Barcode Bulletin
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Standards for Pollen Metabarcoding

Research
Pocket Mouse Conservation

Applications
Barcoding Game Meat
Welcome to our December 2016 issue of the Barcode Bulletin.

This issue once more contains contributions from last year’s conference as the second part of a special issue was published in November. They are supplemented by stories on conservation, meat analysis, and some important dates for next year’s conference.

Enjoy reading,

Dirk Steinke
Editor-in-chief

The Bulletin’s report on the PLOS Case Study of the endangered Pacific pocket mouse diet notes the important collaboration between public, private, and university scientists to complete their analysis. Their success reflects the similarly diverse foundation provided by the San Diego Barcode of Life (SDBOL), a unique regional DNA barcode campaign in a global biodiversity hotspot.

SDBOL leads and partners with San Diego’s innovative and entrepreneurial scientific, corporate, civic, philanthropic, and academic communities and resources to advance mutual goals in biodiversity understanding. Aspiring to be a leading international node and example for exploration, dissemination, and implementation of DNA barcoding and its infrastructure, SDBOL is achieving critical mass as it evolves from and supports IBOL, BIO, and BOLD in their global missions.

The unprecedented DNA barcoding of the San Diego County Plant Atlas at the San Diego Natural History Museum, the first completed of a large globally important flora, leveraged strategic seed funding from Consulate of Canada and Trade Commissioner for Life Sciences, with corporate contributions from ResMed, Inc, and community philanthropy, supporting efforts by BIO, SDNHM, and UCSD faculty and staff.

The USGS paper (Page 15) demonstrates the utility of the publicly accessible Plant Atlas BOLD barcodes to accelerate ecological understanding in both plants and animals. SDBOL Global Malaise Program sequences now exceed 45,000, including over 15,000 from ResMed urban corporate campus, with its own 1000 BINs, 182 unique to the site, and accumulation curve pointing to nearly 2000 species. Upcoming SDBOL efforts are directed to establish San Diego-wide STEAM (Science, Technology, Engineering, Arts and Math) and citizen biodiversity engagement in using LifeScanner and Malaise collections, and further reference barcoding of the County’s remaining ~1300 species of macrofauna.

Written by: Brad Zlotnick
A slide mount of pollen from the pollen baskets of honey bees

Developing Standards for Pollen Metabarcoding

Written by: Stephanie J. Swenson, Volker Wissemann, Birgit Gemeinholzer (Justus Liebig University, Giessen, Germany)

The biological and economic importance of pollen is widely acknowledged. Pollen allergies, both from airborne pollen and food sources, affect up to 30% of the population of industrialized nations, with severity of reaction highly dependent on plant species. In agriculture, plant breeding relies heavily on pollen, and cultivation of up to 35% of the world’s food crops rely on animal-mediated pollination.

Pollen can serve a key role in ecology and evolution research by elucidation of plant-pollinator networks, flower phenology, and the composition of paleontological communities. It is also used to identify the floral origin of honey and to reveal relationships between objects, people, and places in forensic investigations.

Despite this importance, accurate identification is primarily achieved by time consuming manual microscopic pollen grain analyses, which demand special training and expert knowledge. Further confounding this problem is a diminishing number of experts who can reliably determine organisms to species level and misidentifications due to a lack of species-specific characters or homoplasy. This renders these assessments inherently operator dependent and often only allows identification to the genus, subfamily, or family level.

35% of the world’s food crops rely on pollination

Metabarcoding technology has the potential for fast species-level identification of pollen from a wide variety of sources that overcomes many of the limitations of morphological identification.

A few studies have already successfully applied next-generation sequencing (NGS) for identification and quantification of airborne pollen (Kraaijeveld et al. 2015), pollen contents of honey (Bruni et al. 2015, Hawkins et al. 2015, Valentini et al. 2010), and insect-collected pollen (Galimberti et al. 2014, Keller et al. 2015, Richardson et al. 2015, Sickel et al. 2015).

Despite this potential and proven success, several limitations exist that hamper the use of metabarcoding for pollen identification. These limitations include 1) the necessity of a complete database of genetic markers that provide species-level identifications and 2) a lack of standard best practice protocols for...
DNA extraction and sequencing that overcome inhibition and contamination introduced via the method of collection. Without building a solid foundation, these studies are subject to biases introduced in the field, lab, and final analyses.

“We will develop NGS standards for airborne pollen, honey, and insect-collected pollen”

Our GBOL II subproject, funded by the German Federal Ministry of Education and Research (BMBF), aims to develop standard protocols that will enable the use of NGS for pollen identification from a variety of sources and aid in the development of automation of widespread biomonitoring.

We will develop these standards for airborne pollen, honey, and insect-collected pollen (Hymenoptera and Diptera (Syrphidae)). Each of these pollen sources has both unique and shared problems associated with successful sequencing of genetic markers.

Automated processes have to be equally successful and independent of highly varying pollen quantities and sizes, e.g. (i) for temporal variation in quantity and capture success of different instrumentation of airborne pollen (ii) variety-specific pollen content of honey and (iii) the massive discrepancy in amount of pollen collected on and removed from the body of different insect species. These sources also differ in the chemicals and solvents used in collection and retrieval that have the potential of inhibiting DNA extraction.

Furthermore, species-specific delimitation by means of multiple DNA barcoding markers has to be evaluated and tested concerning success in sequencing.
The 6th International Barcode of Life Conference, held in Guelph, Canada in August 2016, showcased a wide diversity of scientific discoveries as well as socio-economically important applications of DNA barcoding and related genetic approaches. Following the conference, many authors are sharing their work in the form of full scientific articles, published across multiple post-conference special issues (see September 2016 Barcode Bulletin for an overview).

I am pleased to announce that Part 2 of Barcodes to Biomes has been recently published in Genome, including 13 articles. Exemplifying the Barcodes to Biomes conference theme, this issue includes works ranging widely in taxonomic and geographic scope, with a particular emphasis on applications and novel methods.

Xu provides a comprehensive overview of the state-of-the art in the DNA barcoding of fungi, reviewing progress, outstanding methodological questions, and the diverse applications of fungal DNA barcoding and metabarcoding. Ashfaq and Hebert review progress in the DNA barcoding of agricultural pests, particularly highlighting the utility of DNA barcode data in light of the many cryptic species complexes among pests. Considering our entire food chain, Littlefair and Clare review progress and prospects for using DNA barcoding and metabarcoding for enhancing food security—from field to table.

With a focus on birds, Barreira et al. review the applications of DNA barcodes for evolutionary studies, including investigating the geography of speciation. Also addressing evolutionary questions, Mitterboeck et al. use publicly available DNA barcode data to investigate rates and patterns of molecular evolution associated with terrestrial-aquatic habitat transitions in insects.

This issue also features among the largest regional barcode libraries published to date for fishes. Steinke et al. build a DNA barcode reference library for the marine fishes of South Africa; their high success rate in linking juveniles and adults indicates a maturing library that can now be used for diverse applications.
Lee et al. are also interested in surveying regional biodiversity and do so in an intriguing way: using blowfly-derived DNA to generate barcodes from mammalian species. Also investigating species detection but in aquatic settings, Lacoursière-Roussel et al. present their progress in studying herpetofauna using environmental DNA (eDNA). (See additional contributions in this Barcode Bulletin for further information about these three studies.)

Metabarcoding—generating DNA barcodes from multiple species or samples simultaneously via high-throughput sequencing—is gaining increasing attention and usage. For example, nearly one-fifth of all contributed abstracts from the 6th Conference related to developing or using high-throughput sequencing approaches (Adamowicz 2015). Clare et al. investigate the consequences of bioinformatics choices for generating Molecular Operational Taxonomic Units (MOTU) and for the conclusions regarding dietary niche overlap of species. While they found that similar ecological conclusions were drawn, varying the bioinformatics choices had large consequences upon MOTU numbers, highlighting that it is vital to consider analysis choices in metabarcoding studies.

Many members of the DNA barcoding community discuss how genetic techniques have many potential benefits for society. However, the translation of knowledge to policy is a complex issue and is not automatic. In a unique contribution to this scientifically-focused special issue, Thomas et al. discuss how DNA barcoding can be formalized as a method for alien invasive species identification, in the context of Canadian policy and law.

Addressing the ground level of pest management, Hodgetts et al. describe real-world case studies from the UK in which DNA barcoding was used for the rapid identification of pests or suspected pests. For example, DNA barcode results provoked a rapid response following the early detection and identification of an agricultural pest; the application of phyto-sanitary methods to the affected agricultural field was shown to be effective.

Finally, Sirianni et al. present their novel method that they term “closed-tube barcoding”. They discuss how their method could form a component of a highly portable and affordable DNA barcoding device.

In sum, parts 1 and 2 of Barcodes to Biomes present a wide-ranging compilation involving researchers working on all 7 continents and in the world’s oceans. Stay tuned for a larger grouping of articles from members of our global research community, to be published as an online virtual special issue of Genome in 2017.
Conservation biologists use a wide variety of tools to survey mammals in tropical forests - camera traps, searching for scat and footprints, interviews with local communities, sightings, hair traps, cage traps, and nets. These conventional tools often require conservationists to scour the forest and search for mammals themselves, and some methods which require physically restraining the mammals are becoming less acceptable from an ethical perspective.

A recently proposed addition to the mammal survey toolbox is mammal DNA detected from the guts of blowflies. This method does not cause stress to the mammals, needs the least ecological or taxonomical expertise, and is potentially able to detect rare and cryptic species. The unfussy blowflies that feed on carcasses, faeces, or wounds of wild animals in tropical forests may save the conservation biologists the work of finding and collecting mammal DNA themselves. It makes sense in theory, but is it a feasible monitoring tool in the real world and how does it compare with the conventional survey tools?

To address these questions, we, together with colleagues from Monash University Malaysia and Rimba, compared blowfly-derived DNA against conventional mammal survey tools (wire cages, nets for capturing bats, hair traps, and scat collection) at Ulu Gombak Forest Reserve, peninsular Malaysia, where there have been recent reports of small- to medium-bodied mammals. Next, we compared the performance of blowfly-derived DNA with the most popular mammal survey tool - camera traps in Tembat Forest Reserve, peninsular Malaysia, where there have been recent records of large-bodied mammals.
Blowfly-derived DNA detected flying and non-flying mammals, representing a wider body size range than the conventional survey tools at Ulu Gombak Forest Reserve. DNA from the dusky leaf monkey, a near-threatened species not previously found in the forest using conventional tools, was detected in blowfly guts. Blowfly-derived DNA also detected more flying or tree-living mammals than those detected by camera traps at Tembat Forest Reserve.

However, different survey methods detected different mammal groups, indicating that using multiple survey tools may be the fastest way to detect the broadest range of mammals. Apart from detection of mammals, DNA of other vertebrate groups was also detected from blowfly guts – birds, fish, lizards, snakes, and turtles.

With further calibration, blowfly-derived DNA may join the list of traditional field methods.
An important issue for the protection of rare and threatened species is to obtain efficient large-scale population size estimates to comply with legal statutes. However, assessment and monitoring of species of concern are challenged by costs, logistics, and negative impacts on target populations. Analysis of environmental DNA (eDNA) is likely to become a revolutionary tool to increase both spatial and temporal scales for monitoring datasets for species of concern.

The eDNA method detects traces of DNA in cellular or extracellular form from sources such as feces, secreted mucous membranes, gametes, and skin cells. Evidence is growing that eDNA can provide information not only on species presence/absence, but also on abundance. Using eDNA might also increase the observation time windows for surveys, enabling multispecies surveys and reducing the need for extensive taxonomic efforts and financial resources.

However, this new data collection approach is challenged by uncertainty related to false positives and false negatives, as well as environmental effects on eDNA quantity. This, in turn, is slowing the integration of eDNA analysis within management and conservation strategies.

We tested a large-scale eDNA monitoring survey to track both amphibians and reptiles, the two taxonomic groups with the highest proportion of declining species. The efficiency of eDNA to detect and quantify amphibian and reptile populations in seven lakes and five rivers using multiple and species-specific primers was compared to a standardized visual survey and an occupancy distribution model. Our results empirically support the effectiveness of eDNA metabarcoding to inform about local herpetological distributions.

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The only inconsistency among the 34 species was the detection of the Northern Watersnake (*Nerodia sipedon*) outside of its known distribution range.
First considered as a false positive result, an observation of this species by a landowner was then reported in the same river section where the water samples were collected. The latter was particularly relevant given that this species is likely to be designated threatened or vulnerable by the provincial government in the near future. Moreover, detection rates provided similar results to standardized visual surveys currently used to develop conservation strategies for the wood turtle, *Glyptemys insculpta* (see Figure to the right), a species protected against illegal collection and trade in most of its distribution range in North America.

Our results provide an empirical demonstration of the effectiveness of the eDNA method both to evaluate species distributions and to provide an effective semi-quantitative tool, provided that assay calibration and standardization are performed. Detection of eDNA is a promising method towards significantly increasing large-scale herpetological conservation efforts. Integrating eDNA within policy decisions will clearly rely on the rigor with which eDNA is used and interpreted. With improved methodology and standards, eDNA will continue improving in reliability and also in credibility with conservation planners.
The publication of the special issue of Genome this November reminded me of very tragic news earlier this year. March 18th, a very dear colleague and long-time collaborator, Allan Connell, died during a diving accident.

Even though Allan did his PhD in Entomology, he had always been interested in fishing from a very young age, and after his retirement he started a culture of collecting and studying fish eggs. He collected, catalogued, reared, and identified thousands of fish eggs at the KwaZulu-Natal coast off Park Rynie. Of course he often came across eggs and larvae he couldn’t identify. Allan described what happened next:

I searched the internet and came across an article in New Scientist about a researcher at the University of Guelph in Canada, who was barcoding cryptic butterflies, to unravel the mystery of very distinguishable larvae on specific host plants giving rise to cryptic adults that few experts could tell apart by traditional taxonomy.

I made contact with the scientist (Paul Hebert) and asked whether it was possible to barcode some of my unknown species. He replied that they were in the process of sourcing funding for the launch of an international effort to barcode the fishes of the world. They asked if I was willing to collect fish from South Africa and in exchange they would barcode my hatched larvae.

I met Allan more than 10 years ago at the inaugural FishBOL meeting, and we started a collaboration that went on until his untimely death. Countless emails went back and forth, and it was great to see how it progressed. I am glad I kept most of those emails as some are wonderful examples of his enthusiasm. He often likened the arrival of new lab results to the opening of Christmas presents because some mysterious larva finally revealed its identity.
In the said special issue of *Genome* we jointly published a paper that summarized the first 10 years of this work. Little did we know that this would become Allan’s legacy. I am grateful that he learned about the acceptance of the paper shortly before his untimely death. The study delivered DNA barcodes for over 5000 individuals representing more than 1000 species of South African fishes. The fact that these specimens represent about 3% of all known fish species and 10% of the fish species barcoded to date is startling as they derive from the efforts of a single researcher, Allan. This effort took decades, but it clearly shows his dedication and ardour. A line from the last email I received from him shows his enthusiasm:

*Visiting you guys in Guelph was an amazing experience, and your generosity could only be repaid by collecting with all the enthusiasm I could muster. That was the easy part, and fun too. And the project continues, now a 28-year data set, with many more accurate and verifiable identifications, and a lot more that await identification, thanks to barcoding. It is a very satisfying feeling to know that even if, presently, I cannot identify a particular egg type, with the barcode captured, it is just a matter of time.*
* separate article in this issue


Phytopathogenic fungi infecting fruit and forest trees like *Phyllosticta* leaf spots, *Melampsora* rusts, or *Ganoderma* root rot are capable of causing significant economic costs. A generous application of fungicides, often prophylactic, however, entails a series of complications.

Apart from potential health hazards during the application and environmental damage, the fungicidal residues on the edible products have to be closely monitored and kept low enough as not to endanger the consumer. This is often time- and labour-consuming and increases production costs.

In this context, the development of a ready-to-use diagnostic tool to accurately detect the species of phytopathogens and endophytic fungi offers a way to allow a more targeted disease control. In order to provide such a tool to screen for present fungal infections, we are in the process of designing a RNA microarray chip, including the establishment of a standardized work- and dataflow. The idea is to not only print a series of microarray chips and test them, but to additionally install a functioning workflow, including automated data analysis, and a dataflow that allows to match results against a relevant database.

To implement this, the probes of the microarray chip will be derived from fungal barcode sequences, hence Internal Transcribed Spacer (ITS rDNA) sequences, which are collected from already available databases and specimens from the GBOL project ‘German Barcode of Life II (GBOL II) – Pilze in Obstbau – und Forstwirtschaft’.

As part of the developmental strategy, the obtained phylogenetic gene markers from the sampled phytopathogenic fungi, along with ‘Next Generation Sequencing’ data providing insights into the community composition of infected relevant trees, will be stored in a dynamic database, allowing export into a variety of dataflows and working environments. Furthermore, the actual test results of the microarrays will be stored in a database in order to provide reference material for the actual field data.
The development of the microarray aims to include a dual probe set approach, combining a set of probes to screen for phylogenetic gene markers and a set of probes to screen for functional genes, which are associated with the expression of pathogenicity factors. The advantage is that, even when the phylogenetic probes do not deliver any meaningful signals, the functional gene probes can still indicate the presence of a potentially unknown pathogenic species.

For more information, see DOI: 10.1139/gen-2015-0185.

» Attention Readers!

The editors of the Barcode Bulletin are always on the lookout for new contributions. If you just published a paper and think it would be something of interest for our readership a short (approximately 500 word) summary with some print-quality images would be most welcome. Perhaps one of your students just published their first work and you think it needs more airtime. Let them know that we are always interested to spread the word about the newest DNA barcoding and biodiversity research.

Similarly, we are also keen to further build our photo database. As you might have noticed we try to make the bulletin as visual as possible. If you have a stock of images you like to share we would be happy to utilize them, proper credit guaranteed.

Let us know at:
barcodebulletin@gmail.com
How do you determine the diet of one of the smallest rodents in North America, particularly if it’s nocturnal? Readers of the Barcode Bulletin may already know the answer. Collect feces and use metabarcoding to identify the plant material they contain. A fortuitous collaboration between federal government, museum, zoo, and academic scientists has now completed the first such analysis for the Pacific pocket mouse (*Perognathus longimembris pacificus*). This critically endangered mouse only occurs in three small populations in coastal Southern California where most of its historic habitat has been destroyed by urbanization.

Scientists from the US Geological Survey have been studying the ecology of the Pacific pocket mouse since 2007 in order to monitor their populations and build the knowledge base for sound management and restoration. In doing so, animals are monitored using both Sherman live traps and “track tubes” which are PVC tubes lined with sand to record tracks to verify use by the Pacific pocket mouse. Fecal pellets deposited in these traps were used for diet analysis. DNA was extracted and PCR amplified using primers for the ITS (Internal Transcribed Spacer), a region often used in plant DNA barcoding. Amplified DNA fragments were subjected to next-generation sequencing to determine identity and frequency of plant ITS sequences.

Fortuitously, a San Diego Barcode of Life project to collect DNA barcodes for all 2600 native and naturalized plant taxa in San Diego County was in progress involving scientists from the University of California San Diego, the San Diego Natural History Museum, and the Biodiversity Institute of Ontario. This project used tissue from herbarium specimens and sequenced three barcode loci, among them part of the ITS region, providing a reference library for this study. From 52 fecal samples, sequences matching 111 plant species representing 74 genera were recovered at a frequency of at least 1% in at least one sample. However, 50% of sequences recovered mapped to just six species in five genera. The most frequent sequence recovered came from millet, used to bait the traps.

"Understanding the diet of an endangered species illuminates the animal’s ecology, habitat requirements, and conservation needs."
Metabarcoding diet studies are in their infancy. One potential problem in interpreting the results of this study concerns the degree to which ITS sequences from different plant species amplify equally. If they do not, then the frequency of a sequence found by metabarcoding may fail to reflect the frequency of that plant in the animal’s diet.

The authors used two methods to assess this. First they constructed mock fecal samples from mixtures of known concentrations of DNA from approximately 20 different plant species. Sequences from most species were recovered at frequencies similar to their representation in mock fecal samples though some were overrepresented and some, particularly species of wild sage, were underrepresented. Second, feces from captive pocket mice that were fed a diet containing seeds and leaves of 15 different wild and domesticated species were examined. Sequences from all but one of the plant species fed to the mice were recovered from feces. Interestingly, the rarest diet species recovered was a wild sage, indicating that these may be difficult to recover, even if they make up a significant proportion of the diet. Taken as a whole, the results confirm that most plants eaten will be detectable by metabarcoding, though there may be some biases in the frequency of detection.

San Diego County sits within the California Floristic Province, a global biodiversity hotspot. Among US counties, San Diego harbors the highest diversity of plant taxa and the most threatened and endangered species of plants and animals. Having DNA barcodes for all plant species enables detailed diet studies of any herbivore whose feces can be collected.

The broad diet recovered from a relatively small sample of fecal pellets in this study indicates we have much to learn, and that barcoding will be a major tool in developing knowledge for species conservation within complex landscapes.
Game meats are a niche market in the United States, providing consumers with exotic offerings such as raccoon stew, camel steak, and alligator tail. These products are often sold at higher prices than traditional meat products, such as beef, pork, and chicken. For example, yak sirloin steak retails for about US $70/kg compared to US $16/kg for beef sirloin steak. However, when meats are sold as cuts or ground products it can be difficult for consumers to verify the actual species. In addition to the economic incentives of game meat mislabeling, there is also a danger for the use of threatened or endangered species in this market.

In order to determine whether mislabeling of game meat products is occurring in the U.S., my research students and I conducted a series of market surveys on whole cuts of meat as well as ground portions. These studies were carried out at Chapman University and published in the journal *Food Control* (Quinto et al., 2016; Kane and Hellberg, 2016).

We used DNA barcoding as the primary tool for identifying the species in these products. In one study, we collected over 50 game meat products from four different online distributors. This study was focused on testing whole cuts of meat, such as steak, stew meat, breast, and roast. Through DNA barcoding, we determined that close to 20% of products were potentially mislabeled. A smaller percentage of samples (9%) contained near-threatened (bison) or threatened (lion) species, but these products were all correctly labeled and legally sold. Some of the products that we determined to be potentially mislabeled included “black bear” meat identified as beaver, “alligator” meat identified as crocodile, “deer” loin chops identified as llama or alpaca, and “yak” or “bison” steak identified as cattle.

Due to historical hybridization between cattle and bison/yak, further testing would be needed to verify mislabeling in these cases.
Alarmingly, over half of the products sold by one of the online distributors were mislabeled. Many of the mislabeling events associated with this distributor had economic incentives, suggesting that mislabeling was intentionally carried out.

In another study, my research group used DNA barcoding to determine species in ground meat products. This study tested both conventional meats and game meats collected from retail outlets as well as online distributors. Due to the potential for species mixtures to be present in ground meats, we used real-time PCR as a supplementary tool when DNA barcoding failed to produce an identification.

DNA barcoding revealed the majority of samples to be correctly labeled, including all ground beef products. However, one sample labeled as yak burgers was identified as domestic cattle, and nine products were found to contain species mixtures not declared on the label. The same online distributor mentioned above with regard to the black bear stew was found in this study to be selling black bear burgers that contained a mixture of beaver and pork.

Another interesting finding was the detection of horsemeat and other undeclared species in products labeled as ground bison and ground lamb. In some instances of mislabeling observed in this study, there was a clear economic incentive, while in others mislabeling appeared to be due to cross-contamination during processing.

Overall, meat sold through online specialty meat distributors was found to be the most frequently mislabeled, while mislabeling of meat sold at supermarkets was only found in one instance.

DNA barcoding has proven to be a valuable tool in the detection of mislabeling of game meat products on the commercial market. Through our research, we identified multiple instances of species substitution and undeclared species mixtures. These findings indicate the need for increased regulatory monitoring and enforcement of game meat mislabeling in the U.S.
In a little less than a year from now the African Centre for DNA Barcoding and the University of Johannesburg will be hosting the 7th International Barcode of Life Conference from 20 - 24 November 2017. This is the first time that this event will be held on the African continent, and the venue chosen is the Nombolo Mdhluli Conference Centre, Skukuza, located within the heart of African wildlife, the Kruger National Park, South Africa.

**IMPORTANT DATES**

- Registration opened: 01 December 2016
- Accommodation booking opened: 01 December 2016
- Call for abstracts: 31 January 2017
- Deadline for submission of abstracts: 31 March 2017
- Notification of acceptance of abstracts: 30 April 2017
- Deadline for early-bird registration: 31 May 2017
- Deadline for online registration: 31 October 2017

Registration is a pre-requisite for booking of accommodation

Accommodation has been reserved at Skukuza, Kruger National Park – all accommodation bookings for the conference have to be made through Jackey Deacon (dot@mpu.co.za).

Do not use any other website or agent.

We look forward to seeing you there!

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**Credits and Contributions**

Editors: Dirk Steinke, Sarah Adamowicz
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The Barcode Bulletin owes its success to the valuable contributions of researchers and enthusiasts within the global DNA barcoding community. If you wish to contribute please contact us at barcodebulletin@gmail.com.