RpoS regulon by a genetic screen that is based upon the differential levels of expression of β-galactosidase expression in wild type and RpoS mutant strains. In the course of this work, we identified, by phage isolation DNA sequencing, over 100 operon fusions that depend on the RpoS sigma factor for expression. Because many of the independent genes identified are members of operons, about 120 genes were found in total and further, since the mutant library we used was estimated to have hits to about half the genes in *E. coli,* the size of the RpoS regulon is likely ~200 genes, the number that is in fairly close agreement with the 200+ genes that we have found by microarray analysis (Patten et al. 2004).

Manipulation of RpoS levels itself may contribute to our understanding of which genes depend on RpoS directly for expression (as opposed to be indirectly controlled through an intermediate regulator). To directly alter cellular levels of RpoS, we have generated constructs that either over express (Chen and Schellhorn, 2003) or attenuate cellular levels of RpoS (Chen et al, 2003). Interestingly, mutations in the *rpoS* gene can be selected (and reverted) under specific conditions which has led us to propose that such mutations may function as a molecular switch to modulate expression of the large RpoS regulon.

Physiological Role(s) of RpoS regulated genes

Andrew Hughes, Daniel Li, Tao Dong, Susan Sullivan

As RpoS controls many seemingly-unrelated metabolic functions, understanding the individual physiological function of each gene is necessary to understand the adaptive process. Catalase regulation (Dong, Li), phosphate utilization (Dong) GABA utilization and regulation of genes of unknown function (Choi, Hughes) are being actively examined using common technologies (gene knockout, gene complementation, enzyme assays and gene

expression detection). We are also using mass spectrometry (chemical biology) to identify subtle changes in metabolite pools in bacterial strains carrying defined mutations.

Vitamin C metabolism

Daniel Li, Thuraya Shaban

Humans (and other primates) are unusual mammals because we lack a key enzyme required for the synthesis of vitamin C. The endogenous human gulonolactone oxidase gene is defective – having been inactivated by mutation about 40 million years ago. Since vitamin C is essential for life, why did we lose this function? To examine this, we cloned murine gulonolactone oxidase gene from a mouse liver cDNA library and used this to construct an adenovirus vector that can express the gulonolactone oxidase activity in human cells (Ha et al, 2004). This adenovirus vector should be useful in pre-clinical gene therapy to examine the role of endogenous vitamin C synthesis in antioxidant physiology of mammals that lack the enzyme (i.e. humans and guinea pigs). Vitamin C is of topical interest, not just because of its importance as an antioxidant, but because of recent findings that it may stimulate embryonic stem cell differentiation and that high affinity transport of this vitamin into essential for post-natal development (mouse models lacking the high affinity transporter die at birth).

Rama S. Singh

Population and evolutionary genetics, molecular evolution and speciation

Laboratory Personnel

Postdoctoral fellows: Wilfried Haerty, Santosh Jagadeeshan. Ph.D. Sanjay Hiremat, Carlo Artieri. Masters. Abha Ajuha, Manhal Younes; *Undergraduates.* Amanda Raben, Alicja Puchta, Sanaa Mahmood; *Lab Assistant.* Aaron Thomson

Funding

Natural Sciences and Engineering Research Council (2000-2006), Natural Sciences and Engineering Research Council Genomics Grant (2000-2006)

Over the last two decades, our laboratory has been focusing on understanding the genetic basis of speciation. We have used both Drosophila and Mammalian models in our investigations to understand and elucidate the genetic mechanisms underlying hybrid sterility and reproductive isolation.

In addition to trying to find out the molecular dynamics of SRR genes, we are also interested in finding out (1) if the evolution of SRR genes is linked to speciation, (2) if SRR genes in males and females, particularly those involved in fertilization, evolve through co-evolution, and (3) if SRR genes are more susceptible to environmental perturbation.

The genetic architecture of hybrid sterility:

One major line of research has focused on understanding and elucidating the genetic basis of Haldane's rule and the genetic architecture of hybrid sterility. Previous approaches to this problem in our laboratory involved the transfer of genetic material (genes, chromosomes) from one species into another. We have identified specific regions of chromosomes as well as a number of genes that may be involved in fertility breakdown in hybrids. This line of investigation is now being pursued using high-resolution microarray technology and comparative genomics to study the architecture of breakdown in gene expression in *Drosophila* hybrids. We are specifically examining the nature of breakdown in testis and ovaries to characterize fertility defects in hybrid males and females. We are now able to categorize genes that are commonly mis-expressed in all hybrids between species of the *D. melanogaster* clade; an important piece of information essential to our understanding of the functional basis of hybrid sterility (Fig 1). These data are now being used to characterize specific functional processes and gene-networks therein that may preferentially be involved in affecting sterility, infertility and inviability.

Faster evolution of Sex and Reproduction Related genes:

Another major line of investigation in our lab is the comparative and functional analysis of Rapidly Evolving Genes (REGs) and asking how rapid evolution relates to the process of speciation. We have been in the leading front and have shown that a) Sex and Reproduction Related (SRR) proteins and genes are evolving faster than non-sex and reproduction related genes (Fig2), b) the reproductive systems have higher proportion of REGs compared to non-reproductive systems and c) more recently we have results suggesting that that sex-specific proteins between very closely related species may have experienced accelerated rates of evolution either during or immediately following speciation. Using mouse and human systems, we have shown that a) sperm specific proteins are evolving rapidly compared to proteins in other tissues (also shown in *Drosophila*) b) sperm proteins on the X chromosome are evolving faster than those on autosomes and c) more recently we showed that there are a higher number of sex specific genes affecting male fertility compared to female fertility. We are conducting further detailed investigations

into how sex and reproduction related genes relate to the process of speciation and also we are also trying to find out Sex and Reproduction related genes are more susceptible to environmental perturbations.

Functional analysis of regulatory gene networks:

We are now focusing on investigating the functional significance these candidate genes in the context of the evolution of male and female infertility. We have also launched investigations to study how candidate gene regulatory networks are broken down in hybrids through the use of transgenic technology. We are also studying the evolution of gene interaction and gene network interaction in human systems, specifically in the context of understanding how brain functions in humans have evolved.

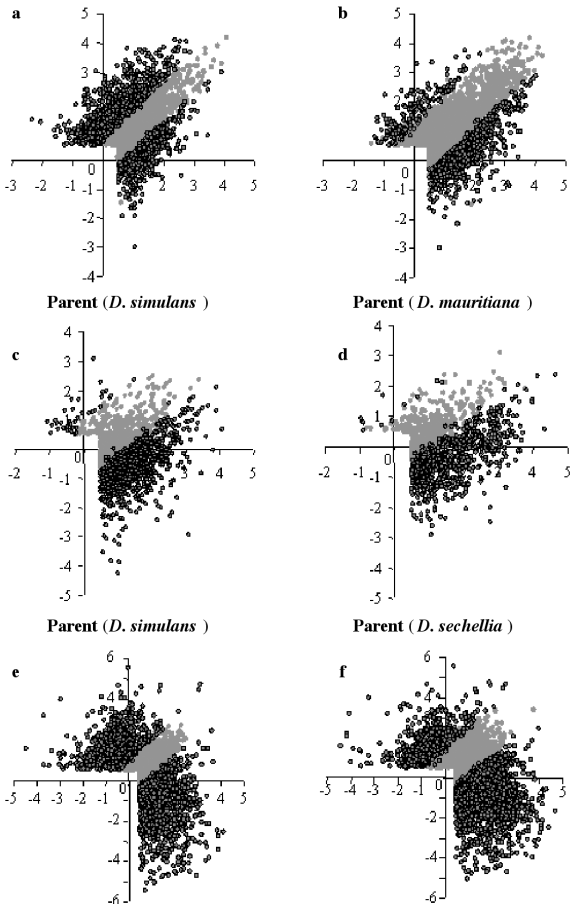


FIGURE 1: Comparison of gene expressions in parental and hybrid testes. a. *D. simulans* vs. hybrid (*D. simulans* females x *D. mauritiana* males). b. *D. mauritiana* vs. hybrid (*D. simulans* females x *D. mauritiana* males). c. *D. simulans* vs. hybrid (*D. simulans* females x *D. sechellia* males). d. *D. sechellia* vs. hybrid (*D. simulans* females x *D. sechellia* males). e. *D. simulans* vs. hybrid (*D. simulans* females x *D. melanogaster* males). f. *D. melanogaster* vs. hybrid (*D. simulans* females x *D. melanogaster* males). Misexpressed male-biased genes are represented in green, all other misexpressed in red, non-misexpressed genes in grey.

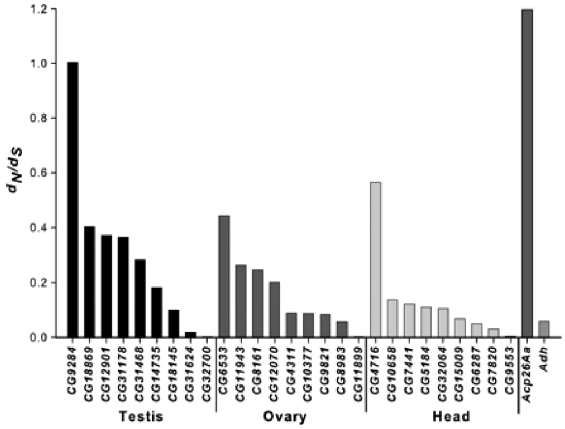
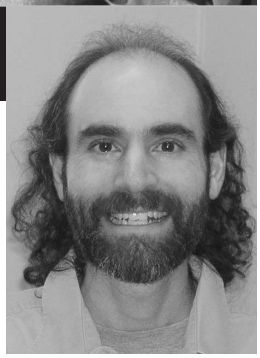


FIGURE 2: Divergence of candidate Rapidly Evolving Genes in testis, ovary and head between *D. melanogaster* and *D. simulans.* dN/dS indicates the proportion of amino acid changing substitutions relative to silent substitutions in a gene.

Jonathan Stone



Computational Biology conducted at multiple heirarchical levels

Laboratory Personnel

Ph.D. Students: Maria Abou Chakra, Marc Colangelo; *Undergraduate Students:* Shahriar Alam, Tahani Al-Rifai, David Cantelmi, Sarah Chahine, Teresa Domladovic, Sandy Faheim, Nancy Fairbairn, Marc Gauvin, Danya Konrad, Jason Mitakidis, Alexandra Pontefract, Parastoo Salehi, Jean Tien, Stephanie Yantsis, Marlena Zdelar

Research Collaborators

Mats Björklund (Uppsala University, Sweden), Brian Hall, (Dalhousie University, Canada), Greg Wray, (Duke University, USA)

Funding

Natural Sciences and Engineering Research Council (2003-2005), Canadian Foundation for Innovation (2004)

Projects involving search algorithms for DNA sequence motifs, gene regulation evolution, cancer growth and oncolytic viral treatment, psychrophile astrobiology, biological pattern formation, skeleton development and evolution, and population breeding structure were advanced.

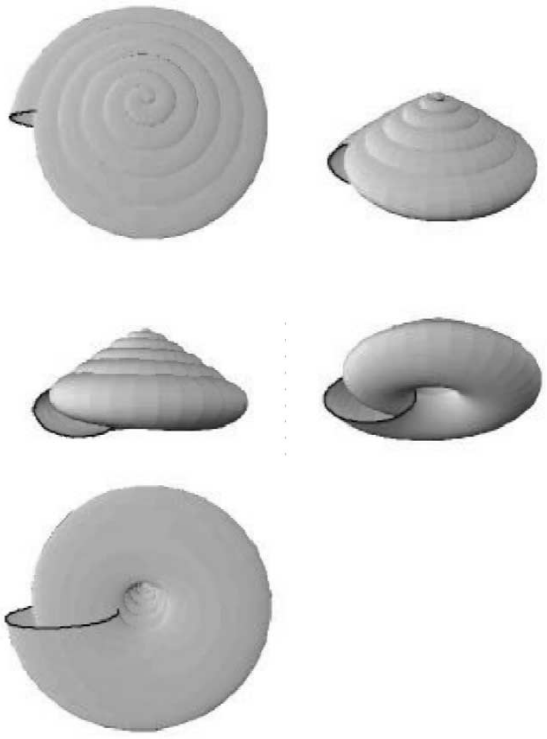


FIGURE: Computer-simulated sundial snail shell observed from different orientations

Elizabeth Weretilnyk

Plant abiotic stress tolerance; Metabolomics; Environmental Genomics; Chemical Biology

Laboratory Personnel

Ph.D. students: David Guevara, Michael BeGora; *M.Sc. students:* Jeffery Dedrick, Amber Gleason; *Undergraduate students:* Andrius Sestokas; *Technical Assistants:* K. Haines, Chris Wang; *Undergraduate lab assistant:* Ingrid Kassner

Research Collaborators

Christian Baron (McMaster University), Turlough Finan (McMaster University), G. Brian Golding (McMaster University), Peter Summers (McMaster University), J-P Xu (McMaster University), Brian McCarry (McMaster University), Trevor Charles (University of Waterloo), Barbara Moffatt (University of Waterloo), Gordon Gray (University of Saskatchewan)

Funding

Performance Plants (2003-2006), NSERC/AAFC Industrial Partner Support Program (2001-2005), NSERC Discovery Grant (2005-2009), Genomic analysis of soil microorganisms (2003-2006), Genome Canada (2003-2005), ORDCF (2003-2007)

My program is directed towards identifying environmental stress tolerance traits in plants using physiological, biochemical, metabolomic and genomic approaches. The molecular basis underlying environmental stress tolerance traits in plants is complex and our understanding of how plants survive (and even thrive) in adverse environments is very incomplete. We are also using metabolomics approaches to help identify functions of uncharacterized gene products in plants and bacteria.

With respect to plant abiotic stress, we have focused on two research objectives: 1) To examine the synthesis and accumulation of the compatible solute glycine betaine by plants subjected to osmotic stress. Our biochemical model has been spinach, a glycine-betaine accumulating plant. 2) In collaboration with G.B. Golding and B. McCarry (Chemistry, McMaster) and G. Gray and B.A. Moffatt (Saskatchewan and Waterloo, respectively), we are studying a highly stress tolerant native plant, *Thellungiella salsuginea.* This plant is a member of the Cruciferae family and is closely related to *Arabidopsis thaliana,* the genetic model plant whose genome has been completely sequenced, and canola which is Canada's most important oilseed crop. A limitation to using Arabidopsis to identify traits associated with environmental stress is that this plant has very little capacity to withstand cold, drought or saline conditions. By contrast, Thellungiella endures freezing temperatures, semiarid conditions and grows on saline and alkaline soils of the Yukon. We have been able to use and benefit greatly from the abundant genetic resources developed for research on Arabidopsis for our studies of stress tolerance in its extremophile relative. *(Dave Guevara, Jeff Dedrick and Ingrid Kassner)*

Choline serves as a precursor for glycine betaine in all multicellular plants studied to date. Despite the ubiquitous nature of choline, not all of the genes encoding enzymes responsible for its synthesis have been identified from plants (or non-plants). We are using functional complementation of a choline-requiring yeast mutant to clone genes involved in choline metabolism. By transforming the mutant with plasmids from an Arabidopsis cDNA library constructed in a yeast expression vector, we can identify cDNAs that "rescue" the yeast mutant by conferring the capacity for it to grow in the absence of added choline. At least two enzymes are S-adenosylmethionine-dependent methyltransferases and kinetic analyses of one such enzyme is underway. Comparisons of the

biochemical properties of these enzymes can identify how their activities contribute to plant growth under non-stress conditions and whether changes in their properties are required to accommodate glycine betaine accumulation under stress. (Michael BeGora and Amber Gleason)

We have analyzed the physiological response of Thellungiella to increasing salinity, to drought imposed by withholding water and during recovery of the plant when watering is resumed following drought. As it is impossible to replicate field conditions in growth cabinets, we have supplemented our comparisons with physiological measurements taken from plants growing in field sites in the Yukon. In all cases, plant tissues were harvested and RNA extracted to generate cDNA libraries and perform microarray analyses (under the direction of our collaborators at Waterloo). In our lab, metabolome profiles of well-watered and stressed plants have been obtained by gas chromatography/mass spectrometry and are being analyzed to identify metabolic phenotypes associated with stress tolerance. Information from these profiles will complement and add value to the information arising from our ongoing physiological and genomics studies with this plant. By all criteria, the physiological data indicates that Thellungiella is extremely drought and salt tolerant and we believe that this plant is as an excellent physiological and genetic model for future studies in plant tolerance to environmental stress. *(Dave Guevara, Jeff Dedrick and Karen Haines)*

Together with Peter Summers (McMaster), we are applying metabolomics approaches to identify the biological roles of genes encoding products of unknown function. We have extracted polar metabolites from bacteria cells and generated comprehensive metabolite profiles by gas chromatography/mass spectrometry that are analyzed using the software program "GASP" developed by Paolo Nuin (PDF, G.B. Golding, supervisor). GASP aligns comparable peaks from successive chromatography runs and allows the user to statistically analyze and display experimental results. The bioinformatics skills and data made available by this project will be readily applicable to metabolomic studies of virtually any organism from bacteria to man. *(K. Haines, A. Sestokas and C. Wang).*

Thellungiella grows on highly alkaline salt flats in the Yukon. In 2005 plants were harvested from a number of field sites for transcriptome and metabolome analysis by researchers at McMaster and Waterloo.

Photo by J. Dedrick

Chris Wood

The Physiology of Transport Processes and Metabolism, and the Aquatic Toxicology of Metals in Fish and Crustaceans

Laboratory Personnel

Postdoctoral Fellows: Dr. Patty Gillis, Dr. Natasha Franklin, Dr. Richard Smith, Dr. Fernando Galvez, Dr. Makiko Kajimura (joint with Dr. Grant McClelland), Dr. Tommy Tsui; *Ph.D. Students:* Michele Nawata, Carol Bucking, John Fitzpatrick (joint with Dr. Sigal Balshine); *M.Sc. Students:* Lara Alves, Adeola Ojo, Karen DeClerk, Monika Patel, Warren Green (joint with Dr. Greg Pyle), Tatiana Kozlova (joint with Dr. Jim McGeer); *Visiting Researchers:* Dr. Pierre Laurent, Dr Ibrahim Messad, Claudine Chevalier, Viviane Prodocimo; *Technicians:* Linda Diao, Sunita Nadella

Research Collaborators

Dr. Grant McClelland (McMaster University), Dr. Pat Chow-Fraser (McMaster University), Dr. Russell Bell (McMaster University), Dr. Jim Kramer (McMaster University), Dr. Colin Seymour (McMaster University), Dr. Carmel Mothersill (McMaster University), Dr Martin Grosell (University of Miami), Dr. Pat Walsh (University of Miami), Dr. Yuxiang Wang (Queens University), Dr. Colin Brauner (University of British Columbia), Dr. Jeff Richards (University of British Columbia), Dr. Pat Wright (University of Guelph), Dr. Michael Wilkie (Wilfrid Laurier University), Dr. Jim McGeer (Natural Resources Canada), Dr. Greg Pyle (Nipissing University), Dr. Ora Johannsson (DFO, Burlington), Dr. Alex Ip (University of Singapore), Dr. Kath Sloman (Plymouth University, UK), Dr Bernardo Baldisserrotto (Brazil), Dr. Adalto Bianchini (Brazil), Dr. Adalberto LuisVal (Brazil), Dr. Sue Clearwater (NIWA, New Zealand), Dr. Gudrun DeBoeck (University of Antwerp, Belgium)

Funding

Natural Sciences and Engineering Research Council Discovery Grant (2002-2007), Natural Sciences and Engineering Research Council, Collaborative Research and Development Grant (2005-2009), Industrial Consortium Co-funding of CRD grant – International Copper Association, Copper Development Association, Nickel Producers Environmental Research Association, International Lead-Zinc Research Organization , Noranda-Falconbridge, Teck Cominco, & Inco (2005-2009), International Copper Association Human Health Program Grant (2004-2005), Natural Sciences and Engineering Research Council Metals in the Human Environment Research Network Grant (2005-2010), Aquanet Research Grant (2005-2006), Canada Research Chair Program (2001-2008)

Our lab studies the basic mechanisms by which ions, nutrients, respiratory gases metabolic wastes, and acid-base equivalents are transported across environmental and internal surfaces in fish and crustaceans, and how these processes are impacted by environmental stressors. In our applied research program, the stressors of interest are waterborne and dietary metals, and our goal is to use data on physiological responses to develop models that can be used to generate more protective and cost-effective environmental regulations for metals. While our starting point is always basic mechanistic physiology, we use tools of molecular biology, proteomics, cell biology, organismic physiology, behavioral analysis, field studies, geochemistry, and modeling to address these questions.

A selection of ongoing projects in the laboratory is listed below:

(i) The role of the gastrointestinal system in ion and acid-base regulation in freshwater and marine fish

(ii) The mechanisms by which dietary metals (Cu, Zn, Ni, Cd, & Ag) are transported by the gastrointestinal tracts of freshwater fish, and the protective actions of naturally occurring cations (Ca, Na)

(iii) Urea transport, aquaporin function, ion and water balance, feeding metabolism, cocoon function and protein metabolism in aestivating lungfish

(iv) Ion and metal transport by reconstructed gill epithelia in primary culture in vivo

(v) The impact of feeding on urea and salt metabolism in ureo-osmotic elasmobranchs, and the role of the rectal gland in homeostasis

(vi) The impact of chronic waterborne and dietary metal exposure on behavioral responses to intraspecific chemical signals in fish

(vii) Ammonia transport processes in the freshwater fish gill

(viii) Metal uptake and depuration in daphnia and chironomids

(ix) Proteomic and molecular analysis of ionoregulatory proteins in the fish gill

(x) Analysis of the mechanism(s) by which natural organic matter ("NOM, DOC") alters the electrical and ion transporting properties of fish and daphnia gills, and its relationship to NOM composition.

(xi) Development of "Biotic Ligand Models" to predict water quality criteria that are protective against acute and chronic metal toxicity to a range of different fish and invertebrate species. Fig. 1 below illustrates one such model.

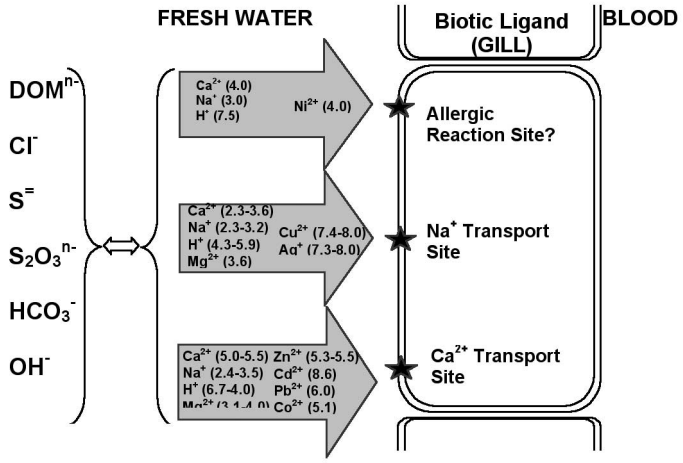


FIGURE: A Biotic Ligand Model showing the binding strengths (log K values) of various metals to the physiological sites of toxicity in the gills of freshwater rainbow trout *(Oncorhynchus mykiss)*. Log K values for competitive, protective binding by certain naturally occurring cations are also shown.

J. P. Xu

Molecular Ecology and Evolutionary Genetics of Microorganisms

Lab Personnel

PhD students: Zhun Yan, Sheng Sun; *M.Sc. students:* Mori Shahid; *Undergraduate students:* Eddie Dang, Lijun Wang, Ashlee Vincent, Ana Kobylinski; *Research associate:* Hong Guo

Research Collaborators

Dr. T. M. Finan (McMaster University), Dr. V. Chaturvedi (New York State Department of Health), Dr. J. Kronstad (University of British Columbia), Dr. Joe Heitman (Duke University), Dr. Christina Hull (University of Wisconsin-Madison)

Funding

Natural Sciences and Engineering Research Council, Discovery (2006-2010), Genome Canada (2003-2006), Premier Research Excellence Award (2002-2007)

The focus of our research is to understand the origins and maintenance of genetic variation in microorganisms, with a special emphasis on fungi. To achieve this goal, we examines microbial populations from the environment, clinics, and laboratory to address a variety of questions, including the rate and effect of spontaneous mutations on medically important traits; the spread of microbes in natural environments and human populations; and the origins of novel strains and species. Our research uses both molecular as well as microscopy and quantitative genetic tools.

The notable discovery from our lab this past year was the identification that sex in microorganisms entails a cost and that the cost was positively correlated to the sexuality. This was the first report of that interacting with sexual partners in facultative sexual microbes has a cost. This study was published in the journal Genetics. Among other places, it was featured in the Toronto Star.*

Our other discoveries include: (i) the identification of a large number of novel genes and DNA fragments among natural strains of the nitrogen-fixing bacterium Sinorhizobium meliloti (published in the journal Applied and Environmental Microbiology); (ii) the Cryptococcal outbreak on Vancouver Island was due to multiple recent migrations of strains; and (iii) the global population of a pathogenic yeast consists a few closely related clonal lineages (in press for Microbiology).

*(www.thestar.com/NASApp/cs/ContentServer?pagename=thestar/Layout/Article_Type1&c=Article&cid=1139611813276&call_pageid=970599119419)

CLA/Teaching Faculty

ASSISTANT PROFESSOR

Kimberley Dej

Regulation of chromosome segregation in *Drosophila melanogaster;* Dynamics of chromosome condensation and sister-chromatid cohesion in mitosis and meiosis

Lovaye Kajiura

Organismal ecology, resource allocation and life history, impact of biotechnology on physiology, endocrinology, nutrition, and behaviour, analysis of the transgenic rat growth hormone mouse model

Peter Summers

Genomics; large-scale screens for gene function by observing changes to metabolic and phenotypic profiles in response to altered gene expression

Kimberley Dej

Regulation of chromosome dynamics during mitosis and meiosis

Research Interests

Cells reproduce by a highly coordinated process of cell division. The integrity of the genome is contingent upon the faithful replication of the DNA and the accurate segregation of the duplicated copies of the genome into the two daughter cells. I am studying the pathways that ensure that sister chromatids separate precisely at anaphase of mitosis. Separation too early or too late can lead to aneuploidy and chromosome breakage. Research has correlated the occurrence of aneuploidy with tumorigenesis.

During mitosis, the large genomic DNA molecules must be compacted so that they can be easily transported on the mitotic spindle. This requires the process of chromosome. Condensation factors form an integral part of the mitotic chromosome, yet the mechanisms of condensation remain elusive. One important component appears to be the pentameric complex called the condensin complex. In all species studied, condensin proteins are associated with condensing chromosomes during mitosis and are involved in proper chromosome dynamics including the segregation of sister chromatids. My postdoctoral studies focussed on a genetic analysis of one subunit of the condensin complex in Drosophila called dCAP-G. These studies revealed dramatic defects in the resolution of sister chromatids and the segregation of chromatids at anaphase. Surprisingly, chromosome compaction was not altered dramatically, however, we found that chromosome condensation is disrupted when DNA replication is absent prior to mitosis.

Genetic analyses of the condensin complex have revealed in yeast and in C. elegans that the condensin complex has numerous varied functions during interphase. Our studies in Drosophila showed that dCAP-G and perhaps the entire complex is involved in the regulation of gene expression in heterochromatic regions of the genome. Currently, studies of dCAP-G are focused on its role in chromosome condensation and chromosome segregation in the meiotic cell divisions of the germ line cells in Drosophila. In addition, we have identified several other genes that are required for the separation of sister chromatids in both mitosis and meiosis, at least one of which interacts genetically with dCAP-G.

Lovaye Kajiura

Organismal ecology, resource allocation and life history, impact of biotechnology on physiology, endocrinology, nutrition, and behaviour

I am the **Level 1 Biology Undergraduate Course Coordinator** and hold a **Teaching Faculty** appointment in the Department of Biology. I am involved in coordinating and teaching the following courses:

BIOLOGY 1A03 and BIOLOGY 1AA3

These courses are designed for students who intend to specialize in Science programs and are required for many higher level courses in the Faculty of Science. The primary goal of these courses is to prepare students academically for subsequent, specialized Biology and Biochemistry courses and to ensure that students acquire skills essential for upper-level biology courses and biology-related fields of study.

BIOLOGY 3Q03

This course gives students theoretical and practical experience with teaching methods in biology and provides an introduction to scientific writing and presentation focusing on cellular and molecular biology concepts and topics. Lecture topics include the following.

Roles of Peer Mentors and Mentees, Ice Breaker Techniques, Presentation Styles and Effective Communication Skills, Learning Styles and Intelligences, Motivating and Inspiring Others, Improving Organization and Time Budgeting Strategies, Lesson Planning, Setting Goals, Evaluating Knowledge and Improving Your Performance, Scientific Writing; Mentoring and Teaching Dossiers, Dealing with Discouraged Individuals, Generating Discussions – Incorporating Facts, Concepts, and Applications

BIOLOGY 3QQ3

This course gives students theoretical and practical experience with teaching methods in biology and provides an introduction to scientific writing and presentation focusing on evolutionary and ecological concepts and topics. Lecture topics include the following.

The Roles of Peer Mentors and Mentees, Motivating and Inspiring Students, Ice Breaker Techniques, Mentoring/Teaching Dossiers, Creating Teaching Models and Aids, Lesson Planning, Evaluating Knowledge: Creating Factual, Conceptual, and Application Questions, Organization: Study Habits and Techniques, Effective Goal Setting, Learning Styles and Intelligences, Designing surveys and evaluations for student feedback, Generating Interactive and Open-Ended Questions, Effective Communication Skills and Presentation Styles, Dealing with Discouraged Students, Effective Listening Skills, Improving Your Performance

Peter Summers

Metabolism in Plants and Bacteria

Thanks to many genome sequencing projects, we know the exact number and the exact sequence of every openreading-frame in many organisms. With a variable degree of confidence these sequences have been annotated with a biological function based on similarities to other sequences. However, to identify the exact function of the proteins coded by DNA, further genetical and biochemical-supporting evidence is often required. I work on the metabolism of carbohydrates, amino acids and secondary compounds. Jointly with other researchers at McMaster we are using biochemical techniques to understand the specific biological role of proteins in plants and bacteria whose functions are currently not fully known. Techniques used range from simple enzymatic assays up to gas chromatography/mass spectrometric analysis of whole extracts of metabolites from an organism. When the biochemical evidence is analyzed in conjunction with genetical and microarray data, we hope that we can add improved identities to the thousands of genes currently labelled as “unknown”, “hypothetical” or “putative”.

Adjunct and Associate Members

ADJUNCT MEMBERS

Gary Chiang, Professor
Department of Biology, Redeemer University College, Ancaster, ON, Canada

My current research involves various aspects of insect physiology. At McMaster University, I am working in collaboration with the O'Donnell laboratory to study the transport of organic anions by Malpighian tubules in a variety of insects. At Redeemer University College, I am using electrophysiology to describe the neuroendocrine regulation of egg production and the motor control of egg-laying in the blood-feeding insect, *Rhodnius prolixus.* I am also applying morphological and electrophysiological techniques to examine the physiology of the western conifer seed bug, *Leptoglossus,* a plant-feeding bug that is closely related to *Rhodnius.*

David A. Galbraith, Assistant Professor
Department of Research and Natural Lands, Royal Botanical Gardens, Hamilton, ON , Canada

I am interested in evolutionary and ecological consequences of the activities of our own species, and interactions among animal and plant species and communities and human populations. To date most of my research has been on the ecology, conservation biology and population biology of reptiles and plants. These groups some important practical and theoretical constraints. Both plants and reptiles are relatively sedentary compared to mammals, birds, and even many insects, and both groups include members which are very long-lived. Both reptiles and plants have been systematically under-represented in public perception of conservation priorities. Plants are often viewed either as a source of raw materials or as habitat for more interesting animals. Reptiles have suffered at best from benign ignorance and at worst from terror and fear. Both reptiles and plants offer opportunities to study the structuring of population genetic information at varying scales, especially as it relates to conservation issues. At present I am collaborating with Prof. Brad White at Trent University on the population genetics of endangered wood poppies *(Stylophorum diphyllum).* I am involved in the development of research and conservation programs at botanical gardens, and in promoting the role of these institutions in support of sustainable development and biodiversity initiatives.

Pierre Laurent, Professor
Department de Morphologie Fonctionnelle et ultrastructurale des Adaptations, Center d'Ecologie et de Physiologie Energetique, CNRS, Strasbourg, France

As a cell biologist I have long been interested in the structure to function relationship in the fish gill in relation to environmental variables, particularly in euryhaline species. In the current project Chris Wood and I combined our complementary expertise and focussed on some cellular responses of ionic regulation during the rapid transfer of the estuarine killifish, *Fundulus heteroclitus,* from sea to fresh water. We are investigating the links between the populations of the different cell types present in the gill and functional changes in branchial ion transport machinery. Experiments combine a range of classical and modern morphological techniques, as well as cell turnover, apotosis, molecular expression, and ion transport studies.

Gary Leppard, Professor
National Water Research Institute, Aquatic Ecosystem Management Research Division, Canada Center for Inland Waters, Burlington, ON

My research interests are in the areas of environmental biochemistry and microbiology. I have been studying the roles of natural and engineered aquatic aggregates (flocs, biofilms) in the transport and fate of contaminants. In concert with these activities, I have developed electron-optical means to analyze the colloidal structure of natural dispersing agents, riverine biofilms and the flocs of water treatment tanks. My research interests have extended into biogeochemistry, wastewater treatment, materials science, X-ray spectromicroscopy and the activities of natural microbial consortia.

James Pringle, Associate Professor
Royal Botanical Gardens, Hamilton, ON, Canada

My work focuses on systematics of the flowering plants, including naming and description of new species, revised classifications, improved identification guides, nomenclature, geographic distribution, and spread of invasive species. My research involves Gentianaceae of the Americas, Syringa, and the history and biography of natural history and field biology. I am also interested in nature interpretation, and teach the course in systematics of the flowering plants in the Ontario Universities Program in Field Biology.

ASSOCIATE MEMBERS

Sigal Balshine, *Assistant Professor,* Psychology, McMaster University

Richard G. Butler, *Professor,* Patholology, McMaster University

Martin Daly, Professor, Psychology, McMaster University

David Earn, *Assistant Professor,* Mathematics and Statistics, McMaster University

Margaret Fahnestock, *Associate Professor,* Psychiatry, McMaster University

Bennett G. Galef, *Professor,* Psychology, McMaster University

Ashok K. Grover, *Professor,* Medicine, McMaster University

Hendrik N. Poinar, *Assistant Professor,* Anthropology, McMaster University

Carl Richards, *Associate Professor,* Pathology, McMaster University

Henry Szechtman, *Professor,* Psychiatry, McMaster University

Eva S. Werstiuk, *Professor,* Medicine, McMaster University

Professors Emeriti/Retired Faculty

Stanley T. Bayley

Douglas Davidson (Adjunct member)

Douglas M. Davies

Allan D. Dingle (Adjunct member)

Frank L. Graham (Distinguished University Professor)

Doris E.N. Jensen

Kenneth A. Kershaw

John Lott

Richard A. Morton (Adjunct member)

Stanley Mak

B. Ann Oaks

Ludvik A. Prevec (Adjunct member)

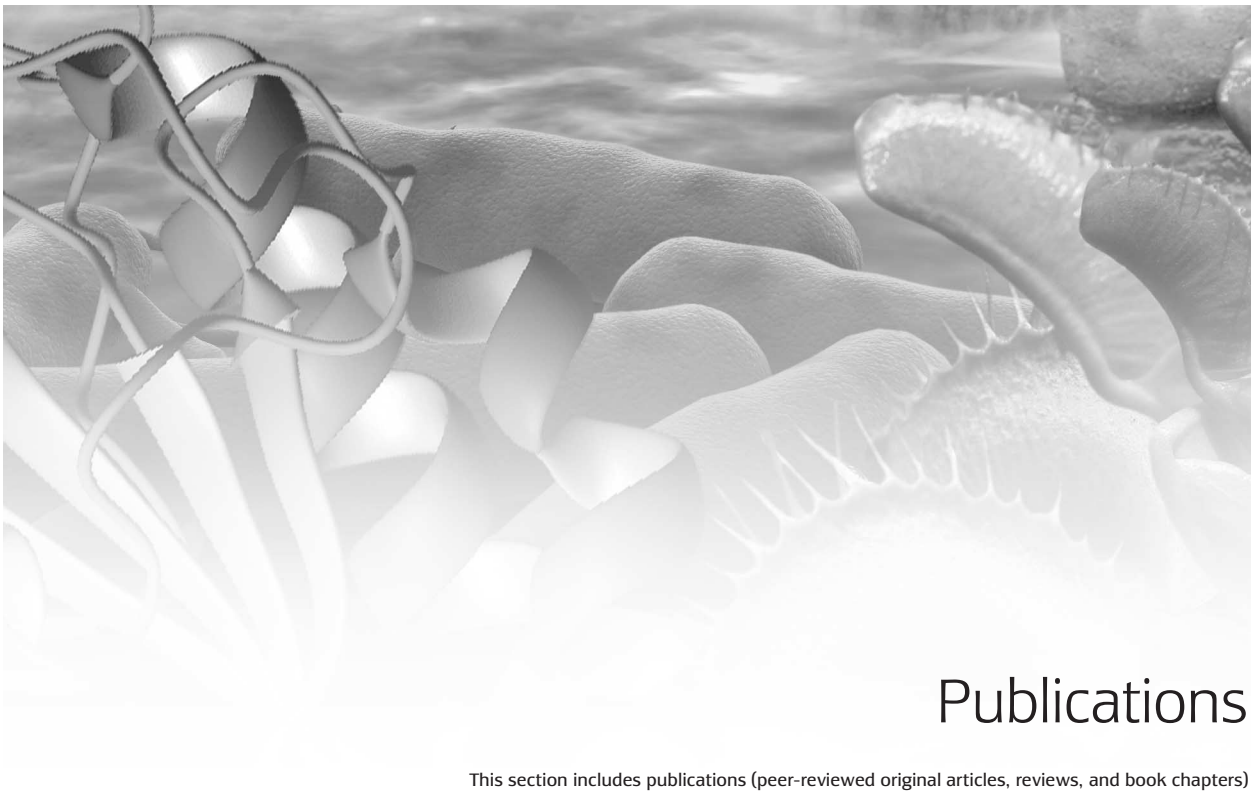
George J. Sorger

François Takahashi

Stephen F.H. Threlkeld

Jean E.M. Westermann

Bradley N. White



Publications

This section includes publications (peer-reviewed original articles, reviews, and book chapters) that have been published or are currently in press. Papers have been listed alphabetically based upon the first author. The names of lab PIs have been bolded.

Baldisserotto, B., J.M. Chowdhury, and **C.M. Wood.** 2005. Effects of dietary calcium and cadmium on cadmium accumulation, calcium and cadmium uptake from the water, and their interactions in juvenile rainbow trout. *Aquat. Toxicol.* 72 : 99 -117.

Baron, C. 2005. From bioremediation to biowarfare: On the impact and mechanism of type IV secretion systems. *FEMS Microbiol. Lett.* 253: 163-170.

Beisner B.E., J. Hovius, A. Hayward, T. N. Romanuk and **J. Kolasa.** 2005. Environmental productivity and biodiversity effects on colonization: Evidence for a sampling effect in rock pool invertebrate communities. *Ecological Invasions* (accepted)

Bianchini, A., R.C. Playle, **C.M. Wood,** and P.J. Walsh. 2005. Mechanism of acute silver toxicity in marine invertebrates. *Aquat. Toxicol.* 72: 67-82.

Bianchini, A., C. Rouleau, and **C.M. Wood.** 2005. Silver accumulation in Daphnia magna in the presence of reactive sulphide. *Aquat. Toxicol.* 72, 339–349.

Bijelic, G. and **M.J. O'Donnell.** 2005. Diuretic factors and second messengers stimulate secretion of the organic cation TEA by the Malpighian tubules of *Drosophila melanogaster. J Insect Physiol.* 51,267-275.

Bijelic, G., N. Kim, and **M.J. O'Donnell.** 2005. Effects of dietary or injected organi cations on larval *Drosophila melanogaster:* Mortality and elimination of tetraethylammonium from the hemolymph. *Archiv. Insect. Biochem. Physiol.* 60(2), 93-103.

Bucking, C. and **C.M. Wood.** 2005. Renal regulation of plasma glucose in the freshwater rainbow trout. *J. Exp. Biol.* 208 : 2731-2739.

Bucking, C.P. and **C.M. Wood.** 2005 Does urea reabsorption occur via the glucose pathway in the kidney of the freshwater rainbow trout? *Fish Physiol. Biochem.* 30: 1-12.

Bulmer, J.T., N. Zacal, and **A.J. Rainbow.** 2005 Persistent cisplatin-induced DNA damage in active genes activates the Jun N-terminal kinase and correlates with cisplatin sensitivity in human cells. *Cancer Chemotherapy and Pharmacology,* 56, 189-198.

C.E. Wong, Y. Li, B.R. Whitty, C. Diaz-Camino, S.R. Akhter, J.E. Brandle, **G.B. Golding, E.A. Weretilnyk,** B.A. Moffatt and M. Griffith, 2005. Expressed sequence tags from the Yukon ecotype of Thellungiella reveal that gene expression in response to cold, drought and salinity shows little overlap. *Plant Molecular Biology* 58:561-574.

C.Rusterucci, Z. Zhao, K.Haines, D.Mellersh, M. Neumann, **R.K. Cameron.** Age-Related Resistance to Pseudomonas syringae pv tomato is associated with the transition to flowering in Arabidopsis and is effective against Peronospora parasitica in a salicylic acid-independent manner. *Physiological & Molecular Plant Pathology,* 66: 222-231, 2005.

Campanucci, V.A. and **C.A. Nurse.** 2005. Biophysical characterization of whole-cell currents in O2-sensitive neurons from the rat glossopharyngeal nerve. *Neuroscience* 132: 437-451.

Campanucci, V.A., S.Brown, K. Hudasek, I. O'Kelly, **C.A. Nurse,** and I.M. Fearon. 2005. O2-sensing by recombinant THIK-1 background K+ channels heterologously expressed in HEK293 cells. *Neuroscience* 135: 1087-1094.

Chowdhury, M.J., B. Baldisserotto, and **C.M. Wood.** 2005 Tissue-specific cadmium and metallothionein levels in rainbow trout chronically acclimated to waterbourne or dietary cadmium. *Arch. Environ. Con. Tox.* 48: 381-390.

Chow-Fraser, P. 2005. Ecosystem response to changes in water level of Lake Ontario marshes lessons from the restoration of Cootes Paradise Marsh. *Hydrobiologia.* 539:189–204

Chow-Fraser, P. 2006. Development of the Wetland Water Quality Index for assessing the quality of Great Lakes coastal wetlands. In: *"Coastal Wetlands of the Laurentian Great Lakes: Health, Habitat and Indicators"* Eds Simon and T.P., Stewart. (In press)

Chow-Fraser, P., K. Kostuk, T. Seilheimer, M. Weimer, T. MacDougall, Theÿsmeÿer. 2006. Effect of wetland quality on sampling bias associated with two fish survey methods for coastal wetlands of the lower Great Lakes. In: *"Coastal Wetlands of the Laurentian Great Lakes: Health, Habitat and Indicators"* Eds Simon and T.P., Stewart. (In press)

Defossez, P.A., K.F. Kelly, G. Filion, F. Magdinier, H. Menoni, C.L. Nordgaard, **J.M. Daniel,** and E. Gilson. The human enhancer-blocker CTCF interacts with the transcription factor Kaiso. 2005 *J. Biol. Chem.* 280: 43017-43023.

Donini A. and **M.J. O'Donnell.** 2005. Analysis of Na^+, Cl^-, K^+, H^+ and NH_4^+ concentration gradients adjacent to the surface of anal papillae of the mosquito Aedes aegypti: application of self-referencing ion-selective microelectrodes. J Exp Biol. 208, 603-610.

Donini, A., M.L. Patrick, G. Bijelic, R.J. Christensen, J.P. Ianowski, M.R. Rheault, and **M.J. O'Donnell.** 2005. Secretion of water and ions by Malpighian tubules of larval mosquitoes: effects of diuretic factors, 2nd messengers and salinity. Physiological and Biochemical Zoology *(accepted)*

Evans, B. J., D. B. Kelley, D. J. Melnick, and D. C. Cannatella. 2005. Evolution of RAG-1 in polyploid clawed frogs. *Molecular Biology and Evolution* 22(5):1193-1207.

Franklin, N.M., C.N. Glover, J.A. Nichol, and **C.M. Wood.** 2005 Calcium/cadmium interactions at uptake surfaces in rainbow trout: waterborne versus dietary routes of exposure. Environ. Toxicol. Chem. 24: 2954-2964.

Fuller, M., T.N. Romanuk, and **J. Kolasa.** 2005. Community structure and metacommunity dynamics of aquatic invertebrates: a test of the neutral theory. Community Ecology. 6: 229-240.

G. Zhu, **G.B. Golding,** and A.M. Dean, 2005. Towards reconstructing an ancient adaptive event. Science 307:1279-1282.

Gill, S.A., M.J. Vonhof, B.J.M. Stutchbury, E.S. Morton, and **J.S. Quinn.** 2005. No evidence for acoustic mate-guarding in duetting buff-breasted wrens *(Thryothorus leucotis).* Behav. Ecol. and Sociobiol.57: 557-565.

Gillis, P., C.M. Wood, J.F. Ranville, P.E. Ross, and **P. Chow-Fraser.** 2006. Bioavailability of sediment-associated Cu and Zn to *D. magna. (Accepted in Aquatic Toxicology).*

Gillis, P.L., P. Chow-Fraser, J.F. Ranville, P.E. Ross, and **C.M. Wood.** 2005. Daphnia need to be gut cleared too: The effect of exposure to and ingestion of metal-contaminated sediment on the gut clearance patterns of *D. magna.* Aquat. Toxicol. 71: 143 -154.

Glover, C., E.F. Pane, and **C.M. Wood.** 2005 Humic substances influence sodium metabolism in the freshwater crustacean *Daphnia magna.* Physiol. Biochem. Zool. 78: 405-416.

Glover, C.N. and **C.M. Wood.** 2005 Physiological characterization of a pH- and calcium dependent sodium uptake mechanism in the freshwater crustacean, *Daphnia magna.* J. Exp. Biol. 208 : 951 – 959.

Glover, C.N. and **C.M. Wood.** 2005 Physiological interactions of silver and humic substances in *Daphnia magna:* effects on reproduction and silver accumulation following an acute silver challenge. Comp. Biochem. Physiol. C. 139 : 273-280.

Glover, C.N. and **C.M. Wood.** 2005. Accumulation and elimination of silver in *Daphnia magna* and the effect of natural organic matter. Aquat. Toxicol. 73 : 406-417.

Glover, C.N. and **C.M. Wood.** 2005. The disruption of *Daphnia magna* sodium metabolism by humic substances: mechanisms of action and effect of humic substance source. Physiol. Biochem. Zool. 78: 1005-1016.

Glover, C.N., R.C. Playle, and **C.M. Wood** 2005. Heterogeneity of natural organic matter amelioration of silver toxicity to *Daphnia magna:* Effect of source and equilibration time. Environ. Toxicol. Chem. 24:2934-2940.

Glover, C.N., S. Sharma, and **C.M. Wood.** 2005. Heterogeneity in physicochemical properties explains differences in silver toxicity amelioration by natural organic matter to *Daphnia magna.* Environ.Toxicol. Chem. 24:2954-2964.

Grosell, M., **C.M. Wood.** Wilson, R.W., Bury, N.R., Hogstrand, C., Rankin,C., Jensen, F.B. 2005 Active bicarbonate secretion plays a role in chloride and water absorption of the European flounder intestine. Am. J. Physiol. 288 R 936 - 946.

Guo, H, S, Sun, **T.M. Finan, J. Xu.** 2005 Novel DNA sequences from natural strains of the nitrogen-fixing symbiotic bacterium *Sinorhizobium meliloti.* Applied and Environ. Microbiol. 71:7130-8.

Hao, W. and **G.B. Golding.** 2006. The fate of laterally transferred genes: Life in the fast lane to adaptation or death. Genome Research *(in press).*

Hao, W. and **G.B. Golding.** 2006. Asymmetrical Evolution of Cytochrome bd Subunits. J. Mol. Evol. *(in press)*

Hassan, J., B. Iyengar, N. Scantlebury, V.R. Moncalvo, **A.R. Campos.** 2005. The photic input pathways that mediate the *Drosophila* larval response to light and circadian rhythmicity are developmentally related but functionally distinct. J Comp Neurol 481::266-275

Höppner, C., A.Carle, D. Sivanesan, S. Hoeppner, and **C. Baron.** 2005 The putative lytic transglycosylase VirB1 from *Brucella* suis interacts with the type IV secretion system core components VirB8, VirB9 and VirB11. Microbiology 151: 3469-3482

Huntley, M., S. Mahmood and **G.B. Golding,** 2005. Simple sequence in proteins. Genome 48: 291-301.

Jagadeeshan S, **R.S. Singh.** 2005 Rapidly evolving genes of Drosophila: differing levels of selective pressure in testis, ovary, and head tissues between sibling species. Mol Biol Evol. 22(9): 1793-801.

Jonz, M.G. and **C.A. Nurse.** 2006. Ontogenesis of oxygen chemoreception in aquatic vertebrates. Respiratory Physiology & Neurobiology. *(In press)*

Jonz, M.G. and **C.A. Nurse.** 2005. Development of oxygen sensing in the gills of zebra fish. J. Exp. Biol. 208: 1537-1549.

Jonz, M.G. and **C.A. Nurse.** 2005. Fishing for O2-chemoreceptors in vertebrates. Physiol. News. 58: PN39-PN40

Kajimura, M. P. J. Walsh, T. P. Mommsen and **C.M. Wood.** 2005. The dogfish shark (Squalus acanthias) increases both hepatic and extra-hepatic ornithine –urea cycle enzyme activities for nitrogen conservation after feeding. Physiol. Biochem. Zool. *(In press)*

Kamunde, C., S. Niyogi, S., and **C.M. Wood.** 2005. Interaction of dietary sodium chloride and waterborne copper in rainbow trout: sodium and chloride homeostasis, copper homeostasis, and chronic copper toxicity. Can J. Fish. Aquat. Sci. 62: 390-399.

Kidd, S.E., H. Guo, K. Bartlett, **J. Xu,** J.W. Kronstad. 2005. Comparative gene genealogies indicate that two clonal lineages of *Cryptococcus gattii* in British Columbia resemble strains from other geographical areas. Eukaryotic Cell. 4, 1629-1638

Kjoss, V. A., M. Grosell, and **C.M. Wood.** 2005. The influence of dietary Na on Cu accumulation in juvenile rainbow trout exposed to combined dietary and waterborne Cu in soft water. Arch. Environ. Con. Tox. 49: 520-527.

Kjoss, V.A., C.N. Kamunde, S. Niyogi, M. Grosell, and **C.M. Wood.** 2005. Dietary Na does not reduce dietary Cu uptake by juvenile rainbow trout. J. Fish Biol. 66: 468-484.

Kjoss, V.A., **C.M. Wood,** and D.G. McDonald. 2005. Effects of different ligands on the bioaccumulation and subsequent depuration of dietary Cu and Zn in juvenile rainbow trout, *Oncorhynchus mykiss.* Can J. Fish. Aquat. Sci. *(In press).*

Kolasa J. and S.T.A. Pickett. 2005. Changing academic perspectives of ecology – a view from within. In (M. Mappin and E. Johnson, eds), Environmental Education or Advocacy: Perspectives of Ecology & Education in Environmental Education. Cambridge University Press. pp.50-71

Kolasa, J. 2005. A community ecology perspective on variability in complex systems: The effects of hierarchy and integration. Ecological Complexity *(in press)*

Kolasa, J. 2005. A personal perspective on discovery. Review of L. Legendre (2004) Scientific research and discovery: process, consequences and practice. Excellence in Ecology 16. International Ecology Institute, Oldendorf/Luhe

Kolasa, J. 2005. Complexity, system integration, and susceptibility to change: biodiversity connection. Ecological Complexity 2 2005 431–442

Kolasa, J. and T.N. Romanuk. 2005. Assembly of unequals in the unequal world of a rock pool metacommunity. In (M. Holyoak, M. A. Leibold and R. D. Holt), Metacommunities: spatial dynamics and ecological communities. University of Chicago Press

Lan, L. and **J. Xu.** Multiple gene genealogical analyses suggest divergence and recent clonal dispersal in the opportunistic human pathogen *Candida guilliermondii.* Microbiology. *(In press)*

Leader, J.P. and **M.J. O'Donnell.** 2005.Transepithelial transport of fluorescent p-glycoprotein and MRP2 substrates by insect Malpighian tubules: Confocal microscopic analysis of secreted fluid droplets. J. Exp. Biol. 208, 4363-4376.

LeMoine, C.M.R., **G.B. McClelland,** Lyons, CN, Mathieu-Costello, O, and Moyes, CD. Control of mitochondrial gene expression in the aging rat myocardium. Biochem. Cell. Biol. *(In Press)*

Lemon J.A., D.R. Boreham, **C.D. Rollo.** 2005. A complex dietary supplement extends longevity of mice. J. Gerontology A Biol. Sci. Med. Sci. 60A:275-279.

Liu, L. and **A.J. Rainbow.** 2005 Pre–UV-treatment of cells results in enhanced host cell reactivation of a UV damaged reporter gene in CHO-AA8 Chinese hamster ovary cells but not in transcription-coupled repair deficient CHO-UV61 cells. Bioscience Reports, 24, 559-576.

Lougheed, V.L. and **P. Chow-Fraser.** 2005. The distribution of zooplankton in coastal wetland complexes of Lake Erie: association with macrophytes and water quality. Proceedings of the Lake Erie Millenium Workshop, Windsor, ON, April 26-28, 1999. *(In press)*

MacDonald, D., K. VanCrey, P. Harrison, P.K. Rangachair, J. Rosenfeld, C. Warren, and **G. Sorger,** Ascaridole-less infusions of Chenopodium ambrosioides contain a nematocide(s) that is (are) not toxic to mammalian smoothe muscle. J. Ethnopharmacol. 92: 215-221.

Macedo, R., **J.S. Quinn** and M. Lima. Reproductive skew and individual strategies: Infanticide or Cooperation? Acta Ethologica. *(In press).*

MacLellan S, L. A. MacLean, R. Zaheer, and **T.M. Finan.** 2006. Promoter prediction and structure in the alpha-proteobacteria Microbiology *(under review)*

MacLellan, S, A.M. MacLean and **T.M. Finan.** 2006. Promoter prediction in the rhizobia. Microbiology 152:1751-63.

MacLellan, S, L. Smallbone, C. Sibley and **T.M. Finan.** 2005. The expression of a novel antisense gene mediates incompatibility within the large *repABC*-family of α proteobacterial plasmids. Molecular Microbiology 55:611-23.

MacMullin, A. and **J. R. Jacobs.** 2006. Slit Coordinates Cardiac Morphogenesis in Drosophila, Dev. Biol. *(in press).*

Matsuo, A.Y.O., **C.M. Wood,** and A.L.Val. 2005 Effects of copper and cadmium on ion transport and gill metal binding in the Amazonian teleost tambaqui *(Colossoma macropomum)* in extremely soft water. Aquat. Toxicol. 74: 351-364.

McClelland, G.B., A. Dalziel, N. Fragoso, and C.D. Moyes. 2005 Muscle remodeling in relation to blood supply: implications for seasonal changes in mitochondrial enzymes J. Exp. Biol. 208: 515-522

Moncalvo, V.G. R., **A.R. Campos.** Genetic dissection of trophic interactions in the larval optic neuropil of *Drosophila melanogaster.* 2005 Dev. Biol. 286: 549-558.

Morgan, T.P., C.M. Guadagnolo, M. Grosell, and **C.M. Wood.** 2005. Effects of water hardness on the physiological responses to chronic waterborne silver exposure in early life stages of rainbow trout *(Oncorhynchus mykiss).* Aquat. Toxicol. 74: 333-350.

Morgan, T.P., C.M. Guadagnolo, M. Grosell, and **C.M. Wood.** 2005. Effects of water hardness on toxicological responses to chronic waterborne silver exposure in early life stages of rainbow trout *(Oncorhynchus mykiss).* Environ. Toxicol. Chem. 24 :1642-1647.

Musters, H., M.A. Huntley, and **R.S. Singh.** 2005. A Genomic Comparison of Faster-Sex, Faster-X, and Faster-Male Evolution between Drosophila melanogaster and Drosophila pseudoobscura. J. Mol. Evol.

Niyogi,S., C.N. Kamunde, and **C.M. Wood.** 2005 Food selection, growth, and physiology in relation to dietary sodium content in rainbow trout (Oncorhynchus mykiss) under chronic waterborne Cu exposure. Aquat. Toxicol. *(In press).*

Nurse, C.A. 2005. Peripheral chemoreceptors: Sensors of metabolic status. In: "Pharmacology and Pathophysiology of the Control of Breathing: eds. Ward, D.S., Dahan, A., Teppema, L., Marcel Dekker Inc., N.Y. Taylor and Francis Informa. N.Y. VOP 202: 1-19.

Nurse, C.A. 2005. Neurotransmission and neuromodulation in the chemosensory carotid body Autonom. Neurosci: Basic & Clinical 120: 1-9.

Nurse, C.A., J. Buttigieg, R. Thompson, M. Zhang, and E. Cutz. 2005. O2-sensing in neuroepithelial and adrenal chromaffin cells. in: *"Signalling pathways in acute oxygen sensing".* Wiley, Chichester (*Novartis Foundation Symposium* 272: p106-118)

O'Donnell M.J. and M.R. Rheault. 2005 Ion-selective microelectrode analysis of salicylate transport by the Malpighian tubules and gut of *Drosophila melanogaster.* J Exp Biol. 208, 93-104.

Pane, E.F., C. Bucking, M. Patel, and **C.M. Wood.** 2005. Renal function in the freshwater rainbow trout *(Oncorhynchus mykiss)* following acute and prolonged exposure to waterborne nickel. Aquat. Toxicol. 72 : 119 -133.

Papaconstantinou M., Y.Wu, H.N. Pretorius, N. Singh, G. Gianfelice, R.M. Tanguay, **A.R. Campos,** and **P.A. Bedard.** 2005. Menin is a regulator of the stress response in *Drosophila melanogaster.* Mol. Cell. Biol. 25: 9960-9972.

Pitsikas, P., M.A. Francis, and **A.J. Rainbow.** 2005 Enhanced reactivation of a UV-damaged reporter gene in pre-UV-treated cells is delayed in Cockayne syndrome cells. J. Photochemistry and Photobiology B: Biology, 81, 89-97.

Rainbow, A.J., P. Pitsikas, C. Caney, I. Boszko, B.C. McKay, and M.A. Francis. 2005. Reactivation of UV-damaged viruses and reporter genes in mammalian cells. In: Regen Drouin, Evelene Sage and Mahmoud Roubhia (Volume Eds.). From DNA photolesions to mutations, skin cancer and cell death. Donat-P. Hader, Giulio Jori (Series Eds.). Comprehensive Series in Photosciences. Amsterdam: Elsevier Science pp. 181-204.

Reddy Marri, P., J.P. Bannantine, M.L. Paustian and **G.B. Golding.** 2006. Lateral Gene Transfer in Mycobacterium avium subspecies paratuberculosis. Canadian Journal of Microbiology *(In press)*

Rheault, M.R., D.M. Debicki, and **M.J. O'Donnell.** 2005. Characterization of tetraethylammonium uptake across the basolateral membrane of the Drosophila Malpighian (renal) tubule. Am. J. Physiol. 289, R495-R504.

Rogers, J.G., M. Patel, K. Gilmour, and **C.M. Wood.** 2005. Mechanisms behind Pb- induced disruption of Na^+ and Cl^- balance in the rainbow trout (Oncorhynchus mykiss). Am. J. Physiol. 289: R463 – R472.

Rollo, C.D. 2005. Review of "Phenotypic integration: Studying the ecology and evolution of complex phenotypes." by M Pigliucci and K Preston (eds.). Oxford University Press. Quart. Rev. Biol.

Romanuk, T.N. and **J. Kolasa.** 2005. Resource limitation, biodiversity, and competitive effects interact to determine the invasibility of rock pool microcosms. Biol Invasions, 7, 711-722

Saltys, H.A., M.G. Jonz, and **C.A. Nurse.** (2006). Comparative studies of gill neuroepithelial cells and their innervation in teleosts and Xenopus tadpoles. Cell Tissue Res 323: 1-10.

Schmaltz, G., C.M. Somers, P. Sharma, & **J.S. Quinn.** Non destructive sampling of maternal DNA from the external shell of bird eggs. Conservation Genetics. *(In press)*

Schmaltz, G., and **J.S. Quinn.** Microsatelite isolation from four avian species comparing two isolation techniques. Molecular Ecology Notes. *(In press)*

Scott, G.R., J.B. Claiborne, S.L. Edwards, P.M. Schulte, and **C.M. Wood.** 2005. Gene expression after freshwater transfer in gills and opercular epithelia of killifish: Insight into divergent mechanisms of ion transport. J. Exp. Biol. 208 : 2719 - 2729.

Shen X-Y., N. Zacal, G. Singh, and **A.J. Rainbow.** 2005 Alterations in mitochondrial and apoptosis regulating gene expression in photodynamic therapy resistant variants of HT29 colon carcinoma cells. Photochem. Photobiol. 81, 306-313.

Sibley C. D., S. R. MacLellan and **T. M. Finan.** 2006. The Sinorhizobium meliloti chromosomal origin of replication. Microbiology 152: 443-455

Singh RS, R.J. Kulathinal. 2005. Male sex drive and the masculinization of the genome. Bioessays. 27(5):518-25.

Sloman, K., D.M. McDonald, J.F. Barimo, O. Lepage, S. Winberg, **C.M. Wood,** and P.J. Walsh. 2005. Does pulsatile urea excretion serve as a social signal in the gulf toadfish, *Opsanus beta?* Physiol. Biochem. Zool. 78, 724 – 735.

Sloman, K.A., O. Lepage, J.T. Rogers, **C.M. Wood,** and S. Winberg. 2005 Socially-mediated differences in brain monoamines in rainbow trout: effect of trace metal contaminants. Aquat. Toxicol. 71 : 237-247

Smith, R.W., **C.M. Wood,** P. Cash, L. Diao, and P. Pärt. 2005. Apolipoprotein A1 is a significant determinant of epithelial integrity in rainbow trout gill cell cultures: a study in functional proteomics. BBA-Proteins and Proteomics. 1749: 81-93

Somers, C.M., J.M. Kwiecien, and **J.S. Quinn.** 2005. A marine fish diet reduces spontaneous lymphoma in outbred Swiss-Webster mice. Leukemia and Lymhphoma 46: 1797-1800.

Somers, C.M., E.V. Valdes, and **J.S. Quinn.** An Approach to Feeding High Percentage Fish Diets to Mice for Human and Wildlife Toxicology Studies. Ecotoxicology and Environmental Safety. *(In press)*

Spring C.M., K.F.Kelly, I. O'Kelly, M. Graham, H.C. Crawford, and **J.M. Daniel.** The catenin $p120^{ctn}$ inhibits Kaiso-mediated Transcriptional Repression of the α-catenin/TCF target gene *matrilysin.* 2005 Exp. Cell Res. 305:253- 265.

Stone, J. and M. Telford. 2005. Fractal dimensions characterizing mammalian teeth. Mammal Review 35:123-128.

Terradot, L., R. Bayliss, C. Oomen, G. Leonard, **C. Baron,** and G. Waksman. 2005 Structures of two core subunits of the bacterial type IV secretion system, VirB8 from *Brucella suis* and ComB10 from *Helicobacter pylori* . Proc.Natl. Acad. Sci. 102: 4596-4601

Torgerson D.G. and **R.S. Singh.** 2005. Enhanced adaptive evolution of sperm-expressed genes on the mammalian X chromosome. Heredity. 96: 39-44.

Torgerson D.G., B.R. Whitty, and **R.S. Singh.** 2005. Sex-specific functional specialization and the evolutionary rates of essential fertility genes. J Mol Evol. 61(5):650-8.

Vogt, R., T.N. Romanuk, and **J. Kolasa.** 2005. Species richness-variability relationships in multi-trophic aquatic microcosms. Oikos *(in press)*

Wei, A., **P. Chow-Fraser.** 2005. Untangling the confounding effects of urbanization and high water level on the cover of emergent vegetation in Cootes Paradise Marsh, a degraded coastal wetland of Lake Ontario. *Hydrobiologia* 544: 1-9

Wong, C.E., Y. Li, A. Labbe, D. Guevara, P. Nuin, B. Whitty, C. Diaz, **G.B. Golding,** G.R. Gray, E.A. Weretilnyk, M. Griffith, and B.A. Moffatt, 2006. Transcriptional Profiling Implicates Novel Interactions Between Abiotic Stress and Hormonal Responses in Thellungiella, a Close Relative of Arabidopsis. Plant Physiology *(In press).*

Wong, C.E., Y. Li, B. Whitty, C. Diaz-Camino, S.R. Akhter, J. Brandle, **G.B. Golding,** E.A. Weretilnyk, B.A. Moffatt and M. Griffith 2005. Expressed sequence tags from the Yukon ecotype of *Thellungiella* reveal little overlap in gene expression in response to cold, drought and high salinity. Plant Mol Biol. 58: 561-574.

Wong, CE, Li Y , Labbe A , Guevara D, Nuin P, Whitty B, Diaz C, **Golding GB,**. Gray, GR **Weretilnyk EA,** Griffith M, and Moffatt BA Transcriptional profiling implicates novel interactions between abiotic stress and hormonal responses in *Thellungiella,* a close relative of Arabidopsis (Plant Physiology, In press)

Wood, C.M., M. Kajimura, T.P. Mommsen, and P.J. Walsh. 2005. Alkaline tide and nitrogen conservation after feeding in the elasmobranch *Squalus acanthius.* J. Exp. Biol.208 : 2693 - 2705.

Wood, C.M., P.J. Walsh, S.F. Chew, and Y.K. Ip. 2005 Greatly elevated urea excretion after air-exposure appears to be carrier-mediated in the slender lungfish *(Protopterus dolloi).* Physiol. Biochem. Zool. 78:893-907.

Wood, C.M., P.J. Walsh, S.F. Chew, Y.K. and Ip. 2005. Ammonia tolerance in the slender lungfish *(Protopterus dolloi);* the importance of environmental acidification. Can. J. Zool. 83: 507-517

Xu, J. 2005. Cost of interacting with sexual partners in a facultative sexual microbe. Genetics. 171:1597-1604.

Xu, J. 2005. The inheritance of organelle genes and genomes: patterns and mechanisms. Genome. 48:951-958.

Xu, J. Microbial ecology in the age of genomics and metagenomics; concepts, tools and recent advances. Molecular Ecology (*In press*).

Yang H.C., J. Cheng, **T.M. Finan,** B.P. Rosen, H. Bhattacharjee. 2005. Novel pathway for arsenic detoxification in the legume symbiont *Sinorhizobium meliloti.* J. Bacteriol.187:6991-7.

Yuan Z.C., R. Zaheer, **T.M. Finan.** 2006. Regulation and properties of PstSCAB, a high affinity, high velocity, phosphate transport system of *Sinorhizobium meliloti.* J. Bacteriol. 188:1089-1102.

Yuan Z.C., R. Zaheer, R. Morton and **T.M. Finan.** 2006. Genome prediction of PhoB regulated promoters in *Sinorhizobium meliloti* and twelve prpteobacteria. Necleic Acid Res. 34:2686-97.

Yuan, Q., A. Carle, C. Gao, D. Sivanesan, K. Aly, C. Höppner, L. Krall, N. Domke, and **C. Baron.** 2005 Identification of the VirB4-VirB8-VirB5-VirB2 pilus assembly sequence of type IV secretion systems. J. Biol. Chem. 280: 26349-26359

Yuan, Z., R. Zaheer, and **T. M. Finan.** 2005. Phosphate limitation induces catalase expression in *Sinorhizobium meliloti, Pseudomonas aeruginosa* and *Agrobacterium tumefaciens.* Molecular Microbiology 58:877-94.

Zacal, N.J., M. Espiritu, G. Singh, and **A.J. Rainbow.** 2005. Increased BNip3 and decreased mutant p53 in cisplatin-sensitive PDT-resistant HT29 cells. Biochemical and Biophysical Research Communications, 331:648-657.

Zacal, N.J., M.A. Francis, and **A.J. Rainbow.** 2005. Enhanced expression from the human cytomegalovirus immediate-early promoter in a non-replicating adenovirus encoded reporter gene following cellular exposure to chemical DNA damaging agents. Biochemical and Biophysical Research Communications, 332: 441-449.

Visitors, Post-doctoral Fellows and Research Associates

Post-doctoral Fellows

Abdo, Zaid (Working with B. Golding)
The barcode of life project: How to determine which species a sequence might originate from.

Azeria, Ermias (Working with J. Kolasa)
Connections Between Island Biogeography And Ecology Of Metacommunities

Donini, Andrew (Working with M.J. O'Donnell)
Ph.D., University of Toronto
Mechanisms of Ion Regulation in Aquatic Insects

Gillis, Patricia (Working with C.M. Wood)
Ph.D., University of Waterloo
Assessing Metal Bioavailability and Routes of Exposure in Aquatic Invertebrates

Haerty, Wilfried (Working with R. Singh)
Ph.D., University of Pierre et Marie Curie, Paris VI
Analysis of genes involved in hybrid male sterility in the Drosophila simulans clade

Kajimura, Makiko (Working with G. McClelland)
Regulation of fat oxidation with environmental stress

Marri, Pradeep Reddy (Working with G.B. Golding)
Ph.D., University of Hyderabad, India.
Comparative Genomics and Lateral Gene Transfer in Bacteria

Paschos, Athanasiios (Working with C. Baron)
Ph.D., Ludwig-Maximilians-University, Munich-Germany
Analysis of interactions between VirB proteins of the Brucella suis type IV secretion system

Singh, Nishi (Working with A. Bedard)
Regulation of the menin tumour suppressor in v-Src transformed cells

Smith, Richard (Working with C.M. Wood)
Branchial proteomics in freshwater fish and Sodium channel expression and copper uptake mechanisms in Xenopus oocytes

Tsui, Tommy (Working with C. Wood)
Cellular and molecular biology of gill transport functions.

Wang, Hong (Working with J. Daniel)
Ph.D., The University of Iowa
Identification of gene targets for novel transcriptional factor-Kaiso

Wu, Yili (Working with: X-D Zhu)
Elucidating the function of DNA repair factors at human telomeres.

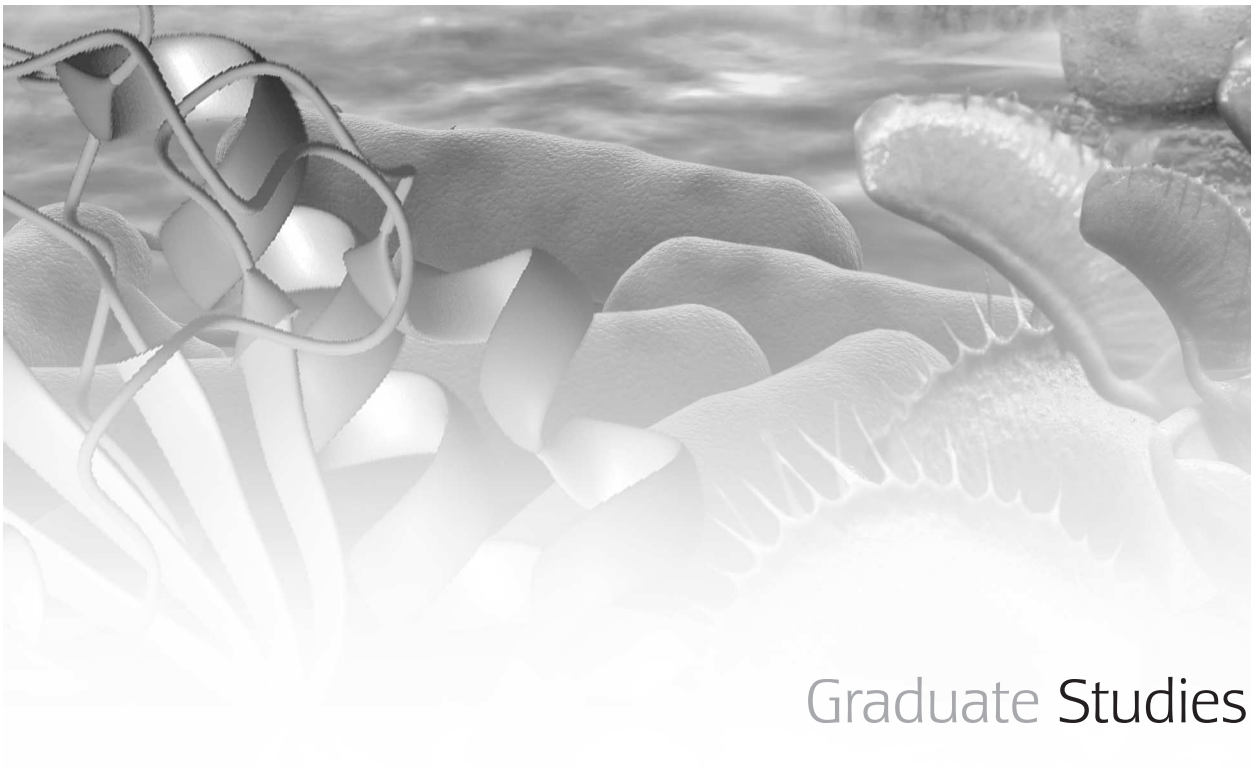
Research Associates

Cheng, Jiujun (Working with T. M. Finan/ G. B. Golding)
Ph.D., University of Wales Swansea
Analysis of bacterial genes of unknown functions

Cowie, Alison (Working with T.M. Finan)
M.Sc., McMaster University
Research project: To assign function to unkown genes of Sinorhizobium meliloti by construction and analysis of an expression library

Zaheer, Rahat (Working with T.M. Finan)
Ph.D., Punjab University, Lahore, Pakistan
Characterization of PhoB regulated genes in Sinorhizobium meliloti

Zhang, Min (Working with C.A. Nurse)
M.D., Shandong University in China,
Chemosensory mechanisms in carotid body and sensory neurons



Graduate Studies

Graduate Program Structure

Programs

The Biology Department offers graduate programmes leading to M.Sc. and Ph.D. degrees. The programmes offer graduate students the opportunity to participate in one of the over thirty faculty research labs. Areas of research cover a broad range and include: biochemistry, bioinformatics, cancer biology, cell biology, developmental biology, population ecology, environmental physiology, evolution, genetics, immunology, microbiology, molecular biology, and others. Often, a research project of any one laboratory involves more than one of these categories.

Students in the Biology graduate programme will enter directly into their chosen research lab in their first year of study. Therefore, students are encouraged to consider their research interests and acquaint themselves with the research programmes of professors in the applicable fields. They then arrange to meet with the professors and discuss the possibility of pursuing a graduate degree in the lab.

The graduate programmes are designed to teach students the research and communication skills required for a successful career as an independent scientist. Many graduates go on to careers in universities, research institutions, or the biotechnology industry, and a growing number choose areas such as consulting, science writing, technology transfer, and patent law.

The average programme length is 2 to 3 years for a M.Sc. and 4 to 5 years for a Ph.D. Currently there are 49 students in the M.Sc. programme and 45 Ph.D. candidates.

M.Sc. degree

The M.Sc. programme requires the submission of a research thesis and is recommended for anyone planning to proceed later to a Ph.D. or otherwise to continue in research.

A candidate for the M.Sc. in Biology must spend at least one calendar year in full-time graduate study at McMaster University and must complete satisfactorily one full graduate course (or two half courses) in biology or related fields. Upon completion of their research, the candidate must present a thesis embodying original results, and have an oral defense before a departmental examining committee.

This is a brief overview of the M.Sc. programme. For details on programme requirements, please see the *Guide to Graduate Studies in Biology at McMaster University* or contact Pat Hayward.

Ph.D. degree

Candidates may enter the programme with an Honours B.Sc. or an M.Sc. It is customary for graduate students holding a bachelor degree to enter a M.Sc., rather than a Ph.D. programme. If the student wishes to proceed to a Ph.D., at the end of an appropriate period of study, they will be asked to submit a critical report on their research to date. The candidate will be examined on this report for evidence of research potential to determine whether they will be granted permission to transfer to the Ph.D. programme.
The requirements to complete a Ph.D. in Biology are:

- Satisfactory completion of at least two and one half full graduate courses beyond the baccalaureate degree in biology or related fields.
- Successful completion of a comprehensive examination designed to test the Ph.D. candidate's breadth of knowledge and competence in biology. The examination will be comprised of two parts: the preparation of a formal research proposal and the presentation of a public seminar, followed by a meeting with the examination committee.
- While not a requirement, most students hold teaching assistantships during their graduate career. The financial remuneration forms a significant part of the graduate stipend and affords the opportunity to learn teaching skills.
- Successful defense of a thesis of original research. Upon completion of their research, a Ph.D. candidate is required to present and defend a thesis embodying the results of their original research.

This is a brief overview of the Ph.D. programme. For details on programme requirements, please see the *Guide to Graduate Studies in Biology at McMaster University* or contact Pat Hayward.

Departmental Participation

The Biology Faculty welcome input from graduate students in matters governing the Department. Graduate students in Biology elect two of their members to attend the regular Departmental faculty meetings, one member to serve on the Graduate Studies Committee, and one member is elected to the Department Curriculum Committee. The Biology Graduate Studies Committee is responsible for maintaining the integrity and academic excellence of the graduate program.

STUDENT SOCIETY ACTIVITIES

Biology Graduate Students' Society

The Biology Graduate Students' Society (BGSS) is comprised of elected graduate students from within the Department of Biology. BGSS members act as representatives for biology graduate students to the department of biology on issues ranging from undergraduate and graduate academics to health and safety. In addition, the BGSS hosts 3 annual social events: the summer picnic, the Welcome Week BBQ and the winter holiday formal the Holly Frolic. Other smaller events and socials we have held in past include karaoke nights, movie/potluck nights, Volleyball tournament, trip to Wonderland, wine tours, free coffee breaks, pumpkin carving contests, and Statistics seminars, and Biology seminars.

Graduate Students Association (GSA)

The mandate of the Graduate Students Association (GSA) is to promote the welfare and interests of McMaster graduate students, to represent the members before the duly elected and appointed authorities of McMaster University, and to promote communication and participation in all matters of common interest between the members of the Association and the members of other student organizations.

The GSA owns and operates the Phoenix restaurant and bar, providing an opportunity for graduate students and other members of the McMaster community to interact in a casual restaurant/pub setting.

The GSA periodically hosts seminars and colloquia, including Graduate Students Day annually. The GSA also provides financial and media support for departmental and faculty seminar days, colloquia, etc.. The GSA also publishes a monthly newsletter, *The GSA Today,* that provides news and information relating to graduate issues and events throughout McMaster University.

Graduate Distinguished Honours

NSERC Doctorial Prize: Patrick Seale

Natural Sciences and Engineering Research Council (NSERC):
Laura Smallbone (Finan)
Stephen Brown (Nurse)
Anhua Wei (Chow-Fraser)
Zhun Yan (Xu) (renewal)

Ontario Graduate Scholarship (OGS):
Richard Piscioneri
Jennifer Kinder (A. Campos)
Nickett Donaldson (J. Daniel)
Michael BeGora (E. Weretilnyk)
Sheng Sun
Michael Lowe

Students Coming to McMaster with Awards:
Warren Green (C. M. Wood) NSERC
Sarah Chiang (H. E.Schelhorn) OGS

Ontario Graduate Scholarship in Science and Technology (OGSST):
John Fitzpatrick (S. Balshine) - Banl of Montreal
Allyson MacLean (T. Finan) - Bank of Montreal
Abraham Yang (S. Igdoura) - Heart & Stroke

U.S. Department of Defence Breast Cancer Research Program: Abena Otchere (J. Daniel)

CIHR: Kevin Kelly (J. Daniel)

Heart and Stroke Scholarship: Jyoti Pande (A. K. Grover)

CONACYT Scholarship: Esau Ruiz Sanchez (M. J. O'Donnell)

Ministry of Science, Research and Technology, Islamic Republic of Iran: Raheleh Masoudi (M. Fahnestock)

Northern Scientific Training Program Grant: David Guevara (E. Weretilnyk)

Faculty of Science, Department of Biology Poster Award – First Place: Kevin Kelly (J. Daniel)

American Association for Cancer Research – Minority Award 2004-05: Abena Otchere (J. Daniel)

Corporate Activities Program Student Travel Grants for 105th American Society of Microbiology General Meeting 2005: Chan Gao (C. Baron)

Degrees conferred, 2005:

Marc J. Champigny, Ph.D.
Transcriptional regulation of neu1 expresssion: Implications for lysosomal storage disease.

Pasqual Cirone, Ph.D.
Immuno-isolation gene therapy: a novel approach to immuno-therapy of cancer.

Randy Elkasabgy, M.Sc.

Jane Elizabeth Fowler, M.Sc.
Expression analysis of ABC transporters in *Sinorhizobium meliloti.*

Timothy Ray Fraser, Ph.D.
Integrating genetic and photo-identification data to assess reproductive success in the North Atlantic right whale *(Eubalaena glacialis).*

Michael G. Jonz, Ph.D.
Structure, function and development of the O2-sensitive neuroepithelial cells of the zebrafish *(Danio revio).*

Shaqil N. Kassam, M.Sc.
The role of the p53 and nucleotide excision repair proteins in the base excision repair of methylene blue plus visible light inducted DNA damage.

Jennifer Kinder, M.Sc.
A functional investigation of the DIP1 gene in *Drosophila melanogaster.*

Jennifer Lemon, Ph.D.
Oxidative stress and aging processes in transgenic growth hormone mice.

Cindy Lentz, M.Sc.
An investigation of territory quality in the smooth-billed ani *(Crotophage ani).*

Heidi Musters, M.Sc.
A genomic comparison of *Drosophila melanogaster* and D-ros-pseudoolscrua: evidence of faster X, faster sex and faster male evolution.

Sunita Rao Nadella, M.Sc.
Dietary uptake of copper in freshwater rainbow trout *(Oncorhynchus mykiss):* A study of mechanisms.

Adeola Ojo
Bioavailability and interactions of metals via the gastrointestinal tract of rainbow trout *(Oncorphynchus mykiss).*

Eric Pane, Ph.D.
Mechanistic analysis of the effects of nickel *Daphnia magna* and rainbow trout.

Adrian P. Rybak, M.Sc.
An examination of UV-induced bystander effects and the repair of a UV-damaged reporter gene in human cells.

Michael Schertzberg, M.Sc.
Regulation of expression the GABDTP operon and utilization of GABA as a fole nitrogen source in *Eschercichia coli.*

Christopher Michael Somers, Ph.D.
Germline Mutations at Expanded Simple Tandem Repeat DNA Loci in Sentinel Mice

Kelly Teal, M.Sc.
Identification and Molecular characterization of dPALS52, the Drosophila orthology of mammalian PALS2.

Dara G. Torgerson, Ph.D.
The molecular evolution of genes expressed in the sperm.

Qing Yuan, Ph.D.
Functional analysis of the roles of VirB4 and VirB5 during t-pilus assembly.

Full-time Students
Ph.D. Students

Abou Chakra, Maria (J. Stone)
Computational Model of Echinoid Skeleton Morphogenesis

Ali, Khaled (C. Baron)
Structure-function analysis of the minor T-pilus component VirB5 from Agrobacterium tumefaciens

Al-daoud, Fadi (R. Cameron)
Microarray/Reverse Genetics to identify genes required for the Age-related resistance response.

Artieri, Carlo (R. Singh)
Evolutionary divergence of gene regulatory elements in closely related species of Drosophila.

Begora, Michael (E. Weretilnyk)
Phosphobase N-methyltransferases involved in phosphocholine synthesis

Brown, Stephen (C. A. Nurse)
The Function of Hypoxia Induced Factors (HIFs) in Acute and Chronic Hypoxia in Rat Adrenomedullary Chromaffin Cells.

Bucking, Carol (C.M. Wood)
The Physiology of Digestion in Rainbow Trout.

Buttigieg, Josef (C. A. Nurse)
Genetics of variation in Sex Comb morphology of males of Drospohila

Capstick, David (M. Elliot)
Aerial development and the role of secreted amyloid-like proteins Streptomyces coelicolor

Craig, Paul (G. McClelland)
Toxigenomics of Zebrafish

Dey, Bijan Kumar (A. R. Campos)
Dissecting the function of the Drosophila disconnected (disco) gene using molecular and genetic approaches

Donaldson, Nickett (J. Daniel)
The novel POZ-ZF protein ZNf131 enhances Kaiso-Mediated Transcriptional Repression via heterodimerization of their POZ domain

Fitzpatrick, John (S. Balshine)

Guevara, David (E. Weretilnyk)
Physiological and metabolic responses of Thellungiella salsuginea toward

Hao, Weilong (G. B. Golding)
Lateral Gene Transfer

Hayward, April (J. Kolasa)
Allometric Scaling at Multiple Scales of Biological Organisation in Aquatic Rock Pool Microcosms

Hiremath, Sanjay (R.S. Singh)

Hossain, Noor (J. R. Jacobs)

Huntley, Melanie (G. B. Golding)
The evolution and origins of protein repeats

Kelly, Kevin (J. Daniel)
Nucleocytoplasmic trafficking and gene regulation of the POZ-ZF transcriptional regulator Kaiso and the catenin p120

MacLean, Allyson (T. M. Finan)
Aromatic acid metabolism in Sinorhizobium meliloti

MacMullin, Allison (J.R. Jacobs)

Maslikowski (A. Bedard)
Identification of promoter units regulated by the v-Src oncogene using approaches of genomics and computational biology

Masoudi, Raheleh (M. Fahnestock)

Moyer, Katie (J.R . Jacobs)

Nawata, Michele (C. Wood)
Mechanisms of ammonia transport in fish

Pande, Jyoti (A. K. Grover)

Pandit, Shubha (J. Kolasa)
Works on the effects of species exchanges among communities on the composition of communities in a model system of microcosms.

Papaconstantinou, Maria (A. Campos)

Patel, Leena (J.R. Jacobs)

Pattison, Susan (S. Igdoura)

Peters, Jason (J.A. Hassell)
Identifying PEA3 target genes

Poduska, Branislava (T. M. Finan)
FRT directed deletions in Sinorhizobium meliloti genome

Robbins, Clinton (C. Richards)

Rodriguez, Moncalvo, Veronica (A. R. Campos)

Ruiz-Sanchez, Esau (M. J. O'Donnell)

Scantlebury, Nadia (A. Campos)
Uses a photobehavioural paradigm to identify and study central neuronal networks and molecules required for the control of locomotion in the Drosophila larva.

Schmaltz, Gregory (J. S. Quinn)
Reproductive skew and competition in the smooth-billed ani (Crotophaga ani)

Seilheimer, Titus (P. Chow-Fraser)
Dimensions of fish habitat in Great Lakes coastal wetlands: water quality, plant diversity, and fish species interactions
Sivanesan, Durga (C. Baron)
Protein-Protein interactions between Brucella suis type IV secretion system components
Sun, Sheng (J.P. Xu)
Population Biology of the Nitrogen-fixing Bacterium Sinorhizobium meliloti
Wang, Lizhen (A. Bedard)
Wei, Anhua (P. Chow-Fraser)
Yan, Zhun (J. P. Xu)
Mating type and Mitochondrial Inheritance in the Human Pathogenic Fungus Cryptococcus neoformans
Yuan, Zechun (T. M. Finan)
Study of phosphate transport and regulation in the nitrogen fixing soil bacterium Sinorhizobium meliloti

Full-time Students
M.Sc. Students

Abha Ahuja (R. S. Singh)
Genetics of variation in Sex Comb morphology of males of Drospohila
Aksenov, Vadim (D. Rollo)
Almardini, Mai (J. Daniel)
Elucidating the role of p120ctn and Kaiso on epithelial-mesenchymal transition and cell migration.
Bechard, Karen (C. Wood)
Trophic transfer of metals from chironomids to fish
Bojanala, Nagagireesh (B. Gupta)
Genetic analysis of the multivulva loci in the nematode Caenorhabditis briggsae
Carviel, Jessie (R. Cameron)
Mapping, cloning and characterization of a potential Age Related Resistance Regulatory gene
Chain, Frederic (B. Evans)
Molecular evolution of duplicate genes in allopolyploid clawed frogs (Xenopus and Silurana)
Chen, Pan (M. Elliot)
Regulation of antibiotic production in Streptomyces coelicolor
Chiang, Sarah (H. Schellhorn)
Development of an evolutionary model for regulons by selecting for increased RpoS-dependent gene expression in Escherichia coli
Chong, Taryne (S. Igdoura)
The impact of sialidase on inflammation mediated cell surface proteins in neurodegeneration.
Clarke, Katie (C. Nurse)
changes in neurotranmsitter receptor expression in the chemosensory carotid body following exposure to chronic stimuli
Croft, Melanie (P. Chow-Fraser)
Relationship between macrophyte and fish community structure in coastal wetlands of the Laurentian Great Lakes
Davis, Kimberly (A. K. Grover)
Dedrick, Jeff (E. Weretilnyk)
Working on the response and recovery of Thellungiella from drought exposure
Dong, Tao (H. E. Schellhorn)
Succinate selection for rpoSS mutations in natural Escherichia coli
Dregoesc, Diana (A. J. Rainbow)
The role of p53 in the transcription-coupled and global genomic sub-pathways of nucleotide excision repair
Gao, Chan (C. Baron)
Gleason, Amber (E. Weretilnyk)
characterizing enzymes associated with phosphatidylcholine biosynthesis in Arabidopsis
Green, Warren (C. Wood)
An olfactory biotic ligand model for predicting sublethal effects of metals on chemosensory function in fish
Gyewu, Daniel (H. Schellhorn)
The role of naturally occurring alleles of rpoS in Escherichia coli
Haiser, Henry (M. Elliot)
Regulation by small RNAs in Streptomyces coelicolor
King, John Paul (S. Igdoura)
Klinck, Joel (C. Wood)
A biotic ligand model for predicting the uptake and toxicity of metals through the gastrointestinal tract of fish
Kostuk, Kristina (P. Chow-Fraser)
Fish-benthos interactions in coastal wetlands: influence of fish sampling methods and plant diversity
Kozlova, Tatiana (C. Wood)
Modelling the acute and chronic effects of nickel in invertebrates

Leach, Derrik (A. Rainbow)
Effects of hypoxia on the repair of DNA damage in lung cells

Lou, Melanie (B. Golding)
studying the molecular evolution of cytochrome oxidase subunit I, the gene chosen for animal barcoding, within insects

Morash, Andrea (G. McClelland)
Regulation of mitochondrial lipid oxidation

Murphy, Guillermo (S. Dudley)

Murphy, Kristina (G. McClelland)
Interactions between exercise capacity and muscle fuel metabolism

O'Neill, Alicia (A. Rainbow/C. Mothersill)
Radiation bystander effects in fish cells

Otchere, Abena (J. Daniel)
The Role of the POZ-ZF Transcription Factor Kaiso in Breast Tumourigenesis

Panyala, Sujatha (B. Gupta)
Molecular genetic study of vulval morphogenesis in C. elegans and related nematode species

Patel, Monika (C. Wood)
Ionoregulation and water balance in the lungfish

Sankey, Jacqueline (D. Boreham)

Sartor, Andrea (T. M. Finan)

Schippers, Marie Pierre (G. McClelland)
Exercise physiology and lifetime performance in honeybees

Setiadi, Iqbal (B. Evans)
Exploring areas of genetic endemism in central Indonesia using amphibians as indicator species. The broader implication of this work is to provide information on the distribution of unique species and populations for use in conservation management this biodiverse region

Shaban, Thuraya (H. Schellhorn)
Expression of Gulo gene I guinea pig using adenovirus

Shahid, Morivard (J.P. Xu)
phenotypic plasticity and hybridization in a fungus

Sharma, Prachi (A. Rainbow)
Effects of combined ionizing radiation and photodynamic therapy treatment on non-small cell lung cancer cells in vitro

Smallbone, Laura (T. M. Finan)
Malic Enzymes: Interacting Proteins and Metabolomics

Szewczyk, Magdalena (A. K. Grover)

Xiao, Shujie (X.D. Zhu)

Yang, Abraham (S. Igdoura)
Role of sialidase in cardiovascular disease

Yasin, Shari (A. Rainbow)
Effects of the DAN mismatch repair genes and hypoxia on the repair of cisplatin -induced DNA damage.

Younes, Manhal (R. Singh)
Sexual selection and the evolution of beauty and human facial attractiveness across cultures

Younes, Mirella (H. Schellhorn)
Comparing the expression of RpoS dependent fusion in GC4468 and MG1655.

Undergraduate Studies

Undergraduate Program Structure

Staff and faculty in the department of Biology teach, support and administer some of the largest courses and degree programmes in the Faculty of Science. We constantly strive to meet the changing academic and social needs of students by offering the most current and innovative means of support available.

Programs

The Biology Department offers the CORE option and two specializations, Genetics and Biodiversity, the interdisciplinary programmes Biology & Psychology, Biology & Mathematics, Molecular Biology and the Co-op options of Biology & Pharmacology and Biology & Genetics.

Core

The Honours Biology (Core) program includes a set of fundamental courses that are shared with other Biology Honours streams. It also permits the greatest flexibility in selection of additional courses. Students will be able to choose biology courses following their own interests, or to develop an interdisciplinary approach to biology that may include obtaining a minor. It provides an excellent background for graduate studies if the student completes a Biology Thesis or Project and chooses Level III and IV courses from Science. Students selecting this programme should be aware that many 3rd and 4th year courses have specific course pre-requisite requirements. Students can switch into the more specialized streams after year 2 if they wish but must satisfy the course requirements of the desired.

Genetics Specialization

Increasingly, biology tools are being applied to the solution of fundamental problems in food production and in the identification and treatment of human disease. Students in the Genetics stream will take a laboratory-centered programme that culminates in an undergraduate thesis in an active research laboratory. Students follow a programme of study that emphasizes practical applications of genetics in the study of human and animal disease, molecular models of development, molecular microbiology, evolutionary processes, gene expression, and the growing field of bioinformatics. Students will obtain practical training in molecular biology laboratory skills, communication skills and will thus be well prepared for a postgraduate career in academia, the health field or in the rapidly developing biotechnology industry.

Biodiversity Specialization

Biodiversity is the diversity of life itself, at all levels of organization from the gene to the ecosystem. Without question, the preservation of biodiversity will be the single greatest challenge for the human race in the 21st century. The goal of the Biodiversity Specialization at McMaster is to train students with the interdisciplinary skills they will need to deal with Biodiversity issues; Students who will have a strong background in basic ecology, evolution, population genetics, and conservation biology. Students will be comfortable dealing with plants, animals, and microorganisms, and will be trained in thinking about the big picture, and about all levels of ecosystem interactions, including the role of humans. To facilitate this process, students will be exposed to two inquiry courses in years II and III. The first course will expose the students to a broad range of ideas and expertise from both inside and outside McMaster, through presentations and discussions with representatives of government, industry, and international conservation and development organizations. The second course will expose students to the range of Biodiversity-related research ongoing at McMaster, and will prepare students for their own research projects in year IV. Graduates of this programme will have the appropriate background to pursue careers in government, academia, and international agencies.

Origins Specialization

The Origins Institute is an intellectual enterprise that promotes, maintains and strengthens interdisciplinary collaboration among researchers who are interested in solving scientific problems concerning 6 origins themes:

- The origin of our universe
- The origin of elements
- The origin of structure of our universe (eg. Solar systems, planets)
- The origin of life
- The origin of species
- The origin of humans

The Specialization in Origins Research curriculum is designed to re-introduce to students through these themes the 19th century ideal "Natural Science" (ie. well-rounded comprehension about the world) but from a modern perspective. Students graduating from the specialization will possess a comprehensive, liberal education in the natural sciences.

Students who are interested in this specialization will enroll in a Core programme in Biochemistry, Biology, Chemistry, Computing and Software, Earth and Environmental Sciences, Mathematics and Statistics, Physics and Astronomy or Psychology and then take the courses required for the Origins Specialization.

Program Enrolment

Programme	1999/00	2000/01	2001/02	2002/03	2003/04*	2004/05*	2005/06*
Biology Core	0	0	0	76	147	236	257
Genetics Specialization	0	0	0	41	80	97	107
Biology/Psychology	101	91	98	92	107	112	128
Biodiversity Specialization	0	0	0	7	15	25	26
Genetics Co-op	0	0	0	0	6	11	17
Molecular Biology	36	37	35	28	23	21	22
Biology/Mathematics	11	9	8	6	5	9	9
Biology/Pharmacology Co-op	40	40	43	46	47	47	54
Arts & Science & Biology	7	8	7	4	4	3	4
TOTALS	**195**	**185**	**191**	**300**	**434**	**561**	**624**

*The statistics of 2003/04, 2004/05, and 2005/06 are yet to be approved by the Office of the Registrar.

Undergraduate Teaching

During the 2004/2005 academic year, Professors, Instructional Assistants and support staff in the Biology Department facilitated courses for students enrolled in every faculty of the University.

Some of the teaching styles, tools and resources that the Biology Department offers are:

- Inquiry Projects
- Problem-Based Learning (PBL)
- 1st Year Biology Skills Labs
- Peer Mentoring programme
- Laboratory-Based Courses (Experimental)
- Senior Project and Thesis courses (62 students participated in 2004)
- Formal, traditional lectures
- Small group tutorials
- Ontario Field Biology Programme (OUFBP)
- Computer-mediated instruction
- Ontario Biology Day
- Biology Undergraduate Symposium (BUS)

Distinguished Honours and Awards

Our students in the undergraduate Biology programmes are some of the best McMaster University has to offer. In 2005, many of our students were recipients of University Scholarships and Awards for their academic excellence and contributions to the community.

Abe Black Memorial Prize:
Katayun Treasurywala

The Burke Memorial Ring:
Katayun Treasurywala

The D. M. Davies Prize:
Priya Sharma

The Jensen Medal:
Paul Cassar

The Ernest Robert MacKenzie Kay Scholarships:
Laura Golding, Jordan Wronzberg, Tracy Kok

The Esther McCandless Memorial Prize:
Tamer Abdelshaheed, Lindzie O'Reilly

The J. J. Miller Prize:
Michelle Melone

Dr. Sina Sazgar Memorial Scholarship:
Priya Sharma

Science Alumni Scholarship:
Laura Golding, Maria-Alexandra Petre

Science Class of '97 Legacy Award:
Sarah Scattalon

Margaret A. Service Book Prize:
Andrea Lam

Stephen F. H. Threlkeld Award:
Christine Kerr

University Prizes for Special Achievment:
Ashlee Vincent

The Valley City Manufacturing Co. Ltd Scholarships:
Maria-Alexandre Petre

Biology Academic Achievement Award:

The Department of Biology bestows this new award upon the top academic achievers in first year Biology 1A03 – Cellular & Molecular Biology. In 2005 27 of these awards were bestowed on 1st year Biology students.

1AA3

Nadia Bashir
Rachel De Catanzaro
Stella Chan
Haman Chaudhry
Nicole Cuevas
Alison Fine
Tiffany Florindo
Timothy Hurley
Rebecca Jarvis
Benjamin Kaiser
Kristen Krysko
Hei-lo Lam
Emma Mazurek
Rebecca McDermott
Melissa Su'en Wu
Fang Yuan
Andrea Lam

1AO3

Christina Emmanuele
Timothy Hurley
Sivanesan Kalaichandran
Navid Khezri
Kristen Krysko
Andrea Lam
Ali Lessan
Emma Mazurek
Patrica Pak
Timothy Soh

Undergraduate Committees and Activities

Biology Society 2005

The Biology Society organized a number of successful events as well as introduced new services and fundraising initiatives. These include,

- Academic events (Meet the Profs, Resume Workshop, Career Nights)
- Social events (Barbeques, Movie Nights, Nature Walks)
- Fundraise for various causes (McMaster Children's Hospital, Women and Children's Shelter)
- Provide discounts offered by Kaplan
- Sell Bioware (past tests for first year and second year courses)

For more information visit the website http://www.msu.mcmaster.ca/clubs/biology/index.htm.

President: Lina Ostrovsky
Vice-president: Neha Maria Egbert
Members: Farhana Alam (Secretary); Jordan Wronzberg (VP Finance); Mark Messih (VP Academic); Jennifer Carroll, Katheen Chung (VP External); Dipannita Basu, Nipa Pandya (VP Fundraising); Aisha Shamas-Din (VP Bioware); Seint Kokokyi (VP Advertising); Nicole Stieber (Member at Large); Silvia Tropea (Upper Year Representative); Abby Sirisegaram (Third Year Representative); Arif Virani, Niraj Kadakia (Second Year Representatives); Meera Nathwani, Rabiya Hasan (First Year Representatives)

Other Undergraduate Societies and Clubs

- BioLinks
- GenetX Society (students in the Biology - Genetics specialization program)
- Bio-Psych Society (students who are in Honours Biology and Psychology)
- McMaster Science School Outreach
- McMaster Science Society

BUGS Committee

The Biology Undergraduate Studies Committee, or BUGS, is a group of faculty, staff and students who meet regularly to discuss and resolve issues involving Undergraduate Studies in the Department of Biology. There are two student representatives on the committee who act as advocates for their fellow students and help address their concerns to the department.

Ontario Biology Day 2005

Ontario Biology Day has become a tradition for senior Biology undergraduate students at McMaster University. The weekend conference is open to students of all Ontario Universities who undertake a senior thesis or project. It is an opportunity for them to reveal their findings and to meet representatives of other schools.

A record number 49 students, 11 faculty and 1 staff member participated in the 18th Annual Ontario Biology Day at the University of Western Ontario in London over the weekend of March 18th-19th, 2004. Students presented talks or participated in poster sessions based on their Senior Projects and Theses.

McMaster Biology students represented the following faculty members' labs:

Department of Biology:

Dr. Robin Cameron	Dr. Roger Jacobs	Dr. Jonathon Stone
Dr. Patricia Chow-Fraser	Dr. Jurek Kolasa	Dr. Chris Wood
Dr. Ben Evans	Dr. Grant McClelland	Dr. Jian-Ping Xu
Dr. Turlough Finan	Dr. Herb Schellhorn	Dr. Xu-Dong Zhu
Dr. Brian Golding	Dr. Rama Singh	

Department of Biochemistry and Biomedical Sciences:
Dr. Radhey Gupta

Department of Psychiatry and Behavioural Neurosciences:
Dr. Margaret Fahnestock Dr. Jane Foster Dr. Ram Mishra

Department of Pathology and Molecular Medicine:
Dr. Laurie Doering Dr. Derek McKay

Department of Medicine:
Dr. Marek Smieja

Department of Medicine/Pediatrics:
Dr. Mark Tamopolosky

The participants agreed that this was a great opportunity to network with students and faculty from other universities with similar or complementary research interests. The Biology department hosted Ontario Biology Day in 1999 and is scheduled to host again in 2006.

Biology Undergraduate Symposium

The Biology Undergraduate Symposium (BUS) was organized for the thesis and project students to present their research project findings to faculty, students, friends and family. This is followed by a gala reception. Submissions covered areas of research as diverse as our department. There were 28 poster submissions and 66 seminar presentations. Of these, six were honoured for being of extremely high quality.

BUS presentation Winners, 2005
Oral presentations:

Michelle Anstey (T. Finan):
Characterization of the Regulation of Protocatechuate genes in Sinorhizobium meliloti by LysR-type transcriptional Regulator, PcaQ.

Menaka Kanagaratnam (B. Golding):
The Metrics of Protein Repeats: From Simulation to Application

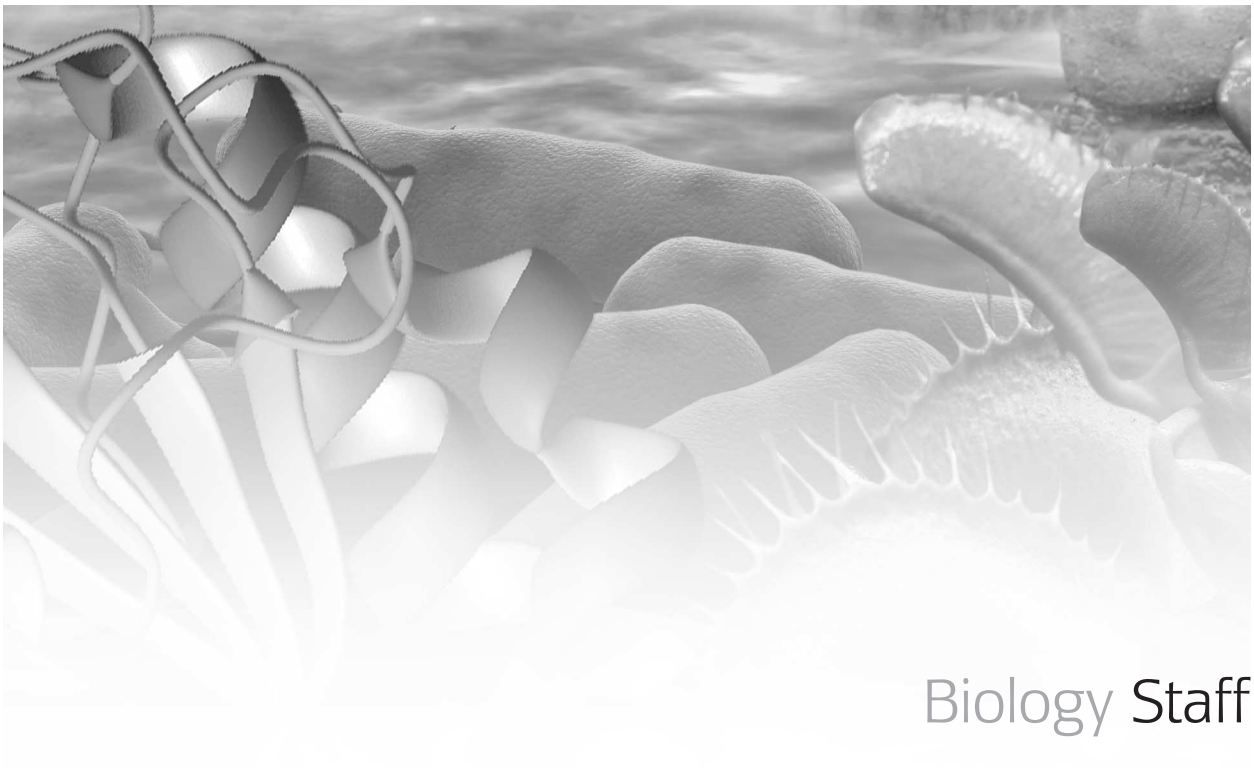
Lindzie O'Reilly (P. Chow-Fraser):
An Investigation of Abiotic Factors Influencing Submersed Macrophyte Colonization in Georgian Bay Wetlands

Poster presentations:

Teresa Domladovac (J. Stone):
Maintenance of Shell Chirality Polymorphism in Amphidromus inversus – A Computational Model

Caroline Gross (S. Balshine-Earn):
Prime real estate for the most invasive bidder: Neogobius melanostomas in Hamilton Harbour

Kevin Skoblenick (R. Mishra):
Role of AP-2 alpha Transcription Factor in the Regulation of Synapsin II Expression by Dopamine D1 and D2 Receptors



Biology Staff

OFFICE PERSONNEL

Name	Position
Marg Biggs	Administrative Secretary
Marge Geroux	Biology Administrator
Kathy Greaves	Administrative Secretary to the Chair & Administrator
Pat Hayward	Administrative Assistant - Graduate
Kathy McIntosh	Administrative Assistant - Undergraduate
Marta Prancho	Administrative Secretary
Barb Reuter	Administrative Secretary

DEPARTMENTAL PERSONNEL

Name	Position
Debbie Bernardo	Glassware Technician / Biomedical Waste
A. Seong Cheong	Undergraduate Laboratory Assistant
Ian Giles	Undergraduate Laboratory Assistant
Rob Gillies	Electronics Specialist
Marvin Gunderman	Technical Coordinator / Instructor of Entomology
Paul Hoffman	Undergraduate Laboratory Assistant
Arif Rawji	Computing Services Coordinator
Klaus Schultes	Electron Microscopy Specialist
Sharon Stray	Undergraduate Laboratory Assistant
Arthur Yeas	Greenhouse Technician

RESEARCH PERSONNEL

Name	Supervisor/Lab
Linda Diao	C. Wood, LS-203
Ying Choy Fong	B. Golding, LS-522
Mihaela Georgescu	R. Jacobs, LS-420
Monica Graham	J. Daniel, LS-321
Hong Guo	J. P. Xu, LS-402
Sally (Yanxia) Li	C. Baron, LS-304
Gregory Rekas	C. Baron, LS-304
Cathy Vollmer	C. Nurse, LS-421
Chris Wang	E. Weretilnyk, LS-521
Ying Wu	A Bedard, LS-419
Natalie Zacal	A. Rainbow, LS-406
Xiaoli Zhao	A. Campos, LS-502

INSTRUCTIONAL ASSISTANTS

The Instructional Assistants act as a bridge between the students and faculty. An Instructional Assistant often runs the lab component of the course, keeps track of all student marks, reschedules students in lab sections and deals with student conflicts.

Name	Course
Lori Ann Goff	Biology 1A03/1AA3, Cellular and Molecular Biology & Biodiversity, Evolution & Ecology; 3Q03/3QQ3 Peer Mentoring in Biology
Thelma Leech	Biology 2D03, Plant Biodiversity; 2B03, Cell Biology
Beryl Piccinin	Biology 1A03/1AA3, Cellular and Molecular Biology & Biodiversity, Evolution & Ecology
Ray Procwat	Biology 2C03, Genetics; 2A03, Integrative Physiology of Animals

Facilities

OVERVIEW

The Department of Biology has a wide range of core facilities that are available to its research labs. These include the insect rooms, the fish facilities and the plant facilities (greenhouse and plant growth chambers). We also have a wide range of imaging equipment available in the Microscope facilities.

MICROSCOPE FACILITIES

These facilities provide scientists with the equipment and training necessary to generate and interpret microscopic images. Faculty and staff with expertise in electron microscopy can help design, conduct and interpret your analyses.

Resources:

Surface Imaging

Samples that are dry, wet or oily can be observed without the aid of any metal coating in our new Environmental SEM (Electroscan 2020 ESEM). Dynamic changes can be studied as samples are subjected to changes in temperature (1500° C), applied tension or compression (up to 1000 pounds and 1000° C) or changes in hydration. Wet or oily samples can viewed on a low-temperature control stage (-5° to + 60° C) or at ambient temperature.

Low-Temperature Preparation

Cryogenic techniques are available for studying samples on Transmission Electron Microscope (TEM).

Image Analysis

Areas, dimensions, volumes and many other features of images can be quantified.

Element Composition

Energy dispersive x-ray (EDX) analysis provides information about elements present in very small areas of the sample. Elemental distributions can sometimes be mapped. Standardless semi-quantitative or fully quantitative results can be obtained.

Interior Imaging

Thin sections (>40 nm) of epoxy resin embedded samples can be viewed for ultrastructure and/or element composition. Wet samples can be frozen, cryosectioned, and the frozen sections observed using a cryostage on our TEM.

Particles and Flocs

Dry particulate samples can be studied for structure and composition. Colloids and flocs can be observed.

Electron Microscope Facility

The Electron Microscope Facility is located on the first floor of the Life Sciences Building. The facility is managed by EM specialist Klaus Schultes. It is equipped with the following:

Confocal microscope

- BIO RAD System attached to a Nikon E800 conventional epi-fluorescence microscope
- Lasers include an Argon Ion (488, 514) and Helium Neon (543)
- Z-drive with a focus resolution of 0.05 microns
- Transmission detector installed
- Dual Photomultipliers
- LaserPix 2D software

Environmental scanning electron microscope

- ESEM 2020
- Full environmental capabilities with LaB6 filament
- Peltier cold stage for viewing wet samples
- Fullam tensile/ 1000 ° C heating stage for compression or tension studies (1000lb, 50lb, & 250 gr load cells and linear transducer) coupled to Mtest windows live readout system.
- Electroscan 1500 ° C heating stage
- Micromanipulator with ability to add liquid or gases to samples in situ
- PGT microanalysis system with PRISM light element detector, semi or full quantitative analysis software/ image analysis software
- VCR recording available with miroVIDEO video digitizing and editing system
- LFD (Large field detector) allows users to view a larger surface area at overall lower magnification

Scanning Transmission electron microscope

- JEOL 1200EX11 STEM
- 120 Kv LaB6 Scanning Transmission Electron Microscope
- Gatan cryo transfer system installed
- Single tilt and double tilt goniometers
- PGT IMIX microanalysis system with beryllium detector, semi and full quatitative software package/ image analysis software

MOLECULAR BIOLOGY FACILITIES

MOBIX lab

The Institute for Molecular Biology and Biotechnology (MOBIX) manages the MOBIX lab, a centre that provides a wide range of molecular biology services to McMaster University. (MOBIX) (See web page www.science.mcmaster.ca/mobix, contact: mobix@mcmaster.ca for more information)

MOBIX Lab is committed to providing diligent service and support in Oligo synthesis, DNA sequencing and fragment analysis with exceptional quality, accuracy and value. We believe in integrity and teamwork in everything we do. We will continue to progress with the purchase and sharing of state-of-the-art equipment and introduction of new services. Mobix Lab is located in the Life Sciences Building, Room B123

Resources:

Oligo Synthesis

Oligos are synthesized on an ABI 394 DNA/RNA Synthesizer, an ABI 3400 DNA/RNA Synthesizer or an ABI 3900 High Throughput DNA Synthesizer.

Sequencing

DNA cycle sequencing in our lab is performed using ABI BigDye terminator chemistry and ABIPRISM® 3730S Genetic Analyzer and ABIPRISM® 3100 Genetic Analyzer. Both Genetic Analyzers are a multi-color fluorescence-based DNA analysis systems fully automated from sample loading to data analysis.

Fragment Analysis

Microsatellite analysis and SNP

Equipment Available

Alpha Imager 2200, Kodak Image Station 440, and Phosphorimager

Phone: 905-525-9140 Ext. 27048
FAX: 905-526-1427
Email: mobixlab@mcmaster.ca

Facility Manager: Galina Kataeva, Ph.D.
Technicians: Liliana DeSousa, B.Sc., Richard Lamb, B.Sc., Leanne Blanchard, M.Sc.

OTHER RESEARCH RESOURCES

Neutron activation analysis (nuclear reactor), Mass spectrometry, High resolution resonance spectrometer.

COMPUTER SERVICES

The Department of Biology has a PC computing lab located in Room 215. During the academic year, student consultants are available for assistance. **Services Coordinator:** Arif Rawji

Hours during the academic year:
Monday - Thursday: 9:15am-8:00pm
Friday: 9:15am-4:00pm

Hours during May - August and during exams
Monday - Friday: 9:15am-4:00pm

ANIMAL FACILITIES

Insect rooms

The LSB has a small insectary used for housing live insects for physiology experiments. The insects include the American cockroach, *Periplaneta americana,* and the true bug *Rhodnius sp.* The former is used in undergraduate physiology labs and the latter in research labs by Dr. Mike O'Donnell.

Marvin Gunderman is our instructor of entomology and curator of biology's insect collection. The collection has pinned specimens from the 1930's right up to 2004 and is thus a valuable resource for presence/absence and range data for insects from mostly southern Ontario. Student collections from Marvin's courses are integrated into the departmental collection ensuring growth. There is a small liquid collection of mostly larvae and pupae. The collection has been used by several researchers for range data, especially the Lepidoptera (butterflies only) and Coleoptera (Coccinellidae and Cicindelidae). **Contact:** Marvin Gunderman

Fish facilities

The aquatic laboratories are a multi-user facility housed in four separate rooms (B101, 575 sq. ft; B102, 185 sq. ft; B109, 200 sq. ft; B112, 895 sq. ft) in the basement of Life Sciences Building. It has the capacity for maintaining fish of various sizes in tanks ranging from 10 - 500 L, as well as conducting experimental procedures and analytical work. The facility currently maintains a variety of fish species including the freshwater rainbow trout (Oncorhynchus mykiss) and yellow perch (Perca flavescens), the tropical zebrafish (Danio rerio), the euryhaline killifish (Fundulus heteroclitus), and the aestivating African lungfish (Protopterus dolloi). In addition to fish, invertebrate cultures are held in B112 including the midge larva, Chironomus riparius and the cladoceran, Daphnia magna. The facility is used in part to study the effects of environmental stressors on homeostatic mechanisms in fish. In particular, the laboratories of Drs. Wood and McClelland are currently performing industrially-supported research to gain a better understanding of impact of metals to aquatic biota. The research is expected to yield valuable information that will be used in the derivation of a new generation of environmental regulations for metals. A large basic research component is focused on understanding basic physiological questions relating to acid-base and ion regulation, and nitrogenous waste excretion. The facility is equipped with a unique swim tunnel, to allow for research on exercise physiology, as well as X-ray equipment, and a Passive Integrated Tagging (PIT) system to enable fish identification and tracking. In the past five years more the 15 undergraduate students, 14 graduate students, 16 postdoctoral fellows and a number of visiting professors have used the facilities to conduct experiments. **Contact:** Chris Wood

PLANT FACILITIES

Greenhouses

The Biology Greenhouse, which is located to the west of The James Stewart Center (formerly Hamilton Hall), is used extensively, for teaching and research purposes. Each year hundreds of students either use the greenhouse in their laboratories or use plants provided by the greenhouse. A number of research projects use green facilities, especially those of Susan Dudley.

Contacts:

Mr. Art Yeas, extension 24284, (yeasart@mcmaster.ca)

Dr. Susan Dudley, extension 24004 (sdudley@mcmaster.ca)

BARC (Bay Area Restoration Council)

Bay Area Restoration Council (BARC) is at the centre of efforts to restore and protect the ecosystem heath of Hamilton Harbour and its watershed. Located in the Life Sciences Building, Room B130F, BARC's Great Lakes and Hamilton Harbour Resource Centre contains 1000's of documents on Great Lakes Clean-up projects, with a particular emphasis on the Hamilton Harbour Remedial Action Plan (RAP), Cootes Paradise marsh and the McMaster Ecowise program. The resource centre is open to visitors most weekdays from 10 am to 3 pm. Students may borrow Items for one week. Volunteer activities and public meetings are listed on the web site: learnlink.mcmaster.ca/barc. Contact: barc@mcmaster.ca or call ext: 27405.

Seminars and Visitors

VISITOR SEMINARS

Biology Seminar Series

Dr. Paul Mains, University of Calgary
Genetic Networks Controlling the C. elegans Embryonic Cytoskeleton. (October 13, 2005)

Dr. Jack Werren, University of Rochester
Wasps, Wings and Wolbachia: Evolutionary Genetics of Nasonia and its Endosymbionts. (October 27, 2005)

Dr. Andy Teng, University of Rochester
Microbes, Innate and Adaptive Immunity and their Playground. (November 10, 2005)

Dr. Charles Despres, Brock University
Plant Immunity: Signaling through the NPR1 Pathway. (November 24, 2005)

Dr. Tom Whittam, Michigan State University
How to Become a Pathogen: Lessons from the Pathogenic Escherichia. (December 8, 2005)

EEE (Evolution, Ecology, Ethology) Seminar Series

Dr. Ryan Gregory, University of Guelph
Why should anyone care about genome size? (October 26, 2005)

Dr. Ben Evans and Dr. Jurek Kolasa, McMaster University
Adventure Seminar Series. (November 2, 2005)

Dr. Tim Westwood, University of Toronto
An evolutionary perspective on the heat shock response. (November 9, 2005)

Dr. Michael Kasumovic
Is bigger better? Explaining the maintenance of phenotypic variation in males. (November 16, 2005)

Dr. William Taylor, University of Waterloo
Exploring pelagic food webs using the phosphorus cycle. (November 30, 2005)

Origins Institute Seminar Series

Dr. Chris Stringer, Natural History Museum, London, UK
The Origin of Our Species. (September 23, 2004)

Dr. Marc Garneau, President of the Canadian Space Agency and Canada's First Astronaut
Finding First Light - Investigating the Origin of the Universe. (October 24, 2004)

Dr. Donald Clayton, Centennial Professor of Physics and Astronomy, Clemson University
The Origin of the Atoms of our World. (4 November 2004)

Dr. Lawrence Krauss, Case Western Reserve University
An Atom from Hamilton - a Cosmic Odyssey. (10 February 2005)

Dr. Christopher P. McKay, NASA Astrobiology Institute
What is life, and how do we search for it on other worlds? (25 May 2005)

EXTERNAL SEMINARS

(Seminars given at outside institution by faculty members of the biology department)

Baron, C.
Department of Biochemistry University of British Columbia
From bioremediation to biowarfare: On the impact and mechanism of type IV secretion systems

58th Annual Brucellosis Research Conference, Merida, Mexico
The Brucella suis type IV secretion system assembles in the cell envelope of the heterologous host Agrobacterium tumefaciens and increases IncQ plasmid pLS1 recipient competence

Bedard, A.
Centre for Functional Genomics, Ontario Cancer Institute, Toronto, Ontario
Control of Menin expression and AP-1 activity by v-Src: Role in cell survival

Cameron, R.
IIIe cycle Meeting on "Systemic signals in plants", Fribourg, Switzerland
Long distance signaling in Systemic Acquired Resistance: on the trail of the elusive long distance SAR signal(s)

American Phytopathological Society Annual Meeting, Quebec City, Quebec
Multiple roles of SA in defense.

Chow-Fraser, P.
10th Annual Wetland Science Forum, Green Bay, Wisconsin
Comparison of recently-developed indicators of wetland quality for coastal wetlands: a basin-wide perspective

Georgian Bay Association 88th Annual General Meeting, Toronto, Ontario
A class of their own: comparison of wetland quality and biodiversity values for eastern Georgian Bay and the North Channel

Ontario Ecology and Ethology Colloquium, Carleton University, Ottawa, Ontario
Improving the relevance of ecology in biodiversity conservation: getting science to the people

Annual Meeting of the International Assoc. for Great Lakes Research, Ann Arbor, Michigan
Comparing catch data using fykenets and boat electrofishing in Georgian Bay: validating results of a gear-comparison study of the Lower Great Lakes

Annual Meeting of the International Assoc. for Great Lakes Research, Ann Arbor, Michigan
Ungangling confounding effects of urbanization and high water level on the cover of emergent vegetation in coastal wetlands of Lake Ontario

Annual Meeting of the International Assoc. for Great Lakes Research, Ann Arbor, Michigan
Multiple-stressor impacts on the fish and plant community of Frenchman's Bay: combined effects of urbanization, water-level fluctuation and mixing with Lake Ontario

Great Lakes Conference and Biennial Meeting, Kingston, Ontario
You don't know what you've got until it's gone: Paradise is here now in Georgian Bay.

Ecological Society of America 90th Annual Meeting, Montreal, Quebec
Basin-wide perspective in assessing quality of fish habitat in Great Lakes coastal wetlands

Ecological Society of America 90th Annual Meeting, Montreal, Quebec
An aggregate response of emergent vegetation to water level fluctuations in Lake Ontario

2nd International Muskie Symposium, Indianapolis, IN
A conceptual model of muskellunge spawning habitat in Georigan Bay, Ontario, Canada

Daniel, J.
Gordon Research Conference on Cell Contact & Adhesion. Andover, NH.
Kaiso and p120ctn in the nucleus: roles in signaling and development

13th IMP Spring Conference & IMBA inaugural Conference, Vienna, Austria.
Convergence of the transcription factor Kaiso and p120ctn on target genes of the Wnt/ catenin/TCF signaling pathway

Dept. of Zoology, University of Toronto, Toronto, Ontario
Convergence of Kaiso and p120ctn on the Wnt/β-catenin signaling pathway

Dept. for Molecular Biomedical Research, VIB - Ghent University, Ghent, Belgium
The transcriptional repressor Kaiso: roles in signaling and development

Dudley, S.
Ecological Society of America, Montreal, Quebec
Response to root competitors and R:FR in soybean.

Society for the Study of Evolution, Fairbanks, Alaska
The role of the maternal environment in the salt tolerance of a locally adapted roadside plant

Elliot, M.
Antimicrobial Research Centre Retreat; Niagara Falls, Ontario
The chaplins and aerial morphogenesis in Streptomyces coelicolor

2nd ASM Conference on Prokaryotic Development, Vancouver, British Columbia
The chaplins of Streptomyces coelicolor: Important developmental proteins that are associated with the Tat secretion pathway

Evans, B.
Conservation International Headquarters, Washington DC
Defining areas of endemism on Sulawesi, Indonesia

University of San Diego, San Diego
Gene duplication in allopolyploid clawed frogs

University of Chicago, Chicago
Gene duplication in allopolyploid clawed frogs

International Herpetology Conference, Cape Town, South Africa
Evolution of allopolyploid clawed frogs

Finan, T.M.
12th International Congress on Molecular Plant-Microbe Interactions. Merida
Functional analysis of the Sinorhizobium meliloti genome.

Canadian Sinorhizobium Genome Consortium – 2005 Inoculant Forum Saskatoon
Understanding Gene Function In Rhizobia.

Golding, G.B.
London NHM
The ability of the BLAST algorithm to aid in the identi cation of species

Royal Astronomical Society of Canada, Ontario Science Center
Origins of Life.

TIGR Microbial Genomics, Halifax, Nova Scotia
Lateral transfer in bacteria

Eastern Great Lakes Meeting Mol. Evolution, University of Toronto
Low complexity sequence is common in proteins

Vancouver Island CIAR meeting
Lateral transfer in bacteria: Tracing the duplication history within proteins

Gupta, B.
International Worm Meeting, Los Angeles, California
Post-genomic resources for C. briggsae: C. briggsae Genetics

Jacobs, R.
University of Toronto, Zoology Department, Toronto, Ontario
Veli- function of a scaffolding protein at the Drosophila neuromuscular junction

Drosophila Research Conference, San Diego
The role of Dorsal closure in heart morphogenesis

Kolasa, J.
2005 Ecological Society of America Annual Meeting
The role, use, and misuse of definitions (with 'disturbance' as a leading example); a case for dialog between semantics and observation.

2005 Ecological Society of America Annual Meeting
Species-area relationships are partly explained by interaction of habitat heterogeneity and species pool.

2005 Ecological Society of America Annual Meeting
Coral reef fish assemblages: contribution of stochastic effects on variation declines over time.

2005 Ecological Society of America Annual Meeting
Allometric scaling at higher levels of biological organization: Evidence from natural aquatic microcosm ecosystems.

McClelland, G.
St. Joseph's Healthcare Regional Respirology Rounds, Firestone Institute for Respiratory Health, Hamilton, Ontario
Determinants and plasticity of oxygen and fuel transport

Canadian Society of Zoologists, Kingston, Ontario
Are there conserved patterns of exercise fuel selection amongst vertebrates?

Nurse C.A.
International Symposium on Arterial Chemoreception, Sendai, Japan
Low-glucose signalling in co-cultures and tissue slices of rat carotid body: neurotransmitter mechanisms

Shandong University School of Medicine, Jinan, Shangdong, China
O2 sensing by adrenal chromaffin cells

O'Donnell, M.
Entomological Society of America, Fort Lauderdale, Florida
Organic anion transport by insect epithelia: Characterization of basolateral salicylate uptake by the Malpighian tubules of Drosophila melanogaster

Canadian Society of Zoologists, 45th Annual Meeting, Kingston, Ontario
Secretion of water and ions by Malpighian tubules of larval mosquitoes: effects of diuretic factors, 2nd messengers and salinity

Quinn, J.
Biology Department, Wilfred Laurier University, Waterloo, Ontario
Kyoto sperm: Germline mutations in gulls and mice exposed to Canadian air pollution

Biology department, York University, Toronto, Ontario
Germline mutations in gulls and mice "in nature": anthropogenic pollution and tandem repeat DNA

Biology department, Trent University, Peterborough, Ontario
Why can't we all just get along? Social cooperation and conflict in joint-nesting smooth-billed anis

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Rainbow, A.J.
State of the Science on Adenovirus – Expert Workshop. Metropolitan Water District of Southern California, Manhattan Beach, California
Repair of UVC-damaged adenovirus and effects of UVC on adenovirus expression

14th International meeting on ADP ribosylation reactions, PARP 2005: Bench to Bedside, Newcastle upon Tyne, UK
PARP-1 knockdown by RNA-interference decreases repair of UV-induced direct and indirect DNA damage

7th Annual Midwest DNA Repair Symposium, Detroit, Michigan, USA.
Role for poly (ADP-ribose) polymerase-1 in the repair of UV-induced DNA damage

7th Annual Midwest DNA Repair Symposium, Detroit, Michigan, USA.
The role of p53 and the XPC gene in base excision repair of DNA damage induced by methylene blue plus visible light in human cells

7th Annual Midwest DNA Repair Symposium, Detroit, Michigan, USA.
Role of the nucleotide excision repair genes in host cell reactivation of a reporter gene damaged by methylene blue plus visible light in Chinese hamster cells

American Association of Cancer research special conference on "Regulation of cell death and oncogenesis, Waikoloa, Hawaii
Increased sensitivity of PDT-resistant HT29 human colon adenocarcinoma cells correlates with increased BNip3 and decreased mutant p53 protein expression levels

30th Annual Lorne Conference on Protein Structure and Function, Cowes, Victoria, Australia
Human cells deficient in transcription-coupled repair show prolonged activation of the jun N-terminal kinase and increased sensitivity following cosplatin treatment

Rollo, C. D.
National Institute of Health (USA) Longevity Consortium Meeting, San Diego.
Body size, growth, aging and free radicals: Lessons from giant mice

Biomarker Pharmaceuticals, Silicon Valley, San Jose California.
A pharmaceutical intervention that extends longevity and abolishes age-related cognitive and brain cell deterioration

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Singh, R.S.
Dept. of Zoology, University of Toronto, Toronto, Ontario
Darwin's Double Dilemma: Sexual Dimorphism and the Problem of Speciation

VIII Eastern Great Lakes Molecular Evolution Meeting, Cornell University.
Characterization of Rapidly Evolving Genes in the Drosophila Genome: sex genes evolve faster

Genomes and Evolution Meeting, Penn State University.
Characterization of Rapidly Evolving Genes in the Drosophila Genome: sex genes evolve faster

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Stone, J.
18th International Conference on Computer Applications in Industry and Engineering Conference, Honolulu, Hawaii
A Complex Dynamic Model for Cancer Growth and Metastasis

2nd Tumor Progression and Therapeutic Resistance Conference, Boston, Massachusetts
A Complex Dynamic Model for Cancer Growth and Metastasis
Origins Institute, McMaster University
Life is What? Astrobiology and The Origins of Life

Weretilnyk, E.
Plant Canada, Edmonton, Alberta
Cloning and biochemical characterization of a novel Arabidopsis thaliana methyltransferase involved in phosphocholine synthesis.

Plant Canada, Edmonton, Alberta
Changes in the physiology and metabolome of Thellungiella salsuginea in response to osmotic stress.

Wood, C.M.
University of Waterloo
The Lake Magadi tilapia, a fish adapted to one of the most extreme aquatic environments on earth

Canada Centre for Inland Waters, Burlington
The Biotic Ligand Model: using comparative physiology to improve environmental regulations

Deakin University, Australia
Metal uptake and toxicity in fish

Bamfield Marine Sciences Centre, Bamfield, B.C.
Modeling metal impacts of fish gills.

University of Alberta
The Biotic Ligand Model-putting physiology into ambient water quality criteria

SETAC N.A. 26th. Annual Meeting Baltimore, MD, USA
How hard is that diet? Implications for metal accumulation and toxicity

32nd Aquatic Toxicity Workshop, Waterloo, Ontario
Pathways of metal uptake and toxicity in fish: putting physiology into environmental regulations

Whole Organism to Mitochondria .Meeting of the Society of Experimental Biology, Barcelona,
The impact of feeding on ionoregulation and acid-base regulation in fish. A tribute to Bob Boutilier

Meeting of the Society of Experimental Biology, Barcelona
The Biotic Ligand Model: putting comparative physiology into environmental regulations. A Tribute to Ted Taylor-Respiratory Physiology

44th Annual Meeting of the Canadian Society of Zoologists, Queen's University, Kingston.
The scale-less carp (Gymnocypris przewalskii): Taking an osmotic holiday in Lake Qinghai

Conference on the Biogeochemistry of Trace Elements. ICOBTE 8th International Adelaide, Australia.
Uptake and toxicity of trace elements to aquatic organisms.

MITHE-RN Annual Research Symposium, Ottawa.
Generation and field validation of chronic Biotic Ligand Models for fish.

Xu, J.P.
Beijing Mycological Symposium. Beijing, China.
Experimental population biology of a basidiomycete yeast

Genetics Society of Canada. Banff, Alberta, Canada.
Mitochondrial inheritance in a fungus

Gordon Research Conference on Quantitative Genetics and Genomics. Ventura, California.
Costs and benefits of hybridization in Cryptococcus neoformans

Zhu, X.D.
Department of Biochemistry, McMaster University
DNA repair complexes at human telomeres: implications for telomere functions


Life@Mac

McMaster University

McMaster University, established in 1887, has occupied its present site in the beautiful west end of Hamilton since 1930. Faculties include those of Science, Engineering, Health Sciences, Humanities, Business and Social Sciences. Full-time student enrolment at McMaster is approximately $17,000 undergraduate and 2,200 graduate students. Collaboration between the various departments of McMaster and studies in interdisciplinary areas are a valuable feature of the scientific research programmes in the University. In the Department of Biology, research may be undertaken entirely within the Department or in conjunction with other Departments such as Anatomy, Biochemistry, Geology & Geography, Pathology, Physics and Psychology.

The University has been building a new Multi-Sport Complex which is scheduled to open in late 2006. This new facility is being built at the north end of the Ivor Wyne Centre. Highlights include: a new wellness and fitness centre that will rank among the best in Canada; the only indoor track in Hamilton, with four 200-metre lanes and sprint lanes; four new squash courts, suitable for international competitions; an additional 15,000 square feet of gymnasium space, double the current capacity; a high performance strength and conditioning area; an indoor climbing wall and cycling studio; multipurpose studios for karate, yoga, dance and tai chi; and an expanded sports medicine and rehabilitation centre. Among the sports activities organized in the University, a renowned Climbing and Caving Club deserves special mention. At appropriate seasons, golf, skiing and sailing are available in the area. Another building project underway is the construction of the New Ronald V. Joyce Stadium In June 2005, Ron Joyce and McMaster University proudly announced Mr. Joyce's gift of $10 million to name the new stadium at McMaster University. The $13 million, 6,000-seat Stadium will create an impressive venue for university football and soccer. It will build on a fan base for university athletics that is already one of the most supportive in the country. It will also position McMaster and Hamilton as the number one destination in the Golden Horseshoe for amateur sporting events, attracting fans and sport tourism dollars into the City.

Visit these links for more information about the University and its facilities and services.
About McMaster: www.mcmaster.ca/welcome/aboutmac.cfm
Relocating to McMaster: www.mcmaster.ca/welcome/relocate/

Hamilton – The City

Hamilton (a city with population ~300,000) is located between Toronto and Niagara Falls. It is situated at the extreme western tip of Lake Ontario. The Niagara Escarpment (locally known as "the mountain), cuts through the city provides an excellent view of the city and its natural harbour. Hamilton is about an hour's drive from Toronto International Airport. In addition, it is less than two hours away from the Buffalo (N.Y.), the closest border of United States.

The city has two major sports activity centres, the Victor K. Copps Coliseum and the Ivor Wynne Stadium. Copps Coliseum is home to the Hamilton Bulldogs hockey team and the stadium is used by the Hamilton Tiger Cats Football team. In addition, Hamilton Place, is one of the finest concert halls in Canada which attracts a variety of plays, musicals, ballets and concerts throughout the year.

The average winter temperature in Hamilton ranges between 0 and -5°C. The snowfalls are lighter compared to the other Canadian cities. The summer temperatures range between 20 to 35°C.

For details about Hamilton, please visit the website: www.myhamilton.ca

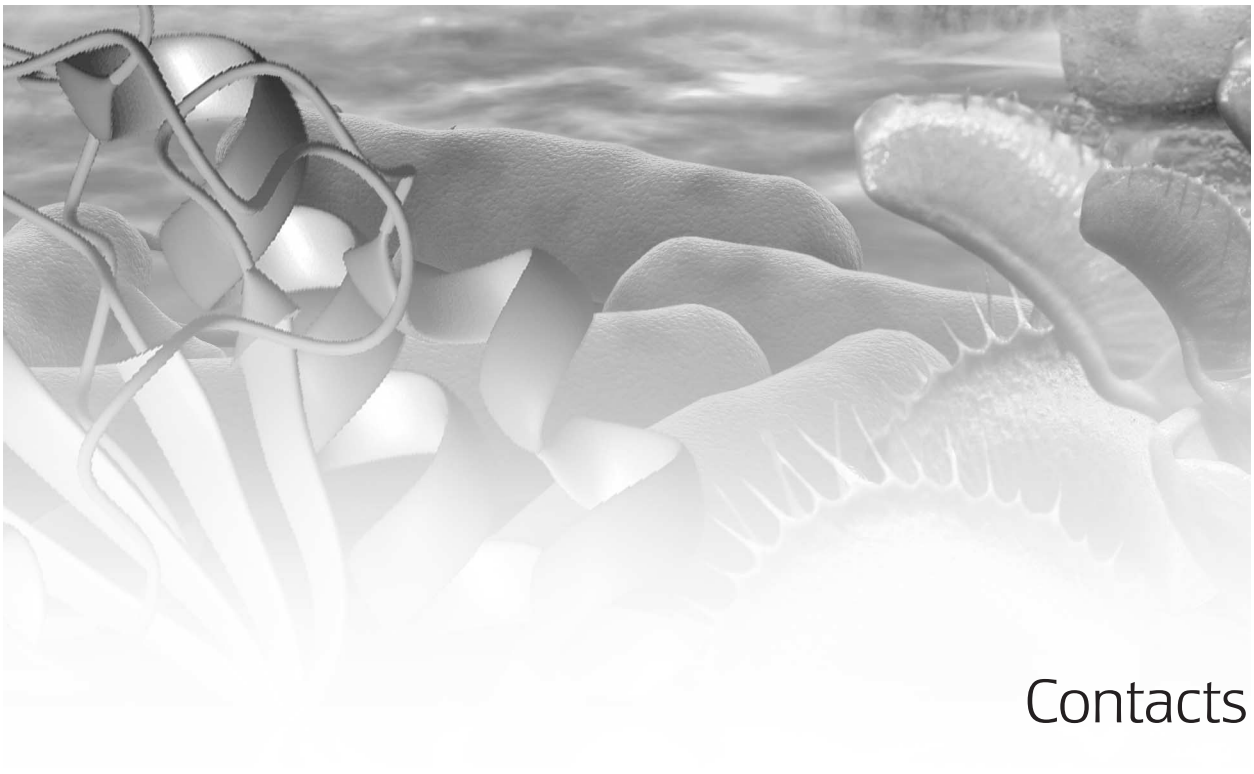
Housing

The housing in Hamilton is generally easy to find around the University campus. Often houses become available when University employees go on research leave. While rents vary depending upon the location and condition of the building, they range between $500 to $2000 per month.

The local newspaper "Hamilton Spectator" is a good source for accommodation advertisements. In addition, the McMaster student housing office (in Wentworth House) also provides help.
Please check out the web site: www.macocho.com/index.cfm.

Transportation

The City and surrounding areas have efficient transportation services. There are many ways in which you can travel in Hamilton. For further information on how to travel to/from and around Hamilton by car, plane, bus, train, bicycle or boat, go to the following **website:** www.tourismhamilton.com/gettingtohamilton



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