

14th Annual  
Biology Graduate Student Symposium  
April 21st - April 22nd, 2022

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## General Schedule

### Thursday, April 21st, 2022

09:00 AM	Oral presentation session I
10:00 AM	Oral presentation session II
11:10 AM	Poster presentation session I
12:00 PM	Lunch break
01:00 PM	Keynote speaker - Dr. Elisabeth Bik
02:30 PM	Oral presentation session III
03:40 PM	Poster presentation session II



Join the conference via Webex on April 21st using the link below:

Meeting link - <https://mun.webex.com/mun/j.php?MTID=ma6c7b01e892e03e013f0e152315c6477>

Password: biology

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### Friday, April 22nd, 2022

09:00 AM	Nature NL
09:20 AM	Edgewise Environmental
09:35 AM	SAEN - Salmonid Association of Eastern NL
09:50 AM	DFO - Department of Fisheries and Oceans



Join the Networking Workshop via Webex on April 22nd using the link below:

Meeting link - <https://mun.webex.com/mun/j.php?MTID=mc8388180565421edc9d6c036316cccd8>

Password: biology

## Land Statement

We would like to respectfully acknowledge the island of Newfoundland as the ancestral homelands of the Mi'kmaq and Beothuk. We also recognize the Inuit of Nunatsiavut and Nunatukavut, and the Innu of Nitassinan, and their ancestors, as the original people of Labrador. We strive for respectful and equitable partnerships with all the people of this province as we work towards true reconciliation and honour this beautiful land together.

We offer this land acknowledgement to recognize Indigenous' peoples continued relationship with their ancestral homelands, and to recognize that when occupying this space we are hosted by Indigenous peoples who have known this land since time immemorial. Acknowledging Indigenous lands is not something we do for performance. We believe the acknowledging of Indigenous lands is central to our learning and is also an important step towards reconciliation.

## Acknowledgments

We would like to thank the Faculty of Science, Department of Biology, School of Graduate Studies and the Ocean Sciences Center for their help in facilitating our annual symposium. Your continued support has allowed the BGSA to provide the graduate student community with opportunities to develop professional skills in a constructive manner, fostering communication and interactions across multiple foci.

## Planning Committee

Arshad Shaikh  
Symposium Chair  
and Host

Johanna Bosch  
Planning and  
Fundraising

Kiana Alfaro  
Planning and  
Networking

Maliya Cassels  
Planning and  
Fundraising

Molly Morrissey  
Communications  
and Advertisement

## Messages of Support

### Dr. Meghan Burchell

Acting Associate Dean (School of Graduate Studies)



In my role as the Associate Dean (acting) for the School of Graduate Studies, I have the pleasure of working directly with graduate students and learning about all of the innovative research that takes place at Memorial University. I want to wish you all congratulations on your academic accomplishments and recognize all of the challenges graduate students have faced during Covid-19. Thank you to all of the members of the Biology Department for contributing your time, skills and knowledge to this event and to the BGSS for bringing the event to the Memorial community. Sharing our research, learning and making new connections is the essence of higher-education and I wish you all the very best in all of your academic endeavours.



### Dr. Travis Fridgen

Dean of Science (Faculty of Science)

It has been more than two years that we have lost the opportunity to travel and communicate the findings of our research at conferences. It is exciting to see this part of our work beginning to return to normal. Scientific communication is, without a doubt, the cornerstone of research. Written and oral communication is not just a means of showing what you have done. Oral communications are especially important to provide a more personal and creative perspective to new and exciting results you are presenting to an audience. It is an opportunity to get instant feedback to progress your work, and to pass on knowledge. The art of oral presentation takes practice and patience. As an audience member, you might try to find where your own work fits in with the work of others, you may be able to help the presenter progress their work, or you may just learn something new which is something we should try to do every day. Congratulations to all of you and the BGSA for participating in and organizing this symposium. It is especially important now when our day-to-day interactions with other scientists are limited. Good luck to presenters and please have a safe conference. Be respectful and be kind in your interactions with one another.

## Messages of Support

### Dr. Paul Marino

Head of Department (Biology)



On behalf of the Department of Biology I welcome all participants and thank them for continuing the tradition of making the Biology Graduate Student Association (BGSA) annual research symposium a significant feature in the life of the Department of Biology. This research symposium brings together graduate students, not only from the Department of Biology, but also graduate students from the Centre for Fisheries Ecosystems Research, Cognitive and Behavioral Ecology, Environmental Science and the Department of Ocean Sciences. The symposium breaks the boundaries among units and highlights the multidisciplinary nature of biological research at Memorial University. The efforts of the BGSA and the graduate students in the participating units are very much appreciated.

### Johanna Bosch

Chair of the BGSA

### Arshad Shaikh

Symposium Chair and Host



It is our honor to welcome all students, faculty, staff, audience members, and our keynote speaker, Dr. Elisabeth Bik, to the 14th annual BGSS. The BGSS was founded to provide graduate students with a platform to present their fascinating research and to learn about the work of their peers. We hope this year's symposium and networking session will help to continue fostering communication and collaboration between individuals of Memorial University and outside organizations, including Nature NL, the Salmonid Association of Eastern Newfoundland (SAEN), Edgewise Environmental, and the Department of Fisheries and Oceans. We would like to thank everyone who has participated in the planning and funding of BGSS, our keynote speaker Dr. Bik, and our peers who have taken time to prepare their presentations for today.

## Keynote Speaker

### Dr. Elisabeth Bik

Elisabeth Bik, PhD, is a Dutch-American microbiologist who has worked for 15 years at Stanford University and 2 years in industry. Since 2019, she is a science integrity volunteer and occasional consultant who scans the biomedical literature for images or other data of concern and has reported over 5,000 scientific papers.

For her work on science communication and exposing threats to research integrity she received the Peter Wildy Prize, the John Maddox Prize, and the Ockham Award.



## Past Keynote Speakers

2021 – Dr. Catherine Cullingham  
Carleton University, Ottawa

2014 – Dr. Diane Orihel  
University of Alberta

2019 – Dr. Joel S. Brown  
University of Illinois

2012 – Dr. Lisette Waits  
University of Idaho

2018 – Dr. Susan Lingle  
University of Winnipeg

2011 – Dr. Stephanie Carlson  
University of California

2017 – Dr. Joe Roman  
University of Vermont

2010 – Dr. John Smol  
Queen's University

2016 – Dr. James Sulikowski  
University of New England

2009 – Dr. Tom Nudds  
University of Guelph

2015 – Dr. Catherine Potvin  
McGill University

2008 – Dr. Tom Chapman  
Memorial University

## Awards Presented

### Joe Brown Award for Excellence in Science Communication

An award of \$100 will be given to the winner based on judges critiques

### Best PhD Oral Presentation

An award of \$50 will be given to the winner based on judges critiques

### Best MSc Oral Presentation

An award of \$50 will be given to the winner based on judges critiques

### Best Poster Presentation

An award of \$50 will be given to the winner based on judges critiques

## Past Award Winners

### Best MSc Oral Presentation

2021 - Sydney M. Collins  
2019 - Jaclyn Aubin (Eco/Evo)  
2019 - Jordan Wight (Cell/Molecular)  
2018 - Ethan Armstrong (Eco/Evo)  
2018 - Jordan Wight (Molecular/Genetics)

### Best PhD Oral Presentation

2021 - Gustavo Diaz-Cruz  
2019 - Danielle Quinn (Eco/Evo)  
2019 - Puvikalyan Pallegar (Cell/Molecular)  
2018 - Quinn Webber (Eco/Evo)  
2018 - Joost Verhoeven (Molecular/Genetics)  
2018 - Sabrina Inkpen (Molecular/Genetics)

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### Joe Brown Award for Excellence in Science Communication

2021 - Joanie Kennah  
2019 - Danielle Quinn  
2018 - Lancy Cheng

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### Best Poster Presentation

2021 - Carlissa Salant  
2019 - Rachel Marshall  
2018 - Juliana Balluffi-Fry

# Morning Schedule

April 21st, 2022

## Oral Presentation Session I

9:00 - 9:05 AM	Introduction	
9:05 - 9:15 AM	Sayani Kundu (PhD in Biology) Genome Editing and Crop Improvement in <i>Vaccinium</i> species	sayanik@mun.ca
9:16 - 9:26 AM	Adam Meyer (PhD in Biology) When does moose marching matter? A theory for context-dependent effects of herbivore trampling on ecosystem nitrogen cycling	gameyer@mun.ca
9:27 - 9:37 AM	Chelsea Malayny (MSc in Environmental Sciences) Estimating calcium carbonate production of cold-water <i>Primnoa resedaeformis</i> gorgonian coral forests on the Northeast Saglek Bank of the Labrador Sea	cjm530@mun.ca
9:38 - 9:48 AM	Alexander Byrne (PhD in Biology) Examination of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> from Canadian Dairy Cattle through phylogenetic and genomic methods	asb068@mun.ca
9:49 - 9:59 AM	Jordan Wight (PhD in Biology) Investigation of Antimicrobial-Resistant <i>E. coli</i> in Aquatic Sediments of Three Urban Waterbodies in St. John's, Newfoundland	jordan.wight@mun.ca

## Oral Presentation Session II

10:00 - 10:05 AM	Break	
10:05 - 10:15 AM	Molly Morrissey (MSc in Biology) Investigating changes over 120+ years in North-east Atlantic marine food webs using seabird feathers	mmmorrissey@mun.ca
10:16 - 10:26 AM	Evan Langille (PhD in Biology) Accelerating purification of gene transfer agents from <i>Rhodobacter capsulatus</i> by monolithic chromatography	ealangille@mun.ca
10:27- 10:37 AM	Nicolas Peñafiel (PhD in Biology) Using genomics to recommend conservation units in wild populations of palms	npenafiel@mun.ca
10:38 - 10:48 AM	Laura Piccirillo (MSc in Environmental Science) A geographic and bathymetric comparison of growth rates and ages in the deep-sea bamboo coral <i>Acanella arbuscula</i> from the Northwest Atlantic and Eastern Canadian Arctic	lpiccirillo@mun.ca
10:49 - 10:59 AM	Jingyu Liu (Post-Doctoral Fellow in Biology) Analysis of <i>Streptomyces</i> volatiles using global molecular networking reveals the presence of many plant-associated metabolites	jingyul@mun.ca
11:00 - 11:10 AM	Johanna Bosch (MSc in Biology) Tracking Population Dynamics of the Northern Gannet ( <i>Morus bassannus</i> ) Nesting Colony in Cape St Mary's Ecological Reserve, Newfoundland, within a ~140-year Sedimentary Record	jlb686@mun.ca



## Poster Presentation Session I

11:10 - 11:15 AM Break

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11:15 - 11:22 AM Jillian McGroaty (MSc in Biology) [jmcgroaty@mun.ca](mailto:jmcgroaty@mun.ca)  
Lichen 'Neighbourhoods' and their Arthropod 'Residents':  
a master's thesis proposal

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11:23 - 11:30 AM Coral San Roman (MSc in Ocean Sciences) [icsanroman@mun.ca](mailto:icsanroman@mun.ca)  
Ecological and Genetic Impacts of Farmed Salmon (*Salmo salar*)  
Introgression Into Wild Populations in Southern Newfoundland

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11:31 - 11:38 AM Ishraq Rahman (PhD in Biology) [ishraqr@mun.ca](mailto:ishraqr@mun.ca)  
A functional gene-array analysis of microbial communities settling  
on microplastics in a peat-draining environment

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11:39 - 11:46 AM Rachael Moran (MSc in Biology) [rbmoran@mun.ca](mailto:rbmoran@mun.ca)  
Predicting the Impacts of Spruce Budworm, Fire, and Moose on  
Ecosystem Productivity at Landscape Extents

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11:47 - 11:54 AM Maliya Cassels (MSc in Biology) [mecassels@mun.ca](mailto:mecassels@mun.ca)  
Paleoecological reconstruction of an Atlantic puffin (*Fratercula*  
*arctica*) colony in the Northeast Atlantic

12:00 - 1:00 PM Lunch Break

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1:00 - 2:30 PM Keynote Speaker Presentation [eliesbik@gmail.com](mailto:eliesbik@gmail.com)  
Dr. Elisabeth Bik

### *The Dark Side of Science: Misconduct in Biomedical Research*

Science builds upon science. Even after peer-review and publication, science papers could still contain images or other data of concern. If not addressed post-publication, papers containing incorrect or even falsified data could lead to wasted time and money spent by other researchers trying to reproduce those results. Several high-profile science misconduct cases have been described, but many more cases remain undetected. Elisabeth Bik is an image forensics detective who left her paid job in industry to search for and report biomedical articles that contain errors or data of concern. She has done a systematic scan of 20,000 papers in 40 journals and found that about 4% of these contained inappropriately duplicated images. In her talk she will present her work and show several types of inappropriately duplicated images and other examples of research misconduct. In addition, she will show how to report scientific papers of concern, and how journals and institutions handle such allegations.

# Afternoon Schedule

April 21st, 2022

## Oral Presentation Session III

- |                |  |                             |
|----------------|--|-----------------------------|
| 2:35 - 2:45 PM | Ze Xuan Ang (MSc in Ocean Sciences)  | zxang@mun.ca                |
|                | Suitability of advanced camera drone technology for submerged kelp mapping   |                             |
| <hr/>          |  |                             |
| 2:46 - 2:56 PM | Kiana Alfaro (MSc in Biology)  | kmalfaro@mun.ca             |
|                | Visualization of Bacteriocytes and Phagocytosis in Symbiotic Thyasirid bivalves  |                             |
| <hr/>          |  |                             |
| 2:57 - 3:07 PM | Sean Basquill (PhD in Biology)   | sean.basquill@novascotia.ca |
|                | Predicting Ecosystem Spatial Organization and Variation across Landscapes – a new direction                                  |                             |
| <hr/>          |  |                             |
| 3:08 - 3:18 PM | Ty Colvin (MSc in Biology)   | tjcolvin@mun.ca             |
|                | Ecosystem Functioning in Seagrass Sediments: Infaunal Response to Seagrass Disturbance                                       |                             |
| <hr/>          |  |                             |
| 3:19 - 3:29 PM | Emilie Dedeban (MSc in Biology)  | ededeban@mun.ca             |
|                | Effects of linear features on fitness in woodland caribou  |                             |
| <hr/>          |  |                             |
| 3:30 - 3:40 PM | Arshad Shaikh (PhD in Biology)   | aashaikh@mun.ca             |
|                | A direct examination of the specialized metabolites associated with ocean sediments from Baffin Island and the Gulf of Maine |                             |

## Poster Presentation Session II

- |                |   |                  |
|----------------|---|------------------|
| 3:40 - 3:45 PM | Break   |                  |
| <hr/>          |   |                  |
| 3:45 - 3:52 PM | Gustavo Diaz Cruz (PhD in Biology)  | gadiacruz@mun.ca |
|                | Regulation of nigericin and geldanamycin biosynthesis in <i>Streptomyces</i> sp. 11-1-2 by N-acetylglucosamine  |                  |
| <hr/>          |   |                  |
| 3:53 - 4:00 PM | Courtney White (MSc in Biology)   | cawhite@mun.ca   |
|                | A paleolimnological reconstruction of Eastern Spruce Budworm ( <i>Choristoneura fumiferana</i> ) outbreak dynamics and vegetation changes in Newfoundland |                  |
| <hr/>          |   |                  |
| 4:01 - 4:08 PM | Ranjan Wagle (MSc in Biology)   | rwagle@mun.ca    |
|                | Alternative artificial incubation system for intensive fry production of <i>Nile tilapia</i> ( <i>Oreochromis niloticus</i> )                             |                  |
| <hr/>          |   |                  |
| 4:09 - 4:16 PM | Hannah Adams (MSc in Biology)   | hadams21@mun.ca  |
|                | Modelling the effects of multiple terrestrial disturbances on small stream ecosystem function   |                  |
| <hr/>          |   |                  |
| 4:17 - 4:24 PM | Veronica Smith (MSc in Biology)   | veronicas@mun.ca |
|                | Are small-scale ecosystem changes from Beothuk inland winter camps captured in Newfoundland lake sediment records?  |                  |
| <hr/>          |   |                  |
| 4:25 - 4:30 PM | Closing Statements  |                  |

# Networking Workshop

April 22nd, 2022

9:00 AM Introduction

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9:05 AM Nature-NL

Nature-NL is a non-profit organization and registered charity promoting the enjoyment and conservation of wildlife and natural resources in NL. They continue to be one of the province's most active environmental organizations and regularly partner with other groups to raise awareness about nature (<https://naturenl.ca/>).



9:20 AM Fisheries and Oceans Canada (DFO)

Fisheries and Oceans Canada (DFO) is a federal institution, responsible for safeguarding our waters and managing Canada's fisheries and oceans resources. DFO helps to ensure healthy and sustainable aquatic ecosystems through habitat protection and sound science (<https://www.dfo-mpo.gc.ca/index-eng.html>).



9:35 AM Edgewise Environmental

EDGEWISE Environmental is a certified women-owned marine environmental consultancy based in NL. They focus on marine mammal and seabird observation, mitigation, and anthropogenic noise solutions; providing tailored training and environmental consulting services across all marine industries (<https://www.edgewiseenvironmental.com/about/>).



9:50 AM Salmonid Association of Eastern NL (SAEN)

The Salmonid Association of Eastern Newfoundland (SAEN) is a conservation group dedicated to the preservation of our province's salmon, trout and other freshwater resources. Since 1979 this group of volunteers has carried out conservation, research, education, and enhancement projects worth over \$10 million (<https://www.saen.org/>).



10:05 hr Question & Answer Period

Take this time to ask any remaining questions you may have regarding the organizations or career paths to take after completing your degree.



## Abstracts

In alphabetical order by first name of the primary author

### When does moose marching matter? A theory for context-dependent effects of herbivore trampling on ecosystem nitrogen cycling

[Adam Meyer](#), [Shawn Leroux](#)

Long term empirical studies have demonstrated strong effects of large mammalian herbivores (LMH) on biogeochemical cycling. However, the direction and magnitude of LMH effects can vary in unintuitive ways across environmental contexts. A lack of general understanding of how LMH impacts on biogeochemical cycling vary in space and time is a key barrier to the field's utility in developing whole-ecosystem management strategies and natural solutions to climate change. To fill this urgent gap in our understanding, there is a need to disentangle the relative contributions of plant consumption, physical trampling, and urination/defecation to the net effect of LMH on soil-mediated biogeochemical cycling across environmental contexts. To this end, we present insights from a mathematical model that explores LMH trampling effects on ecosystem nitrogen cycling.

Mathematical models are useful for disentangling alternative mechanisms underlying complex systems. The model tracks nitrogen through a simplified ecosystem with both biotic and abiotic nitrogen pools. Through analytical and graphical analyses, we discover that both the direction and magnitude of herbivore trampling effects depends on the relative sensitivity of two detritivore-related pathways; intrinsic nutrient recycling rate and intrinsic mortality rate, to trampling. Further, depending on which functional pathway is most affected, detritivore biomass and net nitrogen recycling can be coupled or uncoupled. Thus, an important part of understanding trampling effects across environmental contexts is knowing which detritivore-related pathways of nitrogen recycling are more sensitive to trampling. Our model provides testable predictions to guide future progress in empirical studies.

Contact: [gameyer@mun.ca](mailto:gameyer@mun.ca)

### Examination of *Mycobacterium avium subsp. paratuberculosis* from Canadian Dairy Cattle through phylogenetic and genomic methods

[Alexander Byrne](#), [Kapil Tahlan](#), [S everine Ollier](#), [Nathalie Bissonnette](#)

*Mycobacterium avium subsp. paratuberculosis* (MAP) is the pathogenic organism responsible for the development of Johne's disease in ruminants. MAP is typically categorized into two broad groups; Type I and Type II with additional subgroups such as Type III also previously described. Further subtyping can be performed the examination of discriminatory repeat regions such as short sequence repeats (SSR) and variable number tandem repeats (VNTR) or using whole-genome sequencing (WGS) to allow for an in-depth examination of the MAP genome at the single nucleotide polymorphism (SNP) level. Analysis of the pangenome also allows for the identification of core, accessory, and unique genes within select strains. The goal of this project was to perform WGS on strains from farms located in Ontario and Quebec and examine them through a variety of analysis methods including SSR, VNTR, SNP and pangenome analysis. A total of 67 isolates were processed from 20 herds in farms located in Quebec and Ontario, with DNA, alongside, 9 select RefSeq strains. Complete SSR and VNTR results were obtained from 65 of the 76 isolates, with the remaining 11 having at least one ambiguous locus. Of these 65, 53 unique patterns could be identified between combined SSR and VNTR typing. Pangenome analysis of 71 of the selected isolates identified 4167 core genes, 1158 accessory genes and 694 genes unique to specific strains were identified. The combined results show that while MAP isolates are highly similar, unique SNPs, repeats and genes suggest in-herd heterogeneity which may alter disease dynamics.

Contact: [asb068@mun.ca](mailto:asb068@mun.ca)

## A direct examination of the specialized metabolites associated with ocean sediments from Baffin Island and the Gulf of Maine

[Arshad A. Shaikh](#), [Joost T. P. Verhoeven](#), [Suzanne C. Dufour](#), [Kapil Tahlan](#)

Specialized metabolites produced by various species found in the ocean sediments display a wide range of clinically relevant bioactivities, including antimicrobial, anticancer, antiviral, and anti-inflammatory. Due to the limitation of growing these species in vitro or mimicking their natural habitat, yet little is known about their potential to produce such compounds, including those that could benefit humankind. However, new mass spectrometry data analysis methods such as global natural products social molecular networking and in silico structure prediction have been developed to discover these potentials in recent years. In the current study, ocean sediments were collected from Baffin Island and the Gulf of Maine, and their organic solvent extracts were examined directly to identify the specialized metabolites. Here, we report 12 predicted specialized metabolites of different classes found at the two locations produced by bacteria, fungi, soft corals, ascidians, and marine sponges. The in silico structure prediction tool could not predict approximately 7% of the spectral features, suggesting the presence of the novel specialized metabolites at both locations. The current study examines the sediments directly using untargeted metabolomics to unveil the specialized metabolites in the marine environment and encourages the same investigation to determine what is produced in situ.

Contact: [aashaikh@mun.ca](mailto:aashaikh@mun.ca)

## Estimating calcium carbonate production of cold-water *Primnoa resedaeformis* gorgonian coral forests on the Northeast Saglek Bank of the Labrador Sea.

[Chelsea Malayny](#), [Evan Edinger](#), [Bárbara de Moura Neves](#), [Laura Picirillo](#)

Calcium carbonate (CaCO<sub>3</sub>) production in cold-water octocorals (CWOC) remains largely unexplored, with a particular knowledge gap in the NW Atlantic. This study provides the first estimate of CaCO<sub>3</sub> production rates of a large gorgonian species, *Primnoa resedaeformis*, in the NE Saglek Bank region of the Labrador Sea. Per-coral and per-unit area CaCO<sub>3</sub> production rates by *P. resedaeformis* in the region were calculated using twenty-six (26) colonies and remote operated vehicle (ROV) video footage collected during the 2021 CCGS Amundsen expedition. Per-coral CaCO<sub>3</sub> production rates were calculated by dividing individual calcified colony weight by age, revealing an estimated average production rate of  $2.5 \pm 0.6$  g CaCO<sub>3</sub> ind<sup>-1</sup> y<sup>-1</sup>. Linear regressions found both per-coral % CaCO<sub>3</sub> composition and CaCO<sub>3</sub> production rate to be dependent on colony size. Per-unit area CaCO<sub>3</sub> production rates were calculated for each ROV dive site by multiplying average per-coral production rates by respective abundance density at each site, which was calculated via ROV video transect analysis. This revealed an average production rate of  $0.4 \pm 0.1$  g m<sup>-2</sup> y<sup>-1</sup> by *P. resedaeformis* across study sites. Total CaCO<sub>3</sub> production by *P. resedaeformis* in the NE Saglek bank region was calculated using coral bycatch data from the Northern Shrimp Survey together with site specific CaCO<sub>3</sub> rate estimates, finding an estimated CaCO<sub>3</sub> production rate of  $0.1 \pm 0.04$  g m<sup>-2</sup> y<sup>-1</sup>. The results from this analysis show that CaCO<sub>3</sub> production by CWOCs in the NW Atlantic is lower than previously predicted. Despite their ecological importance, CWOCs in the NW Atlantic make a modest contribution to calcium carbonate production.

Contact: [cjm530@mun.ca](mailto:cjm530@mun.ca)

## Ecological and Genetic Impacts of Farmed Salmon (*Salmo salar*) Introgression Into Wild Populations in Southern Newfoundland

[Coral San Roman](#), [Ian R. Bradbury](#), [Samantha E. Crowley](#), [Steven J. Duffy](#),  
[Shahinur S. Islam](#), [Ian A. Fleming](#)

Farming of Atlantic Salmon (*Salmo salar*) has resulted in highly domesticated individuals, with notable genetic and phenotypic differences relative to their wild counterparts. Therefore, understanding how genetic interactions with farm escapees affect wild populations at local scales is essential. Here, survival, growth, and the genetic impacts of farmed salmon introgression on a wild population in a natural environment in Southern Newfoundland were measured. A release experiment was conducted in three sites in the Garnish River system in the Burin Peninsula. Four cross types were released in July of 2018 (wild, farmed, farm-mother hybrids [FFhyb], and wild-mother hybrids [WFhyb]). At recapture the proportion of wild, farmed, and hybrid individuals was quantified and their differences in survival and growth were analyzed. Furthermore, the differences in survival over time among families of each cross type were studied. Survival differed among cross types in certain sites, with farmed and WFhyb having higher odds of recapture. Size at recapture differed among cross types in sites 1 and 3 (mean length:  $p < 0.001$ ; mean weight:  $p < 0.001$ ). Farmed and WFhyb were significantly larger than wild and F♀hyb, with no notable differences between one another. The family analyses demonstrated that the composition of families remained consistent from 0+ to 1+ and then to 2+. These results indicate that direct genetic interactions between farmed and wild Atlantic Salmon can impact the survival and fitness of wild populations, contributing to their decline over the last decades.

Contact: [icsanroman@mun.ca](mailto:icsanroman@mun.ca)

## A paleolimnological reconstruction of Eastern Spruce Budworm (*Choristoneura fumiferana*) outbreak dynamics and vegetation changes in Newfoundland

[Courtney White](#), [Les Cwynar](#), [Shawn Leroux](#), [Amy Hurford](#), [Bo Zhang](#),  
[Kathryn Hargan](#)

Defoliating insects, although naturally occurring, impact the long-term productivity and quality of the forests they infest. In Newfoundland (NL) and the greater Atlantic Canada, forestry is a significant component of the economy, making understanding forest pest outbreaks an ecological and economic priority. Eastern Spruce Budworm (ESB) has significantly impacted Canadian forests and, of all pest defoliators, often cause the greatest damage to coniferous trees. During Newfoundland's last outbreak (1972-1992) 90% of forests were impacted, reaching epidemic levels of infestation. However, ESB outbreak data has only been collected in the province since 1949, making the future pattern of outbreaks and biophysical conditions required difficult to predict based on current monitoring data. This study analyzed and quantified multiple sedimentary proxies of ESB from within four sediment cores collected from lakes across Newfoundland using paleolimnological techniques. We tested current methodologies for isolating moth wing scales from sediments to quantify (1) the frequency and intensity of historical ESB outbreaks in Newfoundland and (2) the difference between outbreak dynamics at low and high elevations within Gros Morne National Park. Additionally, sedimentary pollen data were collected to explore the historical impacts of ESB and other pest defoliators on Newfoundland forests. Using this data, we will compare how elevation, climate, human intervention strategies, and vegetation dynamics have affected ESB outbreak dynamics over time.

Contact: [cawhite@mun.ca](mailto:cawhite@mun.ca)

## Effects of linear features on fitness in woodland caribou

[Emilie Dedeban](#), [Quinn M.R. Webber](#), [Julie W. Turner](#), [Hance E. Ellington](#), [Eric Vander Wal](#)

Human disturbances increase worldwide and have led to serious and irreversible consequences on natural ecosystems. Linear features are defined as cleared stretches of land and are distinct sources of habitat fragmentation. Human disturbances can modify the environmental perception of an animal and therefore cause variation in the expression of behaviour. In turn, these alterations can negatively affect reproductive success, impacting the viability of a population. Migratory woodland caribou (*Rangifer tarandus*) are at the heart of these concerns raised by anthropogenic development in northern regions because they represent a key species of this ecosystem. Using an integrated step selection analysis, I will assess the individual behavioural response of the woodland caribou population in Newfoundland to linear features and the consequences on fitness.

Contact: [ededeban@mun.ca](mailto:ededeban@mun.ca)

## Accelerating purification of gene transfer agents from *Rhodobacter capsulatus* by monolithic chromatography

[Evan Langille](#), [Andrew Lang](#)

Gene transfer agents (GTAs) are a phage-like particles that uniquely transfer fragments of genomic DNA between cells of a bacterial species. GTAs have a capsid head in which DNA is packaged, and a tail with tail fibres that assist in binding to recipient cells. A hurdle faced in understanding how GTAs function and interact with cells is the ability to purify GTAs from various bacterial species across a broad range of culture media and growth conditions and at varying abundances. We present a novel method for purification of GTAs from *Rhodobacter capsulatus* using a two-step chromatographic purification process. Many species, including *R. capsulatus*, produce the most GTA when they are grown anaerobically photoheterotrophically. This adds challenges to purifying GTAs as photosynthetic membrane vesicles are present in high abundance. Additionally, as the release of GTAs is lytic in nature, cytoplasmic contents interfere with separation. Also, extracellular polysaccharides are produced in high quantities, complicating pelleting of cells and filtering the culture supernatants. The final product of our purification process has high purity and remains functional, allowing for downstream applications, such as biochemical assays, qPCR and NGS, to further understand these particles. This methodology is much improved over previous methods such as ultracentrifugation and PEG or iron precipitation. The purification process can be carried out at room temperature and takes less than two hours to go from the bacterial culture to highly pure, concentrated GTAs. This purification process will be used to answer many outstanding questions about the relative abundance, packaging, structure and other details of GTAs from *R. capsulatus* and related species.

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## Regulation of nigericin and geldanamycin biosynthesis in *Streptomyces* sp. 11-1-2 by N-acetylglucosamine

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Like many other members of the *Streptomyces* genus, the plant-pathogenic strain *Streptomyces* sp. 11-1-2 can produce a myriad of specialized metabolites, including the phytotoxins nigericin and geldanamycin. The biosynthesis of these compounds is often regulated in response to changes in environmental conditions, which can provide a competitive advantage in natural settings. Under nutrient-limiting conditions, the compound N-acetylglucosamine (NAG), part of the bacterial cell wall, is used as a carbon and nitrogen source; additionally, it acts as an elicitor/inhibitor of specialized metabolites in *Streptomyces* strains. This study evaluated the response of the phytotoxins nigericin and geldanamycin biosynthesis in 11-1-2 to a range of NAG concentrations added to two culture media. Organic culture extracts obtained from 14-day old agar plates with different NAG concentrations were evaluated using reverse-phase high-performance liquid chromatography (RP-HPLC) and liquid chromatography-mass spectrometry (LC-MS). Increasing concentrations of NAG resulted in decreased biosynthesis of both phytotoxins. Moreover, two intermediates, one for each phytotoxin, were also detected. These intermediates, which are predicted to be abierixin and 15-hydroxygeldanamycin, presented a similar trend as the main metabolites. Interestingly, nigericin and its intermediate were detected in both media, yet, the geldanamycin intermediate was found only in one medium. Altogether, these results represent a regulation mechanism at the nutritional level in 11-1-2, which can have implications in plant-microbe interactions.

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## Modelling the effects of multiple terrestrial disturbances on small stream ecosystem function

[Hannah Adams](#)

Human activity has impacted ecosystems for centuries, altering important habitats and resulting in biodiversity loss, climate change, and modified global nutrient cycles. Mitigating and managing environmental change has thus become an increasingly important task, but the complexity of ecosystem dynamics makes it an ongoing challenge. Meta-ecosystem theory is a novel framework for explaining how ecosystems are connected throughout the landscape by flows of energy, matter, and organisms. Meta-ecosystem models can predict properties that arise from connections among ecosystems (i.e., productivity and ecosystem stability), but are challenging to restrict to the finite spatial and temporal scales required for real-world application. I am applying a meta-ecosystem model to the island of Newfoundland, studying how disturbances in a terrestrial ecosystem impact the functioning of small streams. My objectives are to 1) empirically measure the impact of terrestrial disturbances on stream function; 2) use the data from 1) to empirically parameterize a terrestrial-aquatic meta-ecosystem model that considers disturbances associated with moose browsing, spruce budworm defoliation, ATV trails on small streams; and 3) use the model to make predictions about stream productivity under different disturbance scenarios. The model predictions will inform moose and spruce budworm management and trail development on the island and create a framework for similar models to be used for wildlife management policies. Including meta-ecosystem models in landscape management allows us to strike a balance between societal and ecological benefits and concerns, enabling informed decision making and adding to our understanding of the indirect effects disturbances have across space and time.

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## A functional gene-array analysis of microbial communities settling on microplastics in a peat-draining environment

[Ishraq Rahman](#), [Aazani Mujahid](#), [Enzo Palombo](#), [Moritz Müller](#)

Concerns about microplastic (MP) pollution arise from the rafting potential of these durable particles which potentially propagate harmful chemicals and bacteria across wide spatial gradients. While many studies have been conducted in the marine environment, knowledge of MPs in coastal and freshwater systems is limited. For this study, we exposed two MPs (polyethylene terephthalate and polylactic acid) to the undisturbed peat-draining Maludam River in Malaysia, for 6 months. The microbial communities on these MPs and the surrounding water were sequenced by MiSeq, while the genetic responses of these communities were assessed by GeoChip 5.0S. Microbial communities were dominated by the phyla Proteobacteria, Acidobacteria and Actinobacteria. Metabolic processes involved with carbon, nitrogen, sulfur, metal homeostasis, organic remediation and virulence had significantly different gene expression among the communities on MPs and in the surrounding water. Our study is the first to look at changes in gene expression of whole plastisphere communities.

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## Lichen 'Neighbourhoods' and their Arthropod 'Residents': a master's thesis proposal

[Jillian McGroarty](#), [Dr. Yolanda Wiersma](#), [Dr. Troy McMullin](#), [Dr. Tom Chapman](#)

The global decline in arthropods due to increasing human disturbances and the effects of the climate crisis is one of the most widely discussed and distressing problems that ecologists face today. Arthropods play critical roles in ecosystem functioning as pollinators, decomposers, nutrient cyclers, and food sources for higher trophic levels. In many forest ecosystems, arthropods depend on lichens for food, oviposition sites, protection, camouflage, and structure-building.

Lichens, formed by the symbiotic relationships of a fungus with an alga and/or cyanobacterium, are an incredibly diverse group that often grow in multispecies assemblages. The species diversity and corresponding trait variation within the assemblage result in the formation of unique and elaborate lichen communities which drive forest biogeochemistry process and interact with ecosystem fauna. The resulting network of physical and biotic interactions can hence be thought of as a micro-ecosystem, or a lichen 'neighbourhood'.

The primary aim of this study is to investigate the relationship between lichen 'neighbourhoods' and arthropod 'residents' in forest stands on the Avalon Peninsula, Newfoundland. My thesis will yield insight into the arthropod groups that are found within these communities, as well as how arthropod diversity changes depending on the composition and situation of the lichen assemblages, through the exploration of lichen, tree, and forest stand characteristics. Lichens are notable in the ecological community as a tool for air quality bioindication. However, if arthropod communities are influenced by lichen community composition, these 'neighbourhoods' may also provide an indicator of arthropod diversity, in turn supplying valuable knowledge for arthropod conservation.

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## Analysis of *Streptomyces* volatilomes using global molecular networking reveals the presence of many plant-associated metabolites

[Jingyu Liu](#), [Jody-Ann Clarke](#), [Sean McCann](#), [N. Kirk Hillier](#) and [Kapil Tahlan](#)

The *Streptomyces* produce a wide variety of specialized metabolites, some of which are used for communication or competition for resources in their natural environments. In addition, many natural products used in medicine and industry are derived from the *Streptomyces*, and there has been interest in their capacity to produce volatile organic compounds (VOCs) for different applications. Recently, a machine-learning workflow called MSHub/GNPS was developed, which enables auto-deconvolution of GC-MS data, molecular networking and library search capabilities, but it has not been applied to microbial volatilomes. In this study, 131 *Streptomyces* isolates from the island of Newfoundland were phylogenetically typed, and 37 were selected for VOC analysis using a combination of conventional and MSHub/GNPS based approaches. The number of unknown VOCs detected by the two methods was higher than those annotated, suggesting that many novel VOCs remain to be identified yet. More than half of the VOCs annotated with high confidence by the two approaches are plant-associated, many with reported bioactivities such as insect behavior modulation. Details regarding the properties and reported functions of such VOCs are described.

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## Tracking Population Dynamics of the Northern Gannet (*Morus bassannus*) Nesting Colony in Cape St Mary's Ecological Reserve, NL, within a ~140-year Sedimentary Record

[Johanna Bosch](#), [Inmaculada Álvarez-Manzaneda](#), [John Smol](#), [Neal Michelutti](#), [Greg Robertson](#), [Greg Robertson](#), [Andrew Lang](#), [Kathryn Hargan](#)

Seabirds play a large role in the transfer of marine-derived nutrients from their feeding grounds back to their nesting colonies and can be linked to biological and chemical shifts in nearby ponds, which can be tracked in sediment profiles. While many bacterial and fungal species are preserved within sediments, little is known about the impacts ornithogenic nutrients have on sediment microbiomes. Thus, our objectives are to: (1) compare the bacterial taxa found within seabird fecal samples to those in pond sediments to identify indicator species for reconstructing seabird population trends; and (2) compare the presence of indicator taxa to more commonly applied proxies in paleolimnology. Our study site, located in Cape St. Mary's Ecological Reserve (Newfoundland, Canada) contains approximately 64,000 nesting seabirds, primarily northern gannet (*Morus bassannus*), but also black-legged kittiwake (*Rissa tridactyla*). As a first step to meeting our objectives, we infer historical changes in the size of the nesting colony using sedimentary chlorophyll a, diatom assemblages, stable-nitrogen isotopes, and metal(loid)s in the dated cores collected from an "impact" pond 240 m away from the nesting site, and a "reference" site, not receiving nutrients, 2.56 km away from the colony.

We also performed metagenomic and ribosomal gene amplicon sequencing on DNA isolated from both sediment samples and fecal samples of gannets to conduct a comparative analysis of microbial abundance between sample types. Overall, our goal is to extend current knowledge concerning long-term seabird population shifts within Cape St. Mary's Ecological Reserve and extend the suite of proxies available to reconstruct seabird populations to include metagenomic techniques.

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## Investigation of Antimicrobial-Resistant *E. coli* in Aquatic Sediments of Three Urban Waterbodies in St. John's, Newfoundland

[Jordan Wight](#), [Alexander S. Byrne](#), [Kapil Tahlan](#) & [Andrew S. Lang](#)

Antimicrobial resistance (AMR) is an ever-present and growing problem in the treatment of infectious diseases, with infections caused by drug-resistant infections projected to kill 10 million people per year by 2050. Detection of antibiotic-resistant bacteria in the environment is therefore a critical aspect for understanding the prevalence of resistance outside of the clinical setting, as detection in the environment indicates that resistance is likely already widespread. We isolated antimicrobial-resistant *Escherichia coli* from aquatic sediments of three urban waterbodies at fifteen timepoints between 2018 and 2019. Strains were screened against a panel of antimicrobials belonging to nine diverse classes and their population structure and genetic determinants of resistance were investigated. We found that the *E. coli* communities at each site were composed of different dominant phylotypes and also showed distinct patterns of antimicrobial and multidrug resistance. We found that resistance to clinically important antibiotics such as amoxicillin, cefotaxime, and ciprofloxacin was widespread, while no resistance to the “last-line” antibiotics amikacin, meropenem, or fosfomycin was found. With a special focus on cephalosporin-resistant strains, the extended-spectrum  $\beta$ -lactamase genes blaCMY, blaTEM, and several variants of blaCTX-M were detected, though only at certain sites. All blaCTX-M-harbouring strains were multidrug resistant and predominantly belonged to phylogroup B2, indicating a probable clinical setting as the source. Our findings indicate that, despite the close proximity of these waterbodies to each other and their common use by both resident and migratory birds, the sources of *E. coli* for the three lakes are distinct. Overall, environmental persistence of bacteria and horizontal gene transfer likely play important roles in the resistance patterns observed in these environments.

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## Visualization of Bacteriocytes and Phagocytosis in Symbiotic Thyasirid Bivalves

[Kiana Alfaro](#), [Suzanne Dufour](#)

The Thyasiridae is a family of small clams found in cold marine sediments worldwide. Some thyasirids are mixotrophic, obtaining nutrients from both particulate (deposit or suspension) feeding and from symbiotic sulfur-oxidizing bacteria. Thyasirid symbionts are extracellular and maintained among the microvilli of gill cells called bacteriocytes. Based on ultrastructural observations, thyasirids obtain nutrients from symbionts through periodic phagocytosis and lysis of symbionts. *Thyasira* cf. *gouldi* from the subarctic fjord of Bonne Bay, Newfoundland display temporal variance in symbiont abundance, which is lowest in the spring and highest in the fall. However, it is unknown whether the nutritional reliance of thyasirids on their symbionts correlates with symbiont abundance. Here, we employ laser scanning confocal microscopy to perform live cell imaging of fluorescently-labeled symbionts, host actin and lysosomes to visualize interactions between symbionts and bacteriocytes. Specific goals are to: 1) quantify the percent space occupied by phagocytotic structures in individual bacteriocytes; 2) compare the relative space occupied by phagocytotic vacuoles in spring and fall months. We expect a greater percentage of space occupied by phagocytotic structures in bacteriocytes in the fall months. This work will help understand the temporal dynamics of energy inputs in symbiotic animals from seasonal environments.

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## A geographic and bathymetric comparison of growth rates and ages in the deep-sea bamboo coral *Acanella arbuscula* from the Northwest Atlantic and Eastern Canadian Arctic

[Laura Piccirillo](#), [Evan Edinger](#), [Bárbara de Moura Neves](#), [Meghan Burchell](#), [Graham D. Layne](#)

Deep-sea corals often provide habitat for invertebrates and fish, and can have high longevities and slow growth rates. However, their growth and success are threatened by anthropogenic activities, specifically bottom contact fishing. The small bamboo coral *Acanella arbuscula* is one of the most abundant and widespread deep-sea coral species in the Northwest Atlantic and Eastern Canadian Arctic, but little is known about the species growth rates and longevity. To address this lack of knowledge, 105 colonies of *A. arbuscula* previously collected from different regions in the NW Atlantic were used to compare growth rates and age with geographic and bathymetric variables, and 10 additional colonies were collected on the SE Baffin Slope (Davis Strait) at ~1300m depth in 2021 using a remotely operated vehicle. Longevity and growth rates were determined primarily from growth ring counts at the proteinaceous nodes of the coral skeletons, and validated with LA-AMS bomb-14C dating. The species exhibited major and minor growth banding, with 3-12 minor growth rings per major ring. Based on relationships of major and minor rings with size metrics, major rings were determined to represent annual banding in the species. Growth ring counts in *A. arbuscula* indicate ages of 9-29 years, radial growth rates of 0.025-0.16 mm·year<sup>-1</sup>, and linear growth rates of 1.9-16.1 mm·year<sup>-1</sup>. A weak negative relationship exists between depth, and growth rate and age. Radial growth rates were fastest, yet colonies were youngest in Davis Strait, while growth rates were slowest, yet colonies were oldest in the SW Grand Banks.

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## Paleoecological reconstruction of an Atlantic puffin (*Fratercula arctica*) colony in the Northeast Atlantic

[Maliya Cassels](#), [Kathryn Hargan](#)

Understanding the long-term histories of seabird nesting colonies can clarify colony dynamics and the drivers of population change. Atlantic Puffins (*Fratercula arctica*) are listed by the IUCN as a globally Vulnerable species; yet we lack long-term monitoring data to identify the main stressors which contribute to population fluctuations. We used a sediment core from a pond in an Atlantic Puffin colony on an island off the northeast coast of Newfoundland with ~ 15,400 breeding pairs to examine changes in the puffin population at this site since ~ 1730 AD. The beginning of our sediment record coincides with permanent human settlement in the area. We are measuring proxies for puffin abundance throughout the sediment record, including sedimentary chlorophyll-a, subfossil diatoms, metal(loid) concentrations, fecal lipids, and stable isotopes of nitrogen ( $\delta^{15}\text{N}$ ), total carbon ( $\delta^{13}\text{C}$ ), and organic carbon. Together, these proxies will provide a history of the puffin population at this site over the past 290 years.

In comparison to a nearby pond not influenced by seabirds, the puffin impacted pond had lower pH, higher conductivity, and elevated concentrations of dissolved organic carbon, nitrogen, and phosphorus. The puffin pond also had  $\delta^{15}\text{N}$  and  $\delta^{13}\text{C}$  stable isotope values indicating seabird presence from the beginning of the sediment record, with an increase in abundance around the year 2000. This is a decade after the human use of these islands greatly decreased due to the moratorium on the Newfoundland cod fishery. The use of gillnets in the area and bycatch of diving seabirds also decreased at this time due to decreased fishing.

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## Investigating changes over 120+ years in North-east Atlantic marine food webs using seabird feathers

[Molly Morrissey](#), [Kathryn Hargan](#), [Alex Bond](#)

Studying marine food web structures proves logistically challenging due to the sheer size of the world's oceans. Seabirds have emerged as excellent indicators of marine food webs because of their nearly exclusive marine diets and their proximity to humans during the breeding season. Stable isotope technology is frequently employed for long-term diet studies. Stable isotope values within tissues of a consumer are direct indicators of foods eaten while those tissues develop, with nitrogen-15 being particularly useful in diet studies because it indicates an organism's trophic position. Here, we investigate long-term (120+ years) marine food web changes in the North-east Atlantic waters near Newfoundland by conducting stable isotope analyses of feathers of Newfoundland breeders Atlantic puffin (*Fratercula arctica*, n = 37) and Leach's storm-petrel (*Oceanodroma leucorhoa*, n = 34). Seabird feathers were collected from Canadian museums and from independent collections of fellow researchers. Birds were restricted to adults collected during the breeding season. Feathers grown during the breeding season represent non-breeding (winter) diets. We utilize both bulk and amino-acid specific stable isotope analyses to investigate changes in  $\delta^{15}\text{N}$  over time in seabird feathers. Preliminary results show bulk stable  $\delta^{15}\text{N}$  values for Leach's storm-petrels from 1904 to 2019 and increasing  $\delta^{15}\text{N}$  values for Atlantic puffins from 1899-2021. Future analysis will relate puffin  $\delta^{15}\text{N}$  values to  $\delta^{15}\text{N}$  values of potential prey populations, creating a timeline of changes in dominant puffin prey. Furthermore, amino-acid specific stable isotopes will elicit whether changes in bulk  $\delta^{15}\text{N}$  in puffins is related to a change in puffin diet or a change in  $\delta^{15}\text{N}$  values at the base of the food web, or both.

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## Using genomics to recommend conservation units in wild populations of palms

[Nicolás Peñafiel](#), [Julissa Roncal](#)

The Tropical Andes of South America are home to an astounding number of plant species. Among them, several palm lineages have found in this hotspot opportunities for dispersal and/or speciation. Palms of the genus *Parajubaea*, however, represent a special Andean case of low diversification with only three species recognized despite the genus' origin 22 million years ago. Two of them, *P. torallyi* and *P. sunkha*, are endemic to Bolivia and are listed as endangered by the IUCN since they show restricted ranges, where they face rapid habitat degradation and limited regeneration. In the present study, we used a Genotyping-by-Sequencing approach to genotype 194 individuals from three populations of *P. sunkha* and six of *P. torallyi* to infer their genetic diversity, genetic structure, and phylogenetic history, and to inform the designation of conservation units within each species. Our results corroborate the distinction between the two Bolivian species, that had been established on morphological characters alone, and indicate that *P. torallyi* is a taxon derived from *P. sunkha*. All palm populations had an excess of heterozygotes suggesting that loss of genetic diversity due to inbreeding is not a threat for *Parajubaea*. Within *P. torallyi*, we identify three management units that correspond to the three main genetic groups observed. For *P. sunkha*, we suggest treating all populations as a single management unit, in spite of the evidence of admixture from two genetic groups.

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## Predicting the Impacts of Spruce Budworm, Fire, and Moose on Ecosystem Productivity at Landscape Extents

[Rachael Moran](#), [Dr. Shawn Leroux](#)

Forest fires and eastern spruce budworm are both natural disturbances on the island of Newfoundland that create canopy openings in the eastern boreal forest. These openings allow for natural forest regeneration, with highly palatable, fast-growing deciduous and coniferous trees (e.g., white birch (*Betula papyrifera*) and balsam fir (*Abies balsamea*)) growing into the canopy. These initial disturbances provide ample forage resources for moose. However, when moose herbivory follows natural disturbances it can suppress forest regeneration, leading to an impact on net ecosystem productivity and the forest's ability to store carbon.

The purpose of this project is to evaluate the impacts of spruce budworm, fire, and moose on the ecosystem productivity of boreal forests. To address this, we will measure carbon stocks and plant-available nitrogen under relative and combined disturbance scenarios in Gros Morne National Park and Terra Nova National Park. We will then use statistical models and remotely sensed predictor variables to scale these site-level measurements to the landscape level to predict the effects of these disturbances on productivity at broader extents.

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## Alternative artificial incubation system for intensive fry production of Nile tilapia (*Oreochromis niloticus*)

[Ranjan Wagle](#), [Narayan Prasad Pandit](#) and [Rahul Ranjan](#)

Jar incubation system is a well established artificial incubation system for intensive fry production of Nile tilapia. However, this system needs special hatchery structure and huge amount of water for circulation of eggs. The present study aimed to explore a simple, economic and water efficient alternative incubation system appropriate for small-scale hatchery operators. Two incubation systems, i.e. atkin incubation system and aquarium incubation system were compared with jar incubation systems in terms of water use, hatching rate and subsequent survival of larvae. Results showed that the amount of water used was significantly higher in atkin ( $127.0 \pm 3.1$  m<sup>3</sup>) and jar ( $36.8 \pm 4.9$  m<sup>3</sup>) incubation systems compared to aquarium ( $0.05 \pm 0.0$  m<sup>3</sup>) incubation system. The hatching percentage was significantly higher in jar incubation system ( $95.5 \pm 0.6\%$ ) compared to aquarium ( $65.2 \pm 7.7\%$ ) and atkin ( $57.8 \pm 2.2\%$ ) incubation systems. Hatching tended to occur slightly earlier in the jar incubator than other systems. After 7 days of rearing, the mean larval survival rate was highest in jar incubation ( $96.9 \pm 0.5\%$ ), intermediate in aquarium incubation ( $90.9 \pm 3.4\%$ ) and lowest in atkin incubation ( $81.0 \pm 3.1$ ) system ( $P < 0.05$ ). The dissolved oxygen was significantly higher in aquarium ( $6.1 \pm 0.0$  mg/L) than jar ( $3.0 \pm 0.0$  mg/L) and atkin ( $3.0 \pm 0.1$  mg/L) incubation systems. Further experiments indicated that about 5000 eggs can be successfully hatched with a hatching rate of 95% and reared to swim-up fry in in 50 L size glass aquarium with water exchange twice daily. This system is best suited for incubation of late stage eggs and rearing of newly hatched larvae up to free swimming stage. The results indicate that aquarium incubation can be used as an alternative of jar incubation system for Nile tilapia eggs, especially in water scarce areas.

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## Genome Editing and Crop Improvement in *Vaccinium* species

[Sayani Kundu](#), [Samir C. Debnath](#)

Berries like huckleberry, blueberry, lingonberry, cranberry etc. belongs to the *Vaccinium* genus of Ericaceae family which is the large group of flowering plants, commonly known as the heath or heather family. They are well-known and economically important especially for its phenolic content, anthocyanin content, antioxidant potential and also for their other abundant health benefits. However, since global climate changes have a considerable impact on beneficial food supply programs. Therefore the importance of epigenetic studies in agriculture needs to be addressed. It will not only prove beneficial for the cultivars but also for the people that depend on them. For cutting-edge research in plant model species along with the benefit of crop quality improvement, role of genome editing plays a pivotal role with addition of valuable traits and removal of undesirable traits.

The gene editing technologies enables to alter the regulation of gene expression in a pre-determined region and facilitates novel insights into the functional genomics of that species. These techniques are useful for accelerating the breeding of many small fruit crops like blueberries, huckleberries. The aim of this study is to evaluate the CRISPR/Cas9- system based genome editing, transcriptome sequencing, genome editing technologies (GET), genome editing mediated by site specific recombinase or a site-specific nuclease (SSN) system of the *Vaccinium* species. For improvement of crops genome editing is most the versatile tool.

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## Predicting Ecosystem Spatial Organization and Variation across Landscapes – a new direction

[Sean P. Basquill](#) and [Shawn J. Leroux](#)

Conservation planners and regulatory authorities are increasingly reliant on predictive models to ensure environmental decisions are informed by objective assessments of contemporary and near-future circumstances. However, while predictive biodiversity models are generally well developed, and frequently integrated into conservation decision-making, spatial models formulated for predicting regional patterns of ecosystem diversity and distribution, and for modelling patterns within and among ecosystems, have not been operationalized. The scarcity of such models, marks a concerning gap in the scientific community's ability to make spatially explicit ecosystem predictions across landscapes, and more broadly for supporting the conservation of biodiversity and ecosystem functions amidst escalating uncertainties facing decision makers. To fill this gap in predictive capacity, we propose a novel conceptual framework for predictive spatial modelling of ecosystem pattern, at regional landscape extents. Our framework differs from others in that it accords biotic and abiotic constituents equally, commensurate with their joint mechanistic influence on ecosystem assembly and geography. Furthermore, it ascribes space as the keystone within which assembly outcomes are both realized and organized. The framework offers conservation decision-makers a novel approach for predicting and understanding ecosystem spatial patterns, and a basis to forecast ecosystem geography and persistence.

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## Ecosystem Functioning in Seagrass Sediments: Infaunal Response to Seagrass Disturbance

[Ty Colvin](#) and [Paul Snelgrove](#)

Eelgrass, *Zostera marina*, spans coastlines of the Northern Hemisphere and supports many ecosystem processes, particularly nutrient regeneration and carbon remineralization. Eelgrass beds also accumulate organic matter, providing an energy source for microbes and associated infaunal macroinvertebrates, which potentially interact to alter nutrient and carbon cycling. In Newfoundland, invasive green crab threaten eelgrass beds as they uproot eelgrass when foraging, thus reducing eelgrass cover. In order to evaluate the effects of disturbance of eelgrass habitat over a 3-month period, we removed small patches of eelgrass and monitored the macrofaunal community and flux rate responses in sediment cores, comparing them to cores in undisturbed eelgrass and adjacent unvegetated sediments. The infaunal communities of the disturbed pits differed from both undisturbed eelgrass and unvegetated communities initially, becoming more similar to both over time. Total infaunal abundance was higher in undisturbed eelgrass and unvegetated sediments initially, with both declining over the season. Initially low abundances in disturbed patches recovered to numbers similar to those in the undisturbed treatments, suggesting that both the community and abundances were recovering from the disturbance. Oxygen consumption was highest in eelgrass sediments, with lower consumption in disturbed patches and unvegetated sediments. Flux rates of ammonium, nitrate, and silicate were similar across treatments. In contrast, phosphate influx was initially higher in disturbed and unvegetated sediments, becoming similar to eelgrass sediments over time. This research emphasizes the importance of seagrass for structuring infaunal communities, and gives insight into the connections between infaunal diversity, seagrass, and nutrient cycling.

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## Are small-scale ecosystem changes from Beothuk inland winter camps captured in Newfoundland lake sediment records?

[Veronica Smith](#) and [Dr. Kathryn Hargan](#)

Fecal stanols and sterols are a source-specific paleolimnological population proxy that is gaining in popularity as it enables more direct comparisons between population reconstructions and environmental data. By obtaining population and environmental data from the same sediment cores, multiproxy approaches are more reliably compared to each other; allowing us to analyze ecosystem stressors, adaptability, and elasticity in relation to human interference to determine efficient courses of mitigation. Russell's Point on Dildo Pond, Newfoundland is a well-studied archaeological Beothuk winter camp that has a history of pre-European Indigenous use, Indigenous-European interaction, and a history of seasonal caribou migration and hunting. Two sediment cores will be taken downstream of Russell's Point and analyzed fecal stanols and sterols, stable isotopes, metals, and  $^{14}\text{C}$ -carbon to understand how ancient ecosystems responded to the interference of ancient humans. These paleolimnological proxies will be compared with archaeological records to provide a multiproxy understanding of environmental responses from Beothuk occupation and hunting practice in Newfoundland. My objectives are to identify and date the window of human presence at Dildo Pond and to validate the use of fecal stanols and sterols as a reliable proxy for tracking past Indigenous settlements on lakes in Newfoundland. My hypothesis is that the fecal stanol and sterol proxy will identify camp occupation dates on Dildo Pond that correspond with archaeological data but will expand the window of human presence as the current occupation window is dependent on the presence of  $^{14}\text{C}$ -carbon of the oldest artifacts/animal bones at Russell's Point.

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## Suitability of advanced camera drone technology for submerged kelp mapping

[Ze Xuan Ang](#) and [Patrick Gagnon](#)

Advanced camera drones are increasingly used for marine habitat mapping purposes, yet the accuracy of classified maps heavily hinges on the complexity of the target habitat and proper selection of drone parameters. We examined the relative importance of spatial and spectral resolutions of imagery, and bathymetry as an additional layer of classification information, to the mapping of completely submerged kelp beds in Newfoundland, eastern Canada. RGB drone imagery (Phantom 4 RTK, DJI) with  $25\text{ cm pixel}^{-1}$  spatial resolution and supervised classification scheme yielded the highest overall accuracy (96%) and kappa coefficient (0.89) of kelp habitat maps among the five spatial resolutions tested (3.3, 10, 25, 50, and  $100\text{ cm pixel}^{-1}$ ). Three-band multispectral satellite imagery (Pléiades-1A) with  $50\text{ cm pixel}^{-1}$  spatial resolution yielded lower overall accuracy (76%) than drone imagery with the same spatial resolution. Integration of seabed bathymetry inferred from drone imagery and from in situ measurements with a recreational echo sounder increased the overall classification accuracy of the satellite imagery by ~1% and 5%, respectively. These preliminary results suggest that RGB drone imagery with  $100\text{ cm pixel}^{-1}$  and below provides reliable classification maps for submerged Newfoundland kelp beds, outperforming multispectral (spectrally more sophisticated) satellite imagery with a slightly larger lower spatial resolution.

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