ISSUE NO. 1 // FALL 2018

# RESEARCH Magazine

College of Biological Science

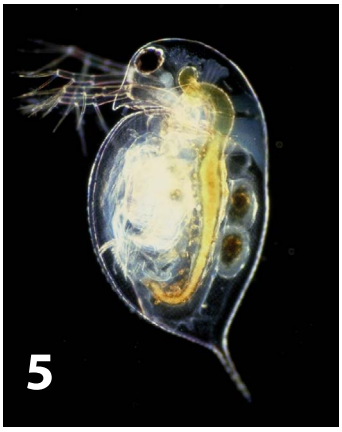
Gaining virtual insights into the molecular structure of the brain

Unravelling the complexities of ecosystem stability

Feeling the pain: Assessing tools to measure patient pain

# Contents







@UofGCBS


**SCRIBE WRITERS**

Danielle Bourque
Andrea Brumwell
Daniel Cervone
Sandra Clark
Evan Despond
Louis Gasparini
Elizabeth Johnston
Michael Lim
Xinjie (Lois) Lin
Gaelan Melanson
Devin McCarthy
Emma Plater
Kevin Romanick
Olivia Roscow
Sidra Sarfaraz
Anjali Silva
Stephen Van Drunen
Adrienne Wan
Xueqi (Sharon) Wang

**EDITOR** Sarah Bates

**DESIGN** Hillary Dort

**PHOTOS** Karen White (p. 8)
Sydney Pearce (p. 19)

**CONSULTANTS** Owen Roberts
Ian Smith
Hannah Collinson

# Message from the Dean

**Welcome to the inaugural issue of the College of Biological Science's Research Magazine**.

This collection of research stories highlights just some of the leading-edge research taking place in the college as part of our core mission to expand our understanding of life, from DNA and cells to complex ecosystems. In this issue, you will learn about exciting discoveries such as a novel cell-trafficking protein with a potential role in cancer (p. 20) and an unexpected culprit behind backaches (p.11). You'll also read about a new technique to measure the impact of water pollutants on aquatic organisms (p. 5) and how droughts and floods may reduce the ability of peatlands to absorb carbon dioxide (p. 22), among many other newsworthy findings.

I'm especially pleased to note that all the research stories showcased here were contributed by CBS's own graduate students. These students are the founding cohort of our SCRIBE program (Students Communicating Research in Biology Education), a new and successful initiative that sees graduate students in the college take an active role in translating and communicating research results for non-specialist audiences.

This is an exciting time in CBS. We are now one year into our 2018-2023 strategic plan, which outlines our mission to be a globally-recognized hub for biological research and scholarship with a unique focus on the student experience. As we take stock of our progress to date, it strikes me that this magazine reflects our achievements towards a number of our strategic priorities. Not only do these stories speak to our efforts to strive for excellence in biology research and produce graduates that are in high demand, but by sharing and celebrating these discoveries with each other and the wider CBS community, I believe it will also help strengthen our sense of common identity.

Happy reading, and I look forwarding to sharing more of our research successes in the future.

**Jonathan Newman**
Dean, College of Biological Science
University of Guelph

### ABOUT CBS RESEARCH

- Globally-recognized research programs in integrative biology, human health and nutritional sciences, and molecular and cellular biology
- World-class research facilities including the Advanced Analysis Centre and Biodiversity Institute of Ontario
- 100 full-time faculty
- 6 Canada Research Chairs and 2 University Research Leadership Chairs
- 4500 undergraduate students
- 300 graduate students
- Over 90 full-time research staff
- $15 million annually in research funding

# DRINK YOUR BEETS

## How beetroot juice improves cardiovascular health

**By Anjali Silva**

Drinking nitrate-containing beetroot juice can improve cardiovascular health by altering signals from the brain, according to a study from a team of researchers in the Department of Human Health and Nutritional Sciences led by Prof. Philip Millar.

Nitrate in beetroot juice is already known to lower blood pressure. The nitrate can be converted to nitric oxide, which causes blood vessels to dilate and in doing so, reduces blood pressure. But nitric oxide also regulates the nerve signals from the brain that cause blood vessels to constrict.

"We know that nitric oxide can dilate blood vessels, but we wanted to know if part of that dilation is caused by decreased constriction signals from the nervous system," says Millar.

Millar and his team asked young, healthy men and women to drink beetroot juice with high nitrate or beetroot juice with no nitrate (a placebo) in what is called a "crossover" study. A crossover can be a particularly informative type of study because instead of having one group of people do one treatment and another group do a different treatment, the same subjects undergo both treatments. Blood pressure and heart rate were measured before and after consumption of both types of beetroot juice. The team also measured neural signals from the brain (known as "sympathetic outflow") to a nerve in each subject's leg.

Although no differences were found in blood pressure in these healthy subjects, the results showed that nerve impulses to blood vessels in the muscle were lower for those that consumed beetroot juice with high nitrate compared to the placebo.

The findings indicate that dietary nitrate can evoke a neural response, lessening the sympathetic outflow from the brain. It is an important discovery, because heightened neural signaling or "elevated sympathetic outflow" is a hallmark of clinical conditions like high blood pressure or heart failure.

"Many of the drugs prescribed today for cardiovascular disorders act on the blood vessels," notes Millar. "But we don't have many therapies to target elevated central sympathetic outflow. These findings offer a potential avenue to investigate a new type of treatment."

In other words, dietary nitrate could someday be used to treat the central "source" of abnormal neural signals associated with cardiovascular disease.

In future, Millar and his team plan to study the long-term effects of dietary nitrate supplementation to see if bigger or sustained effects can be elicited.

Karam Notay and Anthony Incognito also contributed to the study. Funding was provided by the Natural Science and Engineering Research Council of Canada, the Canada Foundation for Innovation, and the Ontario Ministry of Research, Innovation and Science.

This research was published in the *American Journal of Physiology - Heart and Circulatory Physiology*.

# A new take on an old pollution problem in Canada's lakes

## By Evan Despond

Human activities may be more damaging to aquatic life in Canada's lakes than previously thought, according to a team of researchers in the Department of Integrative Biology.

Profs. Andreas Heyland and Teri Crease, along with graduate student Andrew Liorti, studied the interaction of calcium and copper in *Daphnia pulex* (see image bottom left), a crustacean commonly found in freshwater planktonic communities. Calcium is an essential mineral to aquatic organisms with hard exoskeletons or shells, but pollution and deforestation have acidified many bodies of water, leading to low levels of calcium. In contrast, copper is a heavy metal that is toxic to living organisms and – due to mining activities and anti-fouling boat coatings – is now a common contaminant in some lakes.

"I've always been very interested in better understanding the impact that humans have on ecosystems," says Heyland.

He and colleagues examined how sub-lethal doses of copper could negatively affect the growth and lifespan of *Daphnia*. The team developed a new technique for monitoring individual animals automatically over time, using time-lapse photography to reveal the exact time of death in a specific assay. With this setup, *D. pulex* were exposed to different combinations of copper and calcium, both at high and low levels. The team found that the most deadly combination was low copper plus low calcium, while high levels of calcium seemed to protect the creatures from copper.

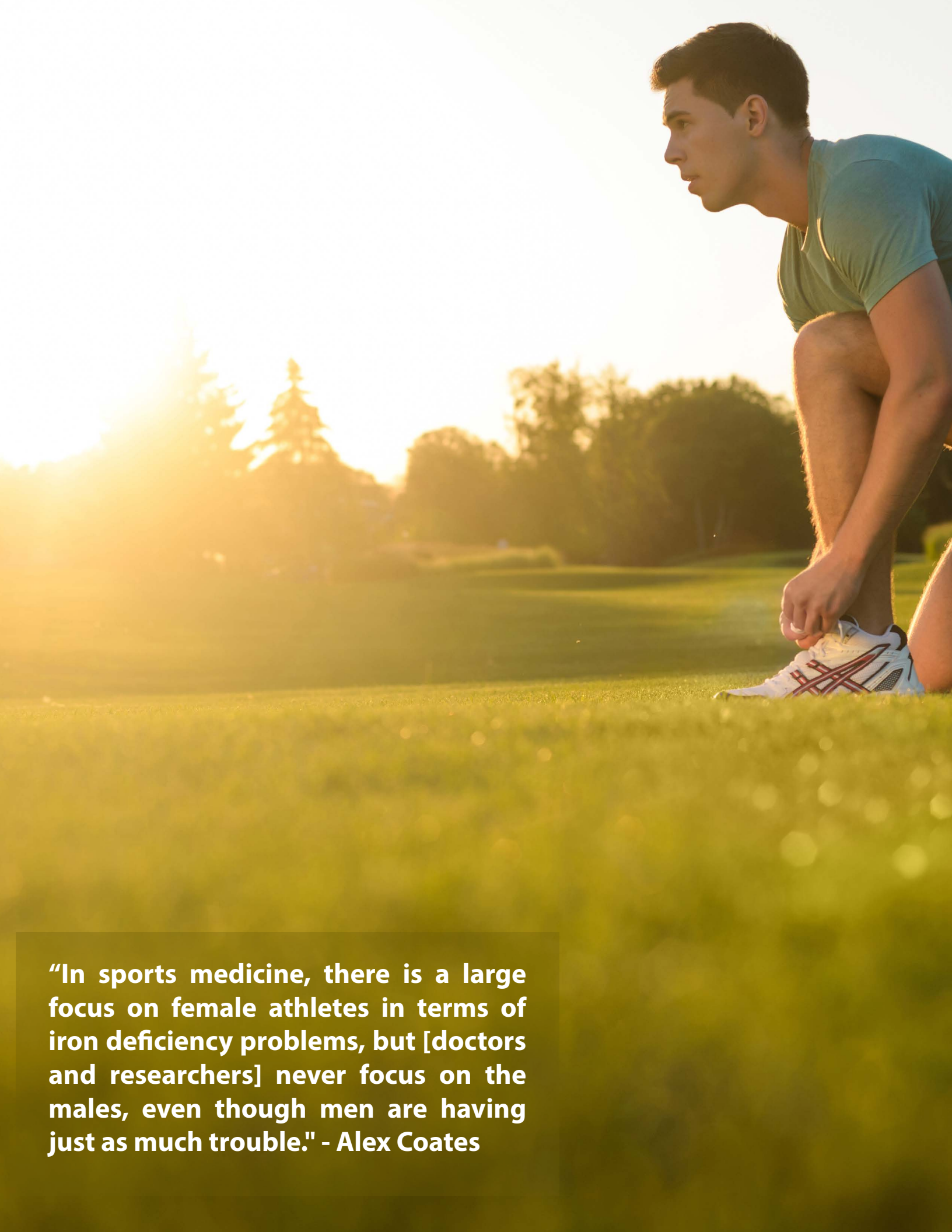
These results indicate that lakes with low levels of calcium that are also contaminated with copper may be much harsher places for *Daphnia* and other crustaceans to live. This could result in them dying off, leaving less food for larger animals, or cause copper to accumulate in higher predators.

The study is the first to look at copper and calcium interaction in *D. pulex*, and it also examined the uptake kinetics of these two metals. While the results still do not explain exactly how the two compounds interact, the team was intrigued to see that there is an interaction.

"Everyone knows about a variety of heavy metals, but while levels for many of them have been significantly reduced in freshwater ecosystems, copper remains a problem," says Heyland.

The study highlights the need to look at a variety of factors when assessing the impact of activities like mining, because the effects of some pollutants may not be obvious. Future research may look at long-term studies to see whether this impacts other life stages such as adults, or try to understand how the interaction works.

This research was funded by Natural Sciences and Engineering Research Council and published in the *Journal of Limnology*.



**“In sports medicine, there is a large focus on female athletes in terms of iron deficiency problems, but [doctors and researchers] never focus on the males, even though men are having just as much trouble." - Alex Coates**

# Iron deficiencies more common in elite athletes than previously thought

## By Adrienne Wan

Elite endurance athletes, particularly males, are more prone to iron deficiency than previously thought, according to a team of researchers led by Prof. Jamie Burr in the Department of Human Health and Nutritional Sciences.

Training at the elite level can lead to both iron deficiency (ID), which is defined by low iron levels in the blood, and iron deficient anemia (IDA), which is characterized by both low iron and low hemoglobin levels. Hemoglobin is an iron-containing protein in red blood cells that is critical for carrying oxygen to the body's tissues.

"In sports medicine, there is a large focus on female athletes in terms of iron deficiency problems, but [doctors and researchers] never focus on the males… even though men are having just as much trouble," says graduate student Alex Coates, who was lead author on the study.

Coates and her colleagues in the Human Performance and Health Research Lab analyzed blood samples from 38 elite runners and triathletes, looking at both iron and hemoglobin levels to determine the prevalence of ID and IDA. They found that 60 per cent of female and 38 per cent of male triathletes had one or more episodes of ID, while the same was true for 56 per cent of female and 31 per cent of male runners. These figures were much higher than what has been previously reported in the literature, say the researchers.

Even more surprisingly, there was a higher incidence of IDA with male elite athletes than their female counterparts (20-25 per cent in males compared to only 0-6.3 per cent in females), although there was no clear explanation as to why this was the case.

The higher than expected incidence of iron deficiencies in elite athletes – a group that undergoes frequent and regular monitoring of health and performance – underscores the challenge faced by many of them when it comes to maintaining adequate levels of iron, which is essential to athletic performance.

Low iron levels can be caused by a number of things, such as foot-strike hemolysis (the destruction of red blood cells when a runner's foot hits the ground), frequent use of nonsteroidal anti-inflammatory drugs, loss through urine and sweat, or nutrient insufficiencies in one's diet. High levels of a hormone called hepcidin, which increases after a workout, can also reduce iron absorption and tends to counteract the benefits of iron supplementation.

As part of the study, the athletes completed a questionnaire regarding their iron supplementing habits. The researchers found that supplementation was not correlated to an increase in blood iron or hemoglobin levels. The results highlight that there is still work to do to help elite athletes manage their iron levels.

"We need to figure out a better iron supplementation protocol," says Coates. She notes that a smaller, more frequent dose of iron, such as a 40-60 mg dose every other day, may allow for better iron absorption compared to a much higher dose taken less often. Additionally, a diet rich in a variety of nutrients and sufficient caloric intake may also help athletes prevent IDA.

Margo Mountjoy from the Health and Performance Centre also contributed to the study. This work was funded by Athletics Canada and NSERC.

This research was published in the *Clinical Journal of Sport Medicine*.

# A Luman recruitment factor dose a day may help keep herpes away

**By Michael Lim**

A research team led by Prof. Ray Lu in the Department of Molecular and Cellular Biology has uncovered a compound that may keep herpes simplex virus-1 (HSV-1) from reactivating in infected individuals.

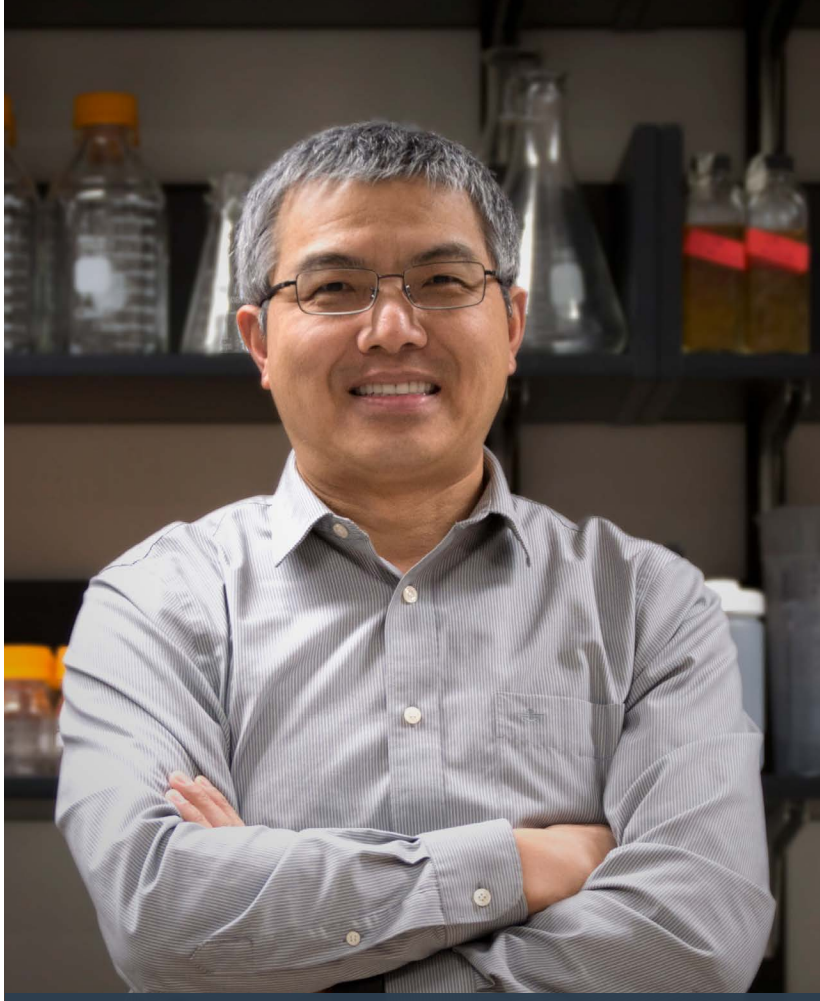
HSV-1, or oral herpes, is incredibly wide-spread. According to the World Health Organization, roughly 67 per cent of people under the age of 50 are infected with the virus, which cycles through active and latent periods of infection. There is no known cure for HSV-1, but Lu and his team have found that a molecule known as Luman recruitment factor (LRF) may keep HSV-1 inactive.

When active, HSV-1 produces “messenger RNA”, or mRNA, which is then used to make proteins that lead to symptoms within its host. But when HSV-1 is inactive, it produces little to no mRNA, and no proteins.

This is where LRF comes in. Lu and former PhD student Timothy Audas were interested in LRF as a potential transcription factor for HSV-1. A transcription factor is something that can increase or decrease mRNA levels of their targets, and Lu and Audas wondered if altering LRF levels could help reduce the symptoms of HSV-1 infection.

Working with fellow graduate students Philip Hardy-Smith, Jenna Penney, and Tiegh Taylor, Audas looked at the effect of different LRF levels within human embryonic kidney cells infected with HSV-1. The results were clear: increasing LRF levels resulted in much lower HSV-1 mRNA levels. That means that administering LRF to people infected with HSV-1 may help keep the virus in its latent form, and may even serve as a type of ‘cure’.

This is potentially great news for those infected with HSV-1. While most infected individuals show no or mild symptoms, HSV can have more severe and frequent symptoms in immunocompromised individuals (for example, those receiving an organ transplant, or with an advanced HIV infection) or cause long-term neural damage or death in newborns.



**“I’ve always been interested in viruses and how they regulate their genes. HSV-1 was especially interesting due to its latency ability.” - Prof. Ray Lu**

*Photo credit: Karen White*

But the LRF story doesn’t end there. Lu has also recently identified additional roles for LRF in stress signaling and behaviour. Mice that were genetically modified to express no LRF, and thus are more strongly affected by HSV-1 infections, displayed "blunted" stress responses, with fewer behaviours attributed to anxiety. This may signify a reduced ability to properly respond to stress in the absence of LRF. As such, Lu and his current graduate students have shifted their focus from strictly HSV-1 studies, to better understanding the widespread effects of LRF on the stress response and behaviour of whole organisms.

“I never expected to go from working on cells to behavioural studies,” says Lu. “I suppose that’s just the nature of science.”

Funding for this research came from the Canadian Institutes for Health Research, and the Natural Sciences and Engineering Research Council of Canada, with a plasmid provided by Johanna Zilliacus (Karolinska Institutet).

This research was published in the *European Journal of Cell Biology*.

# Helping the monarch butterfly with milkweed restoration

**By Louis Gasparini**

Monarch butterfly populations have been rapidly declining for over 20 years, but recent findings by a team of integrative biology researchers could pave the way to help these iconic insects rebound.

Led by Prof. Ryan Norris, the team monitored monarch butterfly habitats in southern Ontario and found that monarchs lay more eggs in patches of milkweed near agricultural landscapes. The findings can be used to plan milkweed restoration efforts to benefit monarchs.

"There is an ongoing conflict between agriculture and milkweed," says Norris, noting that milkweed has long been viewed as an unwanted weed in farmers' fields.

Monarch butterflies lay their eggs exclusively on milkweed plants. The amount of available milkweed, however, has dropped drastically due to the widespread use of herbicides in parts of Canada and the United States. In particular, herbicide-tolerant crops that allow the use of a broad spectrum herbicide known as glyphosate is contributing to the loss of milkweed. Fewer milkweed plants means that monarchs have fewer places to lay their eggs, resulting in a decline in monarch populations.

Increasing the amount of milkweed available in the right places could help monarch numbers rise, so Norris and his team set out to determine where the butterflies prefer to lay their eggs.

The team examined milkweed in 26 locations in southwestern Ontario over two years, looking to find monarch eggs and caterpillars. They focused on milkweed in three types of areas: road-side patches, agricultural fields, and natural areas such as meadows. They found significantly more monarch eggs in milkweed patches located close to agriculture than in patches next to roads or in the wild. They also found that the number of monarch eggs was dependent on the size of the patch, and how many milkweed plants were in the patch; monarchs prefer to lay their eggs in smaller patches near agriculture, where milkweed plants are more spaced out.

The results may help stop the decline of the monarch butterfly by guiding conservation programs to restore milkweed plants and provide the best egg laying habitat. For example, the findings could be used to plan incentive programs that reward farmers for growing milkweed on the borders of their fields.

**"Conserving monarchs is a learning opportunity for other species we also hope to conserve," says Norris.**

By working to conserve monarchs and other species in decline, researchers such as Norris and his team hope to help preserve Canada's biodiversity for future generations.

Other contributors to the study include Grace Pitman from the Department of Integrative Biology, and Dr. Tyler Flockhart from the University of Maryland. Funding was provided by Syngenta Canada Inc. and the Natural Sciences and Engineering Council of Canada.

This research was published in *Biological Conservation*.

# GETTING TO THE ROOT OF LOWER BACK ACHES

## By Xueqi Sharon Wang

Suffering from a stiff lower back? It may not be your back muscles causing the problem, says a team of researchers in the Department of Human Health and Nutritional Sciences.

Lower back pain is among the most common debilitating health problems, and those who suffer are quick to blame their back muscles. But a recent study led by Prof. Stephen Brown has found back muscles will actually become less stiff to try and compensate for what can sometimes be the real culprit behind a sore back: a stiff spine.

"People who have chronic back pain often have back muscles degenerated or with abnormal functions," says Brown. "But we don't know if the chronic back pain developing over time is causing the muscle to degenerate, or if there is something fundamentally different in the muscle that is predisposed to developing a back problem."

The muscles of the back play an important role in both the prevention and the rehabilitation of back problems. The spine and associated skeletal muscles provide support, strength and mobility for daily motions, such as walking, lifting and exercising, which makes them susceptible to injury. Muscles can react to a low back injury by increasing their activity and creating a sensation of stiffness, but it may also be possible for them to adapt in a different way.

"In response to low back injuries, your body is adapting or remodelling," says Brown. "If this is a maladaptive response, which means it is negative, then we need to fix or reverse that remodelling processes. However, it's possible that the changes in the muscle are a positive response to back injuries."

To find out, Brown and his team performed a trial with lab mice to test whether a stiff, less mobile spine causes changes in the stiffness of the surrounding muscles. Using a special strain of mice with spines hardened from excess calcium deposits, they showed that back muscles were less stiff in these mice compared to those with normal spines. And, in contrast to previous studies, the team found that the biggest changes in the muscles were not seen in the extracellular matrix in the connective tissues around the muscle cells, but within the cells themselves.

"We think these changes in the spinal muscles are most likely to be a negative response," concludes Brown. "But we still need to run more trials to test if what we've found is unique to the strain of mice used in our study, or if it's universally observed regardless of the source of the spine stiffness."

The next step, says Brown, is to move on to more fundamental questions regarding human health. For example, when people say their back feels stiff, is that directly related to physical changes in the spine? And if the spine is indeed stiffer, then what's going on with the back muscles? With over 80 per cent of adults claiming to have experienced some levels of lower back pain in their lifetime, answers to these questions promise to yield important information for many of us.

The project was funded by the Natural Sciences and Engineering Research Council and the Canadian Institutes of Health Research. This research was published in the journal *Spine*.

# “Junk” DNA predicts body size in seed shrimp

**By Olivia Roscow**

It turns out that size does matter, say researchers in the Department of Integrative Biology who have discovered that the size of a tiny sea creature’s genome may influence its body size.

A genome is the entire set of DNA and genes that an animal possesses - but not all of this DNA has an obvious purpose. For example, up to 98 per cent of the human genome has no known function. The mystery surrounding the presence of non-coding, or “junk”, DNA is formally referred to by biologists as the “C-value enigma.”

Prof. Ryan Gregory and his research team are spearheading attempts to find out the purpose of junk DNA, where it comes from, and why it is so abundant. The team has worked with flies, hummingbirds, and now seed shrimp in order to find out if there is a relationship between amount of junk DNA and traits such as body size, metabolism, and development.

“Grasshoppers have genomes five to six times larger than humans,” says Gregory. “It raises interesting questions about what’s going on.”

In the case of seed shrimp—tiny crustaceans just 1 to 3 mm in size—genome size seems to influence body size. Gregory and his team looked at 46 seed shrimp species and found that the larger the genome, the bigger the seed shrimp. It follows a similar pattern to what has been observed in other animals with determinate growth – that is, animals that grow in body size by increasing their cell volumes rather than the number of cells. Larger genomes may lead to increased cell sizes, which might explain how genome size could predict eventual body size for some animals.

In contrast, Gregory and his team found no relationship between genome size and habitat type of the seed shrimp, as marine and freshwater species did not differ significantly in their genome size. However, genome size may still influence other traits that have not yet been investigated, such as life span.

*An ostrocod or “seed shrimp”. Photo credit: Anna33 at English Wikipedia.*

According to Gregory, junk DNA can provide insights into the degree that noncoding DNA influences the growth and development of many animals. Some forms of noncoding DNA can influence the expression of other genes while others have no apparent function at all, yet it appears that even the presence of apparently non-functional DNA can still affect many biological traits. He and his lab will remain at the forefront of probing the C-value enigma as they continue to explore the genomes of ever more diverse animals to unravel the secrets of junk DNA.

"I get to work from the genome up [animals] and from the genome down [genes]… there’s a lot of diversity doing this kind of work,” says Gregory.

This research was funded by the National Sciences and Engineering Research Council of Canada (NSERC), the National Science Foundation, the Research Mentorship Program, and the Australian Museum.

This research was published in the *Journal of Heredity*.

# Human activity impacts wolf predatory behaviour in northern Ontario

**By Kevin Romanick**

Humans have long been known for having a major influence on animal habitats. Now, a new study by researchers in the Department of Integrative Biology has shown that human activity can also influence how a predator thinks and hunts.

In one of the largest studies of its kind, Prof. John Fryxell and his research team tracked wolves in northern Ontario during a three-year span, as well as their preferred prey, moose. The group found that the wolves base their movement around moose habitats, which is heavily influenced by human activity.

“We’re trying to get inside the mind of the wolves to understand how these animals make decisions that impact their survival,” says Fryxell.

Fryxell and his colleagues fitted 49 wolves from over 30 packs with GPS tracking collars that enabled the team to follow the animals’ movements. Moose numbers were also measured using aerial techniques to survey over 40,000 square kilometers of land.

Moose are drawn to areas where logging and other human activity has disturbed the land, because it facilitates the growth of shrubs and leafy brush that moose like to eat. In areas like this where moose are abundant, wolves use the land to directly track the moose.

*continues on next page*

But in remote, undisturbed areas where deciduous shrubs and trees are few and far between, so are the moose. The wolves do not encounter enough prey to survive by direct tracking, and they require more efficient ways to maximize encounters with moose. So, the wolves make use of linear paths, such as frozen lakes and man-made access roads to get to and from moose habitats.

Wolves in northern Ontario concentrate their predatory efforts on moose, but they will take down any vulnerable caribou that crosses their path. To see how caribou fit into the picture, the team also used GPS to track 124 caribou. Interestingly, they found that the caribou avoided moose habitat even more strongly than they avoided the wolves' travel routes. In other words, caribou isolate themselves from the moose to avoid wolf predation.

These findings highlight how human destruction of natural habitats can change animal behaviour at the population level.

"Sustaining the boreal forest is on a lot of agendas. This work relates to the necessity of maintaining habitats," says Fryxell.

The study paves the way for future researchers tracking animal behaviour. To track so many animals across such a vast landscape, the team developed new tracking analysis methods that will enable other large multispecies studies in the future.

This project was funded by the Forest Ecosystem Science Cooperative, Natural Sciences and Engineering Research Council of Canada, Ontario Ministry of Natural Resources, and the National Research Council of Canada.

This research was published in *Ecosphere*.

# Superbugs soon to meet their match

## By Danielle Bourque

To defeat a superbug you have to know its kryptonite, and scientists in the Department of Molecular and Cellular Biology have taken big steps to describe it.

Prof. Anthony Clarke and PhD student David Sychantha spent three years characterizing "OatA", a weapon that antibiotic-resistant superbugs such as *Staphylococcus aureus* and *Streptococcus pneumoniae* use to shield themselves from attack by human immune systems.

"This is one of the most impressive papers I've published," says Clarke. "We took what was already known in the field and applied it in a new way."

Superbugs are disease-causing bacteria that are resistant to our current selection of antibiotics. They can't be killed outright.

But scientists like Clarke and Sychantha are approaching this problem by investigating targets that may weaken superbug's defences, so that human immune systems can finish the bacteria off. One of these defence targets is O-acetyltransferase, or "OatA" for short.

OatA is an enzyme—a molecule that speeds up processes happening in and around a cell. When a bacterial infection is underway, OatA modifies a compound called peptidoglycan (PG) that forms the cell wall. PG maintains the bacterial cell's structure and keeps it alive. But when OatA modifies PG with acetyl groups, that wall also becomes a shield against attack from the human immune system.

In the case of human health, the best defence is a good offence. If PG is the superbug's shield, then lysosymes are the human hosts' enzymatic swords that slice through it, causing bacteria cells to burst open.

But when PG is modified by OatA, lysosymes cannot break through the barrier and kill the bacteria. Knowing OatA's structure—and how that structure modifies PG—are the keys to designing new drugs that can stop OatA from working and give human immune systems a fighting chance against superbugs.

Getting this information wasn't easy. Scientists have known about OatA for a decade, and about peptidoglycan O-acetylation for over 60 years, but because PG doesn't naturally dissolve in water, investigating both pure OatA and PG together in a test tube environment was previously very difficult.

By engineering their structures to encourage dissolving, Sychantha was able to examine the interaction between OatA and PG outside of the cell for the first time. He also captured OatA's previously unknown crystalline form, using specialized facilities for high-resolution molecular imaging at The Hospital for Sick Children in Toronto.

"Getting three years worth of PhD work published feels pretty good," says Sychantha, who is the lead author of the publication. "This is an important step forward in the battle against antibiotic-resistant superbugs."

The search for OatA's kryptonite has already begun in Prof. Clarke's lab.

Contributors to the project include: Carys Jones (University of Guelph); Dustin Little and Lynne Howell (University of Toronto); Patrick Moynihan (University of Birmingham); Howard Robinson (Brookhaven National Laboratory); Nicola Galley, David Roper, and Christopher Dowson (University of Warwick). This study was funded by grants from GlycoNet (a Canadian National Centre of Excellence); and the Canadian Institutes of Health Research (CIHR).

This research was published in *PLOS Pathogens*.

# GUT BACTERIA:
## Unsung heroes in the fight against disease

**By Emma Plater**

Gut bacteria may play a vital role in protecting premature infants from a rare but severe condition, according to a study by researchers in the Department of Molecular and Cellular Biology.

"We are realizing how important the gut is to health," says Prof. Emma Allen-Vercoe, who collaborated with colleagues at Sick Kids Research Institute and the Baylor Research Institute on the study. "It could be considered a vital organ."

Idiopathic hypertrophic pyloric stenosis is a condition that leads to elevated blood pressure and projectile vomiting in infants. While the condition often resolves spontaneously, nourishment is a serious concern during its course. It is caused by a lack of tetrahydrobiopterin (BH-4), a substance important to many biochemical pathways in the human body. In premature infants BH-4 can be missing, leading to temporary but severe health problems.

Allen-Vercoe and colleagues made two important discoveries. First, in mice with BH-4 artificially removed prior to birth, they found that BH-4 is present in the mice by the time they reach adulthood. Second, they determined that BH-4 is produced in the adult human gut by a type of bacteria called Actinobacteria. The findings confirm that BH-4 is produced by gut microbes, and suggest that these specific bacteria could serve as a form of therapeutic treatment for premature infants with the condition.

According to Allen-Vercoe, the human gut ecosystem is fully developed by age three. The environment the infant is exposed to, both in the womb and after birth, contributes to this microbial ecosystem. But premature infants do not have the same exposure to bacteria, which may be why BH-4 deficiency is most commonly seen in this group and usually disappears by adulthood.

"In addition to helping infants affected by this condition, this discovery leads to the question of which other substances can be provided to the gut to help with other conditions."

In fact, the question is just the tip of the iceberg in scientists' understanding of the role of the human gut and health and disease. For example, in the age of antibiotic use, how much of their microbial ecosystem might someone be missing after a round of antibiotics, and how might this impact individual's health? Can a person take a "pill" to reintroduce specific bacteria and treat certain conditions?

Allen-Vercoe and her colleagues are continuing to probe the fascinating relationship between gut microbes and human health. "It's exciting research," she notes.

This work was made possible by a grant from the Canadian Institutes of Health Research. The research team comprised of Dr. Jaques Belik, Yulia Shifrin and Jinqyi Pan from Sick Kids Research Institute, Erland Arning and Teodoro Bottiglieri from the Baylor Research Institute in Texas, and Michelle C Daigneualt from the University of Guelph.

This research was published in *Scientific Reports*.

# Gaining virtual insights into the molecular structure of the brain

Using an advanced computing network to visualize interactions between two key proteins has brought researchers in the Department of Molecular and Cellular Biology one step closer to understanding the molecular structure of the white matter of the brain – findings that could also lead to important insights regarding the onset of multiple sclerosis (MS).

A team led by Prof. George Harauz used the Shared Hierarchical Academic Research Computing Network (SHARCNET) facility at the University of Guelph to better understand how myelin, the protective coating of the central nervous system that breaks down in MS, develops. The advanced molecular modelling techniques enabled by SHARCNET allowed the team to visualize the interaction between two proteins: myelin binding protein (MBP) and Fyn-SH3, each essential to the health of myelin.

“Our work has been driven by the desire to understand better at the molecular level how myelin is assembled in the healthy brain and how it degenerates in the MS brain,” says Harauz.

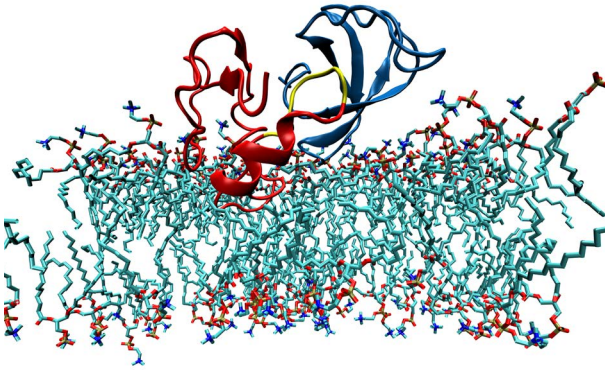
MS ultimately involves an autoimmune attack where myelin is depleted and can’t fully repair itself. Because myelin upholds the body’s communication system by enabling nerves to transmit properly, its breakdown leads to MS symptoms such as pain, numbness, and loss of coordination. Harauz’s team believes it is crucial to first understand how myelin develops, in order to then begin to understand why it can’t regenerate itself fully in MS.

Former University of Guelph research associates Dr. Kyrylo Bessonov and Dr. Kenrick Vassal led the modeling efforts, spending almost four years delving into the complex molecular world of myelin formation.

The team had previously carried out cell-based research that showed the central region of MBP is the target of phosphorylation – a process that modifies the protein’s structure and interactions with other cellular components. Knowing that phosphorylation would change MBP’s interaction with Fyn-SH3, they investigated whether improper signalling between these proteins is the reason why remyelination ultimately fails in the MS brain.

*Photo credit: Sydney Pearce, SPARK*

The virtual modelling program available on SHARCNET allowed them to develop a protein model to visualize, in 3D, how phosphorylation can change the interactions between MBP and Fyn-SH3.



*Computer visualization of proteins involved in myelin formation. Image courtesy of G. Hauraz.*

The importance of using molecular modelling becomes clear: while experimental data that comes from cellular and biochemical research is essential to understanding these interactions, it can be costly and time-consuming, and in general is only indirectly able to contribute to visualizing these interactions. Publicly available computing infrastructure such as SHARCNET allows researchers all over Canada, including the Harauz lab, to run longer simulations while focusing on specific questions.

"This is one step towards modelling more complex systems that reflect more closely the true composition of brain myelin, which would be really exciting," says Harauz.

Harauz and his team hope the study can guide efforts to model these interactions further in an increasingly complex environment more closely matched to that of the human brain, and to better understand the implications for diseases such as MS.

The research was funded by the Natural Sciences and Engineering Research Council of Canada and published in *Proteins*.

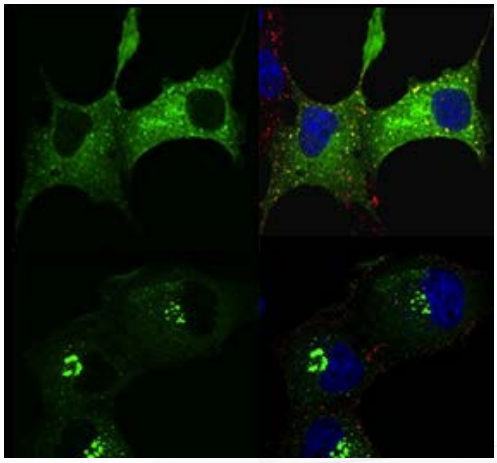
# Study discovers unexpected ability in cell-trafficking protein

**By Daniel Cervone**

A novel cell-trafficking protein may have an unexpected ability to change how certain molecules are transported in and around cells – a finding that could have implications for diseases like cancer, say researchers in the Department of Molecular and Cellular Biology.

Coordinating the way things are commissioned to move around a cell can be tricky business. Despite lacking the defined infrastructure and painted lines that you may find on city streets, the machinery in a human cell is very efficient at getting things where they need to be, particularly when prompted to do so. A family of proteins known as "Shc" proteins play an important role in this process by coupling external stimuli to internal cellular processes.

Now, a team of researchers led by Prof. Nina Jones has shown that a specific Shc protein, "ShcD", behaves differently compared to its family members. Together, Jones and graduate students Melanie Wills and Hayley Lau characterized this new protein and convincingly demonstrated its ability to change cellular trafficking. Namely, the movement of a molecule called epidermal growth factor (EGF).



*Microscopic image of Shc proteins in a cell*

EGF is a protein that promotes cell growth. EGF acts like a "key" that binds to a specific receptor or "lock", EGFR, located on the cell membrane. Once the key fits the lock, this relays a message to other proteins which carry out a very specific effect. The cell can also internalize this "lock and key" complex which either leads to a host of diverse cellular events or gets targeted for death. However, the key can only fit the lock if the lock is available.

Jones and her colleagues used fluorescently-tagged proteins to track how things moved around both healthy and cancer cell lines and subsequently became active in the presence of different Shc proteins. They were astonished to discover that the ShcD protein restrained the EGFR to the center (nucleus) of the cell – sheltered away from where it needed to be to meet with the key at the cell's surface.

"EGFR may have sites that ShcD can regulate, somewhat negating the necessity of a ligand (the key) in its entirety – this intrigues us!" says Lau.

The team also found that in ShcD's presence, the EGFR "lock" tends to be tagged with a molecule called ubiquitin, which is classically considered a signal for its degradation. Lastly, when they modified ShcD's structure so that it more closely resembled other members of the Shc family, it restored ShcD's ability to bring EGFR to the cell surface and bring the key into the cell.

Many human cancers (eg. melanoma, glioma) display higher levels of ShcD and researchers aren't yet sure why.

"ShcD's properties are very unique to this family of proteins," adds Lau. "We're excited to move forward in characterizing it and applying what we learn to a disease model."

The above work was supported by grants from both the Natural Science and Engineering Research Council of Canada (NSERC) and the Brain Tumour Foundation of Canada.

This research was published in the *Journal of Cell Science*.

# Preventing unwanted side effects from a common psychiatric drug

**By Elizabeth Johnston**

Blocking a hormone receptor in the liver may be key in preventing an unwanted side effect of a drug used to treat a range of psychiatric disorders, according to a team of researchers led by Prof. David Wright in the Department of Human Health and Nutritional Science.

The team found that high blood sugar caused by a common antipsychotic drug, olanzapine, can be prevented by blocking receptors for a sugar-regulating hormone known as glucagon. Normally, glucagon tells the liver to release glucose into the blood stream when blood sugar is low and the body needs energy. But in patients taking olanzapine, the liver releases sugar when it is not supposed to, leading to high blood sugar; over time, type 2 diabetes may result.

"We were really interested in examining how antipsychotic drugs cause spikes in blood sugar. A few studies hinted at the possibility of glucagon being involved, but it hadn't really been well tested. We have provided the first evidence showing the link," says Wright.


Wright and his team bred a special colony of genetically-altered mice that lacked liver glucagon receptors, and found that these mice did not experience an increase in blood sugar levels after an olanzapine injection. A second group of mice that still had their glucagon receptors saw a spike in blood sugar after the same injection of olanzapine.

"The ability to block olanzapine-induced increases in blood glucose is exciting. It identifies a mechanism that could be central to this unwanted side effect of the drug," says lead author and graduate student Laura Castellani.

Olanzapine is a second generation antipsychotic used to treat schizophrenia and bi-polar disorder. Increasingly, it is also prescribed for anxiety, as well as attention deficit disorder. Its effect on blood sugar means it can contribute to the onset of diabetes. Wright and other health researchers believe it is important to be able to mitigate the disruptions to sugar metabolism caused by olanzapine and other drugs. In a world where diabetes is already all too common, adding medication to a growing list of causes is a major concern.

The findings from this study provide critical information to pharmaceutical companies designing antipsychotic medications, as well as to those who require olanzapine who may need to make lifestyle changes – such as exercising more - to lessen the negative effects of the drug on their blood sugar levels.

Other contributors to the project include Willem Pepper, Charles Sutton, Jamie Whitfield (Department of Human Health and Nutritional Sciences), and Maureen Charron (Albert Einstein College of Medicine. Funding was provided by the Natural Sciences and Engineering Research Council.

This research was published in the journal of *Psychoneuroendocrinology*.

# Piecing together the climate change puzzle with peatlands

**By Xinjie (Lois) Lin**

Climate change watchers take note: droughts and floods can reduce the ability of peatlands to absorb carbon dioxide, according to a study by Department of Integrative Biology researcher Merritt Turetsky.

Turetsky is part of a consortium of US and Canadian researchers conducting long-term studies on the effects of climate change on northern peatlands. Northern peatlands may cover only three per cent of the global land cover, but they play a big role in the planet's greenhouse gas exchange. They are responsible for around 20 per cent of naturally sourced methane ($CH_4$) in the atmosphere, a potent greenhouse gas, but they also store vast amounts of carbon dioxide ($CO_2$). Now, with several years of data in hand, Turetsky and colleagues have found that droughts and floods can significantly affect the exchange of both greenhouse gases in this important ecosystem.

"Historically, northern peatlands take up more carbon in a year than they release, which helps have a cooling effect on the global climate system," says Turetsky. "But changes to water table depth, soil conditions, and vegetation can tip the balance, changing peatlands from a net carbon 'sink' to a 'source'."

To better understand how unusually wet or dry years can affect carbon cycling in peatlands, Turetsky and her colleagues examined greenhouse gas exchange over nine years in an Alaskan rich fen. The study period included years that were naturally wet and dry, but the team also artificially manipulated the amount of soil moisture by pumping water into some experimental plots, or digging drainage channels around others.

"This study is unique because we conducted a long-term and large-scale field manipulation, so our measured responses are much more realistic than anything that could be conducted more easily in a lab setting," says Turetsky.

As expected, they discovered that drought conditions reduced $CH_4$ emissions. However, droughts also reduced plant photosynthesis, the main mechanism by which peatlands "absorb" $CO_2$ from the atmosphere. The team also found that more severe droughts led to shifts in vegetation, which resulted in a further decrease in photosynthesis and carbon uptake in subsequent years.

In contrast, flood years led to higher $CH_4$ emissions – an increase the researchers say is linked in part to warm temperatures in wet soils, which favours the activity of methane-producing bacteria.

The study provides valuable long-term data that show how the ability of peatland to remove carbon from the atmosphere can change based on moisture status – information that is key to developing accurate climate models.

**"Our ability to predict future changes to our climate and environment is critically dependent on understanding how carbon cycles under different conditions," notes Turetsky.**

Contributors to this project include David Olefeldt (University of Alberta), Eugénie Euskirchens and David McGuire (University of Alaska Fairbanks); Jennifer Harden and Mark Waldrop (U.S. Geological Survey), Evan Kane (USDA Forest Service), and many graduate students and post-doctoral researchers. The project was funded by the National Science Foundations, USDA Forest Service, and the US Geological Survey.

This research was published in *Global Change Biology.*

# Study shows new twist on mind-muscle connection

**By Gaelan Melanson**

Researchers in the Department of Human Health and Nutritional Sciences have gained new insights into the fundamental properties that govern muscle activity and influence our day-to-day movement.

Prof. Geoffrey Power and his research group have discovered a unique interplay between our nervous system and a phenomenon that occurs during muscle contraction known as torque depression.

Muscle contraction is what drives human movement.  For example, the movement associated with taking a drink involves contracting and shortening the bicep muscles. The contraction generates a force called torque that causes the forearm to rotate at the elbow towards your mouth, and allows you to enjoy your morning coffee. But not all muscle contractions are created equal. During contractions where the muscle does not shorten, such as holding a travel mug at waist-level between sips, the muscle generates more torque compared to a muscle that had to shorten to match the same position. The lower amount of  torque generated by shortened muscles is known as torque depression (TD).

According to Power, TD is observable at every level of the muscle, from single muscle fibres to muscles of the entire body, but the interaction between TD and our nervous system during voluntary muscle contractions is not entirely understood.

“TD is a well-known concept that has been around since 1954,” says Power. “But what we don’t know is how TD influences our nervous system. For example, does TD change the way we tell our body to move?”

To answer this question, the team investigated how TD in the leg influences the ability of the brain and spinal cord to transmit voluntary muscle contraction signals. Participants in the study were immobilized and instructed to flex their toes forward 40-degrees to create a TD state in their leg. Electrodes attached to the neck were then used to stimulate transmission of an electrical signal through the spine towards the muscle being contracted. Alternatively, electrical signals from the brain to the flexed muscles were induced by a process called transcranial magnetic stimulation. Detectors placed on each participant's leg were then used to measure the strength of these signals coming from either the brain or spinal cord to their muscles. The experiment was then repeated when the participant’s leg muscle was not experiencing TD.

The researchers discovered that the spine was more “excitable” during TD compared to the brain, and could propagate stronger voluntary muscle contracting signals with less instruction to do so from the brain.

“We are showing that an intrinsic property we thought was limited to muscle actually has a huge implication on our ability to voluntarily generate force,” says Power.

This insight into the mind-muscle connection has many implications for understanding human activity, and could be used to develop a tool to help athletes improve physical performance or aid in rehabilitation of patients who are not able to generate enough muscle force for certain movements.

Jordan Grant and Caleb Sypkes also contributed to the project. Funding was provided by the Natural Sciences and Engineering Research Council. This research was published in *Physiological Reports*.

# From fish farm to fork: Genetics could hold key to farming Arctic charr

**By Devin McCarthy**

Knowledge of the genetic attributes of the fish on your dinner plate may be changing… rapidly.

Evolutionary biologists in the Department of Integrative Biology have made a major advance in decoding the genetic architecture of Arctic charr, an important step toward improving our ability to cultivate the species for human consumption. Arctic charr is a coldwater fish that is closely related to salmon; due to the overwhelming demand for salmon, it is now the focus of a burgeoning aquaculture industry.

“In the long term, this research will help breed Arctic charr with more desirable farming traits,” suggest Profs. Roy Danzmann and Moira Ferguson, who along with team members Cam Nugent, Christine Ouellet, and Anne Easton are developing genetic tools for this species.

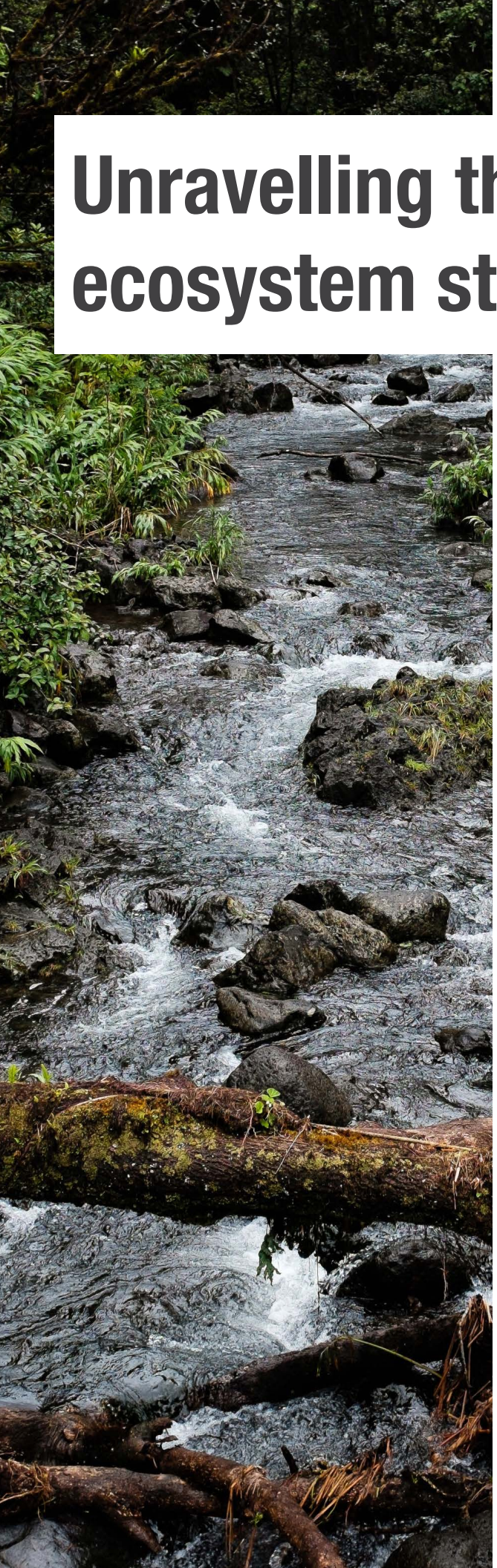
The team developed what is called a genetic linkage map of Arctic charr. This map identifies genes that tend to be inherited together. When enough genes are linked, the order and placement of the genes can be determined. Such a map is a valuable tool for geneticists and evolutionary biologists alike, providing information about the amount of genetic diversity in a species, and how it has diverged genetically from its relatives. It also provides essential information for fish breeders looking to genetically improve the species through selective breeding.

In the case of Arctic charr, fish farmers would like to delay the onset of muscle quality deterioration. Like most animals, Arctic charr prioritize reproduction. However, this species, especially males, invests so much energy into breeding that physical characteristics suffer, including skin and muscle quality. The rapid deterioration in quality when these fish reach reproductive age poses a major challenge to the industry. Currently, fish are harvested before they reach their full size in order to ensure an acceptable consumer product. Selective breeding and techniques such as the production of all-female lines can help address this problem. However, before the species can be made more amenable to farming, scientists must first link specific genes to specific physical traits.

“We eventually want to figure out which genes control which physical traits in Arctic charr,” says Danzmann. He notes that while DNA data can be obtained relatively quickly, it takes years to gather information about the corresponding physical characteristics. Through repeated sets of experiments in Ontario and New Brunswick that relate specific gene variants to physical traits, they hope to provide more information on the genetic markers that will be important in selective breeding programs.

The long-term goal is for fish breeders to use the genetic map to find genes that have an influence on multiple production traits in the species, in addition to flesh quality. Most notable among these other traits would be improvements in disease and stress resistance, and food conversion efficiency. With the enormous potential of Arctic charr to help feed society’s growing demand for fish, genetic improvement of Arctic charr production lines could help transform the industry.

Funding for this project was provided by the Natural Sciences and Engineering Research Council of Canada and the Atlantic Innovation Fund/Atlantic Canada Opportunities Agency. This research was published in *G3: Genes, Genomes, Genetics*.



# Unravelling the complexities of ecosystem stability

**By Sidra Sarfaraz**

Understanding what keeps ecosystems stable is no easy task, but researchers in the Department of Integrative Biology have solved another piece of the puzzle by determining how the age of organisms within a species affects food web stability.

Food webs are like an illustrative map of "who eats who" in an ecosystem, showing all the predator-prey interactions between species. They are an important tool for ecologists, who use them to understand how ecosystems function.

Classic food web theory states that having many interactions between species in an ecosystem helps keep it stable. But, until now, no one has considered how juveniles and adults of the same species with different eating habits – and hence different interactions with other species - might affect food web stability. It turns out that these differences help contribute to the overall stability of an ecosystem.

"Interactions between species are the glue that binds everything, regardless of age," says Prof. Kevin McCann, who conducted the study with PhD student Amanda Caskanette.

The duo used sophisticated mathematical equations to model interactions within food webs. Each equation had variables that represented different components of an ecosystem. The researchers then manipulated the age of the organisms to see how it would affect ecosystem stability, keeping all other variables constant. The model clearly showed that shifts in a predator's food source as it grows to maturity act as a stabilizing force.

Mathematical models simplify the world so scientists can study it. And while they are extremely useful, McCann notes that there are some drawbacks. Research in a real ecosystem will be necessary to gain the most accurate understanding of the impact of age on stability.

Even so, the study is significant because it addresses an ongoing debate in ecology about how the diversity of an ecosystem drives its stability. It is also significant because with growing human impacts on the environment, we may be altering the very things that keep it stable. That is why it is crucial to understand the components of an ecosystem and how they contribute to its stability.

"An ecosystem is like the human body- each part has its own role and helps maintain overall function," explains McCann.

This research was funded by the Natural Sciences and Engineering Research Council of Canada and published in *PLOS ONE*.

# Feeling the pain:

## Assessing tools to measure patient pain

**By Stephen Van Drunen**

Assessing chronic pain in patients can be a tricky business, but researchers in the Department of Human Health and Nutritional Science are working to identify best practices for healthcare professionals.

Chronic pain can lead to changes in the central nervous system that leave patients with a heightened sensitivity to pain. By measuring a person's sensitivity to pain, healthcare workers can better understand a patient's condition – but there is no single accepted method to make this measurement. To address this challenge, Prof. John Srbely and graduate student Emmalee Maracle compared two clinical techniques commonly used to measure an increase in sensitivity or pain – the brush allodynia and Semmes-Weinstein monofilament method. Of the two, the brush allodynia method proved to be the more effective technique.

"Both methods are commonly used by doctors, clinicians, and researchers, but no one had directly compared their sensitivity to detecting changes in sensitivity," says Srbely.

To make the comparison, Srbely and Maracle induced increased sensitivity in student volunteers by applying a chilli pepper-based lotion to the skin on their arm. The sensitivity of these areas was then measured using one of the two pain assessment methods.

For the brush allodynia technique, Srbely and Maracle used a small, fine brush to very gently stimulate the skin's hairs until areas of increased sensitivity were noticed by the patient. In contrast, the Semmes-Weinstein monofilament test used thread-like strands of a known thickness that bend when a certain amount of force is applied. The monofilament strand gently poked the surface of the patient's skin until areas of sensitivity were located.

After testing 20 student volunteers, the results were clear: the brush allodynia technique was a more sensitive and reliable way to measure an increase in pain sensitivity.

Improving the ability of medical practitioners and researchers to assess and treat conditions related to chronic pain is an area of significant interest and need, especially with the increasing incidence of chronic musculoskeletal pain in our rapidly aging population. One in five Canadians suffer from some sort of chronic pain condition, and 65 to 80 per cent of individuals aged 65 and over are afflicted.

"With an aging population, effective assessment and management of chronic pain will be an increasingly important, and expensive, challenge in the future," says Srbely.

This research was published in *Pain Practice*.

Scientists searching for better anti-cancer drugs now have a new target to consider. According to a study from the Department of Molecular and Cellular Biology, inhibition of a protein involved in cell-cell interactions called cadherin-22 could be the next step in improving cancer treatment.

Prof. Jim Uniacke and graduate student Nicole Kelly used molecular engineering to block cadherin-22 in brain and breast cancer cells. By reducing the amounts of cadherin-22 protein, they have gained ground-breaking insights into its role in cancer.

That's where cadherin-22 comes in. Using the results from this study, pharmaceutical scientists can design a drug that inhibits cadherin-22 to reduce cancer progression. Cadherin proteins make attractive drug targets because they are easily accessible on the cell surface.

The team also looked at tumours taken directly from breast and brain cancer patients. High amounts of cadherin-22 were found in bigger tumours and associated with a worse prognosis in patients. According to Uniacke, this means that doctors may be able to use cadherin-22 levels to determine cancer severity and predict how well a patient is going to do.

# Fighting cancer

## Blocking cadherin-22 protein impairs cancer cell migration and invasion

**By Sidra Sarfaraz**

The duo found that cancer cells without cadherin-22 did not move as much as cells with cadherin-22 in a hypoxic or low oxygen environment – the type of conditions that are found in tumours. This means the cancer would be less likely to spread to other parts of the body, a process referred to as metastasis. Cancer cells without cadherin-22 were also less likely to stick together, which would make it easier for the body's immune system to attack the tumour.

"Cadherin-22 is a new protein involved in a hypoxic cancer cell's ability to move," says Uniacke. "Identifying its role in the spread of cancer has given us a new target for treatment."

Hypoxic cells are much harder to treat than other cells in a tumour. They are less likely to be destroyed by chemotherapy or radiation therapy, and more likely to move within the body. Reducing the migration and invasion of hypoxic cancer cells is a key step in treating cancer.

"These findings not only provide mechanistic insight into metastasis, but also provide a new biomarker to diagnose advanced-stage cancer in patients," says Uniacke.

Because Uniacke's team used cancer cells, the door is now open for studies to assess the role of cadherin-22 in animal models. Other types of cancer can also be investigated, since cadherin-22 function could vary among different cancers.

The study offers an exciting new direction for researchers in the battle against a disease that remains a leading cause of death around the world.

Joseph Varga, Erin Specker, Christina Romeo (Molecular and Cellular Biology) and Brenda Coomber (Biomedical Sciences) also contributed to the study. This research was funded by Canadian Institute of Health Research and the Cancer Research Society. It was published in the journal *Oncogene*.


# Gene plays more important role in regulating body fat than previously thought

**By Andrea Brumwell**

The prevalence of obesity in society is a growing concern, and researchers in the Department of Human Health & Nutritional Sciences have made exciting strides to better understand the role of a gene involved in regulating body fat.

Prof. David Mutch and his team study the gene that produces an enzyme called stearoyl-CoA desaturase-1 (SCD1), which is found at higher levels in people with high-fat diets and obesity. In a recent study, graduate student Steven Dragos turned off the gene that produces SCD1 in mice fat cells and found it had a beneficial impact on the conversion and storage of fats.

SCD1 was previously thought to have a single role as an enzyme which helps convert fats into stored energy. But the researchers found that it was actually involved in multiple aspects of fat storage, acting as a "metabolic hub".

"Changes in the activity of this enzyme have far broader repercussions than previously appreciated," says Mutch.

Fats are stored as a molecule known as triacylglycerol (TAG), which is deposited in either visceral (surrounding organs) or subcutaneous (under the skin) adipose tissue reservoirs within the body. Increased visceral or "belly" fat is considered unhealthy due to its location near internal organs, whereas storing extra fat in subcutaneous adipose may be comparatively better for your health. When energy is needed, TAG is broken down into by-products and released into blood, where it can travel to other tissues and organs to provide energy.

But what happens when SCD1 is missing? In mice where the gene for SCD1 was turned off, the team found that TAG storage changed from unhealthy visceral stores to the more beneficial subcutaneous region. They also found that the conversion of broken down fats back into TAG was greatly impaired, and the levels of other genes associated with fat storage were severely depleted.

The results suggest that reducing SCD1 through diet or therapy may be beneficial for overall metabolic health, particularly for people in which the handling of fats is compromised, such as in obesity and type II diabetes.

Mutch is hoping to apply his research to humans by focusing on how the gene for SCD1 interacts with dietary fats, noting that throughout the population different forms of SCD1 exist which have varied abilities to convert fats into storage. As research in this area advances, there may soon come a day where we can tailor our diets based on our type of SCD1 to improve our metabolic health and treat diet-related diseases.

Other contributors to the project include Jessica Ralston and collaborator Catherine Mounier (Université du Québec à Montréal).

This research was published in the *American Journal of Physiology - Cell Physiology.*

# Lake features have big impact on biodiversity and conservation, says study

## By Louis Gasparini

Climate change is turning fish conservation into a pressing issue, but recent findings by researchers in the Department of Integrative Biology may lead to better strategies to preserve freshwater fish in Canadian lakes.

Prof. Andrew MacDougall and his research group have shown how species interactions within fish communities – as well as with the environment – are highly lake specific.

“Humans are affecting the environment in a variety of ways, and there is fear that we may be in the middle of a 6th major extinction event,” says MacDougall, noting that not only is it important to preserve fish that are economically important such as pike, walleye, whitefish, and lake trout, but biodiversity as a whole.

MacDougall and his team analysed data from 721 lakes to determine how factors such as lake depth, water temperature, and the amount of predators affected the diversity of fish found in a given habitat.

Their results showed that interactions between fish species were “context dependant” – that is, they depended heavily on the lake in question. One example is the effect of predation on smaller fish by lake trout. Lake trout prefer colder areas within a lake, so if a lake contains many cold areas, the effects of its predation will be much more pronounced than in lakes with fewer cold areas.

The study further showed that the influence of environmental factors such as temperature also depend largely on the features of the lake itself. For example, the effects of warmer temperatures are more pronounced in shallower water which warms up substantially faster than deeper water. If a lake was to become warmer over time, lake trout might move on in search of new colder waters, changing the predation interactions in the area.

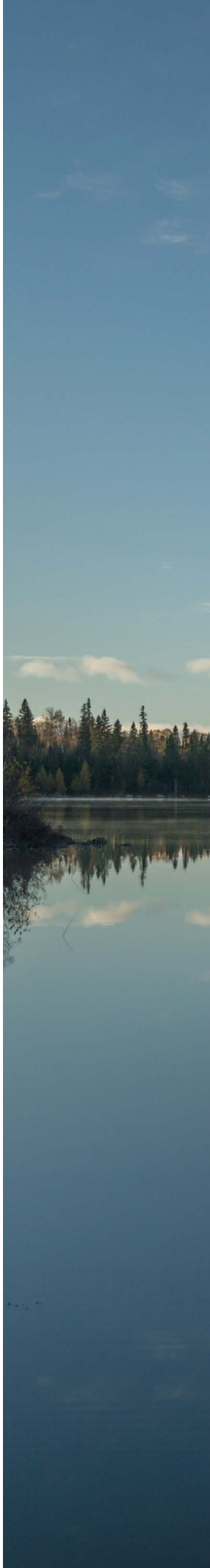
Environmental factors may also facilitate the establishment of invasive species. Factors such as temperature or prey availability can make an environment more susceptible to invasion by species such as the Asian carp, which are currently moving toward the Great Lakes basin.

What this boils down to, say the researchers, is that there is no one-size-fits-all solution when it comes to conserving fish communities in lakes. Choosing the most appropriate management strategy in a particular situation will require that a habitat’s features be carefully considered.

“There is no single formula,” says MacDougall. “Management depends on the lake. Lake size, temperature, and water quality all matter.”

With our lakes and fisheries under increasing threat from global change, the study provides valuable information that can aid the design of conservation strategies to mitigate biodiversity loss and help protect Canada’s native fish.

Significant contributions to this study were made by Prof. Kevin McCann and his lab. Funding was shared between NSERC and University of Guelph’s Canada First Research Excellence Fund project “Food from Thought”. This research was published in *Nature Communications*.



"There is no single formula," says MacDougall. "Management depends on the lake. Lake size, temperature, and water quality all matter."

UNIVERSITY of GUELPH

COLLEGE of BIOLOGICAL SCIENCE

Read more research highlights from the SCRIBE program at uoguelph.ca/cbs