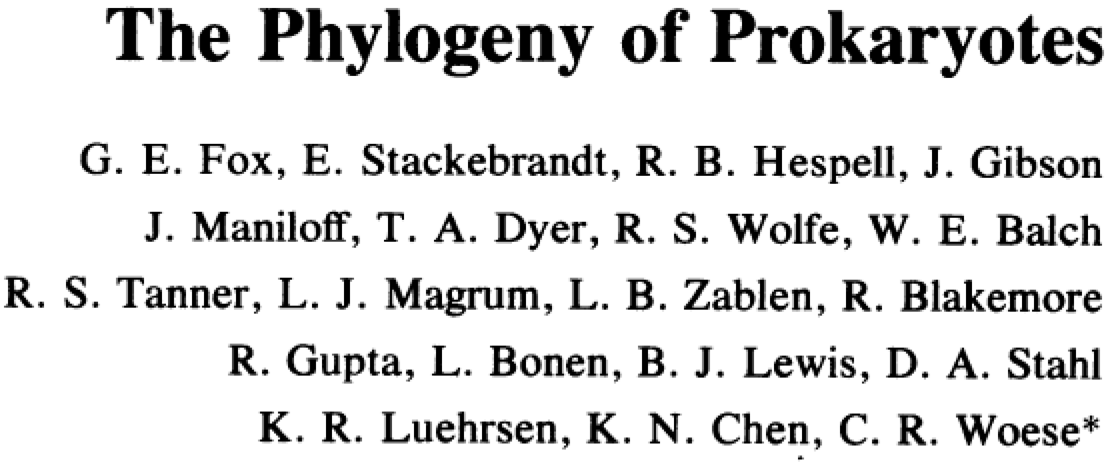
Colecciones biológicas y Códigos de barras de ADN

Identificación de especies

El ADN como herramienta taxonómica

Gen ribosomal 16s



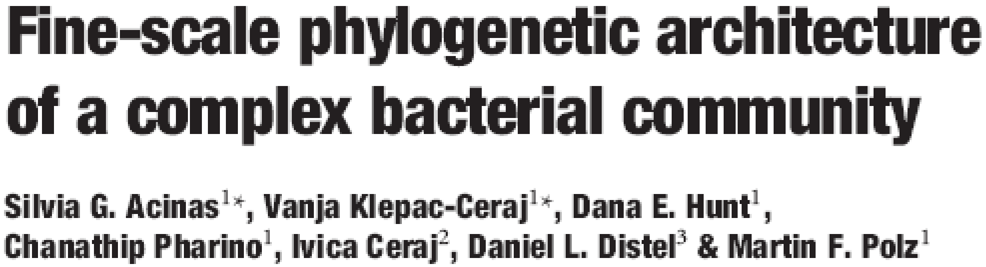
The Phylogeny of Prokaryotes

G. E. Fox, E. Stackebrandt, R. B. Hespell, J. Gibson
J. Maniloff, T. A. Dyer, R. S. Wolfe, W. E. Balch
R. S. Tanner, L. J. Magrum, L. B. Zablen, R. Blakemore
R. Gupta, L. Bonen, B. J. Lewis, D. A. Stahl
K. R. Luehrsen, K. N. Chen, C. R. Woese*

How many species of prokaryotes are there?

Bess B. Ward*

Geosciences Department, Princeton University, Princeton, NJ 08544



Fine-scale phylogenetic architecture of a complex bacterial community

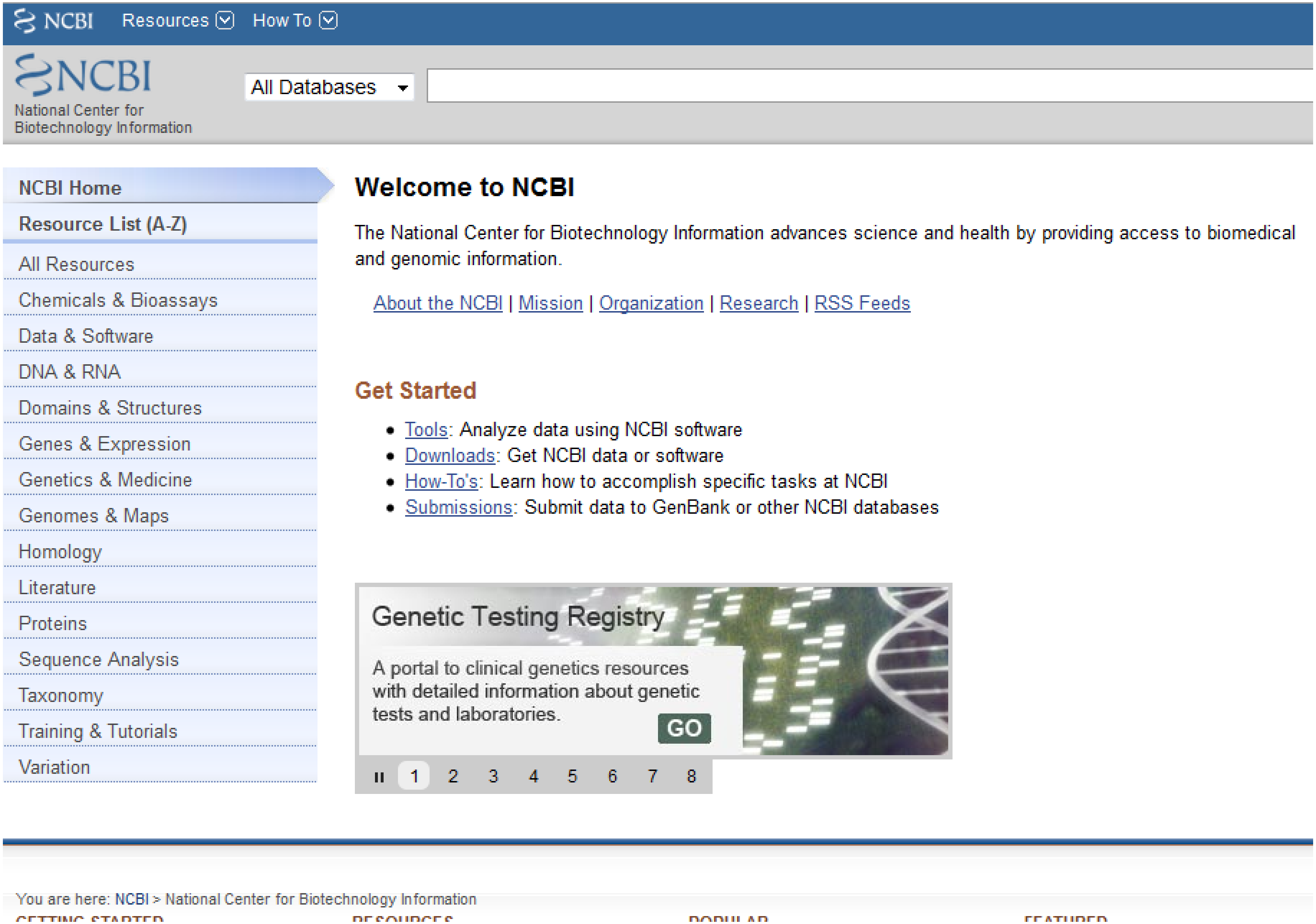
Silvia G. Acinas[1*], Vanja Klepac-Ceraj[1*], Dana E. Hunt[1],
Chanathip Pharino[1], Ivica Ceraj[2], Daniel L. Distel[3] & Martin F. Polz[1]

El ADN como herramienta taxonómica

Ecosystem rooting depth determined with caves and DNA

R. B. JACKSON*†, L. A. MOORE‡§, W. A. HOFFMANN‡¶, W. T. POCKMAN*, AND C. R. LINDER‡

Secuencia ITS



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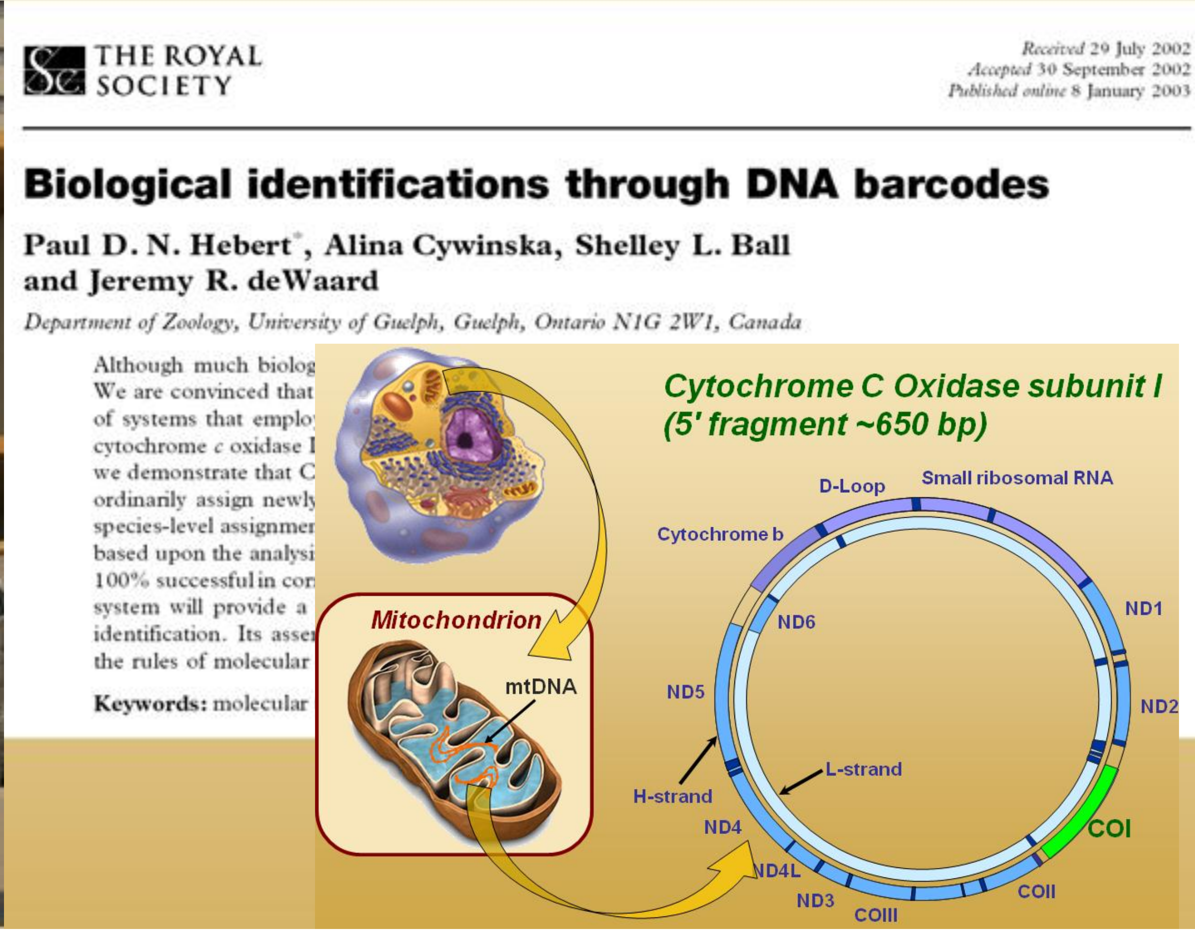
You are here: NCBI > National Center for Biotechnology Information

Códigos de barras de ADN:
Contexto histórico

*cox*1 → código de barras en animales


THE ROYAL
SOCIETY

Received 29 July 2002
Accepted 30 September 2002
Published online 8 January 2003

Biological identifications through DNA barcodes

**Paul D. N. Hebert*, Alina Cywinska, Shelley L. Ball
and Jeremy R. deWaard**

Department of Zoology, University of Guelph, Guelph, Ontario N1G 2W1, Canada

Although much biolog
We are convinced that
of systems that emplo
cytochrome *c* oxidase I
we demonstrate that C
ordinarily assign newly
species-level assignmen
based upon the analysi
100% successful in cor
system will provide a
identification. Its asse
the rules of molecular

Keywords: molecular

Códigos de barras de ADN:
Definición

“**Identificador Universal**”

Utilización de una región génica Estándar

A G C C T

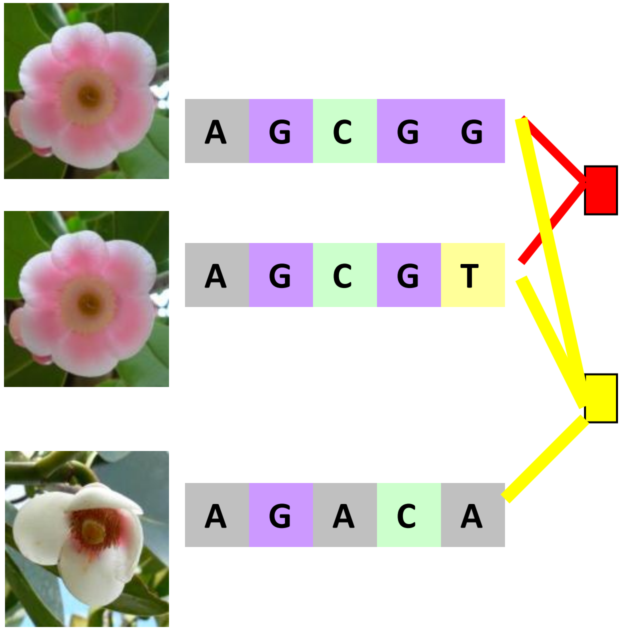
A G C G G

T T A T A

Códigos de barras de ADN: Definición

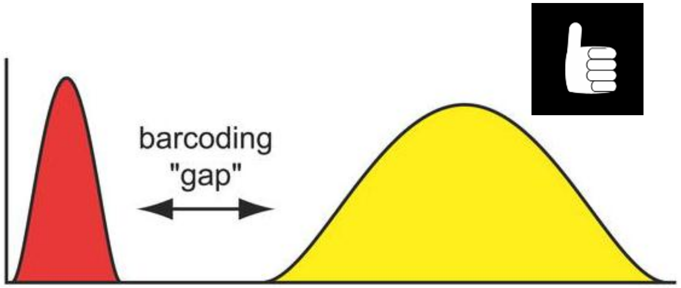
“Identificador Universal”

Variabilidad intraespecífica < Variabilidad interespecífica

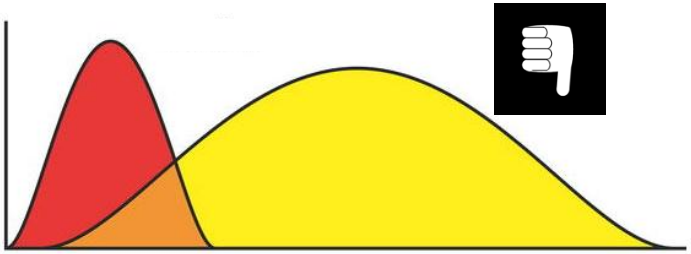


Divergencia intraespecífica

Divergencia entre congenéros



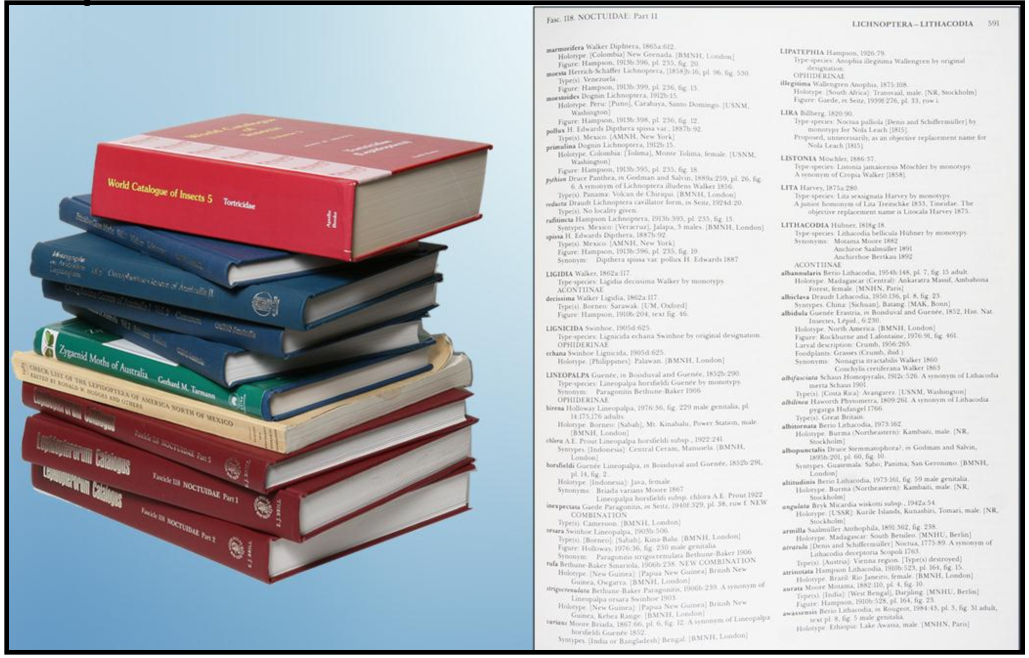
Distancia genética



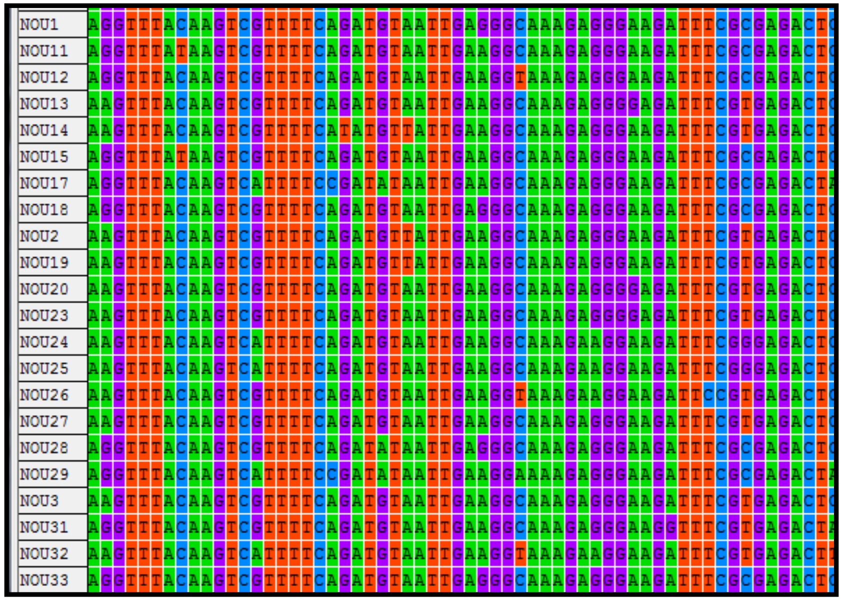
Distancia genética

El ADN como herramienta taxonómica

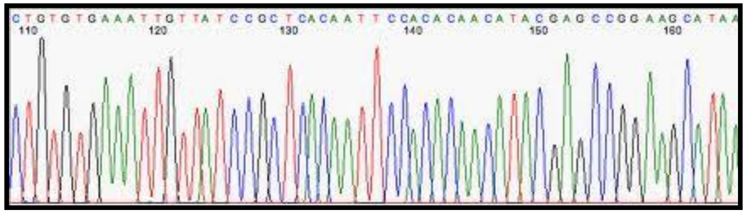
Catálogo morfológico de especies



Catálogo molecular de especie



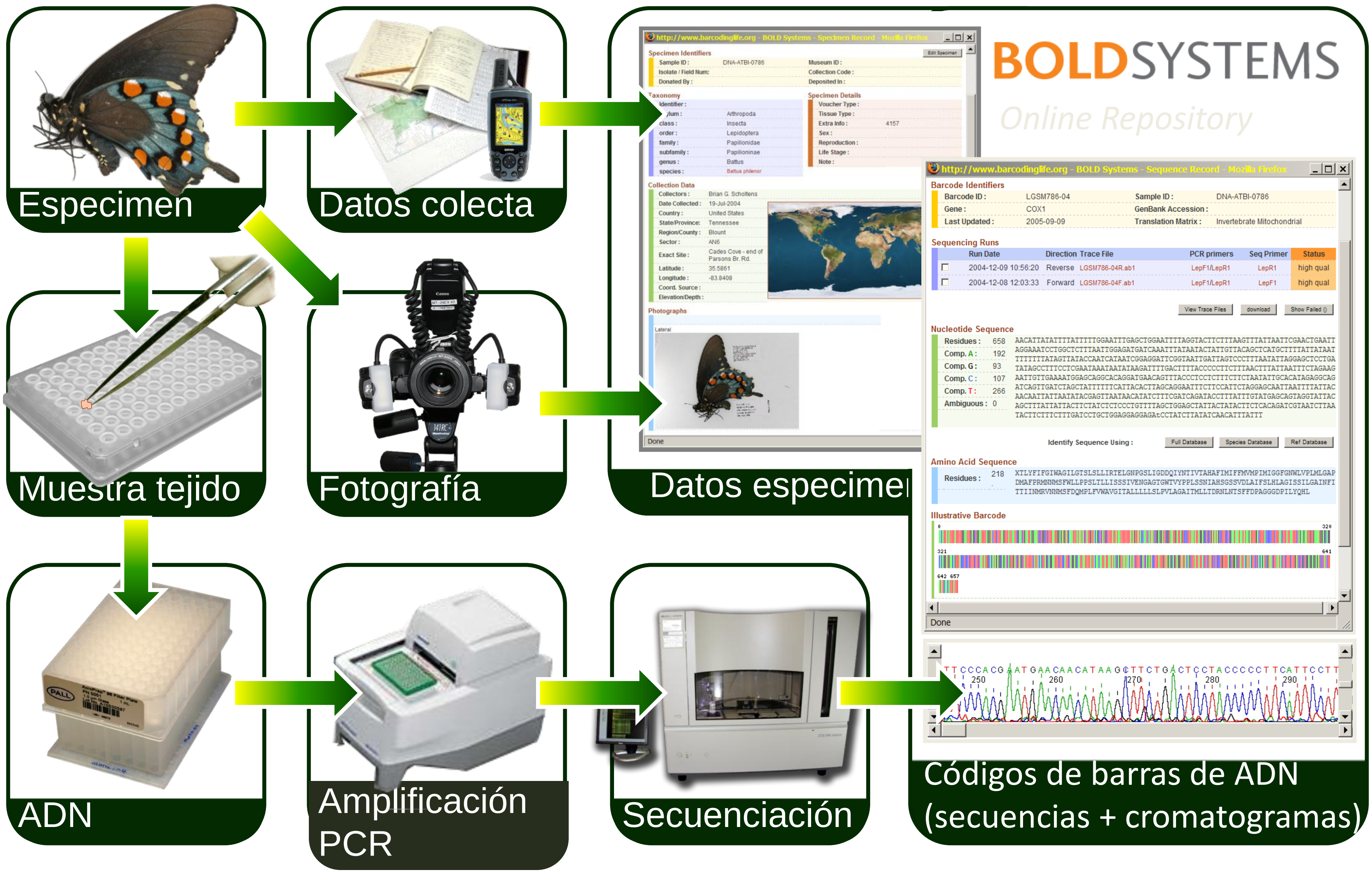
NOU1	AGGTTTACAAGTCGTTTTCAGATGTAATTGAGGGCAAAGAGGGAAGATTTCGCGAGACT
NOU11	AGGTTTATAAGTCGTTTTCAGATGTAATTGAAGGCAAAGAGGGAAGATTTCGCGAGACT
NOU12	AGGTTTACAAGTCGTTTTCAGATGTAATTGAAGGTAAAGAGGGAAGATTTCGCGAGACT
NOU13	AAGTTTACAAGTCGTTTTCAGATGTAATTGAAGGCAAAGAGGGGAGATTTCGTGAGACT
NOU14	AAGTTTACAAGTCGTTTTCATATGTTATTGAAGGCAAAGAGGGAAGATTTCGTGAGACT
NOU15	AGGTTTATAAGTCGTTTTCAGATGTAATTGAAGGCAAAGAGGGAAGATTTCGCGAGACT
NOU17	AGGTTTACAAGTCATTTTCCGATATAATTGAAGGCAAAGAGGGAAGATTTCGCGAGACT
NOU18	AGGTTTACAAGTCGTTTTCAGATGTAATTGAGGGCAAAGAGGGAAGATTTCGCGAGACT
NOU2	AAGTTTACAAGTCGTTTTCAGATGTTATTGAAGGCAAAGAGGGAAGATTTCGTGAGACT
NOU19	AAGTTTACAAGTCGTTTTCAGATGTTATTGAAGGCAAAGAGGGAAGATTTCGTGAGACT
NOU20	AAGTTTACAAGTCGTTTTCAGATGTAATTGAAGGCAAAGAGGGGAGATTTCGTGAGACT
NOU23	AAGTTTACAAGTCGTTTTCAGATGTAATTGAAGGCAAAGAGGGGAGATTTCGTGAGACT
NOU24	AAGTTTACAAGTCATTTTCAGATGTAATTGAAGGCAAAGAAGGAAGATTTCGGGAGACT
NOU25	AAGTTTACAAGTCATTTTCAGATGTAATTGAAGGCAAAGAAGGAAGATTTCGGGAGACT
NOU26	AAGTTTACAAGTCGTTTTCAGATGTAATTGAAGGTAAAGAAGGAAGATTCCGTGAGACT
NOU27	AAGTTTACAAGTCGTTTTCAGATGTAATTGAAGGCAAAGAGGGAAGATTTCGTGAGACT
NOU28	AGGTTTACAAGTCGTTTTCAGATATAATTGAGGGCAAAGAGGGAAGATTTCGCGAGACT
NOU29	AGGTTTACAAGTCATTTTCCGATATAATTGAAGGAAAAGAGGGAAGATTTCGCGAGACT
NOU3	AAGTTTACAAGTCGTTTTCAGATGTAATTGAAGGCAAAGAGGGAAGATTTCGTGAGACT
NOU31	AGGTTTACAAGTCGTTTTCAGATGTAATTGAAGGCAAAGAGGGAAGGTTTCGTGAGACT
NOU32	AAGTTTACAAGTCATTTTCAGATGTAATTGAAGGTAAAGAAGGAAGATTTCGTGAGACT
NOU33	AGGTTTACAAGTCGTTTTCAGATGTAATTGAGGGCAAAGAGGGAAGATTTCGCGAGACT



** Identificar especies previamente descritas

** Descubrir nuevas especies

Catálogo de códigos de barras de ADN



Especimen

Datos colecta

Muestra tejido

Fotografía

Datos especime

ADN

Amplificación PCR

Secuenciación

Códigos de barras de ADN (secuencias + cromatogramas)

http://www.barcodinglife.org - BOLD Systems - Specimen Record - Mozilla Firefox

Specimen Identifiers

Sample ID : DNA-ATBI-0786
Museum ID :
Isolate / Field Num:
Collection Code :
Donated By :
Deposited In :

Taxonomy

Identifier :
ylum : Arthropoda
class : Insecta
order : Lepidoptera
family : Papilionidae
subfamily : Papilioninae
genus : Battus
species : Battus philenor

Specimen Details

Voucher Type :
Tissue Type :
Extra Info : 4157
Sex :
Reproduction :
Life Stage :
Note :

Collection Data

Collectors : Brian G. Scholtens
Date Collected : 19-Jul-2004
Country : United States
State/Province: Tennessee
Region/County : Blount
Sector : AN6
Exact Site : Cades Cove - end of Parsons Br. Rd.
Latitude : 35.5861
Longitude : -83.8408
Coord. Source :
Elevation/Depth :

Photographs

Lateral

Done

http://www.barcodinglife.org - BOLD Systems - Sequence Record - Mozilla Firefox

Barcode Identifiers

Barcode ID : LGSM786-04
Sample ID : DNA-ATBI-0786
Gene : COX1
GenBank Accession :
Last Updated : 2005-09-09
Translation Matrix : Invertebrate Mitochondrial

Sequencing Runs

	Run Date	Direction	Trace File	PCR primers	Seq Primer	Status
☐	2004-12-09 10:56:20	Reverse	LGSM786-04R.ab1	LepF1/LepR1	LepR1	high qual
☐	2004-12-08 12:03:33	Forward	LGSM786-04F.ab1	LepF1/LepR1	LepF1	high qual

Nucleotide Sequence

Residues : 658
Comp. A : 192
Comp. G : 93
Comp. C : 107
Comp. T : 266
Ambiguous : 0

```
AACATTATATTTTATTTTTGGAATTTGAGCTGGAATTTTAGGTACTTCTTTAAGTTTATTAATTCGAACTGAATT
AGGAAATCCTGGCTCTTTAATTGGAGATGATCAAATTTATAATACTATTGTTACAGCTCATGCTTTTATTATAAT
TTTTTTTATAGTTATACCAATCATAATCGGAGGATTCGGTAATTGATTAGTCCCTTTAATATTAGGAGCTCCTGA
TATAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCTTTAACTTTATTAATTTCTAGAAG
AATTGTTGAAAATGGAGCAGGCACAGGATGAACAGTTTACCCTCCTCTTTCTTCTAATATTGCACATAGAGGCAG
ATCAGTTGATCTAGCTATTTTTTCATTACACTTAGCAGGAATTTCTTCCATTCTAGGAGCAATTAATTTTATTAC
AACAATTATTAATATACGAGTTAATAACATATCTTTCGATCAGATACCTTTATTTGTATGAGCAGTAGGTATTAC
AGCTTTATTATTACTTCTATCTCTCCCTGTTTTAGCTGGAGCTATTACTATACTTCTCACAGATCGTAATCTTAA
TACTTCTTTCTTTGATCCTGCTGGAGGAGGAGAtCCTATCTTATATCAACATTTATTT
```

Identify Sequence Using :

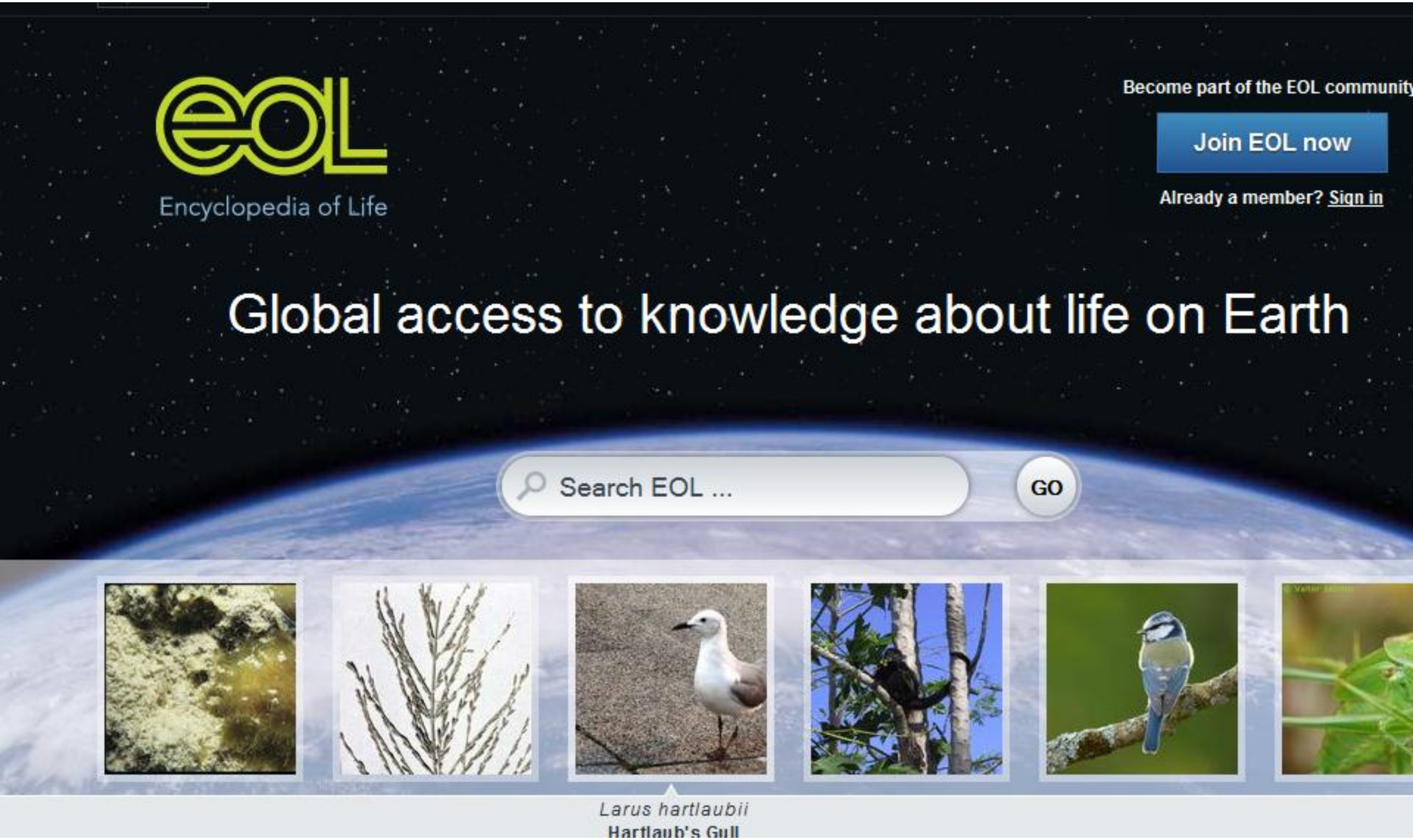
Amino Acid Sequence

Residues : 218

```
XTLYFIFGIWAGILGTSLSLLIRTELGNPGSLIGDDQIYNTIVTAHAFIMIFFMVMPIMIGGFGNWLVPLMLGAP
DMAFPRMNNMSFWLLPPSLTLLISSSIVENGAGTGWTVYPPLSSNIAHSGSSVDLAIFSLHLAGISSILGAINFI
TTIINMRVNNMSFDQMPLFVWAVGITALLLLLSLPVLAGAITMLLTDRNLNTSFFDPAGGGDPILYQHL
```

Illustrative Barcode

Done



Global access to knowledge about life on Earth

Larus hartlaubii
Hartlaub's Gull

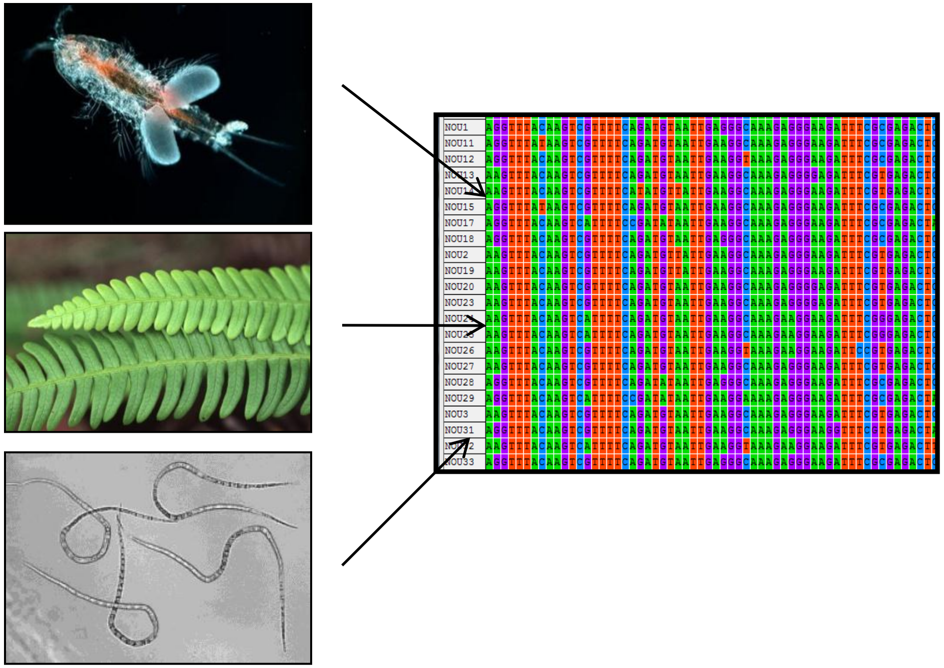
DNA Barcoding: Promise and Pitfalls

Craig Moritz*, Carla Cicero

Democratizing Taxonomy

Imagine a portable DNA barcode scanner that could transform people's relationship with nature. Could such futuristic technology be to biodiversity what the printing press was to literacy?

By Marguerite Holloway



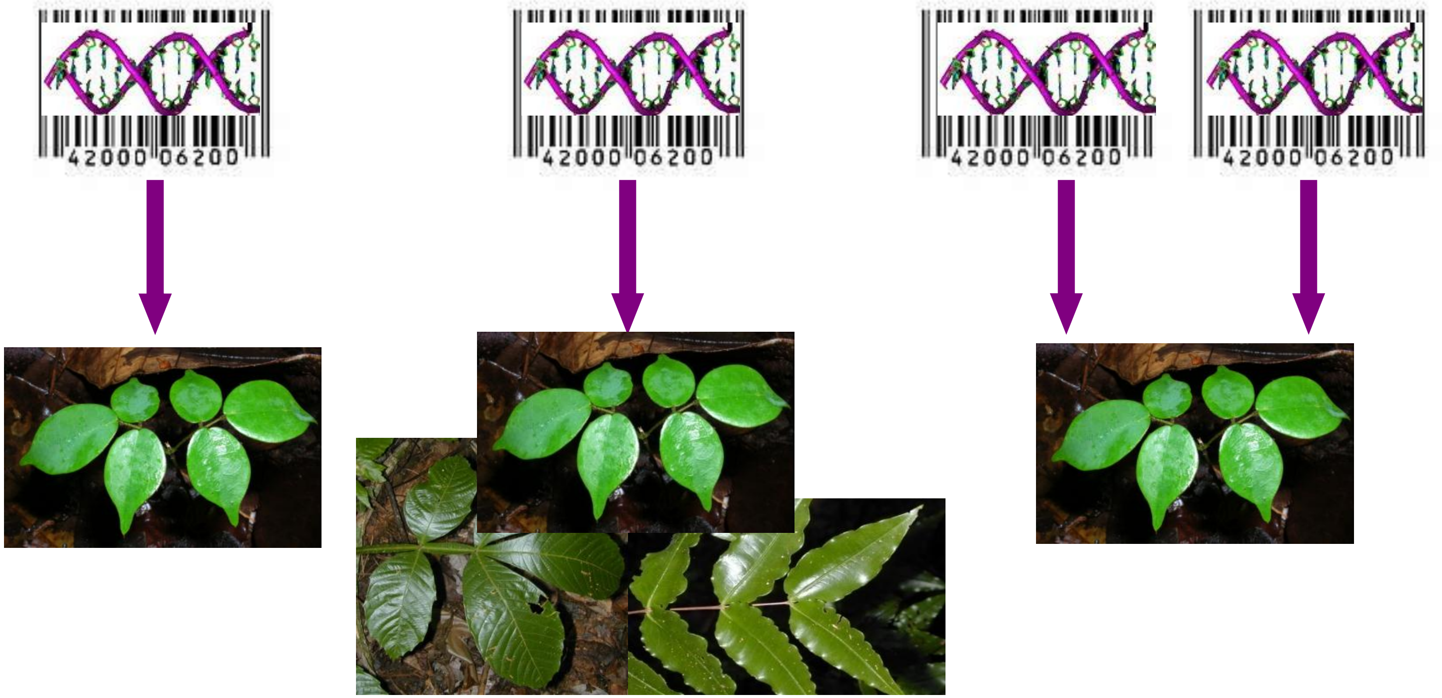
DNA Barcoding: Promise and Pitfalls

Craig Moritz*, Carla Cicero

Encyclopedia of life: should species description equal gene sequence?

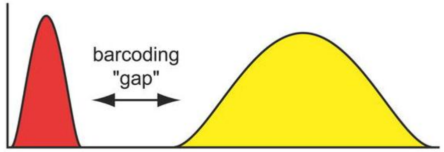
Donat Agosti

American Museum of Natural History and Smithsonian Institution, Eidmattstr. 54, 8032 Zürich, Switzerland



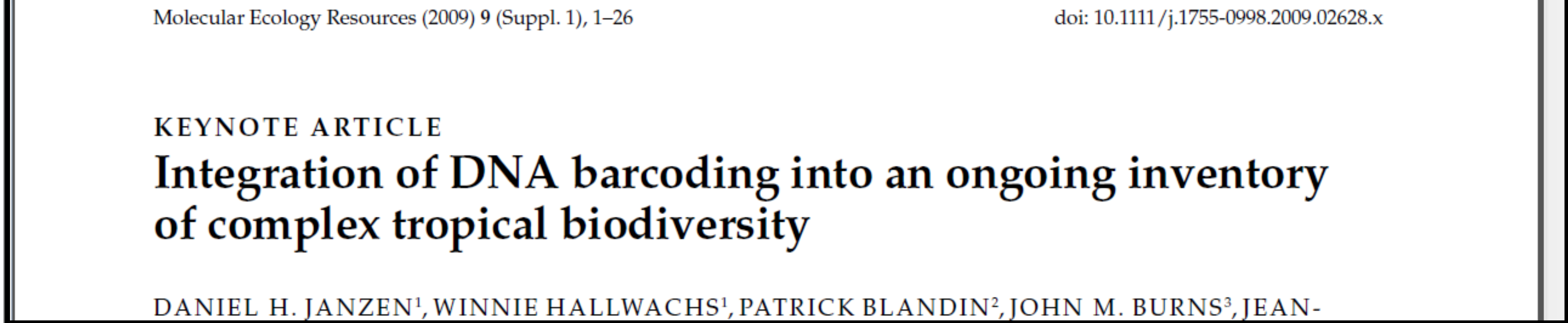
Progreso y aplicaciones

Divergencia del 2% para diferenciar entre las especies




Vireo gilvus

El gen *cox*1 ha permitido una identificación acertada de >95% de las especies de pájaros (*Hebert et al.2003, 2004*)



Molecular Ecology Resources (2009) 9 (Suppl. 1), 1–26 doi: 10.1111/j.1755-0998.2009.02628.x

KEYNOTE ARTICLE

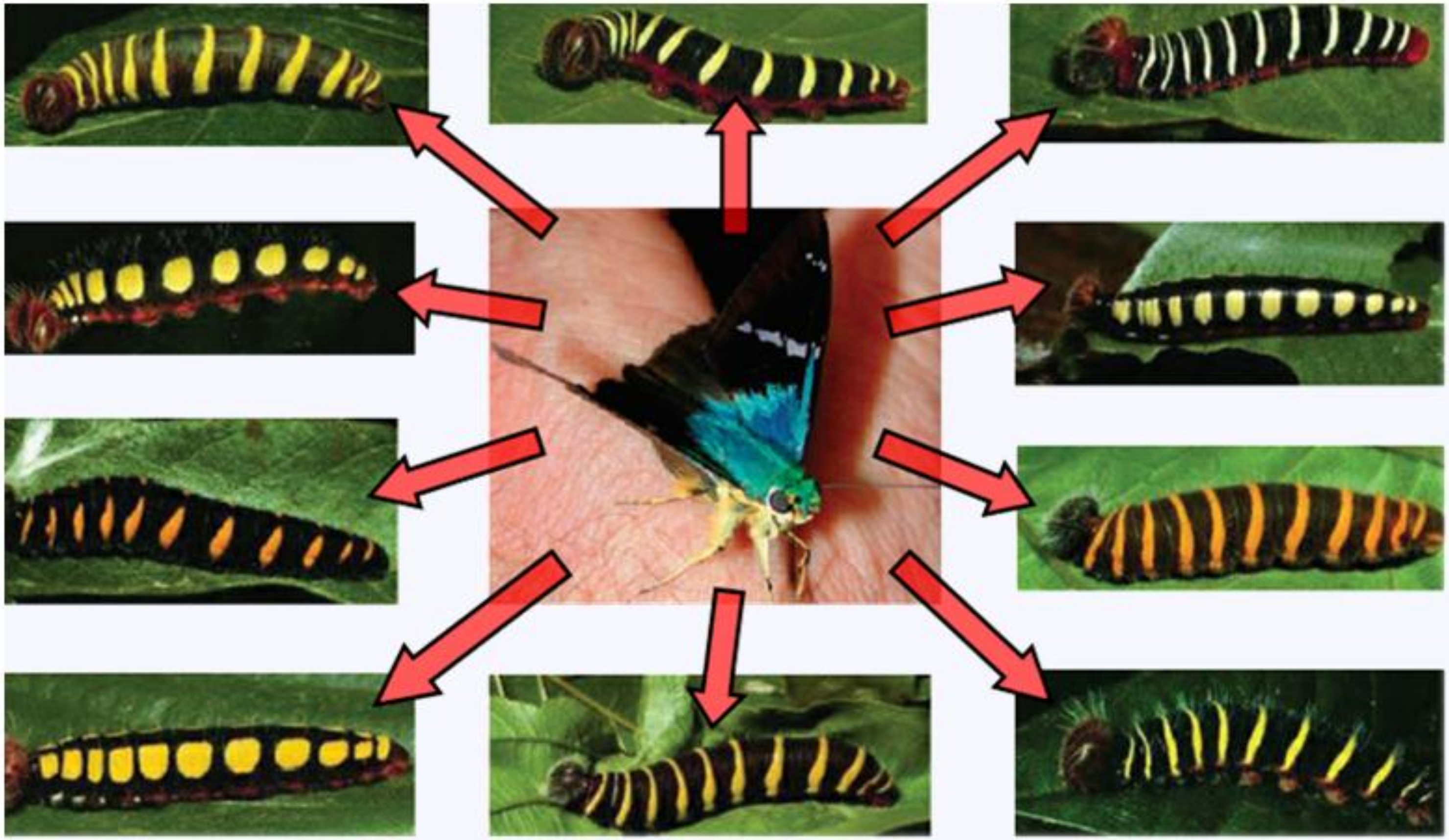
Integration of DNA barcoding into an ongoing inventory of complex tropical biodiversity

DANIEL H. JANZEN[1], WINNIE HALLWACHS[1], PATRICK BLANDIN[2], JOHN M. BURNS[3], JEAN-

Ten species in one: DNA barcoding reveals cryptic species in the neotropical skipper butterfly *Astraptes fulgerator*

Paul D. N. Hebert[*,†], Erin H. Penton[*], John M. Burns[‡], Daniel H. Janzen[§], and Winnie Hallwachs[§]

[*]Department of Zoology, University of Guelph, Guelph, ON, Canada N1G 2W1; [‡]Department of Entomology, National Museum of Natural History, Smithsonian Institution, Washington, DC 20560-0127; and [§]Department of Biology, University of Pennsylvania, Philadelphia, PA 19104



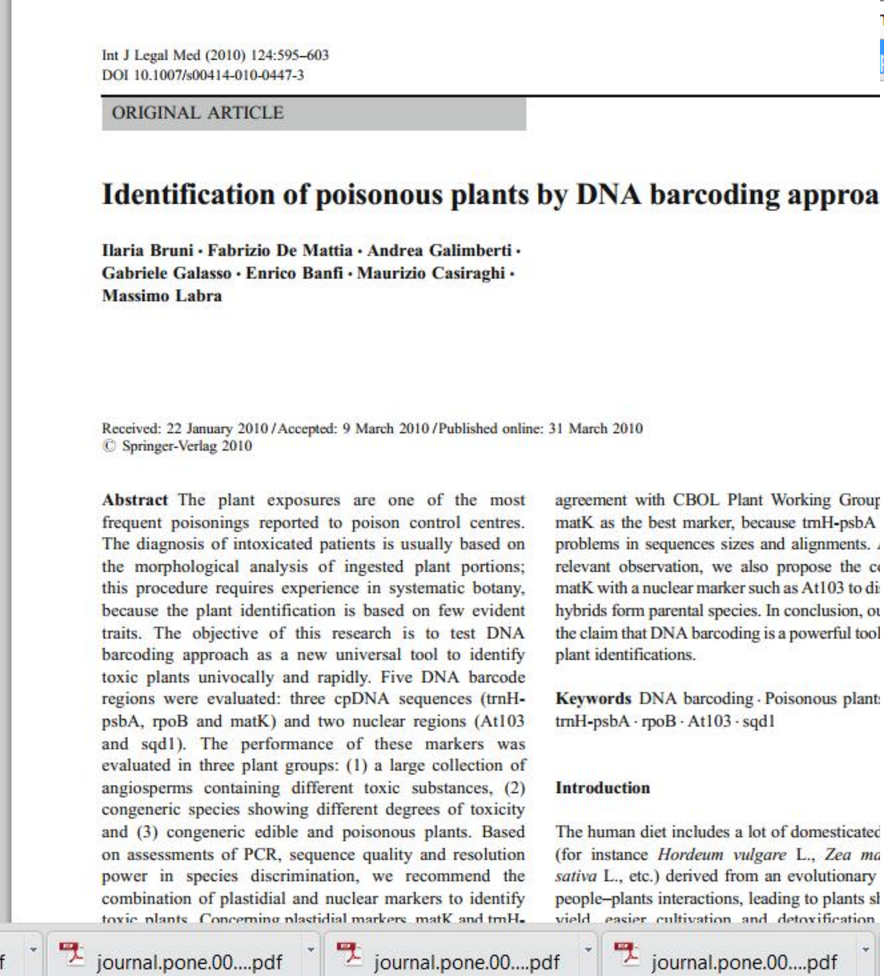
…Otras aplicaciones del código de barras ADN

RESEARCH ARTICLE

OPEN

Validation of the ITS2 Region as a Novel DNA Barcode for Identifying Medicinal Plant Species

Shilin Chen[1*], Hui Yao[1], Jianping Han[1], Chang Liu[2], Jingyuan Song[1*], Linchun Shi[1], Yingjie Zhu[1], Xinye Ma[1], Ting Gao[1], Xiaohui Pang[1], Kun Luo[3], Ying Li[1], Xiwen Li[1], Xiaocheng Jia[1], Yulin Lin[1], Christine Leon[4]



Int J Legal Med (2010) 124:595–603
DOI 10.1007/s00414-010-0447-3

ORIGINAL ARTICLE

Identification of poisonous plants by DNA barcoding approa

Ilaria Bruni · Fabrizio De Mattia · Andrea Galimberti · Gabriele Galasso · Enrico Banfi · Maurizio Casiraghi · Massimo Labra

Received: 22 January 2010 / Accepted: 9 March 2010 / Published online: 31 March 2010
© Springer-Verlag 2010

Abstract The plant exposures are one of the most frequent poisonings reported to poison control centres. The diagnosis of intoxicated patients is usually based on the morphological analysis of ingested plant portions; this procedure requires experience in systematic botany, because the plant identification is based on few evident traits. The objective of this research is to test DNA barcoding approach as a new universal tool to identify toxic plants univocally and rapidly. Five DNA barcode regions were evaluated: three cpDNA sequences (trnH-psbA, rpoB and matK) and two nuclear regions (At103 and sqd1). The performance of these markers was evaluated in three plant groups: (1) a large collection of angiosperms containing different toxic substances, (2) congeneric species showing different degrees of toxicity and (3) congeneric edible and poisonous plants. Based on assessments of PCR, sequence quality and resolution power in species discrimination, we recommend the combination of plastidial and nuclear markers to identify toxic plants. Concerning plastidial markers, matK and trnH-

agreement with CBOL Plant Working Grou
matK as the best marker, because trnH-psbA
problems in sequences sizes and alignments.
relevant observation, we also propose the c
matK with a nuclear marker such as At103 to di
hybrids form parental species. In conclusion, ou
the claim that DNA barcoding is a powerful tool
plant identifications.

Keywords DNA barcoding · Poisonous plant
trnH-psbA · rpoB · At103 · sqd1

Introduction

The human diet includes a lot of domesticated
(for instance *Hordeum vulgare* L., *Zea ma*
sativa L., etc.) derived from an evolutionary
people–plants interactions, leading to plants sl
yield, easier cultivation and detoxification

Why do we need to identify medicinal materials from natural sources?

Medicinal materials from natural sources have been used for centuries in China and other countries. They have been recognized as particularly suitable for treating modern diseases such as cardiovascular diseases, asthma and other long-term illnesses. Substitutes and adulterants are often introduced intentionally or accidentally, thus seriously interfering with their therapeutic effects, even leading to life-threatening poisoning. In 1989, two people in Hong Kong suffered serious neuropathy and encephalopathy after consuming a broth made with the roots of Podophyllum hexandrum, a toxic herb mistaken as Gentiana rigescens. In 2001, 63 people in the Netherlands reported symptoms of general malaise, nausea and vomiting following consumption of an herbal tea, with Japanese star anise (Illicium anisatum) mixed in the product. Aristolochic acid nephropathy has also been reported in Hong Kong, Korea and Belgium due to the erroneous substitution with herbs containing aristolochic acids. From March 2004 to May 2006, it was reported 10 cases of aconite poisoning in Hong Kong were reported. In four of them, the aconite herb was not listed in the written prescription. In 2008, a woman in Singapore suffered from antimuscarinic poisoning consuming brew made with Datura metel, which is a toxic herb mistaken as Rhododendron molle.

MMDBD Statistics

- Species: 1658
- Sequences:31468
- Photos:369
- References:2401

Updated:May 2012

DNA barcoding of medicinal materials

Medicinal materials are traditionally identified by their organoleptic characteristics and other physical properties. However, the differences among related species are sometimes too minute. Chemical analyses may be affected by the physiological and the storage conditions. With the advancement of molecular biology, DNA barcoding has now become a popular means for identification and authentication of plant and animal species. We have established this DNA barcode database for users to retrieve and analyze DNA sequences of medicinal materials. This website includes DNA sequences and information and key references of the medicinal materials recorded in the Pharmacopoeia of the People's Republic of China, American Herbal Pharmacopoeia and other related references. Relevant information of common adulterants and substitutes are also listed. This database provides a web-based platform for storage.

Applications on taxonomy and identification

Taxonomy

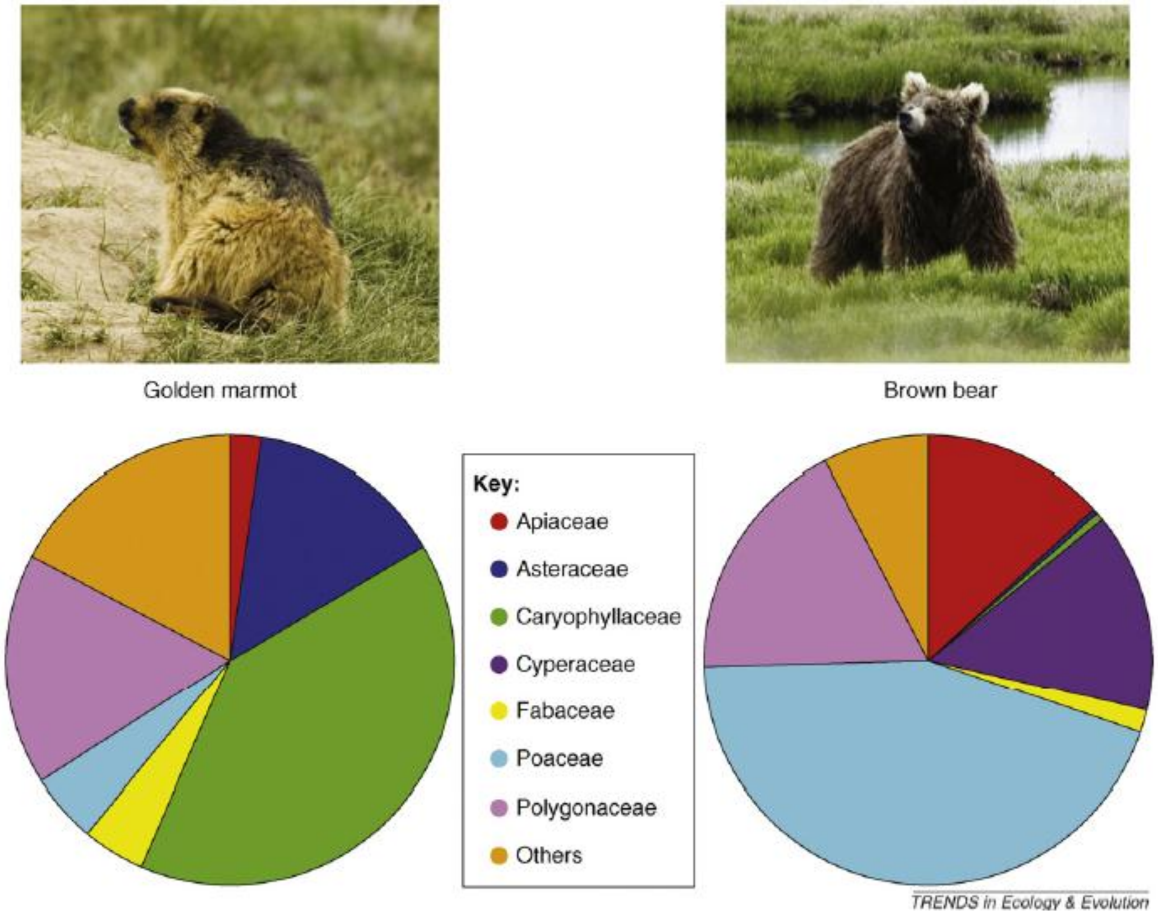
- Law et al. Molecular analyses of the Chinese herb Leigongteng (Tripterygim wilfordii Hook.f.) Phytochemistry (2011) 72:21-26

Identification

- Li et al. Establishment of DNA barcodes for the identification of the botanical sources of the Chinese 'coolin beverage. Food Control (2012) 25:758-766
- Guo et al. Application of DNA barcodes in Hedyotis L. (Spermacoceae, Rubiaceae). Journal of Systematics and Evolution (2011) 49:203-212
- Chan et al. Molecular analyses of Cordyceps gunnii in China. Journal of Food and Drug Analysis (2011) 19:18-25

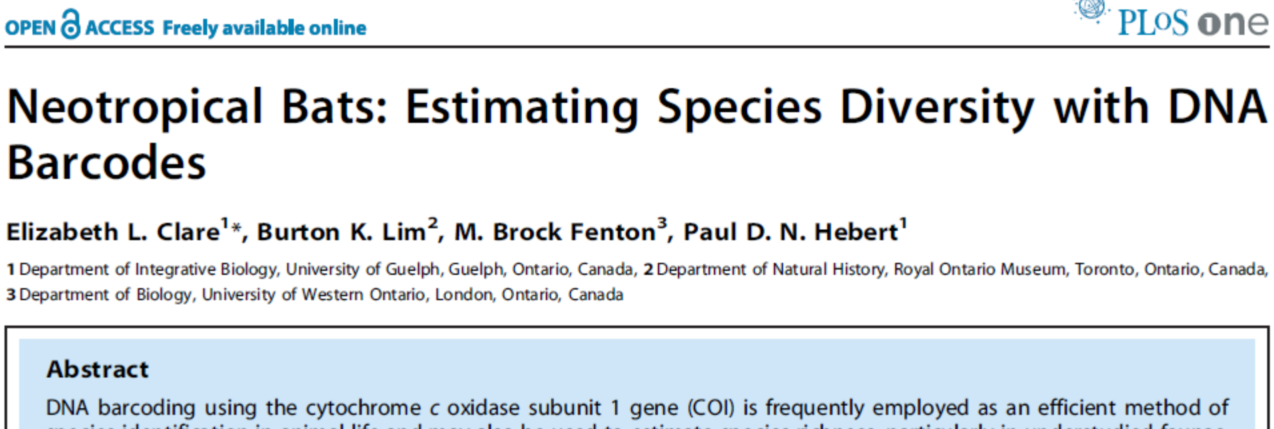
http://137.189.42.34/mherbsdb/index.php

Aplicaciones del código de barras ADN



Valentini et al. Mol. Ecol. Res. 2009

Utilización de Minibarcodes y metabarcoding



OPEN ACCESS Freely available online

PLoS one

Neotropical Bats: Estimating Species Diversity with DNA Barcodes

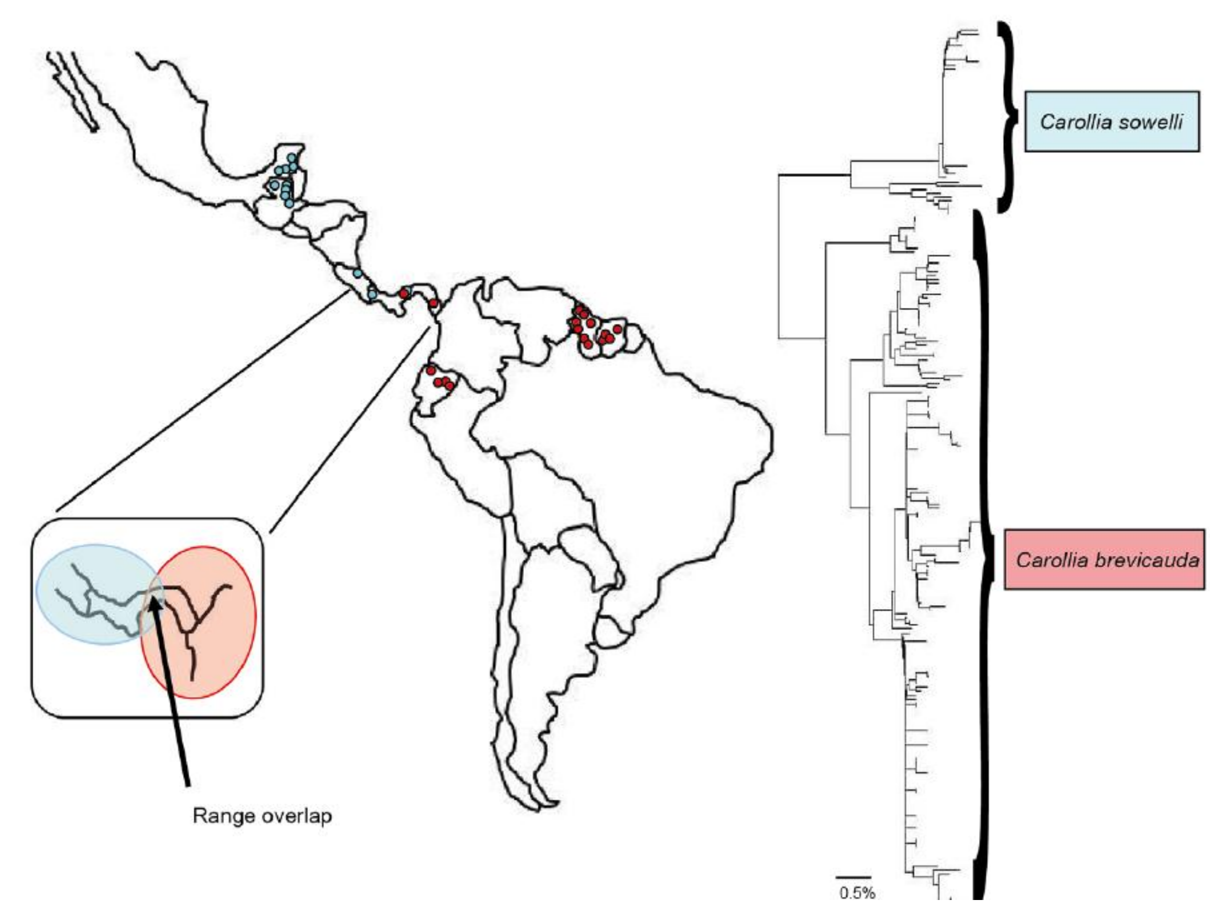
Elizabeth L. Clare[1]*, Burton K. Lim[2], M. Brock Fenton[3], Paul D. N. Hebert[1]

1 Department of Integrative Biology, University of Guelph, Guelph, Ontario, Canada, 2 Department of Natural History, Royal Ontario Museum, Toronto, Ontario, Canada, 3 Department of Biology, University of Western Ontario, London, Ontario, Canada

Abstract

DNA barcoding using the cytochrome *c* oxidase subunit 1 gene (COI) is frequently employed as an efficient method of
species identification in animal life and may also be used t
Despite numerous past demonstrations of the efficiency
barcoding methodologies on a large geographic scale, par
and potential species diversity using DNA barcodes with
Neotropical bats (order Chiroptera). This represents one
group and is certainly the largest to date for land vertebr
geographic distances and across extraordinarily diverse
distinct sets of COI haplotypes making them easily recog
haplotypes. Intraspecific diversity in the region was high
11.79%) with respect to birds, though comparable to othe
intraspecific lineages were identified which may suggest
intraspecific divergence were not good predictors of thei
investigation using complementary molecular technique
data. Our analysis provides strong support for the continue
investigation of bats.

Citation: Clare EL, Lim BK, Fenton MB, Hebert PDN (2011) Neotropical Bats: Es
journal.pone.0022648



OPEN ACCESS Freely available online
PLoS one

Barcoding Nemo: DNA-Based Identifications for the Ornamental Fish Trade

Dirk Steinke[☯]*, **Tyler S. Zemlak**[☯¤], **Paul D. N. Hebert**

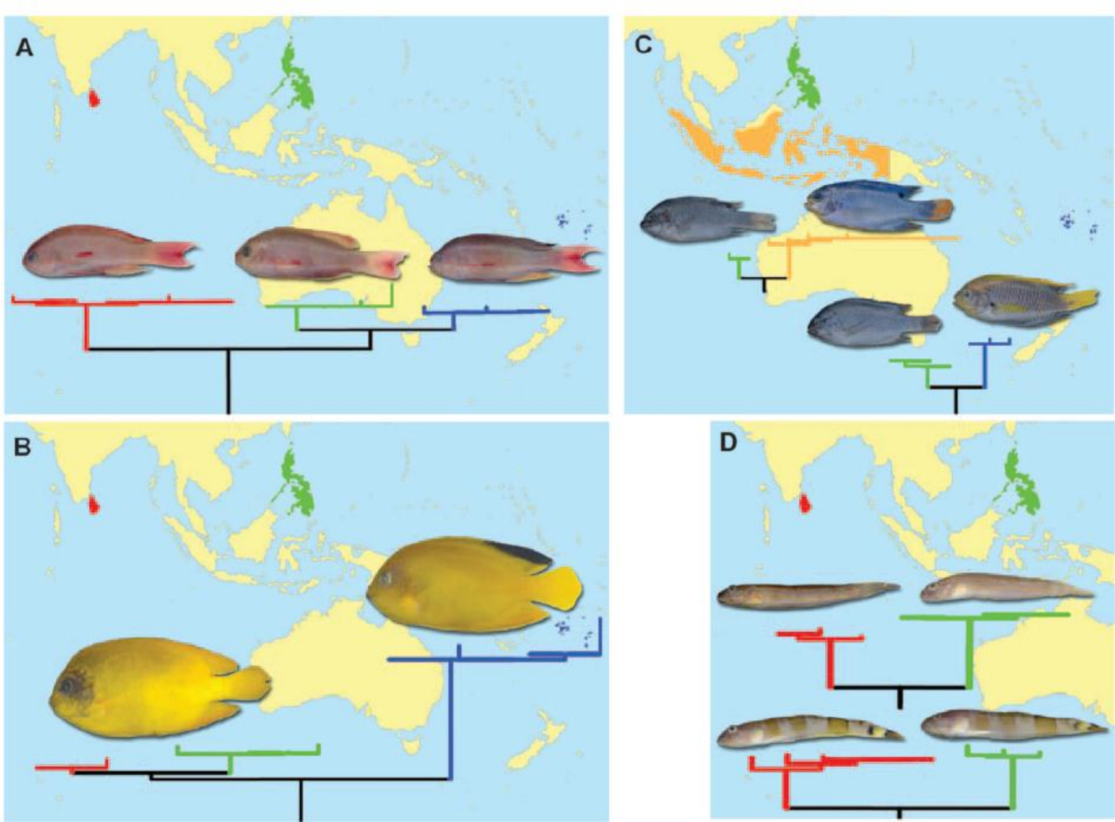
Canadian Centre for DNA Barcoding, Biodiversity Institute of Ontario, University of Guelph, Guelph, Ontario, Canada

Abstract

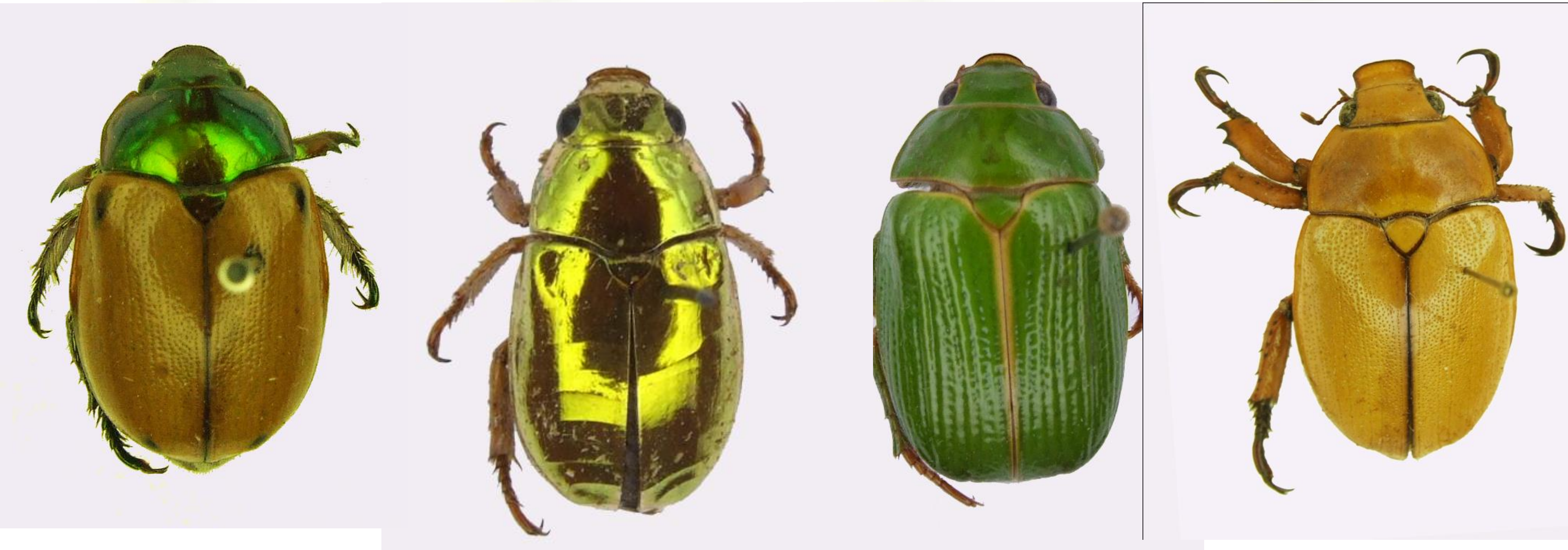
Background: Trade in ornamental fishes represents, by far, the largest route for the importation of exotic vertebrates. There is growing pressure to regulate this trade with the goal of ensuring that species are sustainably harvested and that their point of origin is accurately reported. One important element of such regulation involves easy access to specimen identifications, a task that is currently difficult for all but specialists because of the large number of species involved. The present study represents an important first step in making identifications more accessible by assembling a DNA barcode reference sequence library for nearly half of the ornamental fish species imported into North America.

Methodology/Principal Findings: Analysis of the cytochrome *c* oxidase subunit I (COI) gene from 391 species from 8 coral reef locations revealed that 98% of these species exhibit distinct barcode clusters, allowing their unambiguous identification. Most species showed little intra-specific variation (adjusted m
three lineages showing much more divergence (2.19–6.52%) and likely
contrast, three genera contained a species pair or triad that lacked barcode
young taxa or taxonomic over-splitting.

Conclusions/Significance: Although incomplete, this barcode library alread
the ornamental fish industry, opening a realm of applications linked t
conservation.



Larvas—Adultos (medicina legal)



Forensic botany: species identification of botanical trace evidence using a multigene barcoding approach

Gianmarco Ferri · Milena Alù · Beatrice Corradini ·
Giovanni Beduschi

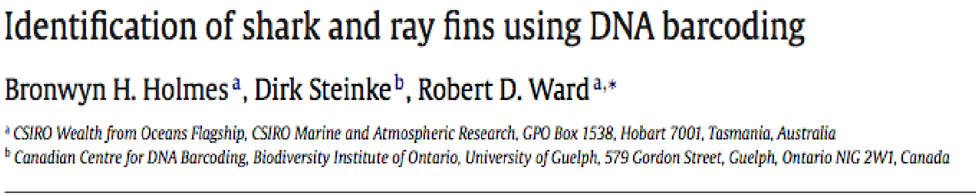
Science News

DNA Analysis Suggests Whale Meat from Sushi Restaurants in L.A., Seoul Originated from Japan

ScienceDaily (Apr. 14, 2010) — An international team of Oregon State University scientists, documentary filmmakers and environmental advocates has uncovered an apparent illegal trade in whalemeat, linking whales killed in Japan's controversial scientific whaling program to sushi restaurants in Seoul, South Korea, and Los Angeles, Calif.

Aplicación de los códigos de barras ADN

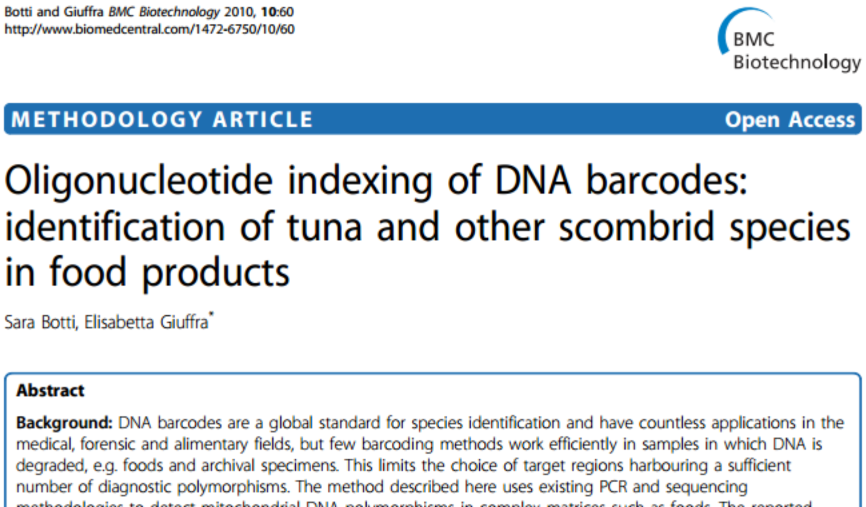
Control de trafico de especies



Identification of shark and ray fins using DNA barcoding

Bronwyn H. Holmes[a], Dirk Steinke[b], Robert D. Ward[a,*]

[a] *CSIRO Wealth from Oceans Flagship, CSIRO Marine and Atmospheric Research, GPO Box 1538, Hobart 7001, Tasmania, Australia*
[b] *Canadian Centre for DNA Barcoding, Biodiversity Institute of Ontario, University of Guelph, 579 Gordon Street, Guelph, Ontario NIG 2W1, Canada*



Botti and Giuffra *BMC Biotechnology* 2010, **10**:60
http://www.biomedcentral.com/1472-6750/10/60

BMC Biotechnology

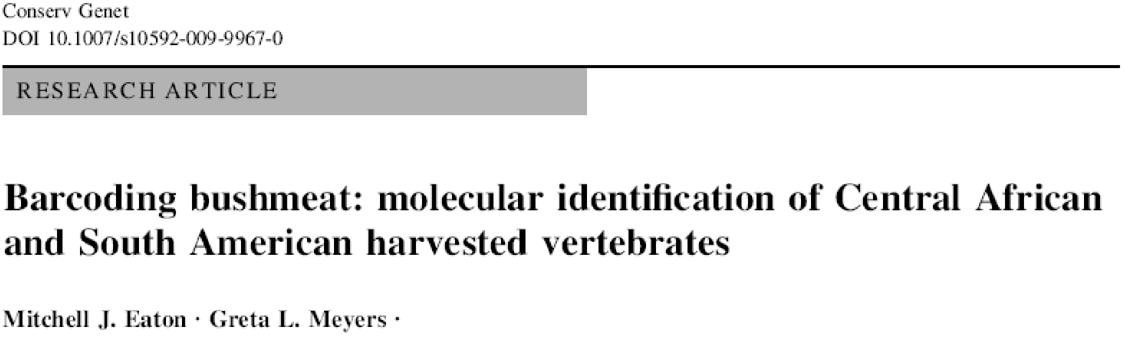
METHODOLOGY ARTICLE **Open Access**

Oligonucleotide indexing of DNA barcodes: identification of tuna and other scombrid species in food products

Sara Botti, Elisabetta Giuffra*

Abstract

Background: DNA barcodes are a global standard for species identification and have countless applications in the medical, forensic and alimentary fields, but few barcoding methods work efficiently in samples in which DNA is degraded, e.g. foods and archival specimens. This limits the choice of target regions harbouring a sufficient number of diagnostic polymorphisms. The method described here uses existing PCR and sequencing



Conserv Genet
DOI 10.1007/s10592-009-9967-0

RESEARCH ARTICLE

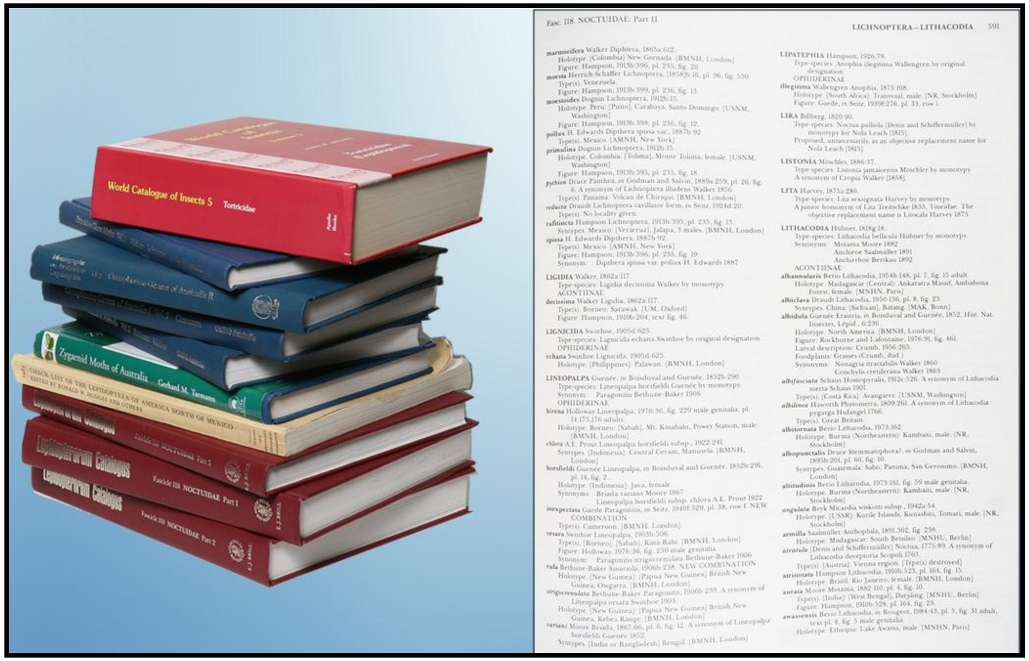
Barcoding bushmeat: molecular identification of Central African and South American harvested vertebrates

Mitchell J. Eaton · Greta L. Meyers ·
Sergios-Orestis Kolokotronis · Matthew S. Leslie ·

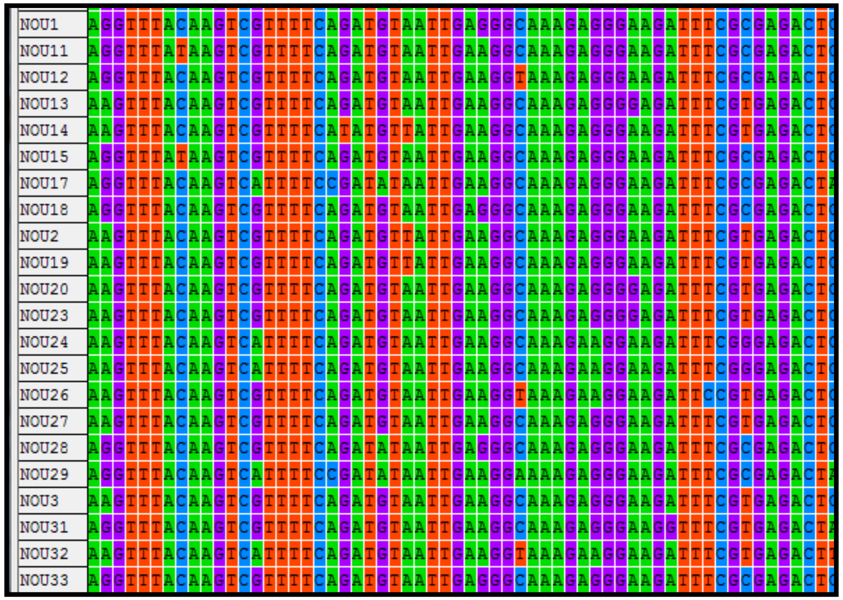
[redacted]

El ADN como herramienta taxonómica

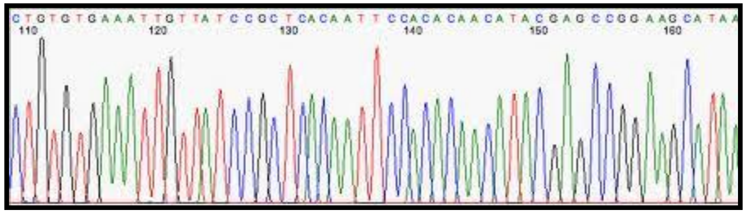
Catálogo morfológico de especies



Catálogo molecular de especies



NOU1	AGGTTTACAAGTCGTTTTCAGATGTAATTGAGGGCAAAGAGGGAAGATTTCGCGAGACT
NOU11	AGGTTTATAAGTCGTTTTCAGATGTAATTGAAGGCAAAGAGGGAAGATTTCGCGAGACT
NOU12	AGGTTTACAAGTCGTTTTCAGATGTAATTGAAGGTAAAGAGGGAAGATTTCGCGAGACT
NOU13	AAGTTTACAAGTCGTTTTCAGATGTAATTGAAGGCAAAGAGGGGAGATTTCGTGAGACT
NOU14	AAGTTTACAAGTCGTTTTCATATGTTATTGAAGGCAAAGAGGGAAGATTTCGTGAGACT
NOU15	AGGTTTATAAGTCGTTTTCAGATGTAATTGAAGGCAAAGAGGGAAGATTTCGCGAGACT
NOU17	AGGTTTACAAGTCATTTTCCGATATAATTGAAGGCAAAGAGGGAAGATTTCGCGAGACT
NOU18	AGGTTTACAAGTCGTTTTCAGATGTAATTGAGGGCAAAGAGGGAAGATTTCGCGAGACT
NOU2	AAGTTTACAAGTCGTTTTCAGATGTTATTGAAGGCAAAGAGGGAAGATTTCGTGAGACT
NOU19	AAGTTTACAAGTCGTTTTCAGATGTTATTGAAGGCAAAGAGGGAAGATTTCGTGAGACT
NOU20	AAGTTTACAAGTCGTTTTCAGATGTAATTGAAGGCAAAGAGGGGAGATTTCGTGAGACT
NOU23	AAGTTTACAAGTCGTTTTCAGATGTAATTGAAGGCAAAGAGGGGAGATTTCGTGAGACT
NOU24	AAGTTTACAAGTCATTTTCAGATGTAATTGAAGGCAAAGAAGGAAGATTTCGGGAGACT
NOU25	AAGTTTACAAGTCATTTTCAGATGTAATTGAAGGCAAAGAAGGAAGATTTCGGGAGACT
NOU26	AAGTTTACAAGTCGTTTTCAGATGTAATTGAAGGTAAAGAAGGAAGATTCCGTGAGACT
NOU27	AAGTTTACAAGTCGTTTTCAGATGTAATTGAAGGCAAAGAGGGAAGATTTCGTGAGACT
NOU28	AGGTTTACAAGTCGTTTTCAGATATAATTGAGGGCAAAGAGGGAAGATTTCGCGAGACT
NOU29	AGGTTTACAAGTCATTTTCCGATATAATTGAAGGAAAAGAGGGAAGATTTCGCGAGACT
NOU3	AAGTTTACAAGTCGTTTTCAGATGTAATTGAAGGCAAAGAGGGAAGATTTCGTGAGACT
NOU31	AGGTTTACAAGTCGTTTTCAGATGTAATTGAAGGCAAAGAGGGAAGGTTTCGTGAGACT
NOU32	AAGTTTACAAGTCATTTTCAGATGTAATTGAAGGTAAAGAAGGAAGATTTCGTGAGACT
NOU33	AGGTTTACAAGTCGTTTTCAGATGTAATTGAGGGCAAAGAGGGAAGATTTCGCGAGACT



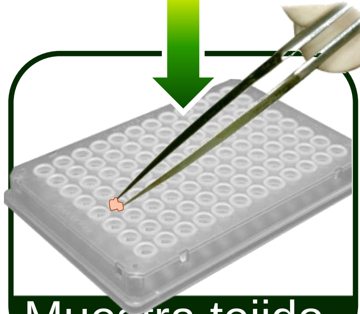
** Identificar especies previamente descritas

** Descubrir nuevas especies

Catálogo de códigos de barras de ADN

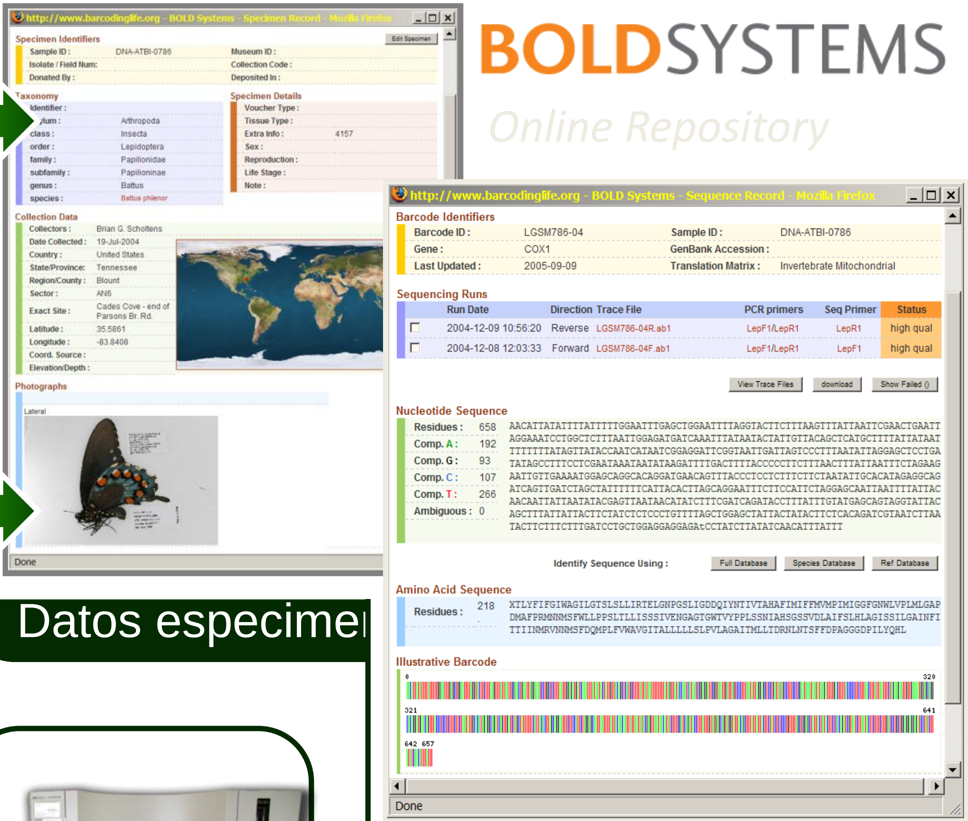
Especimen

Datos colecta



Muestra tejido

Fotografía



http://www.barcodinglife.org - BOLD Systems - Specimen Record - Mozilla Firefox

Specimen Identifiers

Sample ID : DNA-ATBI-0786
Isolate / Field Num:
Donated By :
Museum ID :
Collection Code :
Deposited In :

Taxonomy

Identifier :
lum : Arthropoda
class : Insecta
order : Lepidoptera
family : Papilionidae
subfamily : Papilioninae
genus : Battus
species : Battus philenor

Specimen Details

Voucher Type :
Tissue Type :
Extra Info : 4157
Sex :
Reproduction :
Life Stage :
Note :

Collection Data

Collectors : Brian G. Scholtens
Date Collected : 19-Jul-2004
Country : United States
State/Province: Tennessee
Region/County : Blount
Sector : AN6
Exact Site : Cades Cove - end of Parsons Br. Rd.
Latitude : 35.5861
Longitude : -83.8408
Coord. Source :
Elevation/Depth :

Photographs

Lateral

http://www.barcodinglife.org - BOLD Systems - Sequence Record - Mozilla Firefox

Barcode Identifiers

Barcode ID : LGSM786-04
Gene : COX1
Last Updated : 2005-09-09
Sample ID : DNA-ATBI-0786
GenBank Accession :
Translation Matrix : Invertebrate Mitochondrial

Sequencing Runs

	Run Date	Direction	Trace File	PCR primers	Seq Primer	Status
☐	2004-12-09 10:56:20	Reverse	LGSM786-04R.ab1	LepF1/LepR1	LepR1	high qual
☐	2004-12-08 12:03:33	Forward	LGSM786-04F.ab1	LepF1/LepR1	LepF1	high qual

Nucleotide Sequence

Residues : 658
Comp. A : 192
Comp. G : 93
Comp. C : 107
Comp. T : 266
Ambiguous : 0

```
AACATTATATTTTATTTTTGGAATTTGAGCTGGAATTTTAGGTACTTCTTTAAGTTTATTAATTCGAACTGAATT
AGGAAATCCTGGCTCTTTAATTGGAGATGATCAAATTTATAATACTATTGTTACAGCTCATGCTTTTATTATAAT
TTTTTTTATAGTTATACCAATCATAATCGGAGGATTCGGTAATTGATTAGTCCCTTTAATATTAGGAGCTCCTGA
TATAGCCTTTCCTCGAATAAATAATATAAGATTTTGACTTTTACCCCCTTCTTTAACTTTATTAATTTCTAGAAG
AATTGTTGAAAATGGAGCAGGCACAGGATGAACAGTTTACCCTCCTCTTTCTTCTAATATTGCACATAGAGGCAG
ATCAGTTGATCTAGCTATTTTTTCATTACACTTAGCAGGAATTTCTTCCATTCTAGGAGCAATTAATTTTATTAC
AACAATTATTAATATACGAGTTAATAACATATCTTTCGATCAGATACCTTTATTTGTATGAGCAGTAGGTATTAC
AGCTTTATTATTACTTCTATCTCTCCCTGTTTTAGCTGGAGCTATTACTATACTTCTCACAGATCGTAATCTTAA
TACTTCTTTCTTTGATCCTGCTGGAGGAGGAGAtCCTATCTTATATCAACATTTATTT
```

Identify Sequence Using :

Amino Acid Sequence

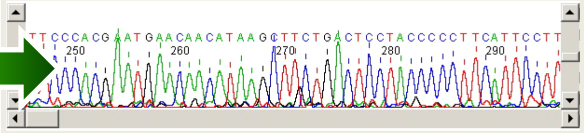
Residues : 218

```
XTLYFIFGIWAGILGTSLSLLIRTELGNPGSLIGDDQIYNTIVTAHAFIMIFFMVMPIMIGGFGNWLVPLMLGAP
DMAFPRMNNMSFWLLPPSLTLLISSSIVENGAGTGWTVYPPLSSNIAHSGSSVDLAIFSLHLAGISSILGAINFI
TTIINMRVNNMSFDQMPLFVWAVGITALLLLLSLPVLAGAITMLLTDRNLNTSFFDPAGGGDPILYQHL
```

Illustrative Barcode

Done

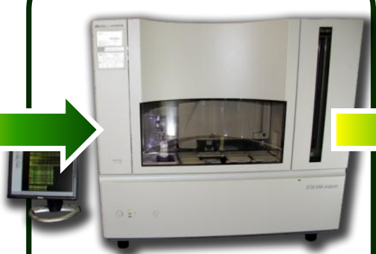
Datos especimen



Códigos de barras de ADN (secuencias + cromatogramas)

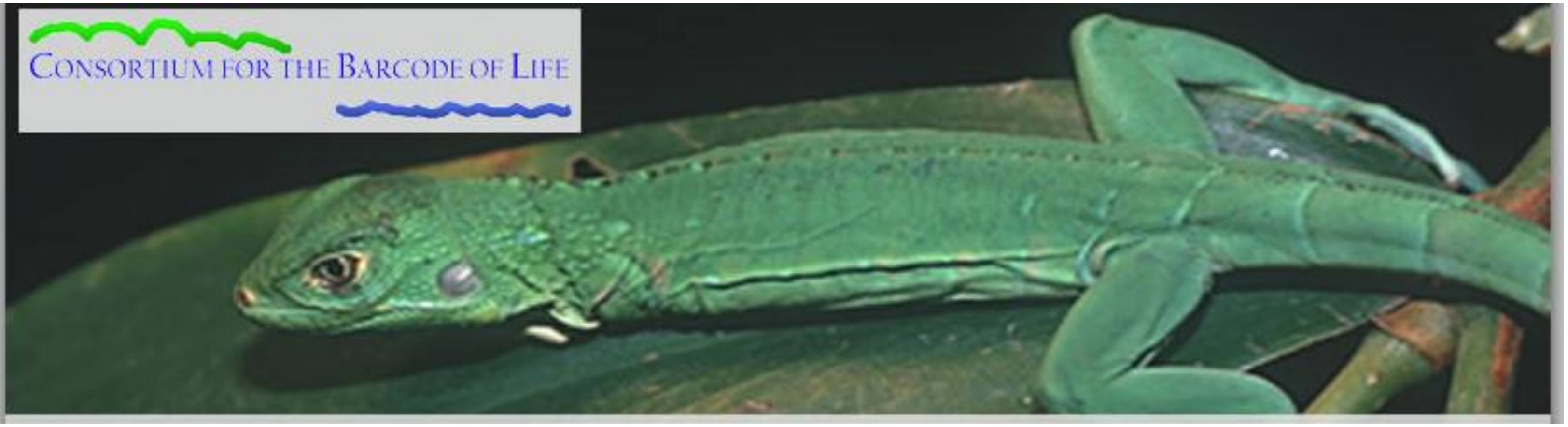
ADN

Amplificación PCR



Secuenciación

Iniciativas internacionales



CBOL

All Birds Barcoding Initiative

Bee-BOL

FISH-BOL

MBI

Mosquito Barcoding Initiative

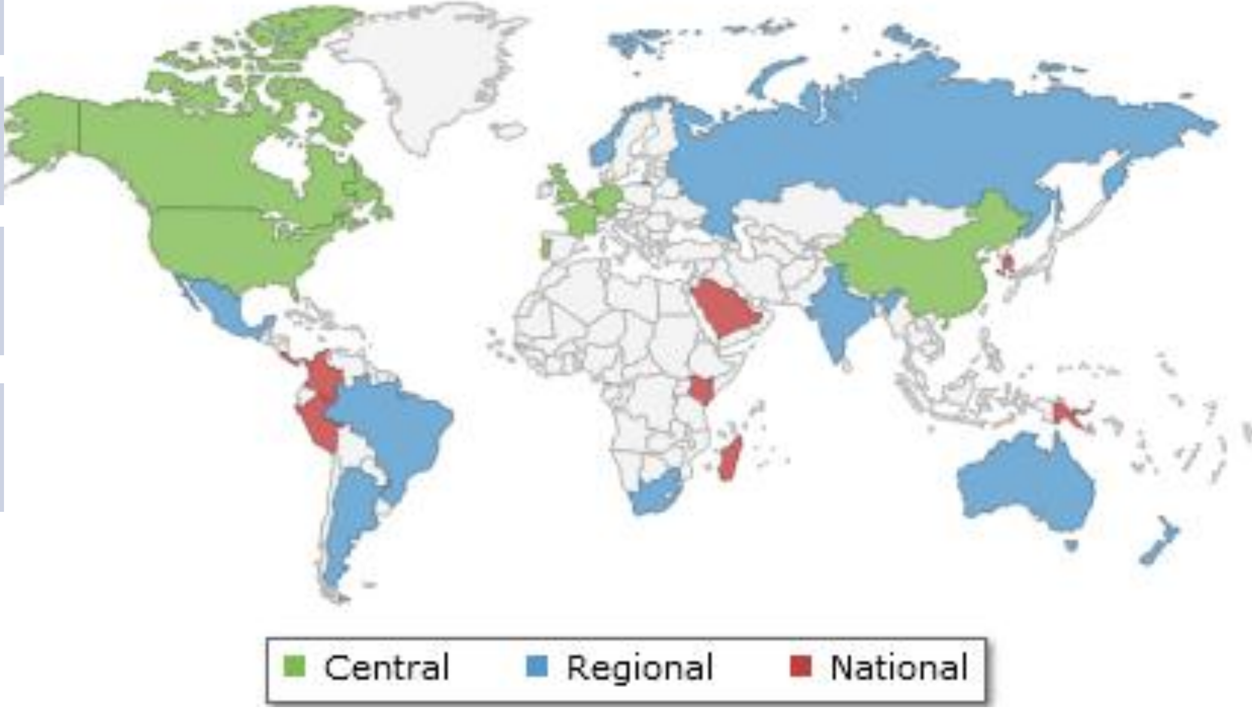
iBOL International Barcode of Life

5 Years

$150M

5M especímenes

500K especies



Central= 25M
Regional=5M
Nacional=1M

TROPICAL
VERTEBRATES
IN A CHANGING
WORLD

APPLICABILITY OF DNA BARCODING TO MUSEUM SPECIMENS OF BIRDS FROM THE DEMOCRATIC REPUBLIC OF THE CONGO

G. Sonet[1], F. C. Breman[2], G. Lenglet[3], M. Louette[4], G. Montañés[3], Z. T. Nagy[1],
J. van Houdt[2], & E. Verheyen[3]

ZooKeys 152: 87–91 (2011)
doi: 10.3897/zookeys.152.2473
www.zookeys.org

DATA PAPER

A peer-reviewed open-access journal
ZooKeys
Launched to accelerate biodiversity research

Project Description: DNA Barcodes of Bird Species in the National Museum of Natural History, Smithsonian Institution, USA

David E. Schindel[1], Mark Y. Stoeckle[2], Chris M. Milensky[3], Michael Trizna[1], Brian K. Schmidt[3], Christina A. Gebhard[3], Gary R. Graves[3,4]

1 *Consortium for the Barcode of Life, MRC-105, National Museum of Natural History, Smithsonian Institution, P. O. Box 37012, Washington, D.C. 20013-7012 USA* **2** *Program for the Human Environment, Rockefeller University, New York, USA* **3** *Department of Vertebrate Zoology, MRC-116, National Museum of Natural History, Smithsonian Institution, P. O. Box 37012, Washington, D.C. 20013-7012 USA* **4** *Center for Macroecology, Evolution and Climate, University of Copenhagen, DK-2100 Copenhagen, Denmark*

Corresponding author: *M. Y. Stoeckle* (mark.stoeckle@rockefeller.edu)

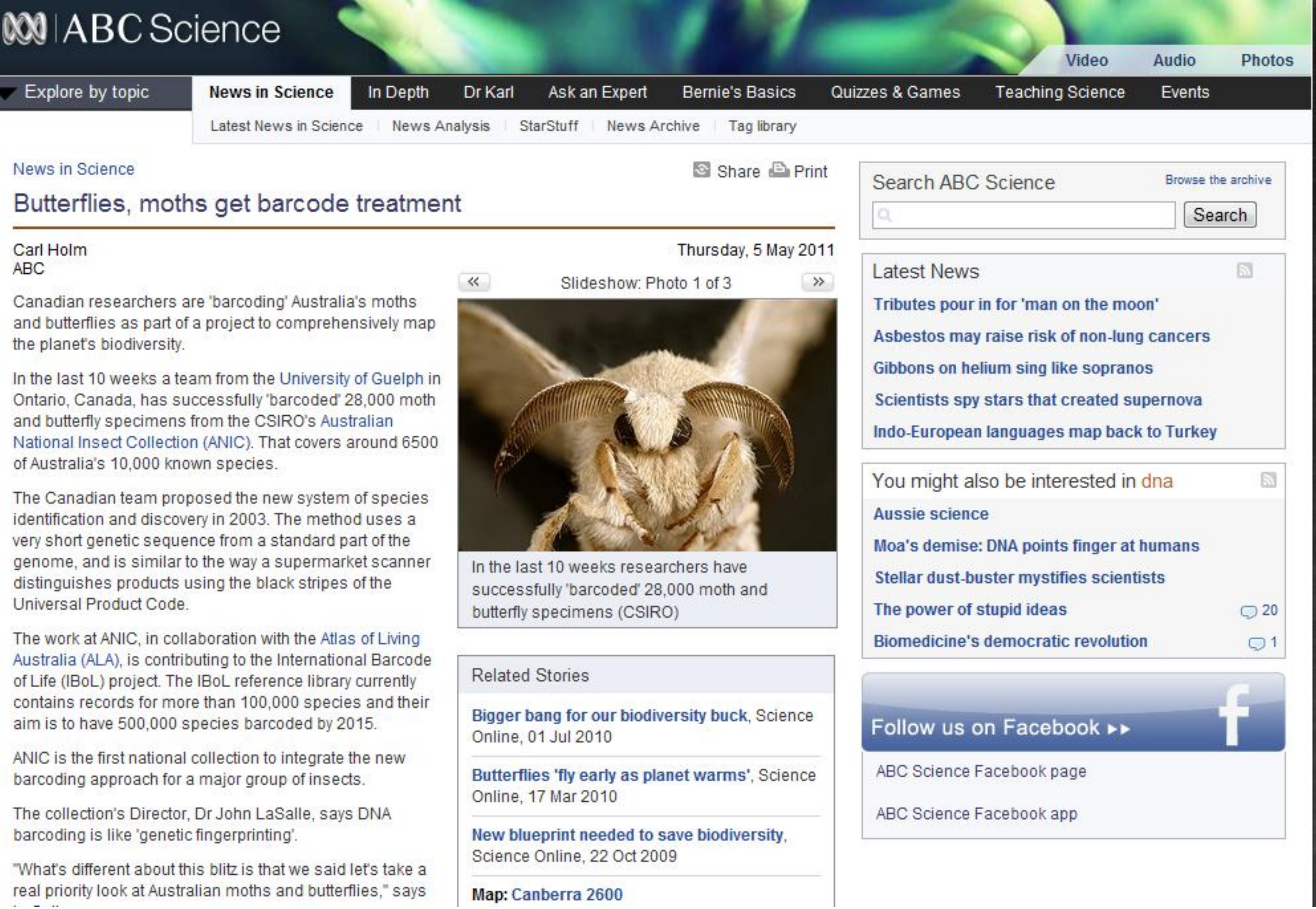
The dataset represents samples from 27 countries (Argentina, Australia, Botswana,

Brazil, Gabon, Greece, Guyana, Iceland, Johnston Atoll, Mariana Islands, Mexico,

Mongolia, Myanmar, Pakistan, Panama, Papua New Guinea, Philippines, Puerto Rico,

Russia, South Korea, St. Vincent, Swaziland, Sweden, United Kingdom, United States,

Uruguay, and the former Soviet Union).



News in Science

Butterflies, moths get barcode treatment

Carl Holm
ABC

Thursday, 5 May 2011

Canadian researchers are 'barcoding' Australia's moths and butterflies as part of a project to comprehensively map the planet's biodiversity.

In the last 10 weeks a team from the University of Guelph in Ontario, Canada, has successfully 'barcoded' 28,000 moth and butterfly specimens from the CSIRO's Australian National Insect Collection (ANIC). That covers around 6500 of Australia's 10,000 known species.

The Canadian team proposed the new system of species identification and discovery in 2003. The method uses a very short genetic sequence from a standard part of the genome, and is similar to the way a supermarket scanner distinguishes products using the black stripes of the Universal Product Code.

The work at ANIC, in collaboration with the Atlas of Living Australia (ALA), is contributing to the International Barcode of Life (IBoL) project. The IBoL reference library currently contains records for more than 100,000 species and their aim is to have 500,000 species barcoded by 2015.

ANIC is the first national collection to integrate the new barcoding approach for a major group of insects.

The collection's Director, Dr John LaSalle, says DNA barcoding is like 'genetic fingerprinting'.

"What's different about this blitz is that we said let's take a real priority look at Australian moths and butterflies," says

In the last 10 weeks researchers have successfully 'barcoded' 28,000 moth and butterfly specimens (CSIRO)

Related Stories

Bigger bang for our biodiversity buck, Science Online, 01 Jul 2010

Butterflies 'fly early as planet warms', Science Online, 17 Mar 2010

New blueprint needed to save biodiversity, Science Online, 22 Oct 2009

Map: **Canberra 2600**

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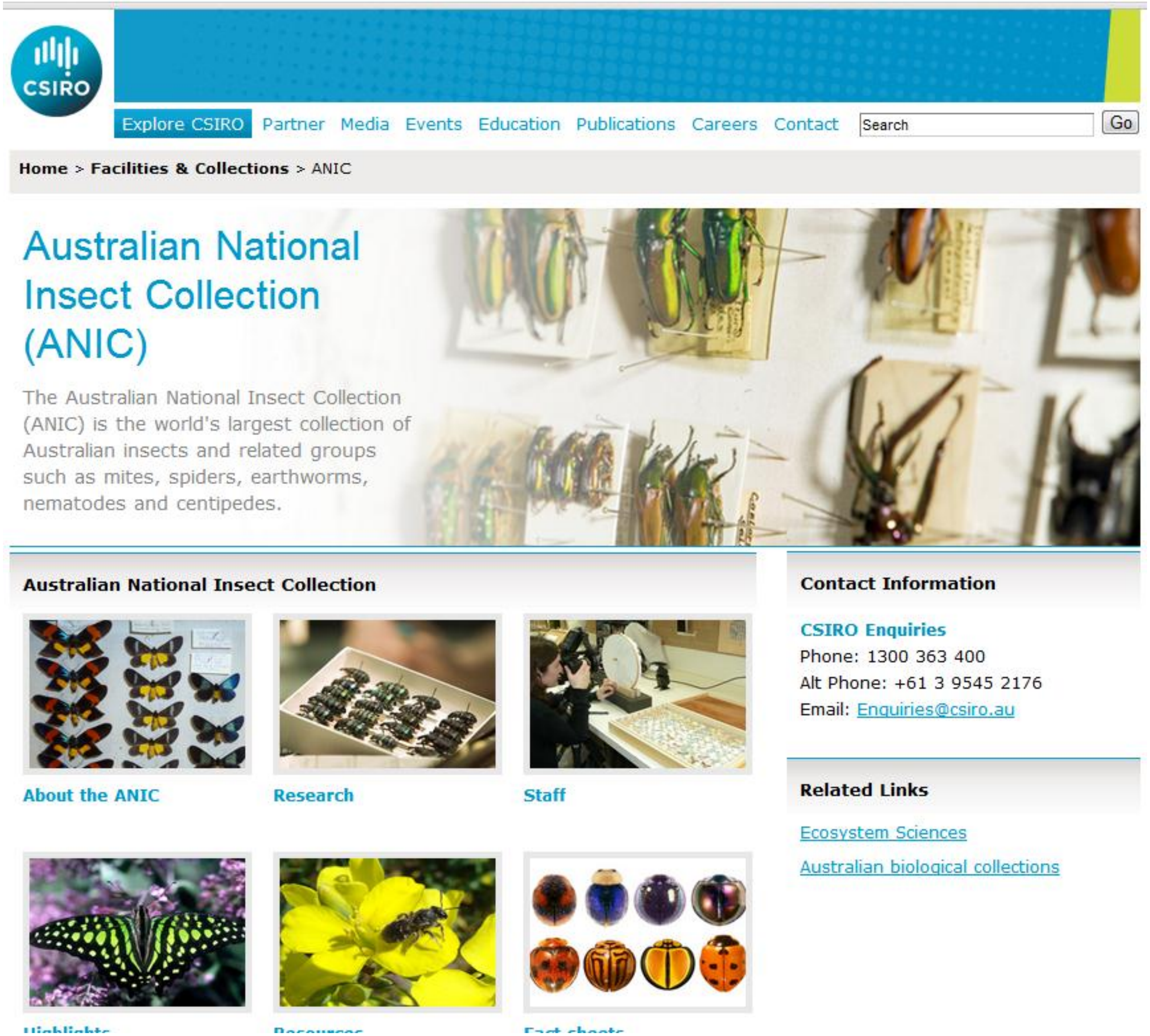

Home > **Facilities & Collections** > ANIC

Australian National Insect Collection (ANIC)

The Australian National Insect Collection (ANIC) is the world's largest collection of Australian insects and related groups such as mites, spiders, earthworms, nematodes and centipedes.

Australian National Insect Collection

About the ANIC

Research

Staff

Highlights

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Contact Information

CSIRO Enquiries
Phone: 1300 363 400
Alt Phone: +61 3 9545 2176
Email: Enquiries@csiro.au

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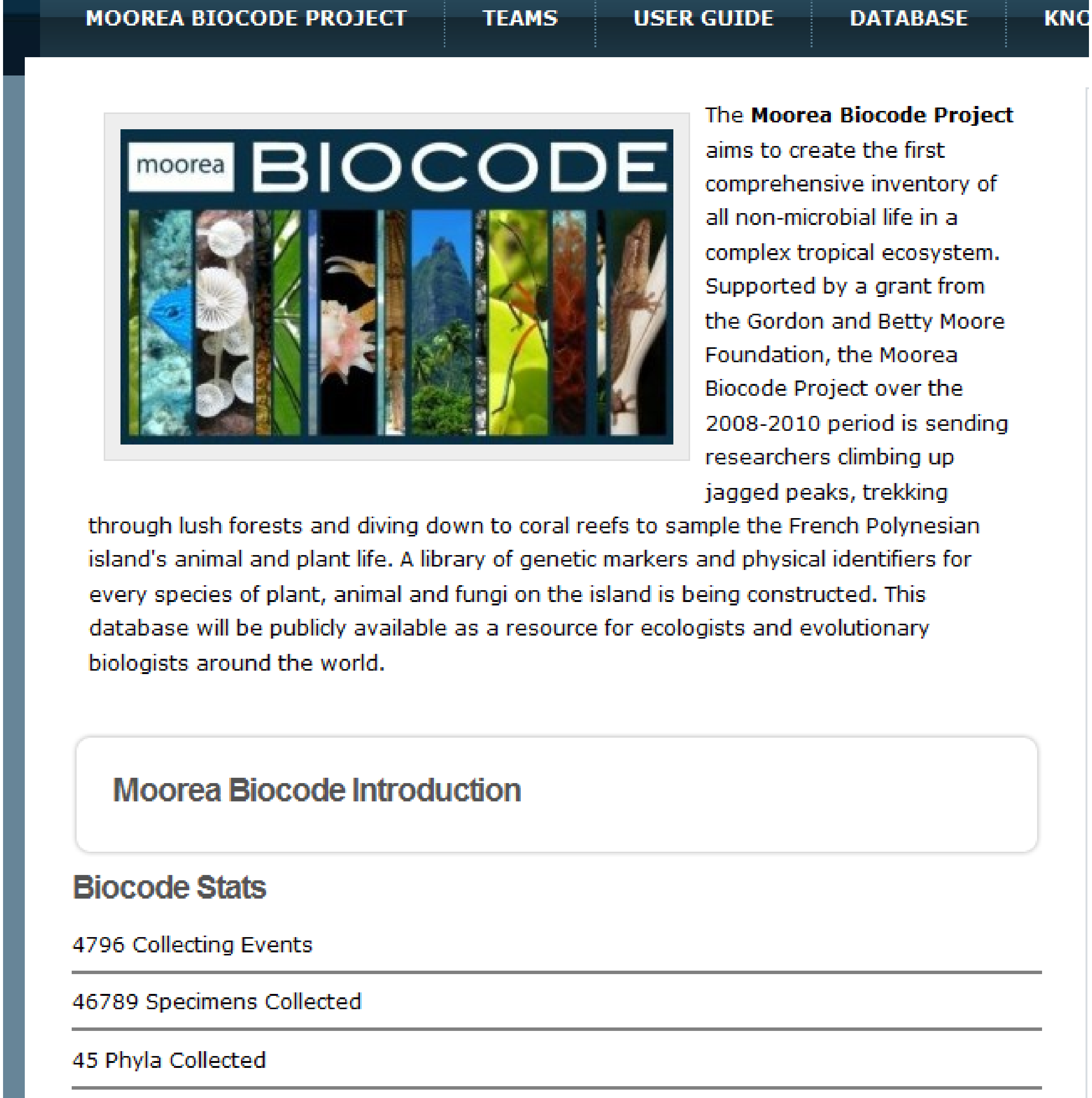
Ecosystem Sciences

Australian biological collections

Otras aplicaciones del DNA barcoding



The **Moorea Biocode Project** aims to create the first comprehensive inventory of all non-microbial life in a complex tropical ecosystem. Supported by a grant from the Gordon and Betty Moore Foundation, the Moorea Biocode Project over the 2008-2010 period is sending researchers climbing up jagged peaks, trekking through lush forests and diving down to coral reefs to sample the French Polynesian island's animal and plant life. A library of genetic markers and physical identifiers for every species of plant, animal and fungi on the island is being constructed. This database will be publicly available as a resource for ecologists and evolutionary biologists around the world.

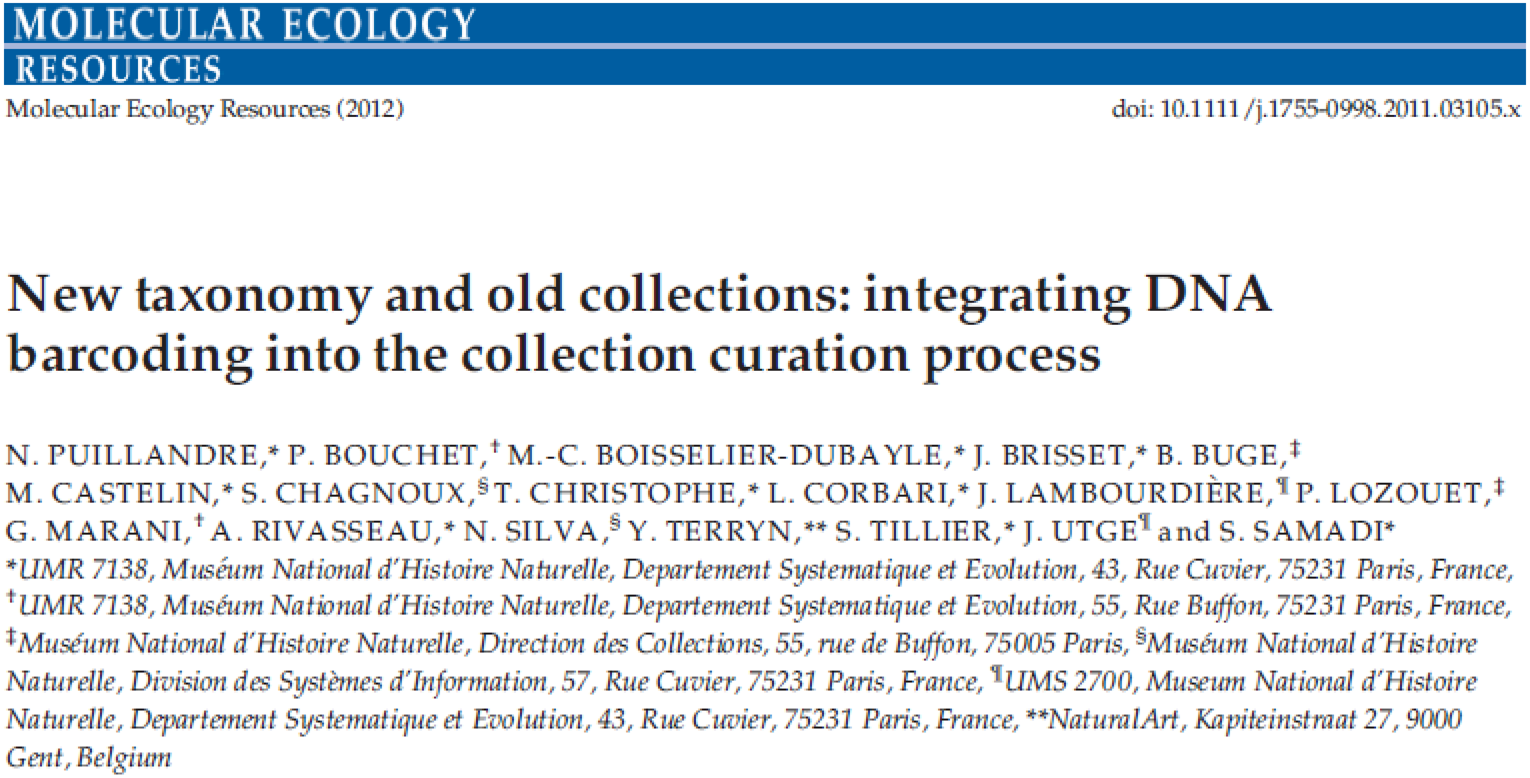
Moorea Biocode Introduction

Biocode Stats

4796 Collecting Events

46789 Specimens Collected

45 Phyla Collected



MOLECULAR ECOLOGY
RESOURCES
Molecular Ecology Resources (2012) doi: 10.1111/j.1755-0998.2011.03105.x

New taxonomy and old collections: integrating DNA barcoding into the collection curation process

N. PUILLANDRE,* P. BOUCHET,† M.-C. BOISSELIER-DUBAYLE,* J. BRISSET,* B. BUGE,‡ M. CASTELIN,* S. CHAGNOUX,§ T. CHRISTOPHE,* L. CORBARI,* J. LAMBOURDIÈRE,¶ P. LOZOUET,‡ G. MARANI,† A. RIVASSEAU,* N. SILVA,§ Y. TERRYN,** S. TILLIER,* J. UTGE¶ and S. SAMADI*
*UMR 7138, Muséum National d'Histoire Naturelle, Departement Systematique et Evolution, 43, Rue Cuvier, 75231 Paris, France, †UMR 7138, Muséum National d'Histoire Naturelle, Departement Systematique et Evolution, 55, Rue Buffon, 75231 Paris, France, ‡Muséum National d'Histoire Naturelle, Direction des Collections, 55, rue de Buffon, 75005 Paris, §Muséum National d'Histoire Naturelle, Division des Systèmes d'Information, 57, Rue Cuvier, 75231 Paris, France, ¶UMS 2700, Museum National d'Histoire Naturelle, Departement Systematique et Evolution, 43, Rue Cuvier, 75231 Paris, France, **NaturalArt, Kapiteinstraat 27, 9000 Gent, Belgium

Workflow,

Importancia de enlazar la muestra con las secuencias y los datos geograficos…..

marine barcode of life

Welcome

"... the only other place comparable to these marvelous nether regions, must surely be naked space itself, out far beyond atmosphere, between the stars, where sunlight has no grip upon the dust and rubbish of planetary air, where the blackness of space, the shining planets, comets, suns, and stars must really be closely akin to the world of life as it appears to the eyes of an awed human being, in the open ocean, one half mile down."
William Beebe, 1934.

MarBOL is an international initiative to enhance our capacity to identify marine life by utilizing DNA Barcoding a new technique for that uses a short DNA sequence from a standardized and agreed-upon position in the genome as a molecular diagnostic for species-level identification. DNA barcode sequences are very short relative to the entire genome and they can be obtained reasonably quickly and cheaply. A part of the mitochondrial gene cytochrome c oxidase subunit 1 (COI) is emerging as the standard barcode region for almost all groups of higher animals. This fragment is 648 nucleotide base pairs long in most groups and is flanked by regions of conserved sequences, making it relatively easy to amplify and analyze. A number of studies have shown that the barcode sequence variability is very low within species (generally less than 1-2%) and that the COI sequences of even closely related species differ by several percent, making it possible to identify species with high confidence.

MarBOL is a joint effort of the Consortium for the Barcode of Life (CBOL) and the Census of Marine Life (CoML). CoML is a global

progress

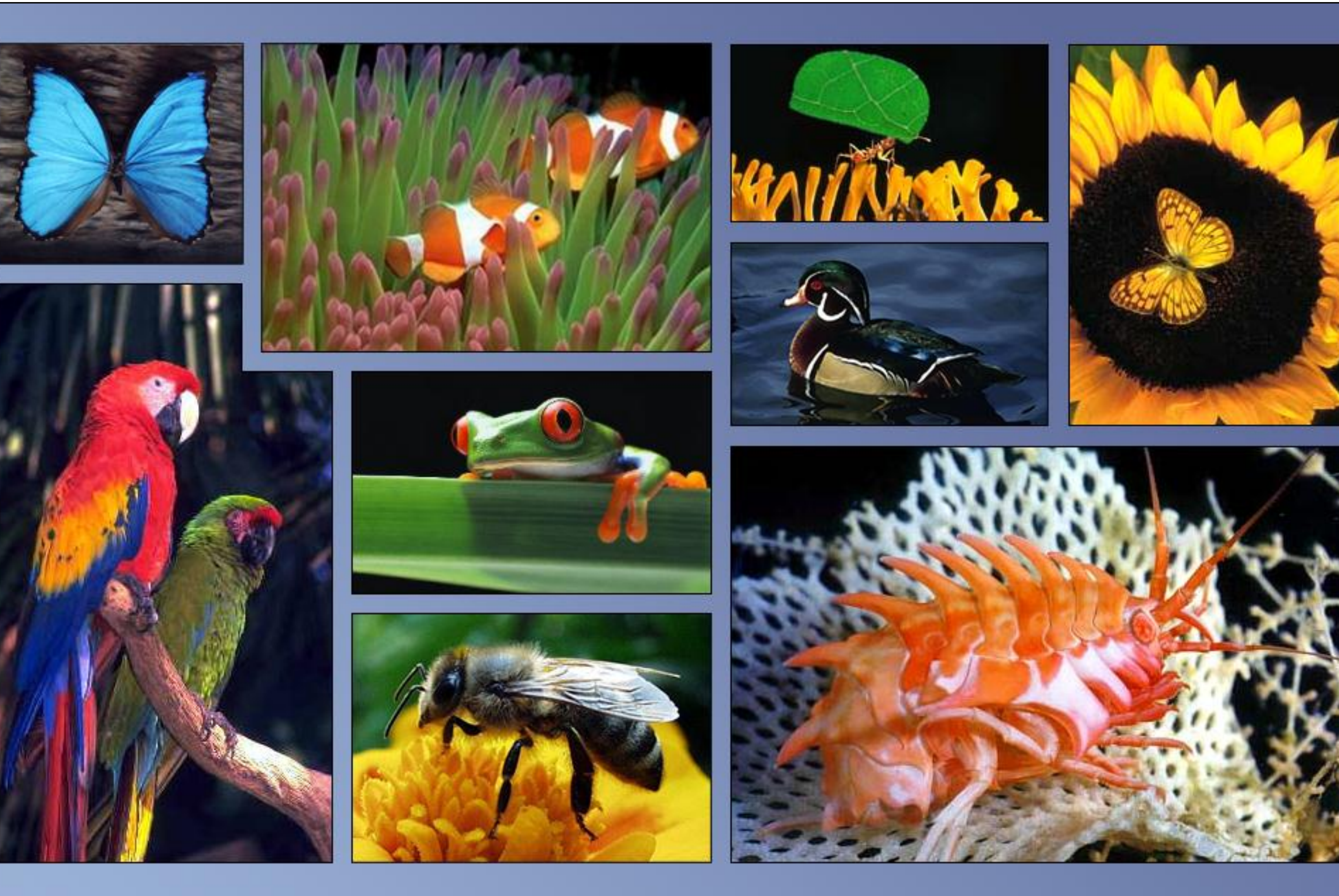
specimens barcoded
37182

species barcoded
6199

View detailed progress reports

explore MarBOL

…iBOL Colombia !



…iBOL Colombia !

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