

Report of the meeting, "ECBOL 2", 2–4 June 2010, organized within EDIT WP 3.4 by ECBOL (Smithsonian Institution (U.S.A), Molecular and Environmental Biology Centre (CMBA) University of Minho (Portugal), CBS-KNAW Fungal Biodiversity Centre (Netherlands) and National Museum of Natural History (France).

Organizing committee:

David Schindel (CBOL, Smithsonian Institution, U.S.A.), Filipe Costa (CBMA, University of Minho, Portugal), Pedro Crous (CBS-KNAW Fungal Biodiversity Centre), Sarah Samadi (National Museum of Natural History, France).

Local organizing committee:

Bjorn Johansson, Cândida Lucas, Cláudia Pascoal, Fernanda Cássio, Luisa Borges, Miguel Pinheiro, Monica Landi, Pedro Gomes, Sara Ferreira, Seena Sahadevan, Sofia Duarte (CMBA, University of Minho), Ronaldo Sousa (CIMAR, University of Minho), Célia Tavares (SPVS, Portuguese Wild Life Society, University of Minho), Cristiane Bastos-Silveira (NMNH, University of Lisbon), Maria Helena Costa (IMAR, New University of Lisbon), Manuela Parente (IMAR, University of Azores).

Scientific committee:

Filipe Costa (CBMA, University of Minho, Portugal), Gary Carvalho (Bangor University, UK), Jan Pawlowski (University of Geneva, Switzerland), Peter Bonants (Wageningen University, Netherlands), Peter Hollingsworth (Royal Botanical Garden, Edinburgh, UK), Mehrdad Haijbaei (University of Guelph, Canada), Ursula Eberhardt (CBS-KNAW Fungal Biodiversity Centre, Netherlands), Wieslaw Bogdanowicz (Polish Academy of Sciences, Poland).

Venue:

B1 Auditorium, CPII Building, University of Minho, Braga, Portugal.

Statistics:

147 participants from 21 countries (27 from 12 EDIT institutions); 9 invited speakers (3 from 3 EDIT institutions); 103 contributed presentations (26 from 12 EDIT institutions) of which 46* oral presentations and 57 posters.

(*Would be 47 presentations but one participant did not arrive)

Aims of the meeting:

- Provide an opportunity for European barcoding groups to interact.

- Present updates on commercial and scientific applications of DNA barcoding initiatives.
- Present new technologies in DNA barcoding initiatives.

Programme:

The programme consisted of scientific presentations and discussion sessions.

Summary of presentations:

Opening session: (invited talks) Stuart Pimm (Duke University) highlighted the rapid rate at which species are becoming extinct with an overview of the global pattern, geographical distribution and the abundances of species of birds and animals. Pimm also emphasized the importance of connecting scattered habitats to prevent the extinction of scarce species in developing countries. David Schindel (CBOL) presented an overview of CBOL activities from the past with future goals of the organization and how it interacts with ECBOL and NELL. Pedro Crous (CBS) gave an overview of ECBOL and NELL activities, highlighting the mission and goals of both networks and future coordination of barcoding activities in Europe. Robert Hanner (University of Guelph) introduced the BOLD database platform as a repository for DNA barcoding information and discussed data sharing, the structure and launch of iBOL. Peter Bonants (Wageningen University) highlighted the importance of accurate identification of quarantine plant pathogens, pests and invasive plants and how developments in DNA barcoding have contributed to this. QBOL aims to barcode voucher specimens of quarantine organisms on the EU Directive and EPPO lists and develop an internet-based database to share with other partners.

Barcoding campaigns and BIOTAS: (invited and contributed talks) Mehrdad Hajibabaei (University of Guelph) outlined advancements in next-generation technologies and their application to barcoding. Nicolas Puillandre (MNHN, Paris), Alessia Cariani (University of Bologna) and Agnès Dettai (MNHN, Paris) reported on the application of DNA barcoding to marine invertebrates and cartilaginous fishes and success obtained with CO1. Rodolphe Rougerie (University of Guelph), David Lees (NHM, London) and Erik van Nieuwerkerken (Naturalis, Leiden) provided informative updates on Lepidoptera DNA barcoding and lesser known Lepidopteran families Micropterigidae and Nepticulidae. The CO1 barcoding gene proved successful in illustrating the biodiversity and identification of cryptic species. A. Manimekalan (Bharathiar University, India) gave an overview of fresh water fish diversity in Western Ghats, India.

Plant barcoding: (invited and contributed talks) Peter Hollingsworth (Royal Botanical Garden, Edinburgh), Sofia Caetano (Switzerland) and Harald Meimberg (University of Porto) provided updates on plant barcoding using chloroplast DNA and some pitfalls

encountered. Hollingsworth also reviewed the process of selecting and refining a plant barcode and its applications, as well as the requirements to push plant barcoding forward.

Fungal barcoding: (contributed talks) Johannes (Ewald) Groenewald (CBS) provided an overview of the progress in barcoding quarantine fungi in the Work Package 2 (fungi) of the QBOL project. Pedro Crous (CBS), Seena Sahadevan (University of Minho), Jozsef Geml (Leiden University) and Nelson Lima (University of Minho) talked about the use of ITS as barcode for various fungal groups and in some instances a secondary barcode, such as calmodulin, would be required. With the exception of Sahadevan’s talk all emphasized the importance of a multi-locus approach to barcoding fungi.

Protist barcoding: (contributed talks) Mónica Moniz (National University Ireland) presented results of a case study validating the use of ITS, SSU and CO1 as barcoding regions of diatoms and found ITS provided a more robust reflection of diatom diversity. Mahdi Bendif (Roscoff), Edward Mitchell (University of Neuchâtel) and Jan Rueness (University of Oslo) highlighted the robustness of CO1 as barcode region to identify the diversity in phytoplankton, shelled amoebae and red algae, respectively. Jonas Zimmermann (University of Berlin) presented results on a fast standardized molecular identification tool using SSU barcodes for diatoms that showed potential in water monitoring.

Data management and analyses: (contributed talks) Robert Vaughan (EMBL-EBI) introduced new services developed by ENA specific for the barcoding community that includes an optimized submission system and validation of barcode data through a keyword, “BARCODE”, that can be controlled by the barcoding community. Vincent Roberts (CBS) introduced a new scientific data management system based on BioloMICS (E-BOLD) that would help ease data management and analyses as well as submissions to BOLD and GenBank. Karl Larsson (University of Oslo) introduced the UNITE database for the molecular identification of fungi (<http://unite.ut.ee>) primarily using ITS sequence data, allowing BLAST type searches and phylogenetic analyses. This session was closed with a discussion panel with the session speakers moderated by Mehrdad Hajibabaei (See below).

Applied barcoding: (invited and contributed talks) Simon Creer (Bangor University) highlighted the restrictions on taxon assessment of microbial eukaryotes using chain termination sequencing and how this can be overcome by second generation sequencing such as 454 Roche environmental metagenetic sequence analyses. Martin Meijer (CBS) reported on the use of ITS barcodes to identify culturable and unculturable fungi in indoor environments by pyrosequencing of dust samples taken from numerous buildings globally. Jan Pawlowski (University of Geneva) presented results on comparisons of two second generation sequencing techniques, 454 and Solexa

technologies, on eukaryotic deep-sea diversity, including cost assessments. Donald Baird (University of New Brunswick) reported on the use of second generation sequencing and phenomics on biomonitoring and how ecological assessments of human impact have become affordable and fast. Joanna Zaluga (Gent University) presented results on developing barcodes for plant pathogenic clavibacters, a quarantine organism, using sequence data as well as MALDI-TOF mass spectrometry. Bart van de Vossen (NPPO, The Netherlands) reported on the development of barcoding protocols for various quarantine organisms for the EU project QBOL as diagnostic tool and validation of data on Q-bank. Neela Enke (University of Berlin) highlighted the importance of correct specimen collection and subsequent treatment of the specimens in the field for further DNA-based study and provided standardized protocols and requirements for specimen collected in the field. Tadeusz Malewski (Polish Academy of Sciences) reported on the successful coupling of real-time PCR and high-resolution melting analyses to identify forensic important blowfly species.

Progress in animal barcoding; Barcoding poorly known animal taxa: (invited and contributed talks) Robert Ward (CSIRO, Australia) gave an overview of FISH-BOL and achievements to date and the importance of barcoding fishes as a diagnostic tool. Federic Sinniger (U.S.A.) presented results of a barcoding-type approach to studying zoanthid diversity from Hawaiian and New Zealand seamounts. Adriana Radulovici (University of Quebec) reported on the success of CO1 as barcoding gene for North Atlantic and Arctic amphipods species identifications and highlighted the importance of including geographical information. Julien April (Laval University) reported on the success achieved with barcoding freshwater fishes in Northern America. Astrid Cruaud (INRA) also reported on the success of using CO1 as barcode to identify figwasps. Charlotte Schoelinck (UPMC) presented the first DNA barcode approach to identifying gill parasites of groupers and how this has helped to identify cryptic species in this group of organisms. Andrea Galimberti (University of Milan) presented results of a barcoding study of Italian bats and the discovery of cryptic species in some genera. Michael Raupach (DZMB) presented results on the effective use of CO1 as barcode for terrestrial and marine arthropods and the use of a secondary gene of the nuclear ribosomal expansion segment. Thibaud Decaens (University of Rouen) reported on the developments of DNA barcoding the soil communities and presented results on barcoding of earthworms and identification of cryptic species within these organisms.

Poster session: The fifty seven posters presented protocols, developments and results obtained based on DNA barcoding and other DNA based identification methods of a large variety of organisms.

Summary of discussion sessions:

Discussion session on Data management and analyses (Moderator: Mehrdad Hajibabaei): The discussion panel consisted of Robert Vaughn (EMBL-EBI), Vincent Roberts (CBS) and Karl Larsson (University of Oslo).

Topics of discussion

1. Quality of data
 2. Availability of data
 3. Improvements and changes to databases
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1. A lot of emphasis was placed on the quality of data provided and deposited into the various databases available for DNA barcoding. All members of the panel, however, emphasized that the quality of the data in the respective databases is not the responsibility of the administrators of the databases, but that of the researcher depositing the data and the barcoding community itself. Quality control of data by database administrators is minimal and therefore the barcoding community should inform them of any mistakes or where entries do not comply with DNA barcoding standards.
 2. Several participants also highlighted the limited availability of barcoding data and urged other barcoding groups to start making data available on the various databases to prevent repetition of work and allow various groups to identify possible collaborations.
 3. Robert Vaughn and Vincent Roberts both stressed that databases are continuously evolving and if any additional fields are required, the barcoding community should not hesitate to contact the administrators of the databases.

Discussion session at closing of meeting (Moderator: David Schindel): the discussion panel consisted of Sarah Samadi (NMNH), Stuart Pimm (Duke University), Jan Pawlowski (University of Geneva), Pedro Crous (CBS) and Filipe Costa (University of Minho).

Issues highlighted (David Schindel):

1. ECBOL and iBOL
 - a. iBOL launch and Scientific Steering Committee in Guelph, 23-25 September
 - b. Goal of \$5M/year for 5 years devoted to barcoding
 - c. Up to \$1M/year by sending specimens to Guelph (\$10 each, data release policy applies)
 - d. TBD: ECBOL involvement in iBOL Working Groups
 - e. How will E-BOLD and BOLD get along?
 - f. Five Europeans leading working groups

2. Observations on ECBOL2 meeting
 - a. Outstanding taxonomic coverage
 - i. Potential global leadership in several major clades
 - b. Strong connections to classical taxonomy
 - i. Support for vouchers
 - ii. Focus on quality of taxonomic identifications
 - c. Support for standardized approach
 - i. Willing to use COI if it's effective
 - ii. Eager to test alternatives to find alternate standards
 - d. Young generation of barcode researchers
3. Status of European barcoding
 - a. Relatively little involvement in global campaigns (exceptions e.g., amphipods, earthworms)
 - b. Except for QBOL, no European-based campaigns
 - c. Despite EU networks of collections (CETAF, EDIT, SYNTHESYS, Species2000), little focus on infrastructure
 - d. Some large field projects (e.g., Mercantour ATBI) but little collection-based barcoding (e.g., CBS)
 - e. Unclear/weak relationship to other funded biodiversity projects that generate collections
 - f. Prominence of small research projects
4. Obstacles
 - a. Data submission to BOLD and GenBank
 - b. Disconnect between barcoding and major collections in museums, herbaria, botanical gardens
 - c. Disconnect between barcoding and European biodiversity informatics initiatives (BioCase, Species2000, etc.)
 - d. Major funding proposals for coordinated projects
5. Next step?
 - a. Improve communication through Connect
 - b. NELL Pipelines and training
 - c. Proposal to ESF for Barcoding Programme
 - d. Barcoding discussion at CETAF?
 - i. Cooperation with SYNTHESYS network
 - ii. Future FP calls for infrastructure?
 - iii. Next big EC proposal, successor to EDIT?

Views of the panel and participants:

- Possibly reconsider the taxonomic classification of microfauna and flora due to a bottle neck effect in naming species and might have to consider an operational species unit system for these organisms.
- Apply for network funding from ESF to allow members of the core group to meet on a regular basis. This will be approximately 100K euro per year for five years.
- Need a strong proposal for large-scale funding of barcoding in Europe with barcoding of specimens in collections of museums and other institutes forming the core of the proposal.
- This meeting was open to new fields, introducing new taxa and new ways of treating and applying barcoding data and allowed participants to get a global view of biodiversity and gave a new perspective on barcoding.
- The meeting highlighted the expansion in researchers doing barcoding in Europe and could therefore allow for more that wishes to be involved in barcoding.
- Need to engage more people by improving communication through a newsletter and dynamic website allowing better integration of barcoding initiatives and help other to get started in barcoding.
- More barcoding workshops are required to engage and help new people in the field of barcoding.