Efficient Mosquito Surveillance using Metabarcoding
Welcome to our December 2017 issue of the Barcode Bulletin.

It has been a while since we published the last issue. This is by no means an indication of a lack of newsworthy items but rather the result of some institutional changes that also affected the editorial team.

But we are back and will resume our old quarterly rhythm to provide you with the newest information from the world of DNA barcoding.

Enjoy reading,

Dirk Steinke
Editor-in-chief

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Arthropod-borne viruses (or “arboviruses”) are responsible for causing a wide variety of human disease and are primarily spread by mosquitoes. To help prevent, detect and control arboviral outbreaks, surveillance programs monitor mosquito populations and arbovirus circulation. Surveillance is often conducted by culturing viruses from mosquito homogenate, prepared from pools of 10 to 50 mosquitoes in a suitable cell culture system.

The mosquitoes are pooled according to species, which is determined using morphological methods via microscopic examination of the specimens. Surveillance programs struggle using this approach during high vector activity, when more than 10,000 mosquitoes can be caught in overnight collection traps. During these periods, Malaise traps often need to be subsampled, which can leave many mosquitoes untested.

Molecular strategies such as DNA barcoding show great promise as an alternative tool for screening large numbers of insect samples. Initially, DNA barcoding was used to identify the species of individual specimens. However, when combined with high-throughput sequencing, DNA barcoding can be used for species identification of bulk samples, such as a surveillance trap. This process is called “metabarcoding” and can also include pathogen detection by using diagnostic markers in addition to the markers used for species identification.

A group of researchers within Agriculture Research Victoria tested the metabarcoding method using mosquitoes from surveillance traps (for full details see Batovska et al. 2017 DOI: 10.1111/1755-0998.12682). Two pools of mosquitoes were prepared – one with 100 mosquitoes, and one with 1000 mosquitoes. Each pool contained three different mosquito species at varying proportions, including a single Aedes notoscriptus mosquito that was infected with Ross River virus (RRV), a zoonotic virus common in Australia that causes joint inflammation and pain in humans.

A short section (269 bp) of cytochrome oxidase I (COI) was used to identify the mosquito species, and virus-specific diagnostic RRV primers were used for pathogen detection.
Metabarcoding was able to successfully detect all three species in each pool, and detect RRV. The sequencing data were also able to provide the approximate abundance of each species in the pooled samples. However, the quantification accuracy was affected by a range of factors, including the barcoding primers and the number of cycles used when amplifying the genes of interest. It is recommended these variables are optimised to the targeted taxa and the size of the pool, prior to testing unknown samples.

The COI barcode database for Victorian mosquitoes (Batovska et al. 2016 DOI: 10.1002/ ece3.2095) was used to detect the species present in the pooled samples. The utility of metabarcoding is dependent on the reference databases available to correlate the sequences produced. As more mosquito species are barcoded, the reference database could be expanded to help detect the spread of species to new geographic regions. The ability to detect the species of one specimen in a pool of 1000 shows how useful metabarcoding would be during an exotic incursion. In this instance sequences for invasive species could be included in the reference database to allow screening of biosecurity traps, even if the insect of interest is thought to be in very low numbers.
Environmental DNA: Detecting a New Macroinvertebrate in the UK

Freshwater habitats are one of the most vulnerable on earth, facing a range of impacts from climate change to localised pollution. Accurate monitoring of species within these systems is increasingly important as we can then determine any harmful impacts. Current monitoring methods rely heavily on specimen collection followed by morphological identification. However, some species such as rare, non-native or invasive species may be missed due to low numbers or cryptic identification features.

The recent revolution in molecular methods offers a great opportunity for conservation and invasion biologists alike. The detection of these species via environmental DNA (eDNA) allows a non-invasive method of collection, extraction and detection of DNA shed by an organism into water, soil or air, without prior collection of the actual specimen.

Using metabarcoding and high-throughput sequencing we screened samples for all macroinvertebrate DNA present. At 65 sites from 8 river catchments in the UK we collected a 3-minute kick-net sample alongside eDNA samples from water and sediment. The kick-net sample was analysed using microscopy and then lysed to form a DNA sample (“smoothie”), which was sequenced alongside the water and sediment eDNA samples.

Our data found an extensive range of aquatic macroinvertebrates within all sample types. However, surprisingly, in a large proportion of the metabarcoding samples, both eDNA and direct DNA smoothie, we also detected a previously unrecorded Gammaridae species – *Gammarus*...
fossarum, which is very common in continental Europe. This species was not found using microscopy. Morphological separation of the UK’s native *G. pulex* and *G. fossarum* can be difficult as it relies on a number of cryptic features (See Figure 1), and the UK guides currently do not feature *G. fossarum*.

To confirm the presence of *G. fossarum* in the UK we carried out further verification steps. We collected samples for morphological identification and Sanger sequencing, and also examined historical specimens. *Gammarus fossarum* was found to be widespread and common in 6 of the 8 catchments we sampled (Figure 2). It is unknown as to the effects *G. fossarum* may have on the native macroinvertebrates including *G. pulex*, and therefore further investigation is required.

Our results demonstrate the huge potential molecular tools have to detect and monitor freshwater species. Using a metabarcoding approach allows samples to be screened for a wide range of taxa, instead of previously targeting single species, allowing a much greater amount of information to be gained from a relative small number of samples. The current research trend into the use of both DNA and eDNA tools is revolutionising how we monitor aquatic systems, allowing detection of invasive, non-native, rare, elusive or cryptic species, which will give us unprecedented insight into what is happening in freshwater systems and therefore the ability to conserve and protect them.

Figure 1: *Gammarus* identification features: *Gammarus fossarum* A male adult specimen, B male uropod III and C male plumose hairs on inside of exopod of uropod III. *Gammarus pulex* features for comparison D uropod III and E plumose hairs on inner and outer edge of exopod of uropod III

Image credit: Drew Constable, Environment Agency

Figure 2: Catchments surveyed as part of the non-targeted metabarcoding study. Blue filled circles indicates new records of previously unrecorded *Gammarus fossarum*. Unfilled circles were surveyed but *G. fossarum* was not detected (Data taken from Blackman et al, 2017).
One of the greatest threats to coastal marine ecosystems is the introduction of non-indigenous species (NIS) that may become invasive. They can outcompete and displace indigenous species, which usually has negative economic effects. This fact justifies scientists’ and also citizens’ efforts towards early detection of exotic species, because undetected introduction events can seriously boost a successful spread into new territories.

Seaweeds are a special case of biological invasions; propagules can easily be transported by vessels (through fouling and/or ballast water) or introduced as accompanying biota of a species of economic interest (i.e. aquaculture). Moreover, intensive monitoring by using morphological analysis alone can be ineffective for invasive seaweed species identification as it leaves cryptic introductions undetected (DOI 10.1111/j.1755-0998.2009.02639).

In the last few years - inspired by G.W. Saunders (University of New Brunswick), who promoted the idea to apply more barcoding efforts to seaweeds and to establish a global DNA barcoding project for algae - we started several research projects to conduct routine NIS screening combining molecular and anatomical methods. The main goal was to update the exotic seaweeds checklist of the Cantabrian Sea (Bay of Biscay).

Asturias is located in the southern part of the bay, an area surrounded by regions with a predominance of boreal species. The average temperature in the Bay of Biscay has increased between 0.6°C and 0.8°C per decade during the last 30 years (IPCC 2007, doi.org/10.1016/j.marenvres.2013.06.006). In addition, this region is home to important traditional aquaculture (including exotic clams and oysters) since the eighteenth century.
We utilized DNA barcoding by using the COI-5P and rbcL genes to identify fresh seaweed samples collected in several locations under anthropogenic disturbances (i.e. marinas and ports). Moreover, we looked back into the FCO herbarium of the University of Oviedo, Spain, (https://herbario.uniovi.es/), where more than 750 sheets of seaweeds have been stored since 1968.

So far, our barcoding findings revealed four non-foliose *Grateloupiap*-like samples from Gijón marina and University of Oviedo FCO Herbarium samples genetically identified as Asian *G. imbricata* Holmes and the Mediterranean *G. filicina* (J.V. Lamouroux) C Agardh, two undetected Halymeniales exotic in this area (DOI 10.2216/15-112.1). Moreover, we have confirmed the presence of exotic Asian seaweeds *Pachymeniopsis gargiuli* S.Y.Kim, Manghisi, Morabito & S.M.Boo and *Grateloupeia turuturu* Yamada on Cantabrian Sea shores (DOI 10.7717/peerj.3116).

The detection of these species through genetic identifications, in both fresh and historical samples, is relevant since these introductions have been overlooked until now. Currently, barcoding is also helping us to determine changes in spatial and seasonal patterns for other seaweeds such as *Codium* sp. that includes invasive seaweeds such as *Codium fragile* (Suringar) Hariot (Skukan et al. in ISBN: 987-84-16664-34-4).

Our results demonstrate the huge potential for molecular methods to detect previously overlooked seaweed species introductions. Furthermore, barcoding really helped to update our view on past and present seaweed species distributions. This information is essential for both risk assessment and management, two key factors in the global fight against biological invasions.

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Increasing market demand for selected food varieties, featuring particular nutritional or organoleptic properties, is accompanied by a rise in food counterfeiting, a phenomenon that is reaching huge proportions. In particular, the substitution of high-value ingredients with similar, but much cheaper, alternatives represents a widespread form of food fraud, which, for some commodities, affects more than 90% of marketed products. For instance, the spice saffron is one among the most counterfeited ingredients on the market, most often substituted or diluted with other yellow spices, such as curcuma.

Processed food loses its identifiable morphology, e.g. powdered spices, and substitution becomes rather easy. The most straightforward method to verify the authenticity of food ingredients is to utilize DNA barcodes. However, timeframes connected to shipment for analysis to an external laboratory are not compatible with durability of perishable food items. Consequently, the great majority of products enter the market without a genetic check for authenticity.

In order to make DNA barcoding more accessible outside specialized laboratories, thus allowing for a more extensive use of the technique in the food sector, we have developed Nanotracer, which combines the barcode concept with nanotechnology tools. Nanotechnology offers several possibilities to simplify detection schemes, reducing instrumental requirement and thereby allowing for portable field tests.

In particular, we have combined a simplified, instrument-free DNA extraction procedure with the amplification by standard, end-point PCR of a short, polymorphic barcode subregion, with a detection strategy based on gold nanoparticles (AuNPs).

The simplified extraction procedure allowed us to obtain a raw DNA extract in a few minutes directly from a raw food sample, in a single, one-tube reaction. This raw DNA extract, which is likely very fragmented, can be robustly used for the subsequent PCR amplification step, as the latter targets very short regions, instead of the full-length barcode.
We amplified these regions by asymmetric PCR and obtained a single-strand amplicon that could readily hybridize (no further processing such as purification or denaturation steps), with universal AuNP probes. AuNPs have the peculiar property of changing their color, from red to dark violet, when the interparticle distance becomes very short. This interesting optical property, combined with a molecular design that exploits universal probes, permitted us to develop a simple, colorimetric detection scheme, which allow the authentication of any food in a few minutes.

The remarkable advantages of this simplified analysis are: minimal instrument requirements (just a standard end-point thermal cycler is needed for the whole test), reduced turnaround time (the complete test is performed in less than 3 hours), universal design (any food item can be identified with the same universal probes), and low cost (less than one euro per test). Notably, the test is suitable to spot even low-percentage contaminants, up to 1% or lower, which would be very difficult to detect using standard sequencing.

Considering its promising features, Nanotracer can thus be appropriate for the genetic analysis of food items in decentralized laboratories, at point-of-sale or along the food supply chain, and holds great prospects of becoming a valuable tool to fight food fraud.
Humpback whales are now regularly seen at the edge of New York Harbor, drawn by vast schools of menhaden. The local waters are recovering their role as critical habitat for fish and other marine life, thanks to decades of environmental efforts aimed at pollution reduction, habitat restoration, and fisheries management. At the same time, increased shipping traffic, ocean noise, aquaculture, and wind farms pose new challenges to the lower Hudson River estuary and surrounding marine waters.

Sustaining ocean life in the midst of changing patterns of human activities will benefit from inexpensive ways to monitor fish and other sea life. Traditional surveys with nets are expensive, requiring big boats, a diverse array of expensive equipment and personnel, and usually focus narrowly on species of economic interest.

We are testing aquatic environmental DNA (eDNA) as a proxy for fish presence and abundance in waters around New York City. As part of the Monmouth University-Rockefeller University Marine Science Policy Initiative, in 2015 we surveyed a dozen urban marine locations, finding eDNA of resident fish species at all sites, and differences among sites consistent with known habitat preferences (NYC/NJ Aquatic Vertebrate eDNA Project). To test whether eDNA detects seasonal differences in fish, we collected weekly samples at two Manhattan sites over six months beginning in January 2016.

One-liter surface water samples were obtained by tossing a bucket over the railings that line the city’s shoreline. Following standard eDNA metabarcoding techniques, DNA was extracted from filtered water samples, amplified with broad-range vertebrate primers, and analyzed by next-generation sequencing.

The target sequence was a 110 base pair fragment of mitochondrial 12S DNA, chosen because the primer binding sites are highly conserved among vertebrates, which helps improve amplification accuracy. The workhorse of DNA barcoding for animals, COI, excels at identifying and distinguishing species, but is so far less suitable for a metabarcoding approach designed to amplify DNA of multiple species in a single reaction.
Rockefeller University post-doc Zachary Charlop-Powers created an analytic pipeline that identified and counted the fish sequences in each of 76 samples. In winter there was very little fish eDNA; then, beginning in early spring, there was a large increase in species detections, coincident with the known movements of fish from southern and offshore locations into the estuary (link to open access PLOS ONE article). Most species abundant by seining were also abundant by eDNA. A surprise was occasional detection of fish commonly consumed but locally rare or absent—Nile tilapia, Atlantic salmon, and European sea bass, for example. We hypothesize these reflect wastewater contamination in the estuary.

Our results highlight the Goldilocks quality of aquatic eDNA; that is, it seems to last just the right amount of time. If it disappeared too quickly, fish couldn’t be detected; if it lasted too long, then seasonal changes would be absent.

Limitations include an incomplete reference library, the cost of sequencing, and the need to batch samples before processing. To improve the library, we obtained 31 specimens from Monmouth University researchers that represent 18 local species with missing or incomplete GenBank 12S entries. With the help of an exceptional local high school student, 12S and COI sequences were obtained from these reference specimens, and deposited in GenBank.

Looking ahead, we aim to better understand aquatic eDNA localization in New York Harbor. We are collecting weekly samples at Coney Island, famed for its hot dogs and amusement park. Coney Island lies in the outer harbor and faces the Atlantic Ocean.

Who knows, it may turn out that NYC beachgoers are swimming with sharks and whales, or at least bits of them in the form of DNA!
Using Taxonomic Consistency for Producing High Quality Barcodes

Written by: B. Rulik, J. Eberle, M.F. Geiger, D. Ahrens, Zoological Research Museum Alexander Koenig, Bonn, Germany

Those who curate or frequently contribute to DNA barcode reference libraries with well-identified material might know the problem: with time and increasing numbers of specimens submitted, it is getting more and more difficult to keep track of taxonomical changes that might have happened in species-rich groups. In addition, it can happen that one made a few submissions, where the uncertainty associated with a particular identification was higher than with other specimens.

In data sets with a few hundred or thousand species and a multitude of specimens thereof submitted by several taxonomists, it soon becomes a challenge to easily identify the problematic records among the full set of DNA barcodes. This becomes even trickier, as the important cross-validation step incorporating already-published DNA barcodes is getting more robust with increasing numbers of independent taxonomist-verified DNA barcodes, which in turn increases data set size.

Confronted with this problem within the German Barcode of Life initiative (GBOL) and in particular while compiling a second, large beetle DNA barcode data release (2,846 species & 13,516 individuals), a new bioinformatics tool for cleaning large data sets was developed and recently published in Methods in Ecology and Evolution.

The bioinformatics pipeline called ‘TaxCI’ runs in R and combines different other R-packages to 1) identify taxonomic inconsistencies in a given tree topology by comparing the species names (or any other chosen class) in each cluster; 2) discriminate between different cases of incongruence taking relative abundance into account and thereby identifying contamination or misidentified specimens; 3) mark those cases in the tree graphically to allow identification even in trees spanning hundreds of pages.

‘TaxCI’ needs approximately 22 hours for checking taxonomic inconsistencies of more than 29k beetle sequences.
In addition to the color flag a penalty score text file for all specimens is created. It lists all potentially misidentified or contaminated samples. If needed, those records can be corrected or removed from the dataset, before entering public data bases and increasing the ‘noise’ therein. For the underlying clustering, ‘TaxCI’ can either use species delimitations from other programs (e.g., mPTP) or performs a user-defined, implemented threshold-based clustering.

The data-processing pipeline was tested intensively with the set of newly generated beetle DNA barcodes (2,846 species & 13,516 individuals) and also as combined data set with previously published data of beetles occurring in Germany as reference (plus 3,514 species & 15,948 individuals). A data revision based on the first run of the tool resulted in a taxonomic match ratio very similar to the one recorded for the already published reference set (92 vs 94%) and substantially increased its quality.

Overall, the new evaluation pipeline for DNA barcode data allows for the rapid and easy identification of inconsistencies in large datasets, which can be dealt with before submitting them to final data repositories such as BOLD or GenBank. Ultimately, this will increase the quality of submitted data and the speed of data submission, while primarily avoiding the deterioration of the performance of the data repositories due to ambiguously identified or contaminated specimens.

For more information, see DOI: 10.1111/2041-210X.12824.
The current global pace of ecosystem changes calls for reliable and efficient acquisition of information on past and present vegetation, in order to project future developments. This is especially true for rapidly transitioning areas such as the arctic-boreal treeline, where boreal forests are expected to expand northwards on a very large spatial scale.

As the treeline is mostly located in very remote areas, long-term observations and even field surveys of current vegetation are challenging. A multidisciplinary research project at the Alfred Wegener Institute in Potsdam is attempting to overcome these difficulties by compiling data from different sources on past and present treeline changes in Siberia.

Past vegetation is classically reconstructed through the analyses of pollen, but DNA stored in sedimentary deposits (sedimentary DNA or sedDNA) is now increasingly being used in paleoecology. This sedDNA stems from organisms living within the lake and in its surroundings, and can potentially offer a highly detailed view on biodiversity changes, but the full evaluation of its power and limitations is far from complete.

Comparisons of pollen and sedDNA from ancient sedimentary deposits have suggested that, in contrast to pollen, the DNA stems from highly local sources (Boessenkool et al. 2014; Jørgensen et al. 2012; Pedersen et al. 2013), and this has been confirmed for modern terrestrial soils (Yoccoz et al. 2012).

To test the sensitivity of lake sedDNA to sub-arctic vegetation composition and diversity, we analysed surface sediment samples from lakes located along a transect crossing the arctic-boreal treeline on the Southern Taymyr peninsula (Niemeyer et al. 2017). To avoid human or riverine impact on lake and its catchments, remote sites were selected that were reached by means of helicopter expedition in summer 2013. We performed DNA metabarcoding and pollen analyses for 31 different lakes, and compared the results to vegetation field surveys.

Overall, sedDNA metabarcoding retrieved the highest taxonomic diversity. Using a specific sequence reference database for arctic and boreal vascular plants and bryophytes (Soininen et al. 2015; Sønstebø et al. 2010; Willerslev et al. 2014), we found that DNA metabarcoding was able to distinguish vegetation types and record a high diversity of terrestrial plants.
et al. 2014), we identified 114 plant taxa in the complete dataset, about half of them to species level. Pollen identified 43 taxa, while the vegetation field surveys recorded 31. All three methods consistently recorded increasing *Larix* percentages from north to south, and ordination results showed a significant fit among all compared pairs of records.

Despite the good overall accordance, the differentiation of vegetation types was not captured equally well by the three methods. The highest distinction was achieved using DNA metabarcoding and vegetation surveys, which gave a clear signal of the position of the treeline, because they in particular separated tundra from forested sites. The pollen record did not show such a clear distinction of vegetation types, which can be explained by the stronger regional input of pollen into the sediments. Certain peculiarities of the data, such as a marked overrepresentation of *Salix* in the DNA metabarcoding record, remain to be addressed in future studies to fully understand the provenance and quantity of the DNA of different taxa.

At this point, our study confirms the reliability of DNA extracted from lake sediments to analyse changes along vegetation gradients, also on relatively small spatial scales. The results in particular show that it is not lake-to-lake differences in the taphonomy but site-to-site differences in the vegetation that dominate the sedDNA signal.

This is a prerequisite for the further routine implementation of sedDNA analyses in paleoecology, and the high richness recovered by the method suggests that it has the potential to uncover vegetation change at a resolution that is not reached by any other available method.
With the still-growing human impact on global ecosystems, monitoring and describing biodiversity has become more and more important. The good news is that the advent of genetic markers for DNA barcoding of life has clearly eased the way how biodiversity can be explored and catalogued. Moreover, even though genetic markers alone are not suitable for the discovery and description of new species, they nevertheless are able to uncover unexpected diversity within taxonomic groups, which may subsequently lead to the description of new species by taxonomists. The choice of the appropriate marker(s) and method of barcoding, however, is still under construction.

More than 1,600,000 GenBank entries (06/2017) for the cytochrome c oxidase 1 (CO1) gene show the immense importance and usage of this mitochondrial marker for species identification in Metazoa, as it has been initially proposed by Hebert et al. in 2003. Currently, the Consortium for the Barcode of Life (CBOL) has agreed on a 648bp CO1 fragment, the so called “Folmer region”, as the universal metazoan marker.

However, in several animal groups this traditional approach has failed to deliver reliable results (e.g. Bergmann et al., 2013), and this might only be solved by the use of additional markers (layered DNA barcoding) or alternative barcoding methods.

A recent study by Rach et al. (2017) compared an unexplored CO1 region (CO1B) to the traditional “Folmer region” in its power and ease of use to discriminate between 23 odonate species in 51 populations. This fragment lies downstream of the “Folmer region” and includes a small part of the tRNA Leu. Overall, the alternative region yielded a more reliable amplification and also more informative characters, providing a better resolution between closely related sister taxa. Because mitochondrial gene order and gene content across insects is relatively conserved (Simon & Hadrys, 2013) and the reverse primer is located in the tRNA Leu, the CO1B region might become a powerful alternative or complement to the traditional “Folmer region” also for other insects.

“...the CO1B region might become a powerful alternative or complement to the traditional “Folmer region”
Animal phyla like Placozoa or Porifera pose another challenge for DNA barcoding using one standardized marker: The fragmentation of CO1 into up to nine exons in Placozoa (Osigus et al., 2017) impedes DNA barcoding of the numerous placozoan cryptic species (Eitel et al., 2013). As an alternative we suggest a truncated COX1 “Folmer region” in addition to the mitochondrial 16S, which represents the best compromise between practicality and high resolution at the species level.

In Porifera, mitochondrial genes evolve slower and the standard “Folmer region” shows an appropriate resolution at the family level but not below. Nevertheless, Erpenbeck et al. (2006) demonstrated that CO1 could also be suitable for lower-level phylogenies of sponges by using an alternative marker region. Later works (e.g. Pöppe et al., 2010 and Erpenbeck et al., 2016) indicated the same problem for identifications at the species level and concluded that a combination with other DNA markers might be necessary in sponges.

In this context it is also noteworthy that traditionally applied distance-based methods for barcoding do not always allow a clear separation of taxonomic entities, because a unified distance threshold across animal phyla does not exist.

To account for this, character-based DNA barcoding has been developed (DeSalle et al., 2005; Rach et al., 2008; Sarkar et al., 2008). Here, a unique set of characters (character states) is generated from a DNA sequence which allows discrimination at different taxonomic levels, including genera, species and even populations.

In an integrative approach, character-based DNA barcoding can even play an important role in the discovery of “cryptic species”. During taxonomic species description, the character states can be included and thus serve as a complement to traditional morphological identification systems. This integrative approach has nicely been tested for the description of the first cryptic dragonfly species (Damm et al., 2010).
Each one of the seven Barcode of Life conferences over the past 14 years had its own style in truly unique settings. The barcode trail traveled through five continents, and each stop assembled an ever-growing crowd of like-minded scientists. In this regard this year’s conference at Kruger National Park in South Africa was no different but it added something to the mix that can perhaps best be described with the old real estate phrase ‘location, location, location’.

Being surrounded by wildlife that many of us knew only from documentaries and textbooks was certainly inspiring for a conference that revolves around biodiversity science. I cannot remember any other conference where participants deliberately got up at four o’clock in the morning to get ready for a game drive or wilderness walk.

Add to all that a wonderful, friendly and endlessly helpful team of volunteers. A large conference in such a setting is quite a challenge, and the local organisers mastered it quite well.

Yes, internet was slow, sometimes painfully slow, but what a small price to pay for something many participants referred to as the experience of a lifetime.

Over 460 participants from 71 nations came to Kruger for four days of conference, and at least half of them participated in one of the pre-conference workshops. For the latter, delegates could choose between several options (Introduction to DNA Barcoding, DNA barcoding natural history collections, and DNA barcoding using high-throughput sequencing platforms).

And the science? There is no doubt that DNA barcoding has matured and left behind old controversies about its usefulness or applicability. Interestingly, some rather old discussions about the choice of marker systems seem to have be fuelled again by the advent of high-throughput sequencing technologies. The ability to do more creates demand for more, and parts of the community begin discussions of the pros and cons of multiple markers, mitochondrial genomes, etc.
Naturally, African-focused biodiversity and conservation topics took centre stage in the scientific program that consisted of 279 talks and 127 posters, but it is remarkable how many contributions showed the use of novel sequencing technologies for eDNA and metabarcoding studies. Fittingly, the conference saw the release of a new bioinformatics platform build by Sujeewan Ratnasingham and his team. mBRAVE was designed to help researchers with metabarcoding analysis. It supports the storage, validation, analysis, and publication of projects based on high-throughput sequencing instruments.

A summary article such as this one can’t do justice to the diversity of presentations and studies at the conference. It can only highlight trends. A more detailed overview prefaces the abstract volume published in Genome. The Barcode Bulletin team will work with delegates on futures articles for the larger audience that didn’t have the opportunity to participate this year. This selection will hopefully showcase how far DNA barcoding developed in the past 15 years.
At the end of this year’s 7th International Barcode of Life conference, Torbjørn Ekrem, member of NorBOL’s steering group, announced that Trondheim will be the venue for the next conference in 2019.

The barcode community will gather June 17 - 20 in this beautiful city at the Trondheim Fjord. At about 63°N it will be the northernmost conference we ever held. It will be at the time around summer solstice with sunrises around 3:00am and the sunset about 20h later. Perfect conditions for an extended conference program.

The local organisers are already busy preparing and the photo shows how excited they are.

Ser deg I Trondheim!

Credits and Contributions

Written by: Dirk Steinke, University of Guelph, Canada

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.