international BARCODE OF LIFE

BARCODE BULLETIN

Vol. 3, No. 3 - Dec 2012

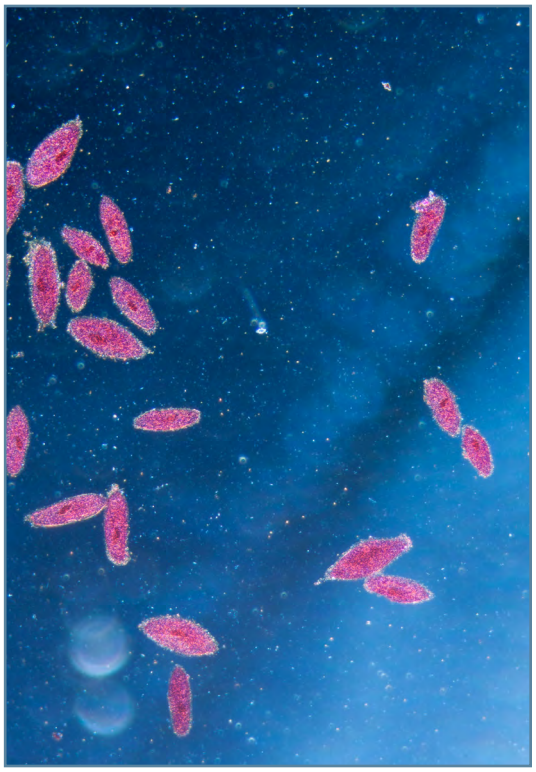
The newsletter of the International Barcode of Life project

Fifth International Barcode of Life Conference to be held in Kunming, China

Our colleagues at the Chinese Academy of Sciences will host the next International Barcode of Life Conference, tentatively planned for October 27-31, 2013, in Kunming. This conference will, once again, bring DNA barcoders from around the world together to showcase and discuss scientific advancements in DNA barcoding and its wide-ranging socio-economic applications. As Kunming is a hub for biodiversity and DNA barcoding research in China, it is an excellent venue for the 5th International Barcode of Life Conference. Stay tuned for more updates about this exciting conference.

DNA Barcode Standards

New community standards adopted for fungi and protists



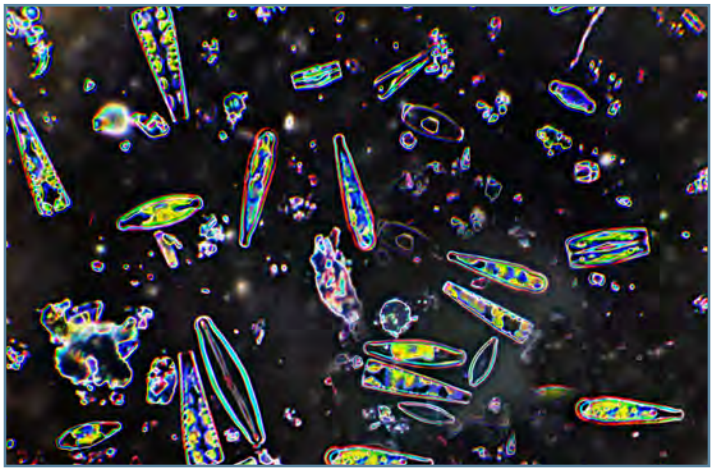
Index:

What is in a DNA barcode?

Editorial feature on DNA barcoding standards

This year saw the designation of standard DNA barcode regions for two major groups of eukaryotes.

In February 2012, the Fungal Barcoding Consortium published a community paper in PNAS that proposed the nuclear ribosomal Internal Transcribed Spacer (ITS) region as a universal DNA barcode marker for Fungi. Nine months later, in November, the CBOL Protist Working Group showed the results of their efforts to identify potential DNA barcode regions across all protist lineages.



Their assessment led to the introduction of a two-step DNA barcoding approach for protistan biodiversity. They propose the V4 region of 18S rDNA as the universal eukaryotic pre-barcode followed by different group-specific barcodes that will have to be defined separately for each major group of protists. This is great news as it signals that all major eukaryotic groups have now been more or less covered by standardized DNA barcode regions.

The ultimate objective of any group tasked with the development of standards in a particular group of organisms is to establish universally applicable criteria to facilitate broad DNA barcode-based species identification and to aid with the discovery of new species.

DNA barcoding uses short standardized genomic sequences to identify species chiefly through PCR amplification by using primers that are applicable for the broadest possible target taxonomic group. For example, many insect groups can be efficiently DNA barcoded by only one primer pair. Reference DNA barcode sequences must be derived from expertly identified voucher specimens deposited in biological collections with online metadata (such as geographic or ecological information) and validated by available online sequence chromatograms.

Effective species-level identification is achieved when interspecific variation exceeds intraspecific variation (often referred to as the barcode gap). Patterns of DNA barcode variation in unknown/undescribed taxa can signal presence of new or cryptic species, which can be verified through integration with other data.

In order to achieve the goal of an effective global DNA barcoding system these standards must be followed. As a consequence of efforts by DNA barcoding community, not only has the International Nucleotide Sequence Database Collaboration (INSDC, consisting of GenBank, the European Molecular Biology Laboratory and the DNA Data Bank of Japan) adopted the data standards proposed by CBOL for barcode data records, it also has empowered CBOL to decide which gene regions can be given BARCODE status.

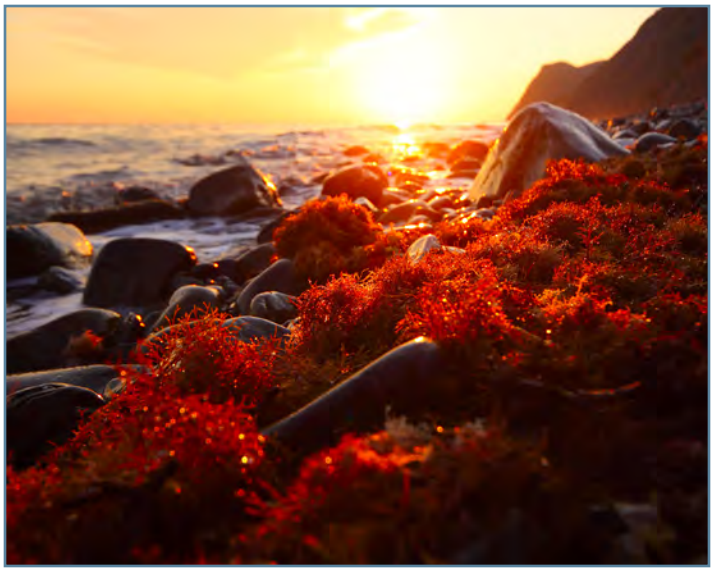
What is in a DNA barcode? -

Continued from page 2

The keyword BARCODE in an INSDC record provides two major advantages for users of the main genetic repositories. On one hand it ensures that only DNA barcode sequences of sufficient quality and collateral information are flagged and thereby promoted. The other advantage is that only a limited number of DNA barcoding regions are used everywhere making research more collaborative and scientifically comparable. Additionally, standardized DNA barcode markers provide a knowledge-base for wide and effective adoption of DNA barcoding in socio-economic applications.

However, an increasing number of studies use non-barcode gene regions and usually they are called DNA barcodes (or other derivatives of the term DNA barcode) referring more to the approach of using a single or a few DNA markers to identify species or even higher taxonomic levels (e.g. family). Unfortunately, this has happened even in groups where several studies have proven that the current DNA barcode standard works well for species-level identification.

We do hope that researchers consider the correct definition of a DNA barcode and do not use the term in situations where DNA barcode criteria are violated.



After almost a decade of development and application, DNA barcoding has become a brand with wide-range scientific and socio-economic impacts. In order to foster even wider applicability and uptake it is critical to protect this brand and prevent generalizations which can lead to divergence from DNA barcoding standards.

As members of the DNA barcoding community, it is important to notify scientific journals on implementing rules on the use of the term DNA barcode or DNA barcoding approach according to adopted DNA barcode standards.

Some of us who have been involved in the process of developing and implementing technical DNA barcode standards know well the difficulty in reaching a scientifically credible consensus backed by comprehensive and high quality data. These two recent papers are great examples of such processes.

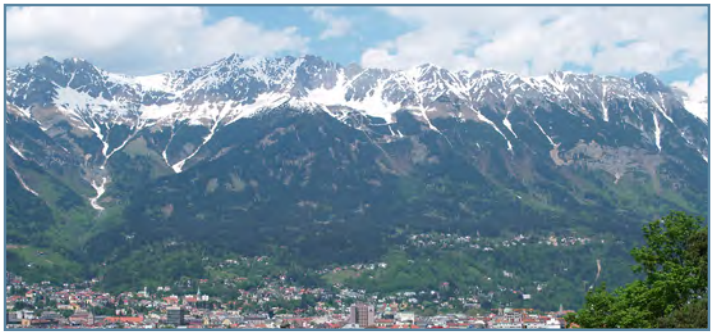
The correct use of the term DNA barcoding would be a respectful gesture to all the researchers involved in the development of a DNA barcode standard and will drive DNA barcoding forward for the benefit of science and society.

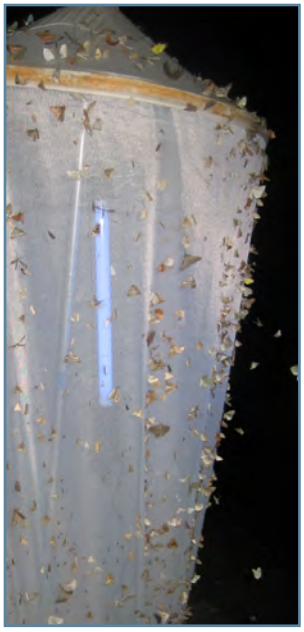
Written by: Mehrdad Hajibabaei and Dirk Steinke

Barcoding Lepidoptera of the Alps:

The search for cryptic diversity

Butterflies and moths represent one of the mega-diverse insect orders in the European Alps, encompassing an estimated 6000 species. First barcoding work by the Tyrolean Federal State Museum Ferdinandeum (Innsbruck, Austria) to build up a complete genetic library started in 2010 and actually included about 2000 species.





In contrast to many other national barcoding initiatives the study area covers a major biogeographic region, shared by 8 Alpine countries. The Alps are among the best known mountain areas in the world and thus scientists were amazed by an unexpected and astonishing amount of cryptic diversity revealed by these early studies.

Taxonomic revision of such problematic taxa represents one of the key issues for conservation of species in a region with increasing environmental issues. Efforts to barcode most of the lepidoptera will be accelerated considerably thanks to funding by the Government of South Tyrol (Italy). A project proposal within the 2nd competition of Scientific Research of the autonomous province Bozen – South Tyrol, was recently approved. The grant will support the search for genetically diverged butterflies and moths north and south of the major ridge of the Alps.

Museums vouchers and collecting in remote alpine areas will be main components to build the final barcode-library. Director Vito Zingerle (photo below on the left) from the Natural History Museum in Bozen and the Scientific coordinator Peter Huemer (right) from the Austrian counterpart expect to collect 2000 species from both sides of the Alps barcoded during the next three years which will provide insights into speciation processes driven by the glacial history of this European biodiversity hotspot.

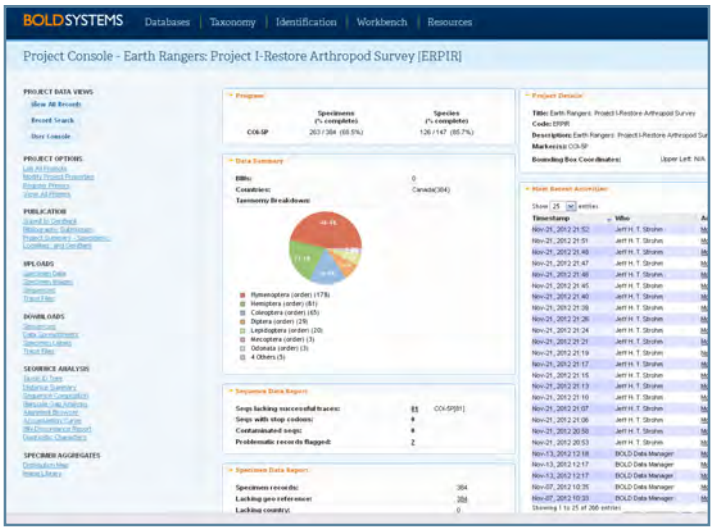
Written by: Peter Huemer

Project iRestore:

Uniquely integrates biodiversity, environmental education, and action

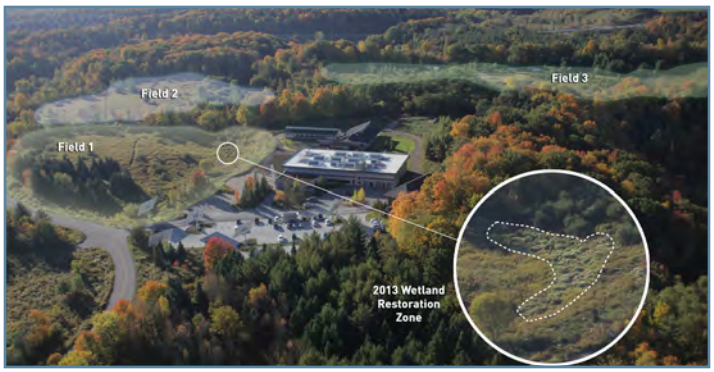
Project iRestore is a long-term habitat restoration project focusing on tallgrass prairie, wetland, and deciduous forest habitat rehabilitation around the Earth Rangers Centre for Sustainability in Woodbridge, Ontario. The primary goals of Project iRestore are native habitat restoration to improve biodiversity in Southern Ontario, and education outreach for conservation and biodiversity awareness and action.

We conduct annual biomonitoring to measure project success (pre, during, and post-habitat restoration) in improving native flora and fauna biodiversity over time. One of our major biomonitoring pillars involves arthropod sampling and DNA barcoding to assist in identification of new species.



BOLDsystems console for arthropods collected in Project iRestore.

In recent years there has been growing recognition of the ecosystem services provided by insects, and because of this insects have become the focus of conservation efforts not seen historically. Furthermore, insects comprise upwards of 50% of known biodiversity, with numerous species yet to be described and new species being discovered in metropolitan areas and schoolyards.



Aerial view of the restoration zone in Woodbridge, Ontario.

We collect insects passively with composite traps at fixed locations. Specimens are sorted to the level of order/infra-order, and insect abundance is assessed by dry weight and number of individuals.

In 2012 our arthropod sampling was generously supported by a MITACS Accelerate Internship to Andrew Frewin, a University of Guelph PhD Biology student in Professor Robert Hanner's lab. So far a total of 385 arthropods were subjected to DNA barcoding. Individuals were pinned, pointed or stored in ethanol, photographed and assigned individual identification numbers.

Expansion plans include a prairie "maintenance" burn in spring 2013, expanding the restored area to include an experimental prairie restoration site where we can examine the effects of different densities of native reseeding and planting on soil characteristics, watershed hydrology, and biodiversity recovery, soil seed bank research, and tree survival to better understand impacts of deer browsing in managed areas.

This project is in partnership with the Biodiversity Institute of Ontario at the University of Guelph, York University, Tallgrass Ontario, Wildfire Specialists, Exquisite Landscaping, and the Toronto and Region Conservation Authority.

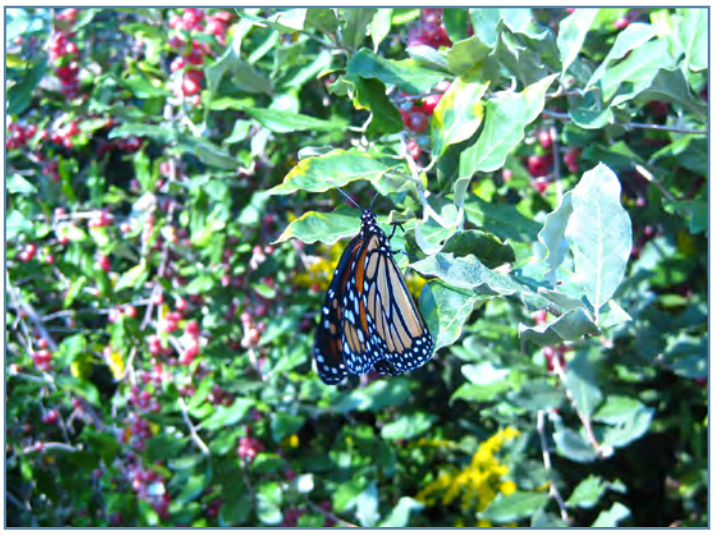
- Continued on page 6

Project iRestore -

Continued from page 5

Project iRestore also forms the basis for a new 2-week undergraduate field course offered through the departments of Biology, Geography, and Environmental Studies at York University. The course teaches senior undergraduate students about field techniques in watershed management and quantifying biodiversity.

Project iRestore confers opportunities to individual and corporate volunteers for science education engagement. Since May 2011, Earth Rangers has used this project as a conduit to help educate 10 undergraduate university students (590.5 hours), 200 corporate volunteers from nine organizations (896 hours), totaling 1,487 hours of outreach engagement.



Written by: Scott Tarof

The National Cockroach Project:

DNA Barcoding the American Cockroach (*Periplaneta americana*)

In 2009, high school students found novel DNA barcode types in American cockroaches (Periplaneta americana) in New York City. This led to a new national project for high school students spearheaded by Mark Stoeckle, Rockefeller University, New York. The goal of the project is to learn more about this feared and despised yet ineradicable urban denizen.

The National Cockroach Project was announced mid December and has put out a call to high school students across the country to sample cockroaches and send them in for barcode sequencing. The main questions of the project are:

- Do American cockroaches differ genetically between cities?
- Do US genetic types match those in other parts of the world?
- Are there genetic types that represent undiscovered look-alike species?

BIObus provides unique opportunities:

Students describe their experiences as part of the crew

The BIObus is the field research vehicle of the Biodiversity Institute of Ontario and, along with a crew of research scientists and biology students, it has travelled to various destinations across North America every summer since 2008 to collect insects and other invertebrates for iBOL.

This summer, the two of us were fortunate enough to participate in the Central-Western Canadian National Parks expedition. On this trip, the BIObus visited 14 National Parks. Five of those parks (Jasper, Banff, Elk Island, Waterton Lakes, and Prince Albert) were visited twice by the bus and crew, each time for a one week period. During our time at these parks we set up various traps and conducted a standardized protocol designed to collect different insects of three distinct habitat types.

Our journey began on July 5th 2012, when we departed Guelph to join the BIObus in Prince Albert National Park. Over two months, we travelled from Guelph in southern Ontario all the way to Pacific Rim National Park on Vancouver Island. Neither of us had driven across Canada before and it was a great experience to see the landscape of our country change around us. We started with the rocky highways of the Canadian Shield in Ontario to the seemingly endless prairies, to the breathtaking Rocky Mountains and finally to the western coast where we dipped our feet in the Pacific Ocean.

The trip gave us great familiarity with entomological field techniques, including setting up malaise, pitfall, intercept, and pan traps. We also applied the knowledge of invertebrate zoology and entomology we gained from our undergraduate studies when it came to sorting and identification of the numerous insects we caught every week.

It was especially interesting to see the environmental changes that happened over the summer when revisiting parks. Plant life changed drastically as did the numbers and species of insects we saw and caught. For example, on our first trip to Prince Albert National Park in early July our vehicle was constantly pelted with deer and horse flies (Tabanidae), and we endured mosquitoes and black flies. However, on our second visit in mid-August we experienced only minimal numbers of mosquitoes. This was a great hands-on experience with the effect of season and location on insect biodiversity.

Aside from insects, we also saw many Canadian mammals. Some were familiar, like beavers and deer, but we also saw mammals we'd never seen before in the wild. In Elk Island National Park we were held up by a large herd of bison on the road (more than once), and in Prince Albert National Park we were lucky enough to see two wolves tracking elk right in our campground.

- Continued on page 8

BIObus provides unique opportunities -

Continued from page 7

Our expedition also encountered black bears, plenty of elk (even two males locking antlers on the shoreline of Waskesiu Lake), red foxes, ground squirrels, prairie dogs and a badger. And once, we even spotted a seal on the ferry ride to Vancouver Island.

We both recently graduated from the University of Guelph with zoology degrees and have a strong interest in entomology, making our position as crew members of the BIObus an ideal summer job and experience. Not only did we get to work outdoors in a field that interests us, we got to see so much of our country and gained valuable work experience along the way.

Our journey didn't end when the BIObus came home for the winter: thanks to this experience, we were both offered one year contracts with BIO.

Written by: Jennifer Gleason & Jonathon Williams

BIObus 2012 Expedition: Sampling was focused in 14 National Parks

1 Pacific Rim National Park
2 Gulf Islands National Park
3 Glacier National Park
4 Jasper National Park
5 Banff National Park
6 Waterton Lakes National Park
7 Elk Island National Park
8 Wood Buffalo National Park
9 Grasslands National Park
10 Prince Albert National Park
11 Riding Mountain National Park
12 Point Pelee National Park
13 Bruce Peninsula National Park
14 Saint Lawrence Islands National Park

Pakistan Barcode Project Progress:

Surpasses the mark of 20K barcodes

DNA barcoding in Pakistan was initiated in April 2010 with the aim to sequence economically important insect species of the country. Sequence data would be used for fast and reliable identification of pest and beneficial insects. Barcode activities gained momentum with funding support from iBOL in January 2012 as part of an initiative to "engage developing nations in iBOL".

These funds have helped to promote and perform DNA barcoding in Pakistan through collaboration between the National Institute for Biotechnology and Genetic Engineering (NIBGE), Faisalabad and the Biodiversity Institute of Ontario (BIO), Canada. This has also increased the capacity of NIBGE and allowed to expand the scope of its barcoding activities by including all arthropod species in its barcode plans.

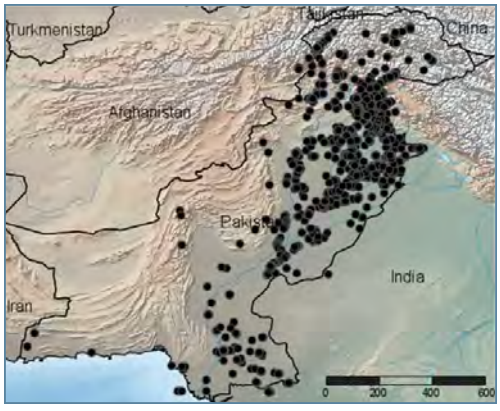
A major emphasis lies on the collection of fresh insect specimens from various geographical areas of Pakistan and to sequence those specimens following standard barcoding protocols.

One of the projects enabled by this funding was launched in July 2012 to perform distributional studies of mosquito species that are vectors for dengue and malaria. Adult and larval mosquito specimens are being collected from various geographical areas, particularly from the urban areas which were recently hit by mosquito-vectored dengue disease.

A group of qualified workers has been trained to handle all steps from collection to tissue sampling. DNA extraction and sequencing is done at BIO. These concerted efforts have resulted in DNA Barcodes for more than 21,000 insect/spider specimens representing roughly 3,500 species. A new specimen repository is under construction at NIBGE which will be ready by early December 2012 and replace the existing smaller facility. It will house and preserve the insect specimens in a more professional way.

Pakistan is now one of the few countries that have started using DNA barcodes for biodiversity analysis and to regularly identify and study the distributional patterns of insects involved in the spread of human and crop diseases.

Written by: Muhammad Ashfaq

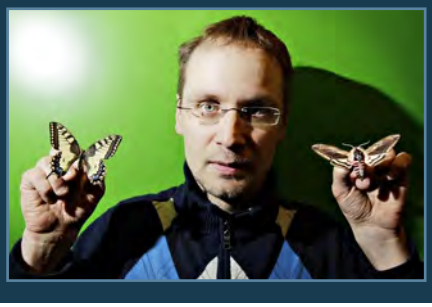


New and Noteworthy:

Latest developments in the world of DNA barcoding

The Ministry of Higher Education, Science and Technology of the Dominican Republic has granted $350,000 to start the Hisp-BOL initiative, a barcoding project to catalog the diversity of the island of Hispanola. The project is led by Dionel López and David Hernandez from the Universidad Central del Este.

Dr. Marko Mutanen has been appointed curator of the invertebrate collections at the Zoological Museum of the University of Oulu, Finland. At present there are about 50,000 vertebrate and two million invertebrate specimens in the museum, with a focus on northern Finnish species. These collections are growing at the rate of several thousand specimens per year.



The Consortium for the Barcode of Life (CBOL) at the Smithsonian Institution was awarded a $3 million Google Impact Awards grant to create and begin implementing DNA Barcoding as an actionable tool for protecting the world's most endangered wildlife. Working with researchers in six developing countries, CBOL plans to build a public library of DNA barcodes that law enforcement officials can use to identify confiscated material. The library is supposed to comprise approximately 2,000 endangered species and 8,000 species that are closely related to them or are commonly confused with them.

The National Science Foundation has awarded $250,000 to the Mount Desert Island Biological Laboratory (MDIBL), the National Park Service (NPS), and the Schoodic Education and Research Center Institute (SERC) for a new project that will involve visitors to the park in hands-on scientific research. The project, called "Pathway to BioTrails," will involve members of the public in monitoring animal and plant species in Acadia National Park and Frenchman Bay using DNA Barcoding.

A project dedicated to the DNA barcoding of Mediterranean Leaf Beetles now has a web site: www.c-bar.org. The Chrysomelidae Barcoding project was developed in partnership with iBOL and aims to create a DNA repository (sequences and specimens database) for the Leaf Beetles of the Mediterranean Region.

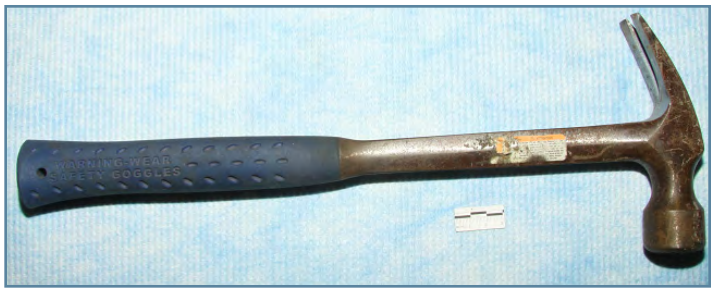
DNA Barcoding Forensics:

Three examples from the Biodiversity Institute of Ontario

Today DNA testing is very common in criminal forensics although it is usually used to establish a connection between a crime scene or a weapon and a suspect. This is done by Short Tandem Repeat (STR) profiling. Only recently DNA Barcoding entered the stage as it provides accurate identification of e.g. animal samples. The following three examples of very different cases showcase the potential applications for DNA Barcoding in a forensic context.

The Hammer

The first case is from an investigation aimed to provide species identification on subsamples taken from a hammer for the Ontario Society for the Prevention of Cruelty to Animals (OSPCA) and Toronto Police Service. Somebody was suspected to have killed a dog with a hammer. Hair and blood samples could perhaps confirm that the hammer owned by the suspect was the weapon.



The CCDB was able to retrieve several short length sequences (mini-barcodes) still long enough to be reliably matched to reference sequences of the domestic dog, *Canis lupus familiaris*. They were also able to retrieve some human DNA from the handle which could have been used for a STR profile.

However, that wasn't even necessary as the suspect confessed when confronted with the initial evidence provided by DNA Barcoding.

Mixed-Meat

In another case two meat samples from the US Food and Drug Administration were sent to the CCDB for species identification.

Analysis provided an accurate identification of the two meat samples using short, medium, and full length barcode regions matched to the BOLD identification library. One was a mixed meat sample with sequences of American Black Bear (*Ursus americanus)*, Lion (*Panthera leo)* in combination with Pig or Wild Boar (*Sus scrofa)*. The other was also a mixed meat sample containing American Black Bear and Lion.

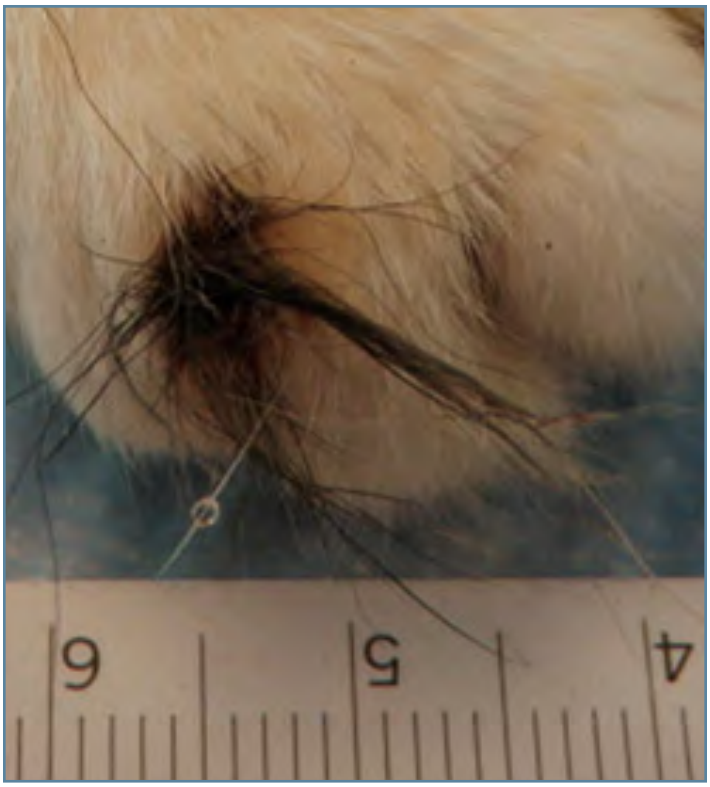
Both the African Lion and the Black Bear aren't currently federally protected endangered species in the US as they qualify as a game meat. It is likely that the FDA just conducted a regular inspection of a game meat retailer.

DNA barcoding forensics -

Continued from page 11

A Cat Paw

The last example describes the DNA analyses on the front paws of a post mortem cat apparently attacked by another animal.



A Veterinary Pathologist from the University of Guelph's Laboratory Services Division had contacted the CCDB as the owners of the cat were specifically interested in having some tufts of black hair visible underneath the deceased cats claws tested for coyote DNA.

It took two attempts at the extraction stage to get some useful results but eventually a the 187 base pair mini barcode and the 421 base pair region of the COI gene were successfully amplified and sequenced.

All the DNA sequences generated matched each other and matched with sequences from *Canis lupus* (grey wolf) as well as *Canis lupus familiaris*, the dog.

Both dog and wolf are too closely related to be reliably separated by short length barcodes but the initial intention was to prove if the cat was killed by a coyote (*Canis latrans*). These occur within the city limits of Guelph and are suspected of a few killings of pet animals. There are unconfirmed reports of wolves in the region but it is rather unlikely that the cat was killed by one.

The dog seems to be a more likely suspect.

Written by: Chris Weland and Dirk Steinke

FISHCODE 2012:

DNA barcoding of fish and marine life

National Training Workshop on DNA Barcoding of Fish and Marine Life – Molecular Analysis and Bioinformatics Approaches.

During three days in September an intensive training workshop for DNA Barcoding was held at Bharathidasan University in Tiruchirappall, India. In preparation for it the organisers had to select 30 applicants from 10 states out of a pool of 150 applications from all over India and from Malaysia and Bangladesh.

Over the three days participants had morning classes on recent developments in DNA Barcoding Research followed by hands on sessions in the afternoon and evening. While the first day of the workshop was dedicated to conventional morphology-based taxonomy, day 2 focused on DNA Barcoding and the application of molecular biological tools in species identification. The 3rd day was devoted to Applications of Bioinformatics Resources in DNA Barcoding research.

The FISHCODE 2012 programme was sponsored by the Department of Biotechnology at the ministry of Science and Technology, the Ministry of Earth Sciences, the council for Scientific and Industrial Research, the Tamilnadu State Council for Science and Technology, the Indian National Science Academy and Bharathidasan University.

Brainstorming Session:

DNA Barcoding for Biodiversity Management

On October 27th in Mumbai, a Brainstorming Session on "DNA Barcoding for Biodiversity Management" was organized by the Central Institute of Fisheries Education (CIFE) in association with National Academy of Agricultural Sciences, New Delhi and Zoological Survey of India. More than fifty leading researchers representing Indian Council of Agricultural Research (ICAR) institutions participated in the session.

Professor W. S. Lakra, Director, CIFE and National Coordinator for DNA Barcoding emphasized the importance of biodiversity characterization and the role of DNA Barcoding for its management and societal benefits. He set out the priorities for immediate networking within the Indian Barcoding community. Among those is the formation of a national steering committee which will lead India to formally join iBOL. The priority submission of barcode data of all current Indian programmes to BOLD was also decided.

Professor Lakra further announced the establishment of a National Centre for DNA Barcoding at the CIFE, Mumbai and the possibility of budgetary support from the Ministry of Agriculture, the Ministry of Science & Technology, and the Government of India for a mega project led by Dr. W. S. Lakra during the XIIth Plan (2012-2017) period of India.

The participants shared their achievements and prepared a draft national project proposal for networking among ICAR institutes, State Agricultural Universities and General Universities.

The Art of DNA Barcoding:

Science and art combine to engage the public in DNA barcoding

Kyoto Prize Laureate Daniel H. Janzen visited San Diego November 11 and 12, 2012 to celebrate the opening of a new exhibit at the San Diego Natural History Museum. BOLD: The Art of DNA Barcoding is a unique interactive exhibition of tropical biodiversity art, science, and technology.

BOLD features innovative Seattle artist Joseph Rossano's biodiversity sculpture series, inspired and accompanied by Janzen's caterpillar and butterfly photographs from Área de Conservación Guanacaste (ACG), Costa Rica. Simulating a near-future where DNA barcoding realizes a vision of reading nature - bioliteracy - via mobile devices, each BOLD piece incorporates its unique genetic sequence identity to bring the species' natural history and science to the viewer.

Janzen updated his renowned biocultural restoration in the ACG on the 3-story screen at the Natural History Museum, for over 250 visitors. Janzen's lecture focused on the role of parataxonomists and other ACG staff in securing the survival of the ACG and its dense and distinctive share of 60% of Costa Rican biodiversity.

He emphasized the key role and interaction with iBOL and the Barcode of Life Datasystems (BOLD). His work in the ACG encompasses 2.5% of the global biodiversity, making him a leading contributor to the iBOL vision of a searchable DNA barcode index of every species on Earth, building towards the approaching day when an inexpensive, ubiquitous, easily used mobile device can "read" nature everywhere. And any species encountered not already a part of the database contributes to its expansion and further discovery.

Image credit: Joseph Rossano

Rossano's artwork vividly depicts how technology influences our understanding of the natural world. The ground-breaking San Diego exhibition features more than 20 original Rossano interactive art pieces and 15 Janzen photomicrographs.

"Beta-tested" at Google headquarters in 2011, BOLD at the SDNHM is presented in partnership with KYOCERA, the Consul of Canada in San Diego, and the Hattie Ettinger Fund at the San Diego Foundation. This installation will remain on display through February 18, 2013.

While iBOL faces difficult challenges in Canadian austerity budgets, the cuts are magnified by their impact on sequencing subsidies for nascent index richness in tropical developing countries, which have just brought their scientific infrastructure.

In an understated surprise, Janzen honored long-time Kyoto Symposium Honorary Chairman Dr. Irwin Jacobs, and his wife, Joan, when he described the key role of barcoding in identifying and understanding the biology of a beautiful new discovery, butterfly species *Opsiphanes jacobsorum*.

Written by: Bradley Zlotnick, MD

The Art of DNA Barcoding:

A few words from Dan Janzen about the exhibition

"I just want to explain a bit more about the exhibit on the wall that you all have just been looking at. Joe came and visited Area de Conservacion Guanacaste (ACG) for a few days, and bumped around with us in the forest, watching us work and hearing about the forest and natural history and taxonomy and DNA barcoding. He did not say a lot, but he was looking for ways to join the artist side of him with the DNA barcoding/science in some sort of combination.

What he hit on is the barcorder's concept that when we look at species, we actually are seeing them only fuzzily. That is on purpose. So you have seen the glass boxes on the walls with a burry image inside, no matter whether you are up close or far away. This represents what you are actually seeing when you look at a butterfly, that YOU think you are seeing very well, and especially if you think you can put a name on its species.

Well, in fact most of us have been deluded into thinking that the name you have is the name for A species. But what barcoding has shown us is that if you take a more focused look at the butterfly, by using its barcode to identify it, you get a more accurate name, thereby sharpening your focus.

The QR code is simply an easy path to where there is a more focused (more accurate, more detailed) look at that butterfly, and especially avoiding confusing it with other species that look the same but really are not because they have different barcodes.

Some day you will be able to drop that barcode into Google and it will go directly to the information on the species with that barcode, on the web, thereby giving you a much more refined/focused view, and therefore a more accurate view, of what is flopping around in front of you. What we do today, in identifying species in nature, is like looking at the vehicles on the freeway from 30,000 feet and calling one a car, another a truck, and another a bus. But if you drop down to 1000 feet, you can say that this one is a 1964 Chevrolet, that one is a Greyhound bus, and the other is an Atlas moving van or a Google photo car.

For some aspects of our interactions with the wild world, perhaps the 30,000 foot view is OK, but for many other aspects, we want to study the beasts from 1000 feet or even less. All buses are not equal. DNA barcoding can give us that."

Image credit: Bradley Zlotnick, MD

The Research Oversight Committee:

Providing strategic direction on research

As was reported in the last issue of the Bulletin, reductions in funding for science linked to the global economic crisis have made it impossible for Genome Canada to sustain its support at the level originally intended. As a consequence iBOL's governance has been streamlined.

The board has appointed a Research Oversight Committee (ROC) whose members are knowledgeable in the program areas but independent of iBOL. The mandate of the ROC is to report to the Funders on the progress being made by the project and make recommendations regarding continued funding as well as to provide advice and guidance to the research team to help ensure that the project achieves its stated objectives and milestones.

To accomplish its mandate the ROC:

1. Monitors quarterly milestones and assesses the progress being made by the Project.
2. Review proposed scientific, GE^{3}LS or management changes to the project and make recommendations to the funders regarding approval.
3. Provide strategic advice to the project team on approaches and directions to aid the project in achieving its high level objectives.
4. Reviews the implementation and effectiveness of the project's management plan and make recommendations aimed at improving management of the project.
5. Identifies issues related to Data Release, GE^{3}LS, Intellectual Property (IP), translation and commercialization of technologies, outcomes and deliverables that arise from the project, where appropriate.

Here we present the members of the ROC:

John McPherson (chair)
Ontario Institute for Cancer Research
Area of Expertise: Genomics

Vivien Bonazzi
National Human Genome Research Institute, Maryland
Area of Expertise: Computational Biology and Bioinformatics

Gary Borisy
Marine Biological Laboratory, Massachusetts
Area of Expertise: Molecular Cell Biology

Mike Bruford
Cardiff School of Biosciences, Wales
Area of Expertise: Biodiversity / Genetic

John Kelly
Ontario Fruit & Vegetable Growers' Association, Canada
Area of Expertise: End User / Applications

Paul Thompson
Michigan State University, Michigan
Area of Expertise: GE^{3}LS

Ben Chalmers
Mining Association of Canada
Area of Expertise: Mining

Top 10 DNA Barcoding Publications 2012

Measured using Publish or Perish

Metrics are largely based on Google Scholar ranking and journal access statistics.

1.
Schoch CL, Seifert KA, Huhndorf S, Robert V, Spouge JL, Levesque CA, Chen W, Consortium FB (2012)
Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi.
Proceedings of the National Academy of Sciences 109: 6241-6246.

2.
Brown SDJ, Collins RA, Boyer S, Lefort M-C, Malumbres-Olarte J, Vink CJ, Chruickshank RH (2012)
Spider: An R package for the analysis of species identity and evolution, with particular reference to DNA barcoding.
Molecular Ecology Resources 12: 562-565.

3.
van Nieukerken EJ, Doorenweerd C, Stokvis FR, Groenenberg DSJ (2012)
DNA barcoding of the leaf-mining moth subgenus *Ectoedemia s.* str. (Lepidoptera: Nepticulidae) with COI and EF1-alpha: two are better than one in recognising cryptic species.
Contributions to Zoology 81: 1-24.

4.
Bienert F, De Danieli S, Miquel C, Coissac E, Poillot C, Brun JJ, Taberlet P (2012) Tracking earthworm communities from soil DNA. Molecular Ecology 21: 2017-2030.

5.
Che J, Chen HM, Yang J-X, Jin J-Q, Jiang K, Yuan Z-Y, Murphy RW, Zhang Y (2012)
Universal COI primers for DNA barcoding amphibians.
Molecular Ecology Resources 12: 247-258.

6.
Nagy ZT, Sonet G, Glaw F, Vences M (2012)
First Large-Scale DNA Barcoding Assessment of Reptiles in the Biodiversity Hotspot of Madagascar, Based on Newly Designed COI Primers.
PLoS ONE 7: e34506.

7.
Hemery LG, Eléaume M, Roussel V, Améziane N, Gallut C, Steinke D, Cruaud C, Couloux A, Wilson NG (2012) Comprehensive sampling reveals circumpolarity and sympatry in seven mitochondrial lineages of the Southern Ocean crinoid species *Promachocrinus kerguelensis* (Echinodermata). Molecular Ecology 21: 2502–2518.

8.
Derocles SAP, Le Ralec A, Plantegenest M, Chaubet B, Cruaud C, Cruaud A, Rasplus JY (2012) Identification of molecular markers for DNA barcoding in the Aphidiinae (Hym. Braconidae). Molecular Ecology Resources 12: 197-208.

9.
Liu Z, Zeng X, Yang D, Chu G, Yuan Z, Chen S (2012)
Applying DNA barcodes for identification of plant species in the family Araliaceae. Gene 499: 76-80.

10.
Vanhaecke D, Garcia de Leaniz C, Gajardo G, Young K, Sanzana J, Orellana G, Fowler D, Howes P, Monzon-Arguello C, Consuegra S (2012)
DNA Barcoding and Microsatellites Help Species Delimitation and Hybrid Identification in Endangered Galaxiid Fishes.
PLoS ONE 7: e32939.

The Barcode Bulletin is the quarterly on-line newsletter of the International Barcode of Life project (iBOL). Send contributions, comments, suggestions, corrections to bulletin@ibol.org

Editors: Mehrdad Hajibabaei and Dirk Steinke
Composition: Suz Bateson
Administrative Support: Vanessa Bouwer