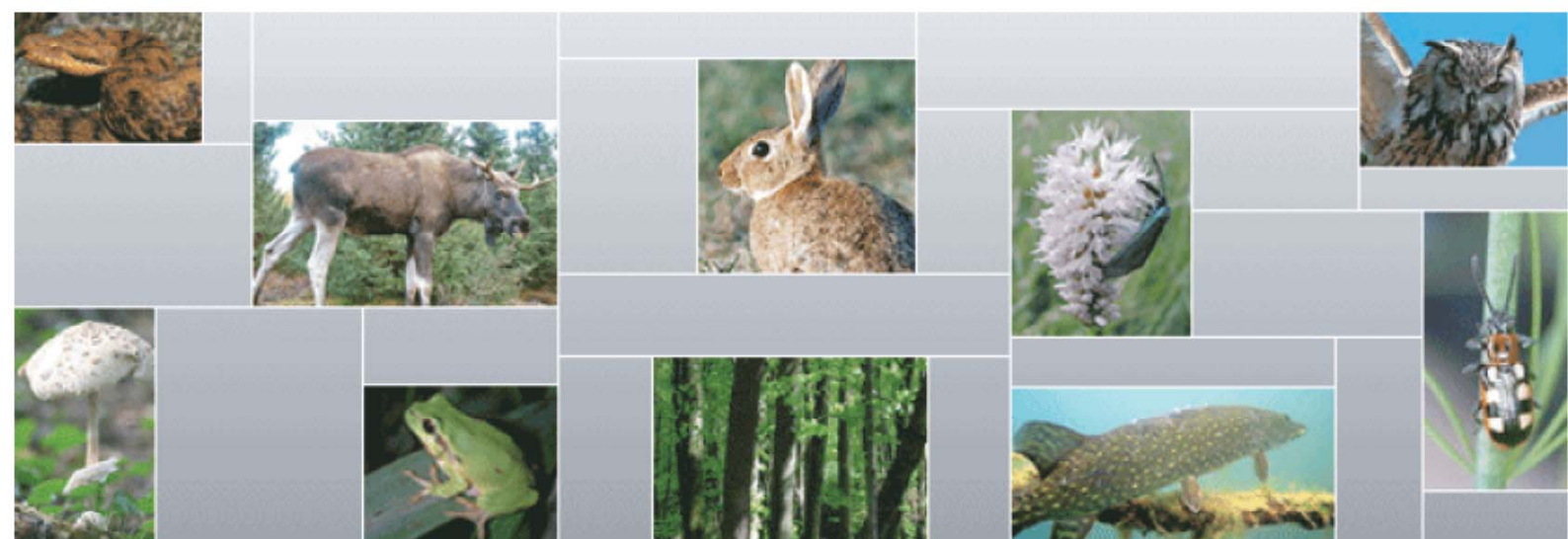


DNA Barcoding in Europe

3-5 October 2007 Leiden, The Netherlands



Scientific Report

Report of the meeting "DNA barcoding in Europe", 3 - 5 Oct. 2007 organized within EDIT WP 3.4 by NLTAf organizations (Centraalbureau voor Schimmelcultures, Naturalis and the Nationaal Herbarium Nederland)

Organizing Committee: Ursula Eberhardt (CBS), Rien van der Linden (CBS), Freek Bakker (NHN/Wageningen UR & CBOL); Local Organizing committee led by Jan van Tol (Naturalis).

Scientific Committee:

Freek T. Bakker (NHN/Wageningen UR & CBOL), Pedro W. Crous (Centraalbureau voor Schimmelcultures, Utrecht), Ursula Eberhardt (Centraalbureau voor Schimmelcultures, Utrecht), Wouter Los (Zoölogisch Museum Amsterdam, University of Amsterdam), Ole Seberg (Natural History Museum of Denmark of the University of Copenhagen), Menno Schilthuizen (Natuurhistorisch Museum 'Naturalis', Leiden), Simon Tillier, (Muséum National d'Histoire Naturelle, Paris), Michel Veuille, (Muséum National d'Histoire Naturelle, Paris), Johann-Wolfgang Wägele (Zoologisches Forschungsmuseum Alexander Koenig, Bonn).

Venue:

"Pesthuis", Naturalis (National Museum of Natural History), Pesthuislaan 7, 2333 BA Leiden, The Netherlands.

Statistics: 148 participants (including organization team) from 22 countries (75 from 18 EDIT institutions); 23 invited speakers (10 from 10 EDIT institutions); 49¹ contributed presentations (18 from 8 EDIT institutions) of which 12¹ oral presentations and 37 posters.

Aims of the meeting:

- Provide a platform where European researchers can interact
- Present commercial and scientific applications of DNA-based identification systems
- Explore funding options, particularly with a view to the 7th European Framework
- Constitute working groups on European aspects of DNA barcoding

Programme

The programme consisted of scientific presentations and discussion sessions.

Summary of the scientific sessions

Status of DNA barcoding (invited talks). Paul Hebert (Univ. Guelph) gave an overview over high throughput DNA barcoding at the Canadian Centre for DNA Barcoding, which can deal with half a million specimens per year, aiming to barcode all animal life in Canada, and beyond, i.e. in iBOL. Frank Bisby (Species 2000 and Catalogue of Life) gave a presentation about how initiatives like Catalogue of Life should supply the taxonomic backbone essential for DNA barcoding, and deliver the default taxonomy browser for the new Encyclopaedia of Life (www.eol.org). Bisby also made a plea for barcoding species globally and by taxon, rather than in a region-by-region approach. Christopher Meyer (Univ. of California, Berkeley) reported on his practical experience from BioCode, an ATBI-project, DNA barcoding the entire island Moorea in French Polynesia. The BioCode project is aimed at providing an insight into taxon dynamics rather than just occurrence and is thus going beyond building a barcode reference library. Meyer referred to the barcode metadata stream, starting from permits and leading to traceable deposits of identified species, enabling the project to metaphorically "put the island in a blender". Costs for collection and barcoding are around 100 dollars per specimen.

¹ The figure would have been plus one, if one speaker had not reported ill.

Applications of DNA Barcoding (invited talks). Hans Helder (Wageningen UR) demonstrated the application of SSU DNA sequences for the identification and quantification of nematodes in the context of soil health. The choice of locus was influenced by the data available for fungi and bacteria co-occurring in soil. Andre Levesque (Agriculture and Agri-Food Canada) showed a variety of DNA barcode based applications to identify plant pathogenic fungi. Barcoding data were also used to make arrays that are ideal tools for ecological studies. Levesque concluded that barcoding heralds a new era for molecular ecology and epidemiology. Astrid Cruad (reading the contribution of Jean-Yves Rasplus, INRA-IRD-CIRAD-SUPAGRO) presented data about the use of barcodes to identify pests. Sequencing of COI & ITS is done in partnership with Genoscope, while RFLPs were also developed as a rapid and cheap tool for species identification. Peter Bonants (Plant Research International, Wageningen) talked about molecular tools for the identification of invasive fungal species (www.portcheck.eu.com), and referred to the new EU call for Plant Health, in which he would be interested to lead a consortium.

DNA Barcoding & Databasing (invited and contributed talks). Mehrdad Hajibabaei (Univ. Guelph – see <http://www.barcodinglife.org/views/login.php>) and Vincent Robert (CBS – see www.mycobank.org) gave short introductions into the DNA barcode assembly workbench BOLD and MycoBank, respectively. Guy Cochrane (EMBL) talked about new developments in the EMBL database for accommodating and searching DNA barcoding data.

“Classical” DNA Barcoding (contributed talks). Filipe Costa (Univ. of Wales, Bangor), Torbjoern Ekrem (Norwegian Univ. of Science & Technology, Trondheim), Urmaz Koljalg (NHM, Tartu), Annette Lee (replacing Yvonne Linton, NHM, London) and Grit Walther (CBS) reported on the application of DNA barcodes for fish, non-biting midges and mosquitoes, ectomycorrhizal and medical fungi. Especially the use of the mobile high-throughput DNA barcoding lab on board the ScholarShip attracted a great deal of interest from participants.

New Technologies (invited talks). Mehrdad Hajibabaei (Univ. Guelph) talked about high throughput DNA barcoding strategies at the CCDB in Guelph and about accessing historic collections for DNA barcoding. Diana Rigola (Keygene) gave an introduction to 454 and Solexa sequencing technologies.

Non-COI Barcoding (invited and contributed talks). Freek Bakker (NHN Wageningen UR/CBOL) outlined the need for (the implementation of) global standards and gave a summary of CBoL’s policy for accepting barcode markers other than COI. Robyn Cowan (RBG Kew) presented the results of a 10-lab collaborative project coordinated by her, aimed at finding optimal loci for the DNA barcoding of plants. Vincent Robert (CBS) showed how insights from comparative genomics may be used to find suitable markers for phylogeny and possibly also for DNA barcoding. Marc Kochzius (Univ. of Bremen) compared three genetic marker systems for their suitability and discriminative power in micro arrays. Julie Hawkins’ (Univ. of Reading) presentation on developing DNA markers for identification of endangered cacti was cancelled due to illness.

Multi-locus Barcoding (contributed talks). Astrid Cruad (INRA-IRD-CIRAD-SUPAGRO), Katerina Fliegerowa (Czech Academy of Sciences), Christian Kubicek (Vienna University of Technology), Nicolas Puillandre and Sarah Samadi (MNHN, Paris) presented data about the added resolution when comparing multiple loci data for the identification of fig wasp, fungal, gastropod and decapod species.

Barcoding the “Invisible” (invited talks). Mark Blaxter (Univ. of Edinburgh) reported on how to DNA barcode in the absence of a stable taxonomy in nematodes, and how discovery of many new groups/clades is expedited by environmental sequencing/DNA barcoding. Birgit Gemeinholzer (BGBM, Berlin) compared the recovery results of different sampling techniques for diatoms. Joerg Peplies (MPI Bremen) showed how rRNA sequencing and hybridization techniques combined are powerful tools for estimating biodiversity of bacteria. Michel Veuille

(MNHN, Paris) talked about a population genetic perspective on how to deal with nascent species in DNA barcoding.

Poster session. Thirty seven posters presented results from a wide variety of organisms with view to DNA barcoding or other sequence-based species identification systems.

Summary of the discussion sessions and related presentations

DNA Barcoding funding opportunities in Europe. Paul Hebert (Univ. Guelph) gave a summary of the iBOL campaign for raising money worldwide that may be matched by Canadian funding for working towards 5 M barcodes in 5 years. Richard Lane (NHM, London) argued in favour of a central European Barcoding facility. Wouter Los (Univ. of Amsterdam) talked about the role of EDIT in initiating an EU DNA barcoding initiative. Willem Wolters (Wageningen UR) informed about existing calls and the realities of applying for EU funding. Cecilia Saccone (ITB-CNR, Bari) reported on DNA barcoding activities in Italy currently worth € 2 M. Richard Lane (Natural History Museum, London), discussed the Joint research Activity in Synthesys 2, which will be focusing on extracting ancient DNA from collections. Wouter Los discussed new opportunities linked to DNA barcoding such as food security, bio-security, early warning systems, environmental quality, wireless biosensors, etc. Leo Kriegsman (Naturalis, Leiden) informed on the November call for Life +, where nature and biodiversity had an allocated budget of 187 Million Euro (deadline end of Nov. 2007).

Discussion topics

- Europe as one of three central nodes in iBOL: can we find \$15 M?
- Do we need a central barcoding facility in Europe?
- Should we go for barcoding museum collections or rather focus on stakeholder needs (agriculture, medicine, trade)?
- Populating local (museum) versus global (BOLD) databases: how do we satisfy our local funders?
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- Organisation of working/funding groups

The outcome of the discussions is included in the general summary.

Summary of the Discussions

1. Coordination

- Promote that different EDIT partners take up responsibility for the different items mentioned below. See also below, working/funding groups
- CBS² to oversee that this happens in a coordinated way. See also below.
- Priority for those activities which require action at the European scale.

2. Website and inventory

Use the website <http://www.ecbol.org> as a (dynamic) inventory of current and planned DNA barcoding activities and as a basis for:

- coordination
- priority setting
- cooperation (for example the working groups)
- targeted EDIT support
- interaction with CBOL
- information on follow-up meetings

² Other WP3 members have indicated interest in sharing this task.

3. Leverage for Genome Canada investment (iBOL)

Note: Europe's obligations in iBOL are explained in detail at

<http://www.dnabarcoding.org/bi/letter.htm> and <http://www.ecbol.org/index.php?page=get-involved-in-ibol-now>. In short, European researchers (as one of three central nodes in iBOL, are challenged to contribute € 18 M of funding applied for and granted or re-dedicated after September 2006 to be spent on DNA barcoding. Along with comparable funding from several regional and local nodes worldwide, these funds will then be matched by Genome Canada.

- All speakers considered aiming at a European contribution to iBOL as advantageous for both the European and worldwide DNA barcoding enterprise.
- Short-term matching must be through existing programmes. Speakers were generally optimistic that the goal could be met or perhaps even have been met.³
- Looking at a 3 to 5 year period of time, national and EU programmes could be initiated through lobbying and setting-up of programmes at the national level. See 5.

4. Large-scale European priorities

- Several contributions stressed that a problem-oriented approach to DNA barcoding is essential in order to attract larger-scale funding and that pure taxonomic ones should be avoided. Suggested problem areas:
 - Public health
 - Biosurveillance: i.e. rapid biodiversity assessment, changes in biodiversity as a response to climatic change
 - Agriculture
 - Invasive organisms
 - Quarantine Organisms
 - Trade
- Barcoding of museum collections
 - Some types of collections accessible to DNA barcoding (i.e. insects, herbarium specimens) while others, i.e. formalin conserved specimens are not.
 - According to experiences from Canada, taxonomists working in collections are the most reliable suppliers maintaining a steady inflow of specimens to the Guelph facility.
 - The short-term impact of DNA barcoding of museum collections outside science is considered to be minor compared to tackling current problem areas. However, the scientists themselves (as one of the most important stakeholder groups for DNA barcoding) would draw major profits from DNA barcoding museum collections.
- Groups lacking their own DNA barcoding campaign
 - Fungi⁴
 - Algae
 - Protists
- Technology development, i.e. FP7 Design studies.
- European central DNA barcoding facility. See below.

³ However, at the time of the discussion the requirements for counting funding for DNA barcoding towards iBOL were not made public. The requirements as they are now known (see the ECBOL and iBOL websites) are such that to our knowledge, none of the projects registered by ECBOL would qualify.

⁴ After the meeting CBOL started negotiating with the international mycologist community worldwide to kick-off the fungal DNA barcoding campaign.

5. Lobbying

With the outcomes of item 4 we have context to start lobbying the European Commission.

Mechanisms are:

- interaction in each country with the national members of the FP7 framework programme committees.
- policy symposiums targeted at policy makers
- dissemination of white papers
- promote that stakeholders and (potential) users will assist in the lobbying

Other targets and mechanisms

- Approach genomics institutions and initiatives in Europe; make them understand that there is a whole research community behind DNA barcoding.
- Interact with Biodiversa. This Eranet for biodiversity research could also be informed via the national members. Should lead to research council money for DNA-barcoding.
- Explore avenues to private funding (i.e. through EuroBioFund).
- Make use of existing calls such as Life+ and Design studies.
- Establish national DNA Barcoding committees (not applicable for all EU countries).

6. Support initiatives

Use part of the EDIT budget to support initiatives amongst partners and staff with seed money for meetings etc to prepare their plans.

[After conference update: plans have been made to put money aside in Wp3 to subsidise planning meetings for a European central DNA barcoding facility and for European campaigns for fungi, algae and protists.]

7. European DNA-barcoding factory

General discussion. The following points were brought up:

- Is additional capacity needed (with view to the existing facilities in Guelph and the Smithsonian)?
- Can we secure the up-keep of facility?
- Are we able to maintain a constant stream of specimens into facility?
- Central facility or dispersed facilities?
- Sequencing capacity exists; lacking is DNA extraction capacity
- Modest costs (5-10 M) of a central DNA barcoding facility compared to many other international projects such as particle accelerators or space telescopes
- Experience from Canada:
 - Facilities not dedicated specifically to DNA barcoding cannot deal with the logistics (specimen processing) of DNA barcoding.
 - No shortage of material observed

Conclusion: There seemed to be a general consensus that a European central DNA barcoding facility would be needed to maintain that European researchers can take active part in advancing DNA barcoding technology and that a constant supply of specimens could be maintained.

Location of a European central DNA barcoding facility:

- The Eastern EU countries (for example in the European middle with Poland, Slovakia, Czechia and Hungary) have a strong position to attract structural funds to construct the factory. This requires:

- Action at their governmental level
- Support from other countries that this should happen.
- As an alternative venue to an Eastern European facility was suggested that a few countries form a consortium and apply for national funds for a DNA barcoding facility.

8. ESFRI Roadmap process (<http://cordis.europa.eu/esfri/home.html>)

In relation (but apart from) getting structural funds for a European central DNA barcoding facility, it can be considered to get in the ESFRI process of their updated Roadmap (with promising new large-scale research infrastructures). It requires that suggestions will be submitted through ESFRI delegated, thus through governments. This would not necessarily confine the choice of location to Eastern Europe.

Local versus global DNA barcoding databases

- CBoL favours a minimalist data standard and GenBank as the ultimate data repository, in which the keyword 'BARCODE' now serves as indicator that all standards have been complied with. For instance, CBoL has made explicit here that accompanying (voucher, GPS, taxonomic) information is linked/available. GenBank/EMBL expect that they can fulfil the needs of the DNA barcoding community also in future.
- The CBoL data standards including the requirement of a specimen and DNA trace files voucher plus information on a new global collection inventory are adopted by INSDC (including GenBank) and appear widely accepted.
- BOLD provides all services commonly needed in DNA barcoding projects, is open to DNA barcoding projects worldwide and can be modified to accommodate special needs. Links to other databases such as UNITE, Mycobank, WASHABEE, etc. are envisaged for the future. The number of mirror sites for BOLD is increasing.
- The multitude of potential uses of DNA barcoding data and accordingly, the variety of different types of connected data or required tools can more easily be served with a spectrum of different databases.
- Technically it is not a problem to integrate between different databases.

Formation of funding/working groups

The seed to the formation of funding/working groups on various aspects of DNA barcoding (funding) was laid at the meeting by starting lists where participants could state their A constantly updated version can be found under <http://www.ecbol.org/index.php?page/funding-groups> .