DNA Barcoding, Capacity Building, and CPM's Mission

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DNA barcoding and forest biosecurity

L.M. Humble, J.R. deWaard, R. Hanner and P.D.N. Hebert

Introduction

The ability to distinguish non-indigenous species (NIS) from native species is critical to the success of any surveillance program. Unfortunately there are numerous problems inherent with detection of NIS including:

- large samples needed to detect NIS when they are present at low levels
- immature life stages often intercepted but usually cannot be fully identified
- often inadequate knowledge of native fauna

We provide examples from forest biosurveillance in Canada showing how these problems can be circumvented by the application of DNA barcoding (DNAB) for species identification.

What is DNA barcoding?

- DNAB uses the sequence variation in a short, standardized DNA fragment to identify organisms
- DNA fragment used for animals is a 658 base pair segment of the mitochondrial gene cytochrome *c* oxidase subunit 1 (COI) (Hebert *et al.* 2003)
- It compares unknown sequences against a reference library of DNA sequences
- It meets or exceeds minimum standards required for diagnostic protocols under ISPM No. 27 (Floyd *et al.* 2010)

Figure 1. Light trapping for nocturnal moths

Biosurveillance for NIS

Methods

- moths sampled with UV lights (Fig. 1)
- a single leg was removed and barcoded using standardized procedures (Fig. 2) (deWaard *et al.* 2009)

Figure 2. Sampling tissue from moths for barcoding

Biosurveillance (cont'd)

Results

The identification engine in the Barcode of Life database (BOLD-ID) was used to obtain initial identifications for the 925 specimens (Fig. 3).

- ~190 species clusters with a 3% sequence divergence cut-off (Hebert *et al.* 2003)
- 124 clusters assigned to species, 61 to genus using BOLD-ID (all species assignments were also confirmed morphologically)
- 66 remaining clusters identified morphologically (the only step in the identification process that required taxonomic specialists)

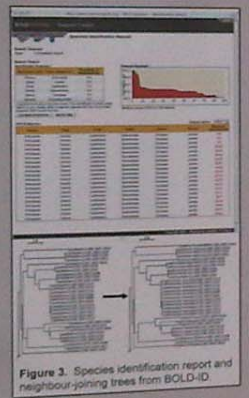

Figure 3. Species identification report and neighbour-joining trees from BOLD-ID

- 31 species and 16% of all moths captured were NIS.
- two NIS, *Argyresthia pruniella* and *Dichelonia histrionana* (Fig. 4), were new introduction records for North America
- two NIS, *Parawannerdomia luteren* and *Priays fraxinella* recorded for the first time from western Canada

DNA barcoding provides an efficient and rapid means of assessing large samples. It enhances both species recognition and the detection of new NIS by:

- minimizing valuable specialist time;
- detecting species at low density

Figure 4. *Argyresthia pruniella* (left) and *Dichelonia histrionana* (right)

Identification of immature life stages

Eggs, larvae or pupae are the most frequently intercepted life stages of many quarantine organisms. They usually cannot be fully identified to species.

- DNA barcodes are invariant during a species development; any life stage can be identified from its DNA sequence

European poplar shoot borer, *Gypsonoma aceriana*, was first reported from North America in 2001

- barcoding of adults in museum collections confirmed its long-term presence in western Canada (Fig. 5)
- barcoding of larvae from delimitation surveys used to define its range in British Columbia (Humble *et al.* 2009)

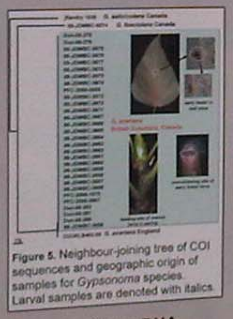

Figure 5. Neighbour-joining tree of COI sequences and geographic origin of samples for *Gypsonoma* species. Larval samples are denoted with italics.

Building DNA reference libraries

DNA barcoding identifies unknown species by comparing their COI sequences to reference sequences derived from reliably identified species sampled from museum collections. Development of the sequence libraries is done in collaboration with taxonomic specialists. Two examples of reference library development follow.

DNA barcoding and forest biosecurity (cont'd)

Building DNA reference libraries

1. *Lymantria* tussock moths

Lymantria includes serious quarantine & forest pests [e.g. gypsy moth (*L. dispar*), pink gypsy moth (*L. mathura*) and nun moth (*L. monacha*)]

- Species are often transported globally as dormant egg masses on vessels and cargo
- DNA reference library constructed for the identification of 36 *Lymantria* spp. (deWaard *et al.* 2010a)

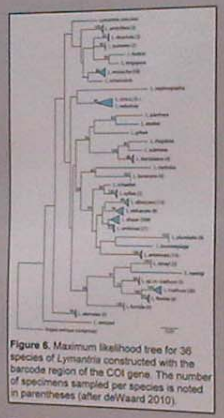

Figure 6. Maximum likelihood tree for 36 species of *Lymantria* constructed with the barcode region of the COI gene. The number of specimens sampled per species is noted in parentheses (after deWaard 2010).

Results

- 518 adult *Lymantria* from 35 countries barcoded (Fig. 6)
- barcode data led to morphological and taxonomic re-evaluation of specimens in two clusters (deWaard *et al.* 2010a)
  - *L.* sp. nr. *mathura* (Fig. 6) now considered to be *L. subpallida*
  - *L. nebulosa* is a valid species distinct from *L. sinica*

Lymantria spp. results (cont'd)

- 142 COI haplotypes identified across all 36 species
- no haplotypes shared between species
- 91 COI haplotypes within *L. dispar*
- haplotypes of Asian subspecies *L. d. asiatica* and *L. d. japonica* cluster separately from European & North American subspecies *L. d. dispar*
  - allows rapid identification of "Asian gypsy moth" recovered from monitoring programs

Geometridae

DNA reference library was developed for the 349 spp. of Geometridae in British Columbia (deWaard 2010).

- specimens from 8 museum collections sampled, databased and imaged; DNA extracted and COI sequenced
- all data is publicly available from the Barcode of Life Data Systems (BOLD) (Ratnasingham and Hebert 2007) in project 'GOBCL – Geometridae of BC Library'

Results

- 2392 COI sequences generated from 400 species in 125 genera
- 374 (93.2%) of the species could reliably be distinguished with barcodes
- only 27 species (6.8%) had undifferentiated or overlapping barcodes
- both a new NIS (Fig. 7) and a new native species for Canada were detected by barcoding museum collections (deWaard *et al.* 2008, 2010b)

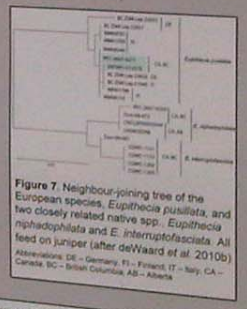

Figure 7. Neighbour-joining tree of the European species, *Eupithecia pusillata*, and two closely related native spp., *Eupithecia niphadophilata* and *E. interruptofasciata*. All feed on juniper (after deWaard *et al.* 2010b)

Abbreviations: DE – Germany, FI – Finland, IT – Italy, CA – Canada, BC – British Columbia, AB – Alberta

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For further information

Please contact the authors (see below) for publications. More information on these and related projects can be obtained from the Canadian Centre for DNA Barcoding - *http://www.ccdb.ca* or the Barcode of Life Data Systems - *http://www.boldsystems.org/views/login.php*.

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INSECT PEST DIAGNOSTICS & SPECIES DISCOVERY UNDER iBOL: THE CASE OF *OROSIUS* LEAFHOPPERS

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International Barcode of Life

Introduction

Orosius Distant (Hemiptera: Cicadellidae) is a leafhopper genus of economic importance in Africa, the Middle East, Asia, Australia and the Pacific. At least half of the eight described species have been reported as vectors of plant pathogens, including phytoplasmas and viruses. Despite their economic importance, the identities and distributions of *Orosius* species are unclear and the genus has a checkered taxonomic history. In addition, like many leafhoppers, only adult males of *Orosius* are identifiable to species. The resulting uncertainty over the identity of vector species has hampered research into phytoplasma transmission and management.

We performed an integrative taxonomic study of the genus in order to provide tools for elucidation of the vector-capability of *Orosius* species. DNA barcodes available for seven of the eight recognised species and several putative novel species were used to group ♂ & ♀ specimens into distinct genetic species clusters using a general mixed Yule-coalescent (GMYC) modeling procedure [1]. These clusters were compared with morphospecies clusters identified through male genitalic characters.

Results & Discussion

Multiple threshold GMYC modeling applied to 97 unique *Orosius* haplotypes identified 18 genetic clusters (Fig.1). These clusters resolved as seven previously described morphospecies, three novel morphospecies and five novel species represented by females only (Fig. 2). Average sequence difference within morphospecies was 14 times less that observed between morphospecies (0.78% vs 11.4%). Monophyly at each morphospecies was well supported by bootstrap analysis. There was strong congruence between species clusters defined by genetic and morphological methods. DNA barcoding was very useful for delineating morphologically cryptic species where male genitalic character variations were subtle (eg., *O. argentatus* vs. *O. orientalis*). Use of ♀ samples in genetic analyses allowed detection of additional putative novel species (Fig. 2).

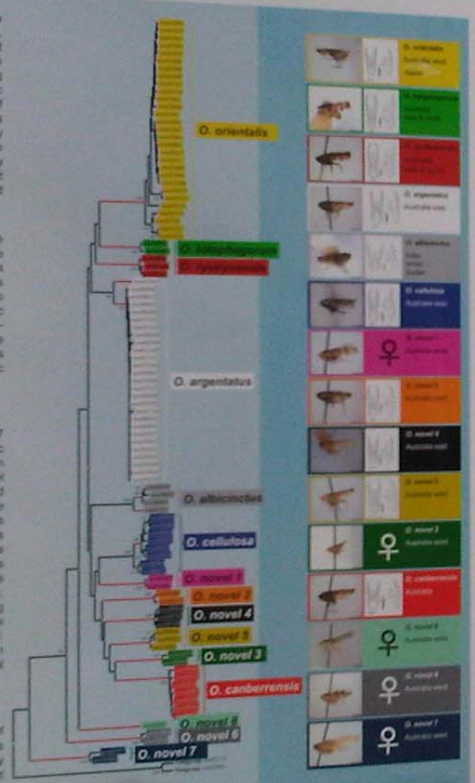

Figure 1. NJ tree of 97 unique *Orosius* haplotypes derived from 179 specimens. Red branches indicate genetic species identified by multiple threshold GMYC model.

Figure 2. *Orosius* morphospecies, male genitalic characters and sample distributions. ♀ = female specimens only, putative novel species delineated exclusively by genetics.

Conclusions

Our study doubles the known species diversity of the genus and clarifies the identity and distributions of the species. The implications of newly discovered cryptic species for studies of plant disease transmission are significant. Our new diagnostic tools can be used as a standard for future investigations of leafhopper-phytoplasma species associations.

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The International Barcode of Life Project

International Barcode of Life

Bringing Genomics to the Battle Against Plant Pests and Invasive Species

The International Barcode of Life Project is building the global infrastructure for rapid, accurate and inexpensive species recognition using a DNA-based identification system. DNA barcoding is a new technology with immense potential for economically, socially and environmentally beneficial applications – none more important than agricultural and forestry pest management, identification of invasive species and customs/border protection. In insect pest outbreaks, the rapid identification of the organism is critical for the implementation of control strategies to minimize lost production. The ability to identify parasitoid species that are either important in controlling outbreaks or in biological control is also crucial.

iBOL Working Group 1.5

Agricultural and Forestry Pests and their Parasitoids

Researchers associated with iBOL Working Group 1.5 are assembling a DNA barcode repository of agricultural and forestry pests and their parasitoids. By 2015, this digital reference library will contain barcodes for at least 20,000 of the most economically important pest species from every region of the world. Despite the broad range of groups involved, a collection of digital records for 23,000 species will provide a comprehensive and extremely effective pest/parasitoid identification system.

Agricultural and Forestry Pests and Their Parasitoids

Group	Species Targets	BOL G1 to G5 Progress Species	BOL G1 to G5 Progress Progress	Overall Progress to Target Species	Overall Progress to Target Progress
True Bugs	8,000	712	14%	2,505	50%
Earwigs	100	18	18%	20	20%
Grasshoppers	500	151	30%	689	138%
Leaveings & kin	500	139	28%	277	55%
Mantises	100	9	9%	155	155%
Parasitic Flies	3,000	955	32%	1,829	61%
Parasitic Hymenoptera	8,000	2,245	28%	6,351	79%
Pest Flies	2,000	874	44%	1,699	85%
Predatory Beetles	4,000	1,515	38%	3,755	94%
Soldiers	700	80	11%	294	41%
Stick Insects	100	23	23%	29	29%
Thrips	1,000	96	10%	200	20%
Grand Total	25,000	6,454	27%	17,758	71%

Revolutionary ID System for Life

DNA barcoding uses sequence variability in a short, standard gene region to tell species apart, permitting the non-experts of their identification.

Protecting Ecosystems

Conservationists are employing DNA barcodes to track shifts in species distribution in response to global warming, pollution, and habitat loss.

Exposing Illegal Trade

Researchers and retailers are using DNA barcodes to verify food items and prevent substitution. Customs officials have a new tool to stop trade in endangered species.

Supporting the Convention on Biological Diversity

iBOL was formally ratified as a program in support of the Convention on Biological Diversity at COP10 on October 20th 2010, in Nagoya, Japan.

An iBOL Highlight

September 25, 2010

The official activation of the International Barcode of Life Project was celebrated at Kenya's famed Oil Creek.

To mark the occasion, the forest was illuminated with the DNA barcode of a Caribbean coral. Coral symbolizes the South American interior.

Spotlight on Kenya

Kenya is rapidly building a barcode reference database of the country's insects. Among the hundreds of species barcoded to date are numerous species of Nymphalidae, including the Mediterranean fruit fly (*Ceratitis capitata*) and several species of cereal stem borers (Noctuidae), economically important pests throughout Africa. Presently, plans include a project that will use DNA barcodes to match pests and their parasitoids to facilitate bio-control assessments.

Spotlight on Mexico

Numerous projects involving DNA barcoding of agricultural pests and invasive species are underway in Mexico.

- Barcoding several species of fruit flies and their parasitoids
- Working with plasmid harvest to produce DNA barcodes
- Using barcoding, GIS and ecological niche modeling to track the invasive Asian Gypsy Moth (*Lymantria dispar*)
- A study of 60 endemic strains of cereal fungi, more than half possessing evidence of virus pathogens

A Rapid and Reliable Diagnostic Protocol

In 2009, the highly degraded specimen was found in a museum's box of British Columbia beetles. A DNA barcode obtained from an antenna removed from the body matched that of a species collected in Mexico. Museum records indicated the Mexican specimen was collected in 1964. Based on this information, researchers were able to locate the correct host plant and rapidly identify a new species, only from a single fragment of leg. Specimens as old as 100 years can now be identified.

Species Identification Matters to All Countries

- Food security and safety
- Border inspection and trade agreements:
  - Agricultural pests/beneficial species
  - Disease vectors/pathogens
  - Endangered/protected species
  - Invasive species
- Ensuring ecosystem services
- Environmental quality assessment
- Documenting/developing genetic resources
- University research in biology

A DNA barcode is a short gene sequence taken from standardized portions of the genome, used to identify species

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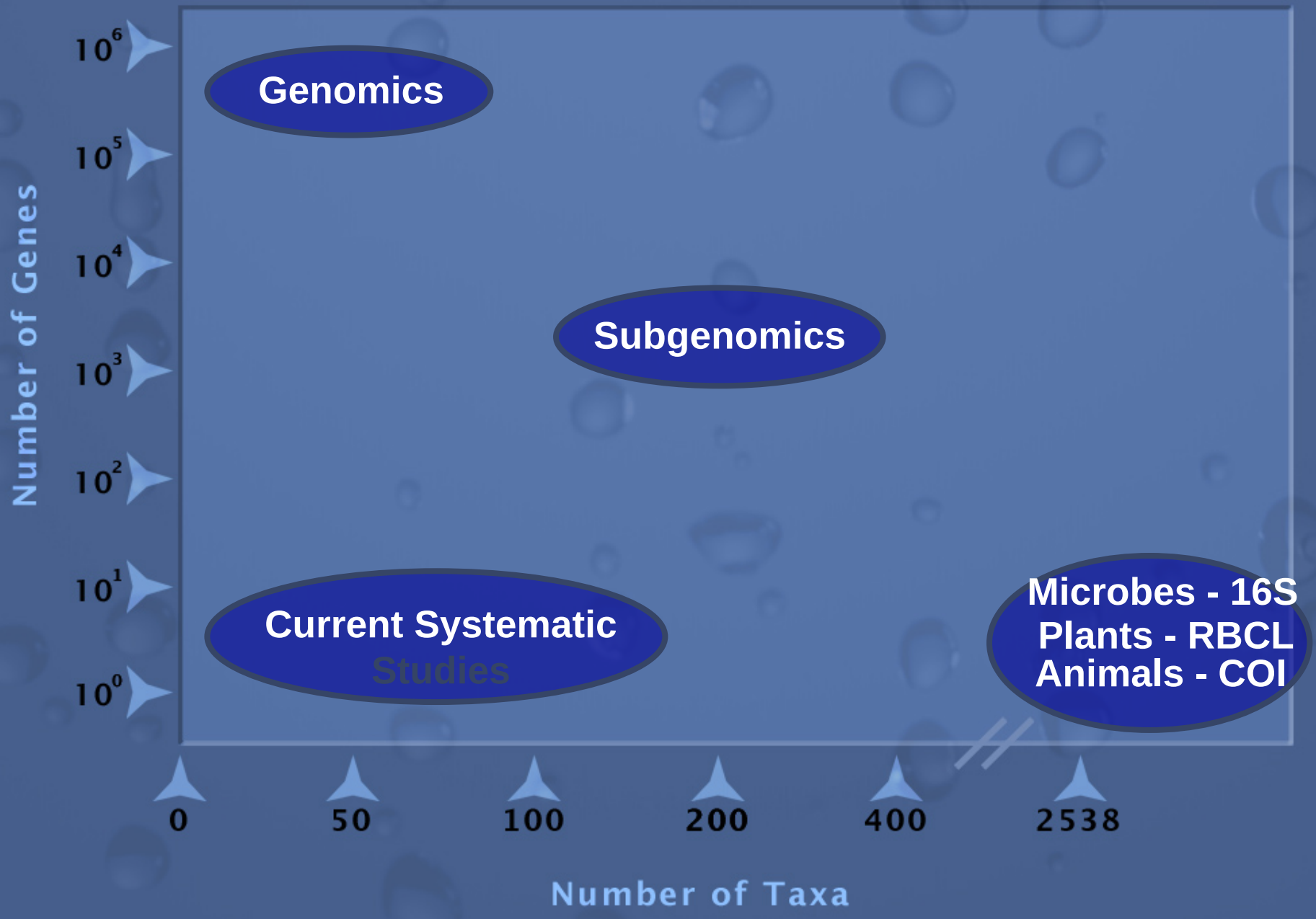
Genomics
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Number of Genes
10^6
10^5
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10^2
10^1
10^0
0
50
100
200
400
2538
Number of Taxa

Associating Life Stages, Processed Parts, Dimorphic Genders

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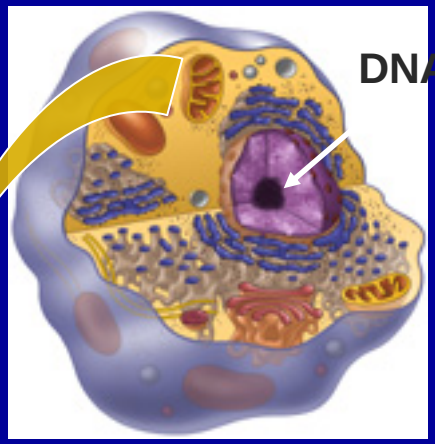
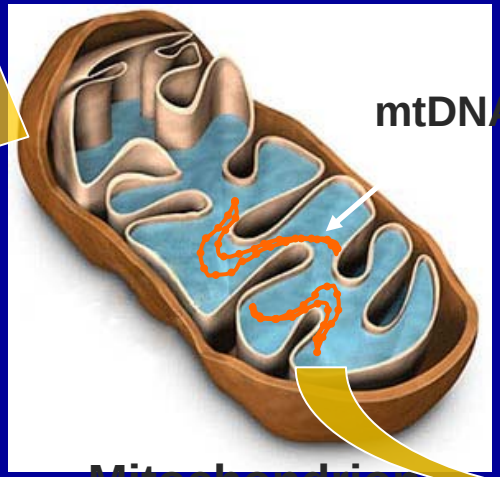
An Internal ID System for All Animals

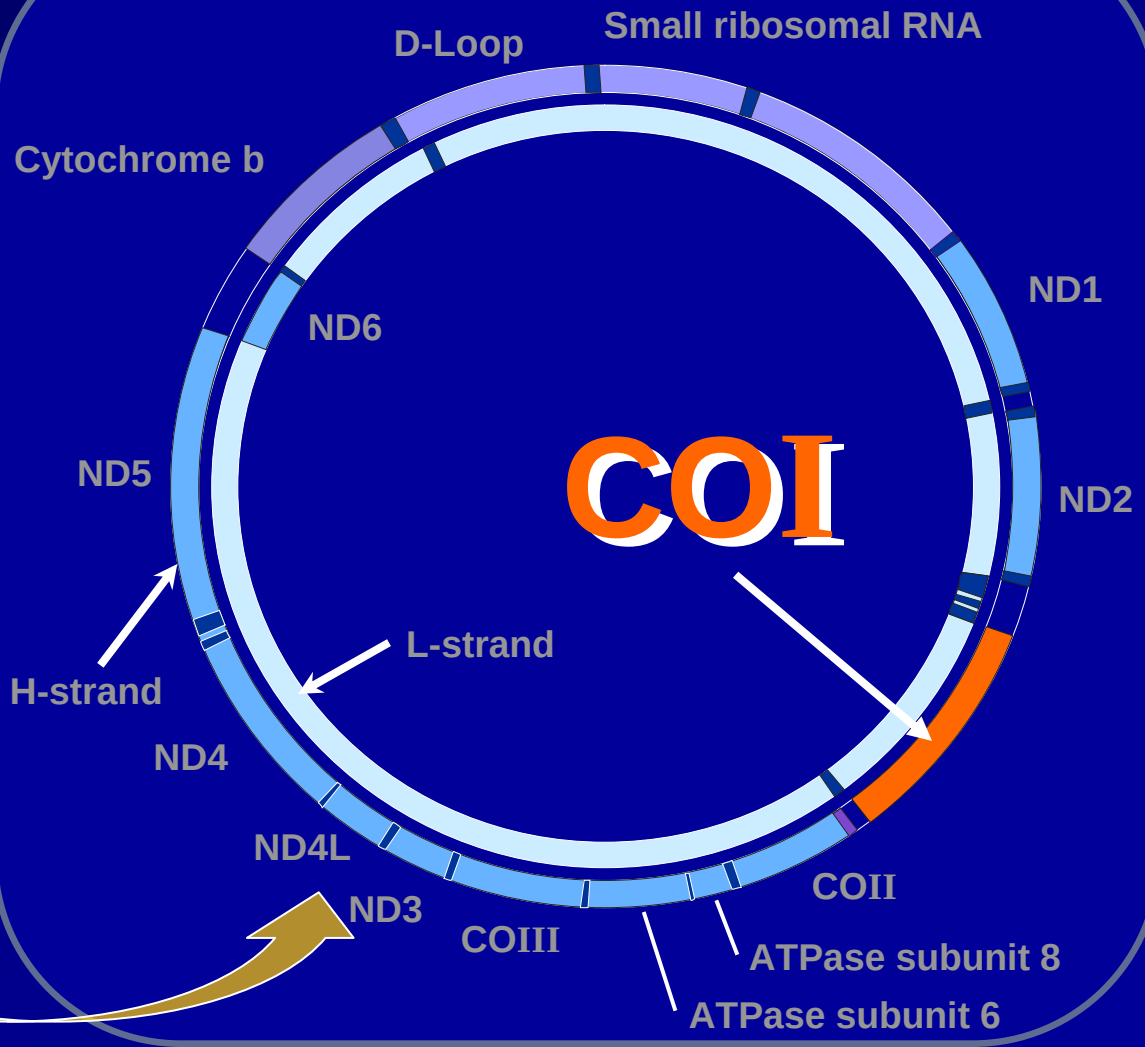


Typical Animal Cell



Mitochondrion

The Mitochondrial Genome



Non-COI regions for other taxa

- Land plants:
  - Chloroplast *matK* and *rbcL* approved Nov 09
  - Non-coding plastid and nuclear regions being explored
- Fungi and protists:
  - CBOL Working Groups convened
  - Recommendations expected in 2010

Biol Invasions
DOI 10.1007/s10530-010-9709-8

PERSPECTIVES AND PARADIGMS

Common goals: policy implications of DNA barcoding as a protocol for identification of arthropod pests

Robin Floyd · João Lima · Jeremy deWaard · Leland Humble · Robert Hanner

"DNA barcoding already meets or exceeds the minimum standards required for diagnostic protocols under ISPM No. 27."

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Barcoding in Diagnostic Protocols

- Applicable to all life stages
- Usable by non-experts
- Well-documented standard lab procedures
- High degree of transparency and repeatability
- Protocols, results, documentation all public and archived
- IDs and specimen comparisons through digital data, objective criteria
- Linkage to reference voucher specimens

Taxonomy

Name, rank and serial number

Biologists want to barcode half a million species in the next five years

THE tale of the unknown goby began in 1982 when Benjamin Victor, of the Ocean Science Foundation in Irvine, California, discovered an unusual fish in a reef in Panama. With only a single specimen he was hard pressed to prove it was a new species, so the fish remained, unnamed, on his desk for 25 years. Then, last year, he was sent an unusual fish larva. Using a new kind of DNA identification called barcoding he showed that it was a younger version of his mystery goby and that both specimens were, indeed, a new species.

DNA barcoding was invented by Paul Hebert of the University of Guelph, in Ontario, Canada, in 2003. His idea was to generate a unique identification tag for each species based on a short stretch of DNA. Separating species would then be a simple which there are at least 3,500 species, many of them hard to tell apart.

So far Dr Linton's team has used the COI gene to distinguish 390 species of mosquito, of which 7% have turned out to be new species. *Anopheles oswaldoi*, for example, was known to be a carrier of malaria in northern, but not southern, Brazil. That was puzzling. DNA barcoding, however, has shown that *A. oswaldoi* is actually four species, of which only one carries malaria. That explains the geographical discrepancy and should also assist efforts to curb the disease in Brazil by allowing the real culprit to be studied in detail.

Fly titles

The mosquito initiative has also had a piece of luck. Using some chemical wiz as medicines. In doing so, they have had to identify a new kind of barcode, as the COI gene is not found in plants.

Another group that could benefit from barcoding are customs officers, says Mark Blaxter, an evolutionary biologist at the University of Edinburgh. For those struggling to prevent the importation of pests or endangered wildlife, rapid and accurate identification tools are essential—particularly when perishable goods are being held up. America's Department of Agriculture is creating barcodes for the world's fruit flies. These are important agricultural pests and often arrive in the country as hard-to-identify larvae, or eggs, on fruit. Another group at the National Chung Hsing University in Taiwan (where hundreds of newly minted experts in the field have just met for the Second International Barcode of Life Conference) have created a prototype barcoding biochip. This is a collection of miniature DNA test sites on a sliver of glass that will rapidly discriminate between four species of fruit flies.

Barcoding's ease of use is also attracting interest from other government agencies. America's Federal Aviation Administration and its air force are working on bird

July 2010 Technical Panel on Diagnostic Protocols Washington, DC

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How Barcoding Works

- First, build a barcode reference library:
  - Well-identified specimen
  - Tissue subsample
  - DNA extraction, PCR amplification
  - DNA sequencing
  - Data submission to GenBank
- Second, use it to identify unknowns:
  - Any unidentified juvenile, adult, fragment, product
  - Tissue sample, DNA, sequencing
  - Comparison with sequences in reference library

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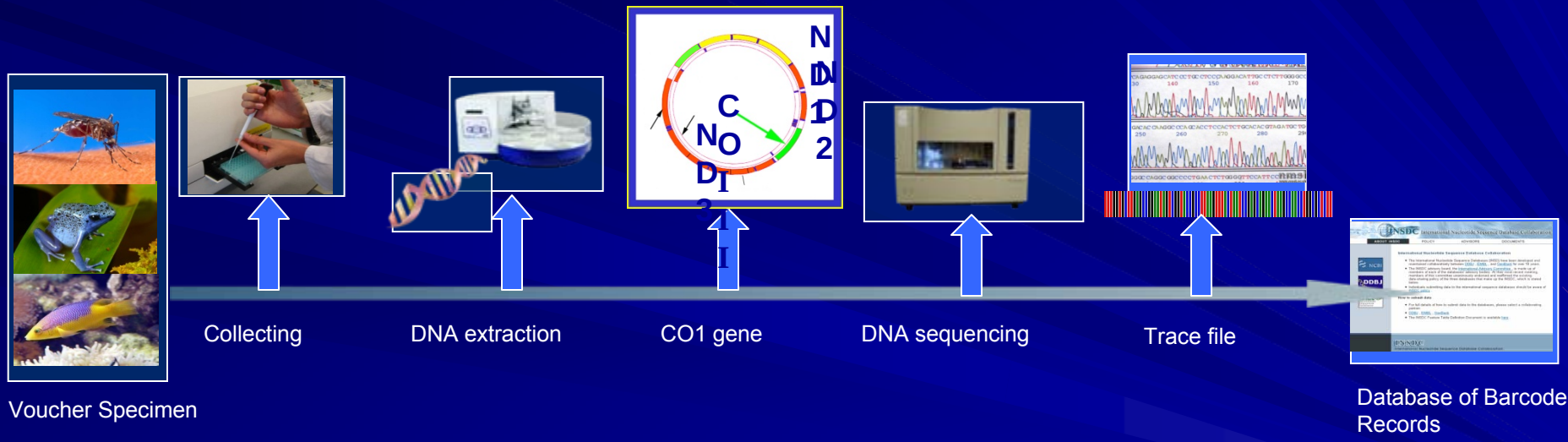
The Barcoding Pipeline

From specimen to sequence to species



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Current Norm: High throughput

Large labs, hundreds of samples per day

Large capacity PCR and sequencing reactions

ABI 3100 capillary automated sequencer

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- US$100-165K purchase
- 150-500 samples per day
- 2-3 hours processing time
- US$3-5 per sample

Technology Development Partnership Goal

The DNA Sequencing Lab of 2013?

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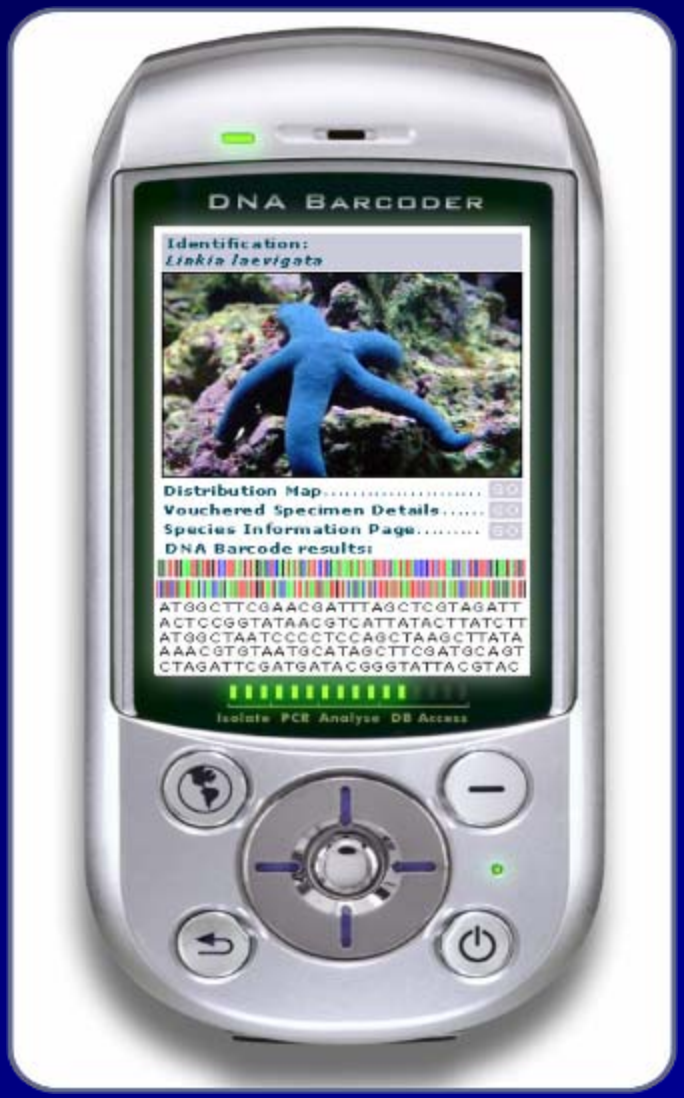
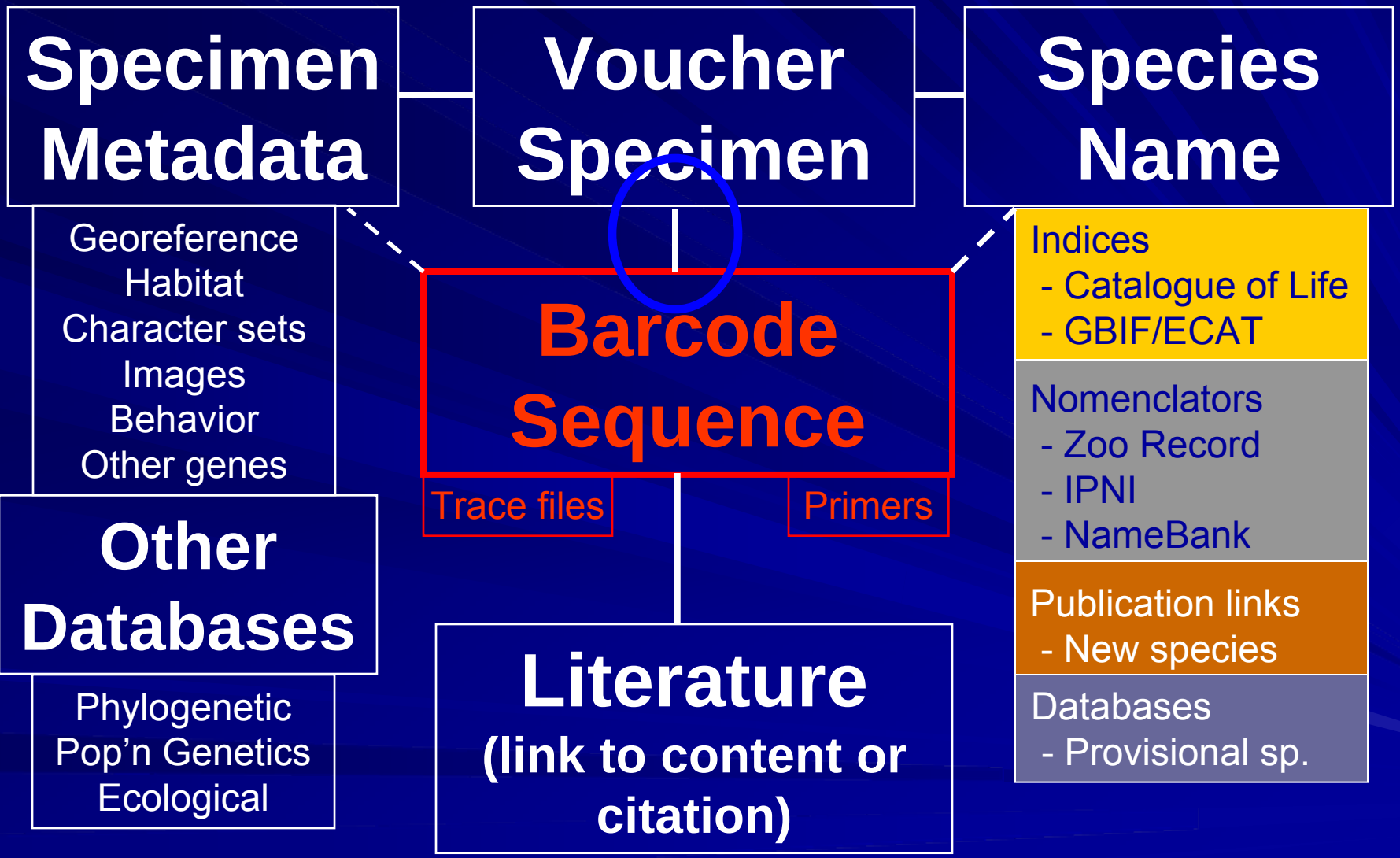
Producing Barcode Data: 201?

Barcode data anywhere, instantly



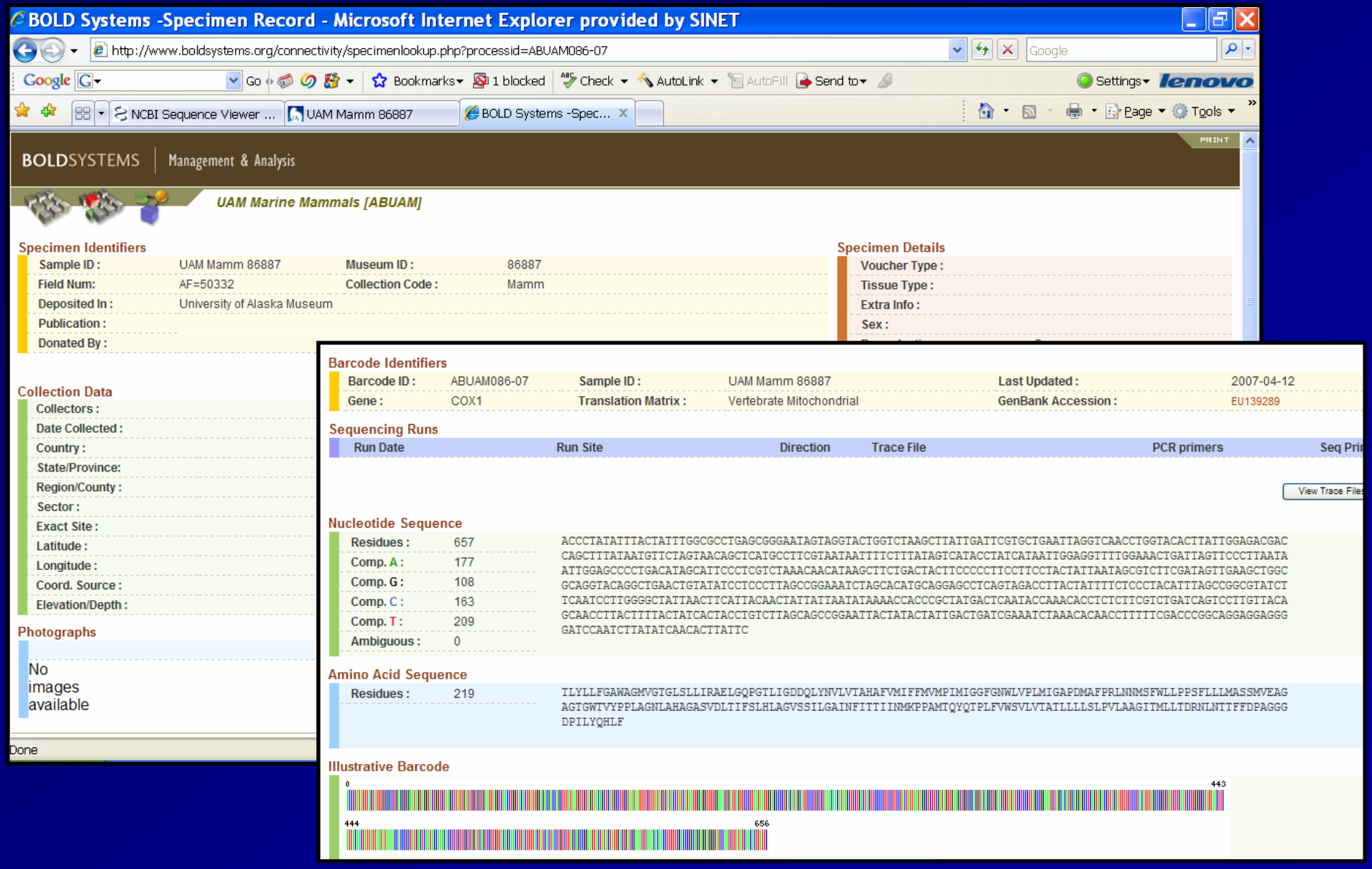
- Data in seconds to minutes
- Pennies per sample
- Link to reference database
- A taxonomic GPS
- Usable by non-specialists

BARCODE Records in INSDC



CONSORTIUM FOR THE BARCODE OF LIFE

1 Million+ records, 100K+ species



Sequence Webpages

BOLDSYSTEM | Management & Analysis

PRINT

Hesperiidae of the ACG 1 [CSCR]

Barcode Identifiers

Barcode ID :	CSCR010-04	Sample ID :	
Gene :	COX1	GenBank Accessi	
Last Updated :		Translation Matrix	

Sequencing Runs

Run Date	Run Site	Direction	Trace File

Nucleotide Sequence

Length :	617
Comp. A :	203
Comp. G :	85
Comp. C :	92
Comp. T :	237
Updated :	2005-09-09

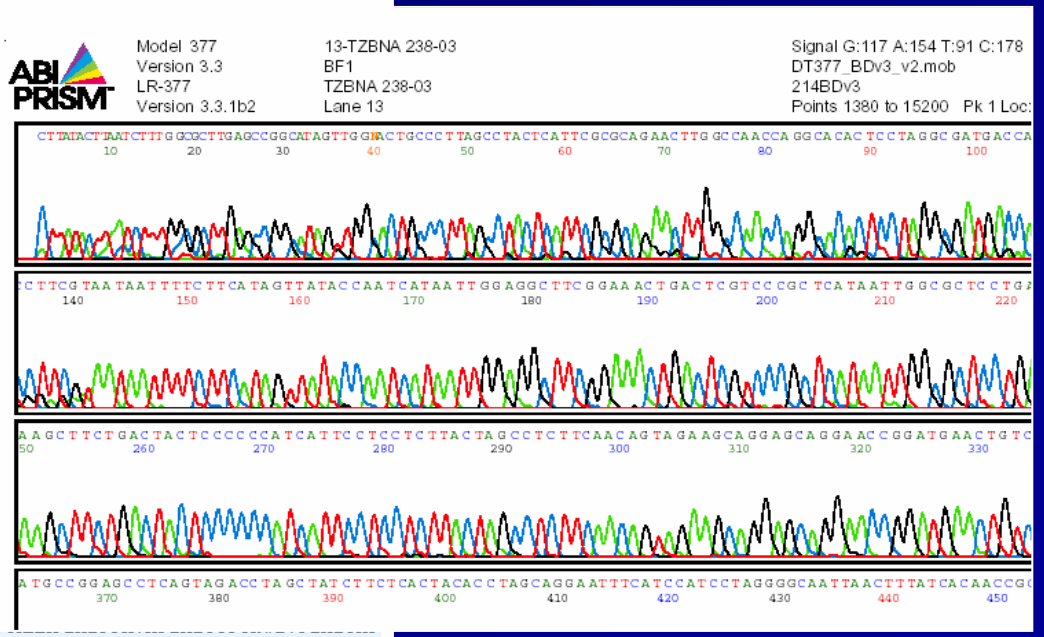
NNAACTTTATATTTTATTTTTGGAATTTGAGCAGGAATAGT
TTAGGTAACCCAGGATCTTTAATTGGAGATGATCAAATTTA
ATTTTTTTTATAGTAATACCAATTATAATTGGAGGATTTGG
GATATAGCATTTCCACGAATAAATAATATAAGATTTTGACT
AGAATTGTAGAAAATGGAGCAGGAACAGGATGAACTGTTTA
TCTTCTGTAGACTTAGCTATTTTTTCATTACATTTAGCAGG
ACAACAATTATTAATATACGAATTAGAAATTTATCATTTGA
ACCGCACTTCTTTTACTTTTATCTTTACCTGTTTTAGCTGG
AATACATCATTCTTGGATCNNNNNNNNNNNNNNNNNNNNN

Amino Acid Sequence

Length :	220

XTLYFIFGIWAGMVGTSLSLLIRTELGNPGSLIGDDQIYNT
DMAFPRMNNMSFWLLPPSLMLLISSSIVENGAGTGWTVYPPLSANIAHQGSSVDLAIFSLHLAGISSILGAINFI
TTIINMRISNLSFDQMPLFVWAVGITALLLLLSLPVLAGAITMLLTDRNLNTSFLDX----------

Illustrative Barcode



Specimen Webpages

BOLDSYSTEMS | Management & Analysis

PRINT

Hesperiidae of the ACG 1 [CSCR]

Specimen Identifiers

Edit Specimen

Sample ID :	02-SRNP-16276	Museum ID :	02-SRNP-16276
Isolate / Field Num:		Collection Code :	
Donated By :		Deposited In :	Smithsonian Institution

Taxonomy

Identifier :	18
phylum :	Arthropoda
class :	Insecta
order :	Lepidoptera
family :	Hesperiidae
subfamily :	Pyrginae
genus :	Anastrus
species :	Anastrus obscurus

Specimen Details

Voucher Type :	
Tissue Type :	
Extra Info :	Pyrginae
Sex :	m
Reproduction :	s
Life Stage :	

Collection Data

Collectors :	Roster Moraga
Date Collected :	12-Jul-2002
Country :	Costa Rica
State/Province:	Guanacaste
Region/County :	Area de Conservacion 276
Sector :	Del Oro
Exact Site :	Uncaria
Latitude :	11.0291
Longitude :	-85.4792
Coord. Source :	
Elevation/Depth :	300

Photographs

Dorsal View

Ventral View

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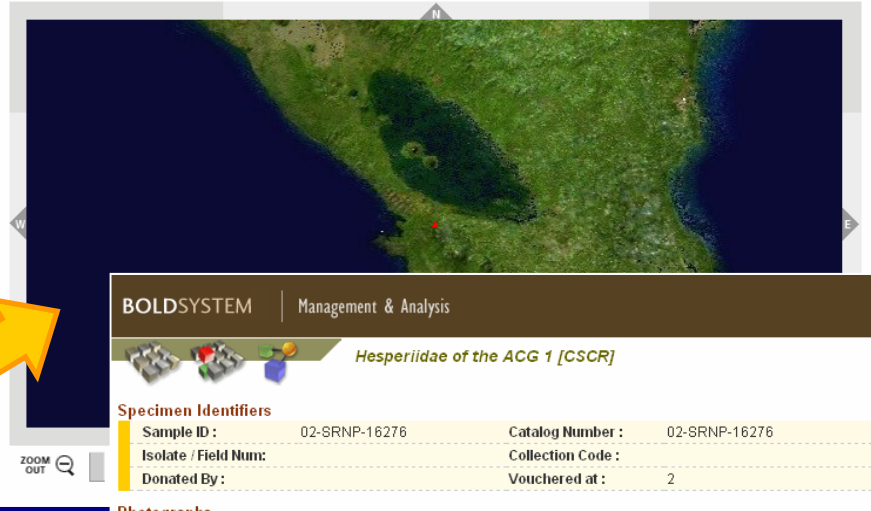
PRINT

Hesperiidae of the ACG 1 [CSCR]



ZOOM OUT

BOLDSYSTEM | Management & Analysis

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Hesperiidae of the ACG 1 [CSCR]

Specimen Identifiers

Sample ID :	02-SRNP-16276	Catalog Number :	02-SRNP-16276
Isolate / Field Num:		Collection Code :	
Donated By :		Vouchered at :	2

Photographs

Dorsal View

Ventral View

EOL Species Pages

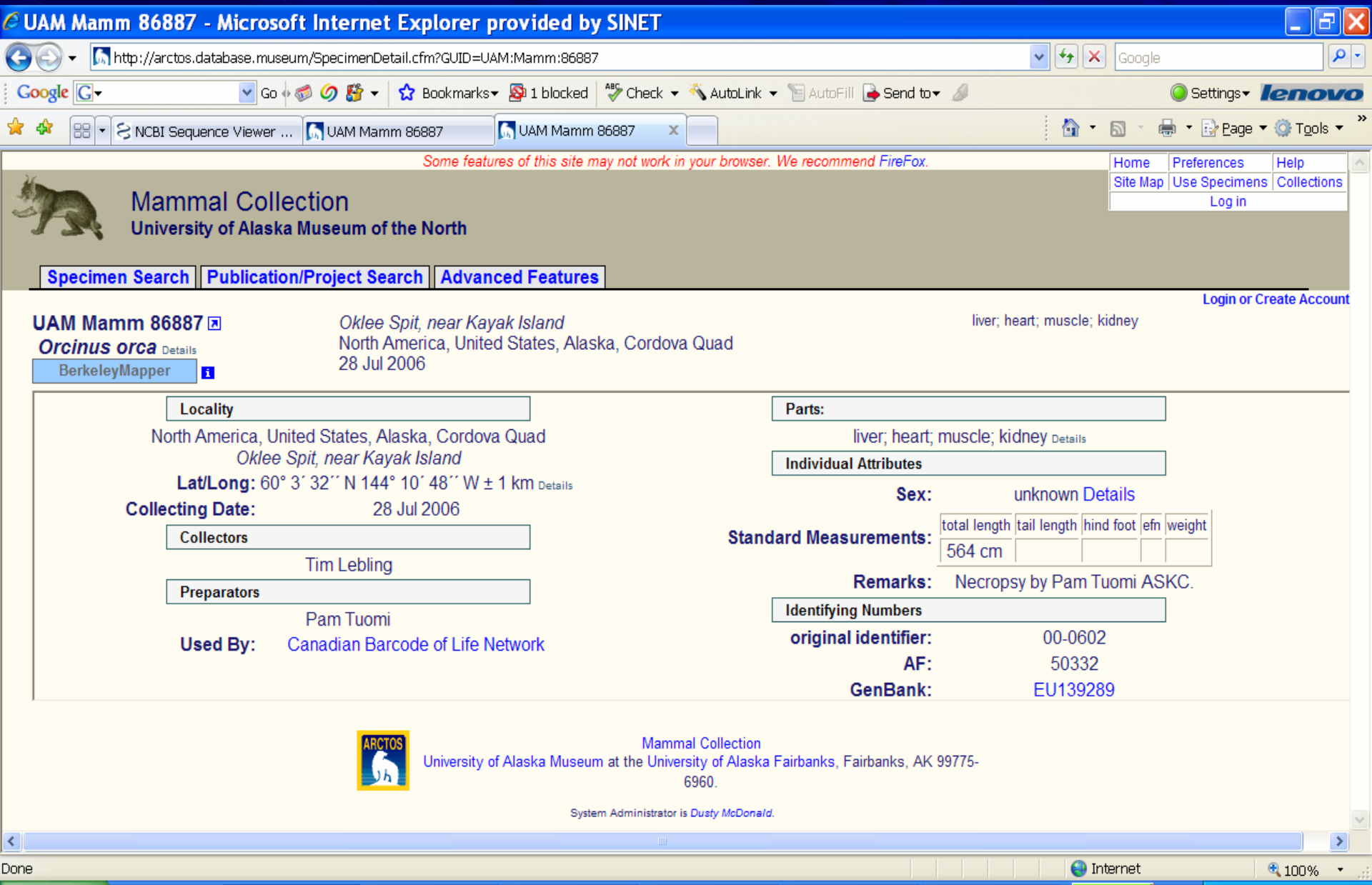
CONSORTIUM FOR THE BARCODE OF LIFE

GenBank, EMBL, and DDBJ

Global, Open Access to Barcode Data

http://www.insdc.org/

Link from GenBank to Museums



How Barcoding Works

- First, build a barcode reference library:
  - Well-identified specimen
  - Tissue subsample
  - DNA extraction, PCR amplification
  - DNA sequencing
  - Data submission to GenBank
- Second, use it to identify unknowns:
  - Any unidentified juvenile, adult, fragment, product
  - Tissue sample, DNA, sequencing
  - Comparison with sequences in reference library

CONSORTIUM FOR THE BARCODE OF LIFE

How Complete is the Barcode Library?

- More than 1 million records in BOLD
- More than 100,000 species represented
- Projects underway in all major groups
- Focus on groups with commercial and societal importance:
  - Agricultural pests
  - Disease vectors
  - Endangered species

CONSORTIUM FOR THE BARCODE OF LIFE

Barcode of Life Community

Consortium for the Barcode of Life

- Promote barcoding as a global standard
- Build participation
- Working Groups
- BARCODE standard
- International Conferences
- Increase production of public BARCODE records

Networks, Projects, Organizations

ECBOL

international BARCODE OF LIFE

BOLDSYSTEMS

QBOL

ABBI

FISH-BOL

Canadian Barcode of Life Network

MBI Mosquito Barcoding Initiative

TBI

CCDB

BIO

Investments in Barcoding

- ~US $5 million per year
  - Smithsonian Laboratories for Analytical Biology
  - Smithsonian barcoding projects
  - Sloan Foundation support for CBOL
  - Project support by USDA, EPA, FDA, FAA…
  - Barcoding in NSF-funded biodiversity grants

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Adoption by Regulators

- USDA, Belgian research projects on fruit flies
  - Plans for submission of Diagnostic Protocols
- Food and Drug Administration
  - Reference barcodes for commercial fish
- Environmental Protection Agency
  - $250K pilot test, water quality bioassessment
- NOAA/NMFS
  - $100K for Gulf of Maine pilot project
  - FISH-BOL workshop with agencies, Taipei, Sept 2007
- Federal Aviation Administration – $500K for birds

Investments in Barcoding

- ~US $5 million per year
- CAN $80 million over 2005-2015
- Commitments of ~CAN $75 million from iBOL partners over 2010-2015
  - 5 million specimens
  - 500K species
  - 25 partner countries
  - Canada, US, EU, China are "central nodes"

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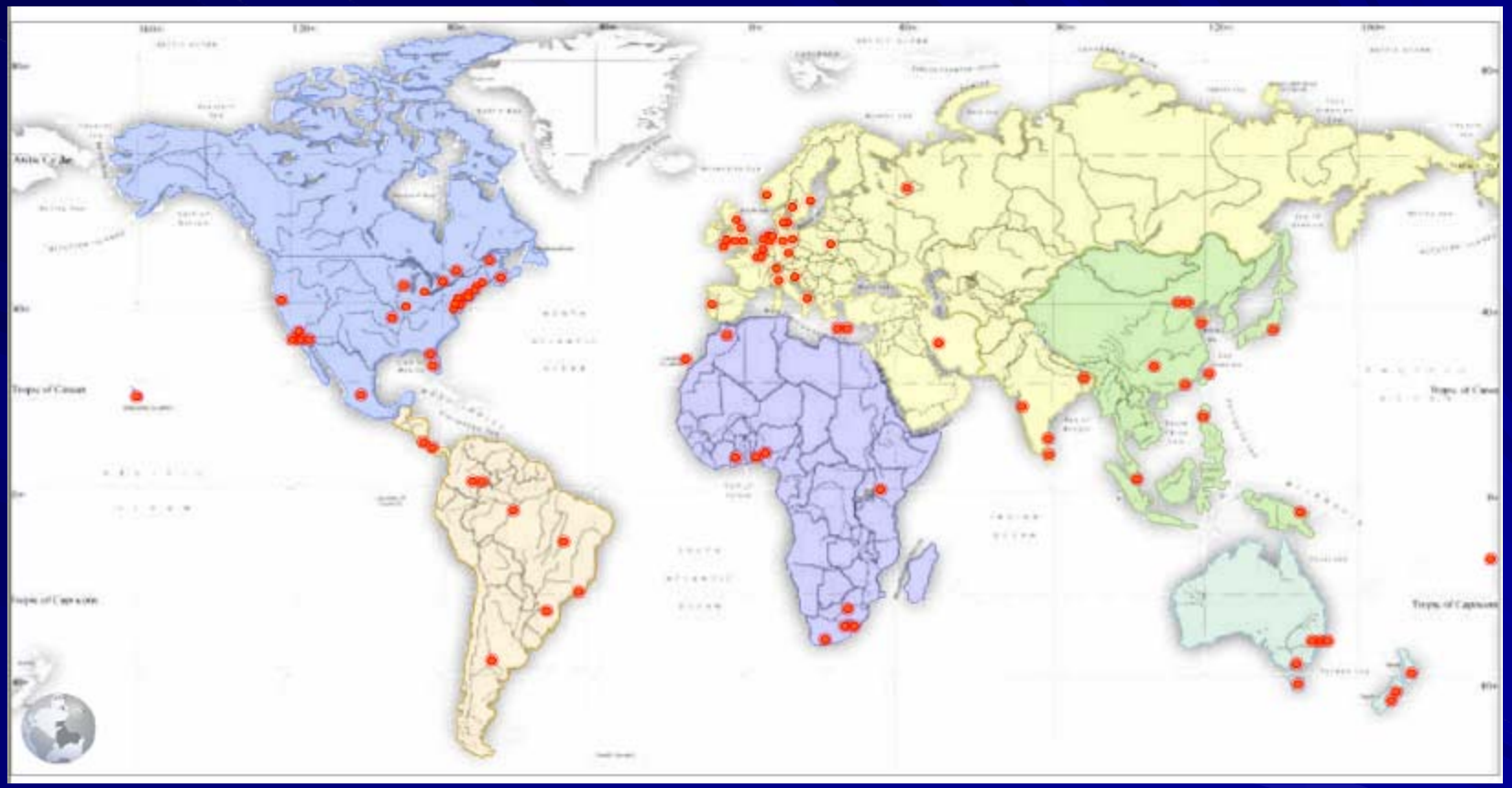
Consortium for the Barcode of Life (CBOL)

- Established May 2004 with Sloan Foundation grant
- Secretariat hosted by Smithsonian Institution
- Now in its fourth two-year funding period
- Workshops, Working Groups, networking, representation/marketing
- Now an international affiliation of 200+ members in 50+ countries:
  - Natural history museums, biodiversity organizations
  - Users: e.g., government agencies
  - Private sector biotech companies, database providers

CBOL Member Organizations: 2010



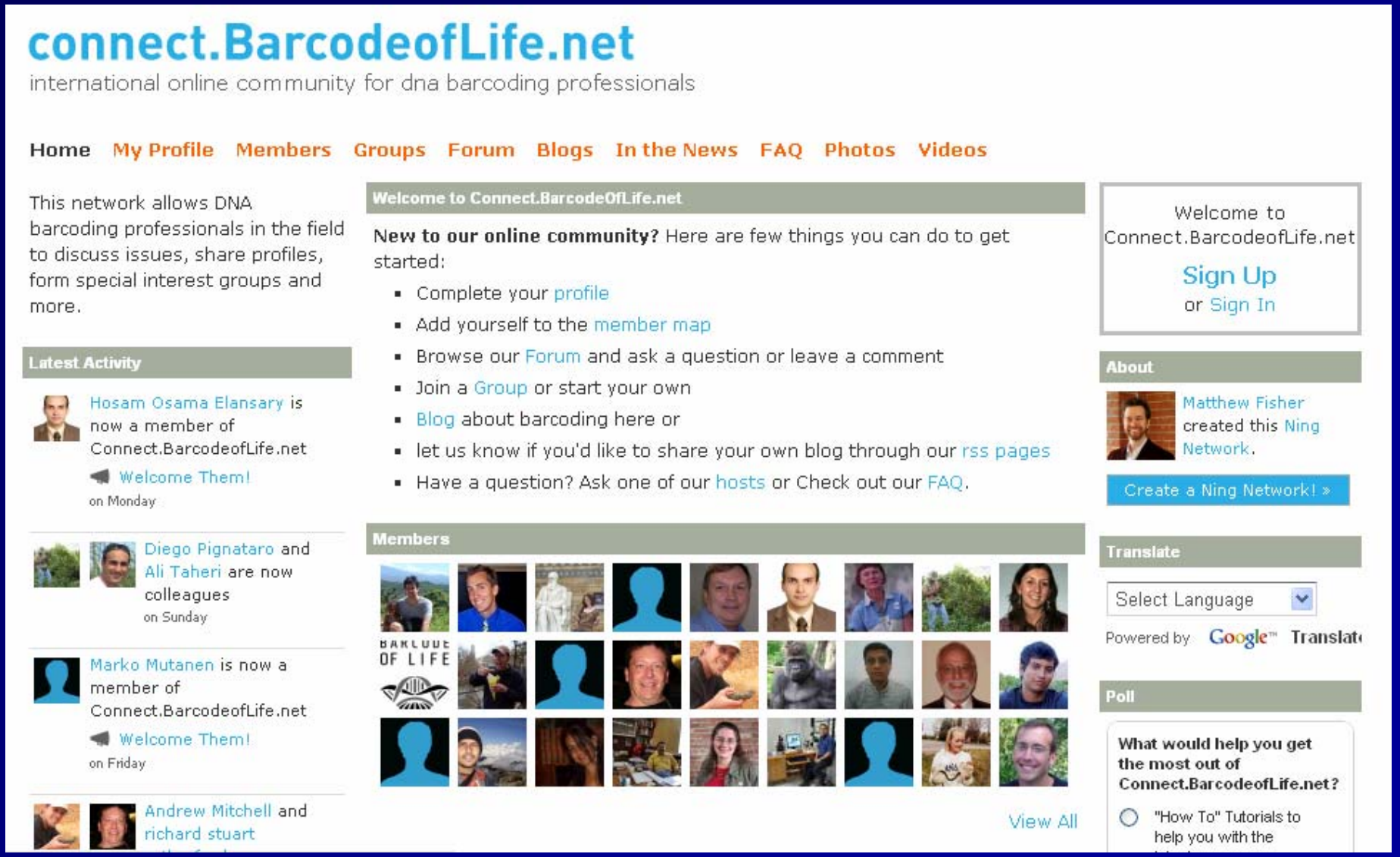
- 200+ Member organizations, 50 countries
- 35+ Member organizations from 20+ developing countries

CONSORTIUM FOR THE BARCODE OF LIFE

Building the Community

- Internal communication through Community Network (http://connect.barcodeoflife.net)
- Outreach communication through
  - o www.barcodeoflife.org
  - o CBOL Webinars
- Coordination with other barcoding projects through CBOL's Implementation Board
- Steering Committee planning meetings
- Assistance in preparing and submitting proposals

Connect.barcodeoflife.org



www.barcodeoflife.org

Barcode of Life

Identifying Species with DNA Barcoding

About | Community | Resources | Events | Partners | News

Community

Barcoding Projects

Barcoding Projects

There are many international barcoding activities dedicated to the development of targeted public reference BARCODE sequence libraries.

FEATURED PROJECTS

Sort By: Title

All Birds Barcoding Initiative (ABBI)

ABBI, the All Birds Barcoding Initiative, is a campaign to collect DNA barcodes from 5 or more individuals of all of the approximately 10,000 bird species in the world. The ABBI DNA barcode library will help speed discovery of new species, open new avenues for scientific investigation, and provide a forensic tool for identifying specimens, including for example tissue fragments from bird-airplane collisions and avian blood samples from biting insects that harbor West Nile virus or other human disease agents.

Project Site

All Fungi Barcoding

All Fungi Barcoding provides up-to-date information on fungal barcoding and facilitates communication and collaboration among researchers interested in fungi.

Project Site

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International Barcode Conferences

- Natural History Museum, London: 2005
- Academia Sinica, Taipei: 2007
- UNAM, Mexico City: 2009
- University of Adelaide, Australia: 2011
- All-Africa Conference: 2012

- 30-60 Travel Bursaries awarded for participants from developing countries

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Challenges

- Raising awareness about barcoding

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Outreach Activities

- Cape Town, South Africa, April 2006, SANBI
  - Scale insects in African agriculture
- Nairobi, Kenya, October 2006
  - Commercial fisheries in Rift Valley lakes
- Brazil, March 2007
  - Hardwood tree species
  - Endangered mammals, reptiles, amphibians
- Taiwan, September 2007
- Nigeria, October 2008
- Beijing, May 2009
- India, November 2010

CONSORTIUM FOR THE BARCODE OF LIFE

Challenges

- √ Raising awareness about barcoding
- Buy-in by national/international authorities
  - Access to study specimens for international research under the Convention on Biological Diversity

DNA Barcoding:

A New Tool for Identifying Biological Specimens and Managing Species Diversity

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ABS Workshop, Museum Koenig

17-19 November 2008

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51 Participants from 24 Countries

Sector		
Research	Agency	Other
29	10	12
56.9%	19.6%	23.5%

Geographic Representation				
OECD	Africa	Latin America	Asia	Pacific
28	8	4	9	2
54.9%	15.7%	7.8%	17.6%	3.9%

Nature magazine
7 October 2010

COMMENT

A researcher prepares to analyse plant samples from the biodiversity-rich regions around Hanoi.

Biology without borders

Fundamental research must not be hampered by an international agreement on sharing the benefits from national biodiversity, says **David Schindel**.

The supreme decision-making body of the United Nations Convention on Biological Diversity (CBD) meets in Nagoya, Japan, on 18–29 October 2010 for its tenth biennial conference. One of the most important items on the agenda is a new protocol which, if enacted, would specify how countries that are parties to the convention control access to their 'genetic resources' (including whole organisms, tissue samples and DNA extracts) and what benefits they can expect from sharing them. The negotiators' focus on genetic resources used to develop commercial products[1] has left non-commercial academic research in a perilous position[2]. One-size-fits-all legislation could have devastating effects on research conducted by foreign and local investigators, and even on the technological growth and economies of developing countries.

According to the CBD, countries can control access to their own species and set the terms for sharing any benefits resulting from their use by foreigners. Since 1993, only 15 of the 193 countries that have ratified the convention have passed legislation and created regulations to control access (another 58 have either legislation or regulations in place; see 'Where countries stand'). Most are hoping for a long-awaited international agreement to set global standards. The tenth Conference of the Parties (COP-10) could provide this.

Just last month, a CBD working group agreed on a new section to the draft protocol, proposed by the European Union and Japan. This directs CBD countries to encourage research that contributes to the conservation and sustainable use of biodiversity. More specifically, it directs them to create simplified access procedures for non-commercial research, with the understanding that mechanisms for handling unanticipated commercial applications may have to be developed. It is crucial that the parties to the convention approve the global access and sharing agreement only if this amendment is included.

SOVEREIGN RIGHTS

The rich biological diversity of many developing countries has long attracted biologists interested in evolution and ecology, as well as researchers looking for compounds that could be developed into products such as drugs and cosmetics. Before the creation of the CBD, most government ministries didn't pay much attention to the collecting ▸

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CBD International Regime for Access and Benefit Sharing

In the development and implementation of their national legislation on access and benefit-sharing, [and on the basis of the sovereign right of Parties who regulate access to genetic resources and its derivatives,] Parties shall:

(a) *Create conditions to **promote and encourage research** which contributes to the conservation and sustainable use of biological diversity, particularly in developing countries, including through **simplified measures on access for non-commercial research purposes**, taking into account the need to address a change of intent for such research*

CONSORTIUM FOR THE BARCODE OF LIFE

Challenges

- √ Raising awareness about barcoding
- Buy-in by national/international authorities
- Start-up funding
  - √ Mexican national barcoding network, equipment and project grants
  - √ Brazilian national funding program
  - √ India national initiative
  - √ South African national network

CONSORTIUM FOR THE BARCODE OF LIFE

Challenges

- √ Raising awareness about barcoding
- Buy-in by national/international authorities
- Start-up funding
- Training
  - √ CBOL training opportunities for researchers, students
  - √ Annual short courses: Buenos Aires, Johannesburg, Paris
  - – Needs to be scaled up
  - – Needs to be extended to regulatory officials, other users

Challenges

- √ Raising awareness about barcoding
- Buy-in by national/international authorities
- Start-up funding
- Training
- Capacity building
  - Specimen repositories
  - Small labs for DNA extraction
  - National/Regional sequencing centers
  - Informatics capabilities

CONSORTIUM FOR THE BARCODE OF LIFE

Fourth International Barcode of Life Conference

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Home

Welcome

The **Consortium for the Barcode of Life** and the **University of Adelaide** invite you to join us in Adelaide, Australia from 28 November - 3 December 2011 for the Fourth International Barcode of Life Conference. Barcoding has seen extraordinary growth since the Mexico City Conference in November 2009 so join participants from around the world for the biggest barcoding event ever!

The organizers have developed this website to provide potential participants, co-sponsors, and other stakeholders with information about the conference. The conference organizers are also eager to have your feedback as we plan the conference so please share your ideas through **Connect, the DNA Barcoding network**. You can do this by using the links found throughout this website.

News Feed

Stay up to date by checking this webpage for new documents. You can also send us an **Expression of Interest** that will put you on an email distribution list, or sign up for an RSS feed by clicking on the icon above. Recently posted documents are:

Connect with the Fourth Conference: Blogs

14/03/2011

In my last blog I introduced the Prepare for the Fourth Conference discussion page and encouraged users to ...

Connect with the Fourth Conference!

04/03/2011

With key information on registration and abstract submission still in development and the conference more ...

Important Dates

University of Adelaide
South Australia
28 November –
3 December 2011

http://www.dnabarcodes2011.org

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