CBG

March 2019
Newsletter

ARCTIC
BIOSCAN

Supported by a contribution from **Polar Knowledge Canada**, our new project in the North – **ARCBIO** – will build the platform necessary to track the state of biodiversity in the Canadian Arctic

See page 4 for interviews with the ARCBIO team.

Visit arcticbioscan.ca for more information, blogs and news about ARCBIO

SPOTLIGHT: Jandir Cruz Santos, Postdoctoral Fellow

Q: Where did you do your Ph.D.?

A: I received my M.Sc. and Ph.D. in entomology at the Universidade Estadual Paulista (UNESP) under the guidance of Professor D. Gilberto Jose de Moraes.

Q: Where did you do grow up?

A: I grew up in the Northeast of Brazil in a city named Arapiraca in the state of Alagoas.

Q: What are you working on here at CBG?

A: I have been working with the phylogeny, biodiversity, and taxonomy of edaphic mites. Here in CBG's collection, there are about 20,000 mites needing identification. My work at this moment consists of identifying this material, developing phylogenies to solve problems between some families and genera, and if possible, describing some new species.

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Director's Note

Dear Colleagues,

I write this message freshly returned from Australia. If my thoughts seem scattered, blame the jet lag. Aside from grabbing a breath in that great southern land, I managed to collect 10,000 specimens whose barcodes will soon be added to BOLD.

While there, I also devoted some time to advancing other matters. As you know, the iBOL Consortium will launch its second project, BIOSCAN, in mid-June in Trondheim. As the CBG will play a lead role in this seven-year, $180 million endeavour, I've been feeling trepidation about its administration.

As a result, I'm very pleased to report that **Donald Hobern**, past Director of the Atlas of Living Australia and current Executive Secretary of the Global Biodiversity Information Facility in Copenhagen, will take up a new position as BIOSCAN's Executive Secretary in mid-April. Donald will be based in Canberra, a very great advantage for BIOSCAN given its global reach, but he will regularly visit the CBG *(first visit March 13 – 18)*.

As you know, the CBG depends on grants to support its operations. Last week, I learned our application to the latest Food From Thought competition was fully funded; this award will provide $7.5 million over the next triennium. As well, last month saw confirmation that Polar Knowledge Canada will provide $1.8 million over the next two years. These two awards will provide about 60 per cent of the funds needed to keep the CBG in full motion, and prospects for additional operating support look bright.

(continued on page 2)

Director's Note (cont.)

However, since we also need support to update our sequencing infrastructure, I visited the Gordon and Betty Moore Foundation in Palo Alto in late January. Based on subsequent discussions with one of their senior Program Officers, the Foundation seems poised to provide a substantial award so we can acquire an ECHO liquid handling system. This $800,000 piece of equipment will allow us to process specimens at a much lower cost and will greatly reduce plastic waste.

Aside from grants to support the CBG core, February also brought confirmation of an $857,000 three-year award to Mehrdad from Genome Canada's Genomic Applications Partnership Program. Because of these awards, it is certain we will do some great science over the next three years (and in the subsequent 20 years with future grants!).

Get ready for fun times!

— Paul Hebert

Spotlight: Jandir Cruz Santos (cont.)

Q: How many new species (and genera) have you found since you started at the CBG in December?

A: I have found about 50 different genera, more than 150 morphospecies and about 30 new species.

Q: What are your main research interests working at the CBG?

A: The use of traditional taxonomy has become increasingly complicated. In light of such difficulties, it becomes necessary to search for tools that facilitate the identification of mites. So, my main interests working at the CBG are to learn more about molecular tools and to improve my knowledge of the phylogeny of mites.

Q: How many families have you created databases for?

A: I have developed databases for the distribution of three mite families (Ascidae, Blattisociidae, Melicharidae) and their associated plant, animal, and soil-inhabiting hosts. Most of these are predatory, and some have great potential to be used as biological control agents for pest mites and small arthropods.

Q: What was the greatest contribution from your Ph.D.?

A: My greatest contribution has been the development of databases that help researchers identify species around the world, and the description of new species of predatory mites that can be used in pest control.

New Faces

Junior Lab Technician - Collections

Mitch is returning after a brief break and will be assisting in imaging and ARCBIO fieldwork.

Laboratory Technician - Genomics

Hayley comes to the CBG from Winnipeg. She holds a BSc in biology and a diploma in biotechnology. She has previously worked in microbiology, studying antibiotic resistance in pathogens. Most recently, she worked in the production of genetically modified Canola through conventional trait integration methods.

Research Associate - Informatics

For the last 4 years, Tony has been a PDF at AIST in Tokyo. His background is in machine learning and statistical methods for genome sequence analysis. Most recently, he worked with allopolyploid plants to develop better methods for expression quantification. At the CBG, Tony will focus on the development of new bioinformatics methodologies, and algorithm/systems development.

Junior Lab Technician - Collections

Shawn is also returning after a break and will be assisting with sample sorting.

Media Team Update

Media team members travelled to Nunavut's Cambridge Bay and Kugluktuk last month to conduct and document the early consultation phase of Arctic BIOSCAN (ARCBIO). Joining Alex Borisenko and U of G anthropologist Tad McIlwraith, our team created digital content to highlight the project in advance of the summer field season. Please visit the new ARCBIO project website for more information.

While visiting Nunavut, the media team took over the official U of G Instagram for a day, sharing stories from the field to promote ARCBIO and its new website. Our stories gained 12,000 views in a single day, and we've been told that this is more than most U of G stories gain in an entire week! Also, since its launch on Feb 25th, the project site has been viewed 900 times.

Media team lead designer, Suz, has also been busy decking out the media office with a new editing and digital media production station. If you have any footage or photos you'd like us to catalogue for the CBG's current or future media projects, we would be happy to ingest and archive them for you.

You'll also notice updates to the iBOL website including updated board member bios, updated BIOSCAN translations, and links to new digital media content. The CBG website is currently being revamped as well.

Mehrdad Hajibabaei made national headlines last month with his new STREAM project funding. Also from the Hajibabaei Lab, we'll promote Katie McGee's soil research in Costa Rica which could have major impacts on policy and planning for forest regeneration projects around the world.

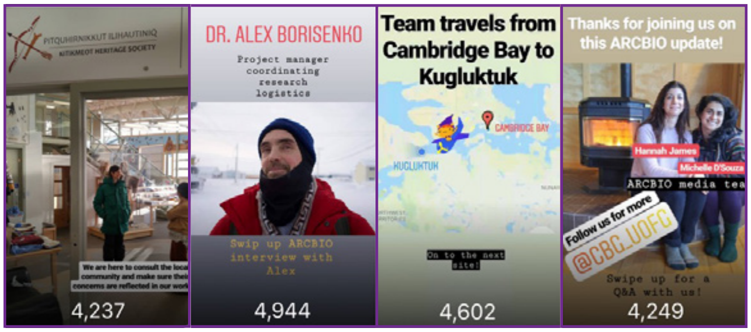
Michelle D'Souza will continue her research with the Kruger Malaise Program, travelling to South Africa's Kruger National Park this month. The media team will document the project, interviewing the scientists and park rangers who are actively involved in sample collection. There is already considerable national media interest, and this project will be instrumental in illustrating iBOL's positive impact on the places and communities where Consortium members work.

This month, we'll be inviting iBOL members to work with us to highlight the many compelling stories across the iBOL network, including the release of the first Barcode Bulletin of 2019. Our aim is to put BIOSCAN on the map not only for the launch in June, but for the duration of its mission.

As always, we would love to hear from you if you have a story idea or are interested in working with us on a project.

— Hannah James

Left to right: Michelle D'Souza, Tad McIlwraith, 'Umingmak' Muskox, Alex Borisenko and Hannah James



We are here to consult the loca community and make sure thei concerns are reflected in our wor

Project manager coordinating research logistics

Swip up ARCBIO interview with Alex

Team travels from Cambridge Bay to Kugluktuk

On to the next site!

Thanks for joining us on this ARCBIO update!

ARCBIO media tea

Follow us for more @CBG_UOFG

Swipe up for a Q&A with us!

ARCBIO takes over U of G's Instagram and racks up thousands of views

Mehrdad tours STREAM project partner WWF

Katie McGee and her colleague Bill Eaton in Costa Rica

One of the 26 Malaise traps in Kruger deployed for 300 days now!

ARCBIO Interviews: Tad McIlwraith & Alex Borisenko

Tad joined the ARCBIO project in January 2019, where he provides advice on ethical research practices to scientific researchers working on ARCBIO. He sits on the University of Guelph's Research Ethics Board and works on oral history projects with First Nations communities in British Columbia.

Q: How did you become involved in ARCBIO?
I got a call one day from Alex Borisenko who said he had found me on the University of Guelph website after searching the words "Indigenous hunting". We set up a meeting over coffee within a few hours and Alex gave me a tour of the Centre for Biodiversity Genomics. He then asked, "Can you go to the Arctic in December?" I did some light edits on the ARCBIO research program proposal and I guess I passed the test! I didn't even know anything about DNA barcoding until Alex called. Being in Nunavut and being part of this project is a privilege.

Q: What interests you about this project?
What interests me about this project? Lots of things. How do scientists work? I've never thought of myself as one. At worst I have a cynical understanding of what it means to be a scientist. I think of information as used in social contexts. I'm interested in how science is done. I'm interested in processes of community engagement, and the connection of science and Indigenous Knowledge Systems, their methodologies and how knowledge systems can be integrated.

Q: As an anthropologist, what will your approach be while working with scientists and other collaborators on this project?
I am going to stay out of the way, try not to break anything, listen as much of possible, and make suggestions where I can. I have long seen my role as a fly on the wall. I am interested in helping people tell their stories. They are the experts and they need their voices heard.

Q: What are you most looking forward to about this first ARCBIO trip?
I'm looking forward to the time shared with my team. My great pleasure is getting to hang out with people of all ages. I am looking forward to meeting Inuit peoples and learning about their perspectives. I also want to feel the winter air and see the winter Arctic. It's cold, but that is part of this wonderful experience.

Q: You came across some interesting documents about Inuit invertebrate knowledge. Do you want to talk about that?
Yes! I came across a study about Indigenous knowledge and insects and wanted to share it with the ARCBIO team. This paper looked at how insects are connected to Inuit oral tradition. The study talked about the importance of small things, the possibility of transformation, the spiritual nature of insects. There is also an entire volume published in 1914 on the insects of the Arctic.

Alex has been involved in ARCBIO from the beginning. He coordinates the project's research logistics and leads the planning mission to identify sampling sites around Cambridge Bay and Kugluktuk, in anticipation of the upcoming field season. Alex traveled to Cambridge Bay in summer 2018 to do a pilot survey.

Q: What is your objective for this first ARCBIO trip?
We'd like to connect with people and organizations that may be interested or have a stake in our project, to inform them about the work we hope to do in the summer and to ask for their input on field sampling design. The local Hunters and Trappers Organizations are among our primary counterparts. We want to make sure there are no concerns and that we maximize the relevance of our planned activities.

Q: What is the purpose of ARCBIO? Why is learning about Arctic biodiversity so important at this moment in time?
Global changes are particularly evident in the Arctic and it is expected that Arctic communities may be disproportionately affected by climatic shifts and increasing economic activity in the North. Fortunately, this is recognized by the Canadian government, which prompted the establishment of Polar Knowledge Canada and its Northern Science and Technology Program. ARCBIO will employ current DNA technology to develop a baseline for the state of arctic biodiversity and set the stage for long-term monitoring efforts. We want to make sure that our project activities serve the needs of communities living in the Canadian Arctic and are informed by them.

Q: What are you most looking forward to about this trip?`
I am excited to meet new people, to tell our story, to hear theirs and to learn the local perspective. A key element of our project is building relationships, and it is a great privilege to be here before the planned field season and to make this personal connection. I am absolutely thrilled by the hospitality of the people I met, their reading of the land and the depth of their understanding of issues around arctic biodiversity.

Q: You have a particular interest in small mammals. Is there something more you are hoping to learn about them through ARCBIO, and if so, what?
Definitely. Small mammals have been studied in these areas, but I hope to glean new information on possible range extensions associated with climate change. I expect that DNA analysis would provide new information about their parasites. Small mammals, such as lemmings or voles, are a critical food source for larger furbearers and some birds, and are also a food supplement for local dogs, meaning they are central to questions about wildlife health and disease, which may affect humans as well. In light of the potential for migration from the south, we might be expecting new parasites and pathogens. Hopefully ARCBIO will allow us to start gathering new ecological information on these characteristic species of the Canadian Arctic.

Collections Unit

News & Announcements

- Jeremy applied with Scott Miller (SI) and Yves Basset (STRI) (with the help of Jayme, Kate and others) to the National Science Foundation's 'Macrosystems Biology and NEON-Enabled Science' competition to fund Malaise trap surveys at 18 NEON sites in the US
- Meredith and Jeremy began making Year Two plans with our Global Genome Initiative counterparts of the GGI-CBG Partnership
- Congrats to Kylee Ronnenberg on being accepted into a master's program at the University of Ontario Institute of Technology

This month, we aim:

To complete:

- A visit to the Lyman Entomological Museum in Quebec to sample specimens for the Arctic BIOSCAN (ARCBIO) project
- Obtaining Nunavut collecting permits for ARCBIO and hiring an ARCBIO field technician
- Processing samples harvested at the ROM and CMN
- Reviewing insect genera lacking a subfamily assignment on BOLD
- Confirming authorship for >2K species names for GGBN release
- Integrating updates to our Access databases for the Sequel workflow quality control checks

To continue:

- Processing the remaining 145 of 193 Kruger Malaise samples
- Working with Laurence Packer and Mike Sharkey to increase generic coverage of Hymenoptera in BOLD

Last month, we completed:

- Processing 50K specimens for year one of the ARCBIO project
- Validating 2M GMP records, that have so far resulted in updates to 1250 BINs (for a total 17K specimen records)
- Reviewing legacy records on BOLD, updating 22K specimen records

Genomics Unit

February was marked by hectic weather patterns that wreaked havoc across the Guelph area and the three snow days had an impact on CCDB operations. Last month, the CCDB processed 42,265 samples through DNA extraction (compared to 54,477 in January) including 10,151 samples that were bidirectionally Sanger sequenced; the remaining DNA extracts were analyzed through the SMRT sequencing workflow.

Method development and optimization:

- We are validating a new version of the SPRI protocol for DNA extraction using a magnetic pin tool. Early testing using a manual procedure demonstrates great promise for significant reduction in the need for manual lysate transfer that is currently a limiting step to scaling up our alkaline lysis protocol
- To improve the audit trail through the 384-well consolidation steps, we have implemented an automated scanning and logging of LIMS barcodes on post-DNA extraction consolidated plates (P1) has been implemented

This month, we aim to:

- Complete analysis of all ARCBIO samples in accordance with the project deliverables for year one
- Continue processing samples from Kruger and other GMP sites
- Complete pre-production testing and roll out of Clarity LIMS functionality for our standard metabarcoding workflow
- Conduct second phase testing of the new SPRI protocol using magnetic rods and Biomek automation
- Finalize validation of single-PCR Sequel workflow for fresh arthropod samples from Malaise traps

Large-scale projects and initiatives:

National Ecological Observation Network (NEON) has committed an additional US$267,980 for DNA barcoding of mosquitoes, beetles, small mammals, and fish samples over the next two years. The new contract will add to NEON's last year contribution of US$169,000 and this work will also be carried out by the CCDB.

Informatics Unit

This month, we aim to complete:

- Continued maintenance to protect services and improve systems:
  - migration to new database server to improve BOLD performance
  - implementation of additional servers to increase analysis capabilities and storage space
  - deprecation of out-of-warranty servers
- Implementation of additional web traffic throttling protocols to improve system performance for priority users of BOLD
- Development of a new BOLD Data Submission Queue system to improve communications and efficiency

Last month, we completed:

- Reviewing and improving data QA/QC protocols for Sequel workflows, with new tools and checkpoints added in collections, genomics, and informatics
- Establishment of a cross-unit Sequel team who will work together to maintain and improve quality of data workflows

Hajibabaei Lab

STREAM

In the field of biology, especially in biodiversity, amateur scientists have been actively participating in research since the 1800's. Often, the driving motivational force behind citizen science involvement is a vested interest in the species being studied or the implications of the research. Biological monitoring (biomonitoring) initiatives repeatedly tick both of these boxes and many previous projects have been successful in attaining large numbers of data-collecting volunteers. Whether it be counting snow hares in the Peak District, 'paparazzi-ing' bumble bees around local wildflower patches or kicking up a riverbed to unearth the hidden wonders of bug communities; citizens have been making science happen across the world.

The growth of citizen science projects, from small enterprises commenced by enthusiastic hobbyists to nationwide or even worldwide monitoring programmes, has largely been the result of both data processing advances and change in perception regarding what public can contribute to scientific research. As with the academic world, citizen science projects are evolving with technology. Biomonitoring methodology has seen the shift from visual identification of species of interest, to the use of DNA as a faster more accurate method of identification. This is particularly important when results from biomonitoring initiatives are used to determine ecosystem health, such as with river biomonitoring.

STREAM project team in the kick off workshop in ECCC facilities, Vancouver, BC

STREAM (Sequencing The Rivers for Environmental Assessment and Monitoring), is a new community-based project which involves DNA metabarcoding analysis of bulk benthic samples from rivers across Canada. Led by the Hajibabaei lab at CBG, STREAM was recently granted $2.6M from Genome Canada (Ontario Genomics) and collaborators including World Wildlife Fund (WWF) Canada, Living Lakes Canada (LLC), Environment and Climate Change Canada (ECCC) and aims to engage members of the public to collect data for monitoring of river health. The STREAM project builds upon 10 years of DNA metabarcoding research at CBG and existing benthic biomonitoring protocols carried out by the Canadian Aquatic Biomonitoring Network (CABIN), which involves kick-netting to collect benthos for identification of macroinvertebrates using microscopes and taxonomic keys. STREAM involves the same protocol for collecting samples, however samples are homogenized and DNA is extracted for next-generation sequencing (NGS) analysis of macroinvertebrate taxa.

Over the next three years, STREAM aims to recruit and train community members to collect at least 1500 bulk samples, through collaborative training videos and outreach materials. The benefits of collaborating with citizens for biomonitoring include both the increased number of samples for analysis, numbers which simply are not possible for researchers to collect independently and the ability to tap into knowledge of local people and Indigenous groups. Through using community groups to collect these bulk benthos samples, macroinvertebrate communities can be determined within numerous catchments, some of which are heavily data-deficient rivers. Benthic invertebrates are targeted for determining the state of the local environment because are sensitive to a variety of physical and environmental disturbances and some orders act as important biological indicators for the health status of rivers. Overall, the STREAM project will allow a database to be established, with all the different macroinvertebrate species which can be found in watersheds nationwide.

An important element of STREAM is to give community groups a sense of stewardship over their local watersheds. By participating in the project, people can gain valuable skills and knowledge in the natural world as well as acquiring responsibility over both data collected and how they, as an ordinary citizen, can actively participate to improve the health of rivers. Data generated through STREAM will be made publicly available through a website portal and numerous dissemination tools and materials will allow members of the public to remain engaged throughout the project and understand how the data they have collected contributes to a better understanding of the health of river systems.

Our understanding of how the natural world functions only improves with extra information. To be able to understand what the effects of environmental issues such as water pollution and climate change have on the macroinvertebrate communities, we need to have an idea of the baseline benthic communities currently existing in rivers across Canada. STREAM will enable an understanding of where different key macroinvertebrate taxa are and the community composition and structure at different geographical levels. From this data, monitoring the long-term responses of benthic macroinvertebrates to change becomes possible, which is fundamental for assessing how rivers as a whole will respond to global environmental change.

— Chloe Robinson and Mehrdad Hajibabaei.

Project partners from ECCC and LLC in a training and sampling event in Smithers, BC.

Steinke Lab

This month, we aim to complete:

- A number of pending manuscripts including a large primer comparison study and the results of the OPP sequencing efforts
- Finding participating schools for the Bees@School program and building Bee Hotels
- Some MinION metabarcoding experiments
- The search for Ultraconserved Element Probes in earthworms
- The first full pipeline to assemble and annotate mitochondrial genomes from various genome sequencing data
- DNA extractions for **a lot** of pollen samples

Publications & Presentations

RESEARCH LABS | GENOMICS | COLLECTIONS | INFORMATICS

Braukmann TW, **Ivanova NV**, **Prosser SW**, **Elbrecht V**, **Steinke D**, **Ratnasingham S**, **deWaard JR**, **Sones JE**, **Zakharov EV** and **Hebert PDN** (2019) Metabarcoding a diverse arthropod mock community. *Molecular Ecology Resources.* Doi:10.1111/1755-0998.13008

Shehata HR, Bourque D, **Steinke D**, Chen S, Hanner RH (2018). Survey of mislabelling across finfish supply chain reveals mislabelling both outside and within Canada. *Food Research International, In press.* Doi:10.1016/j.foodres.2018.12.047