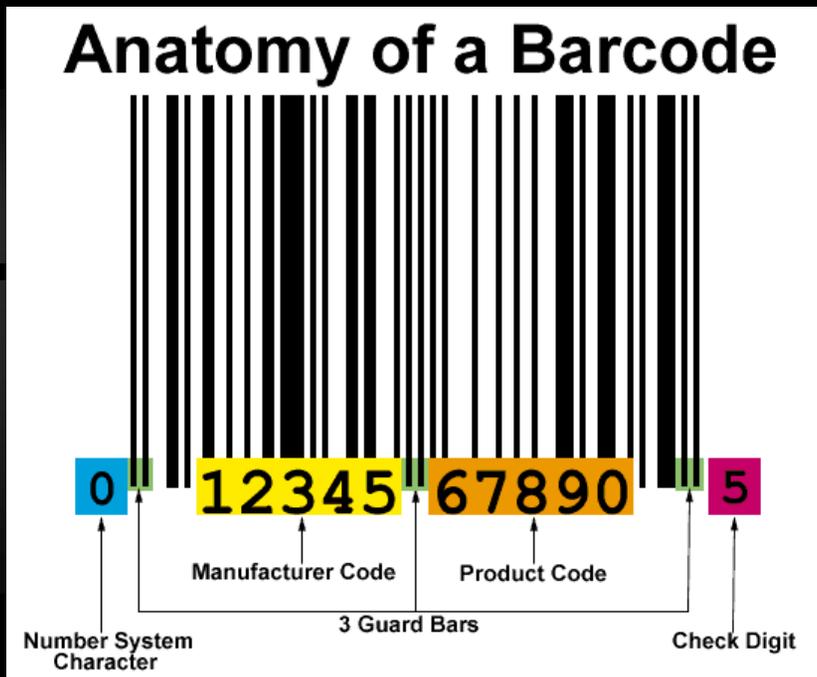


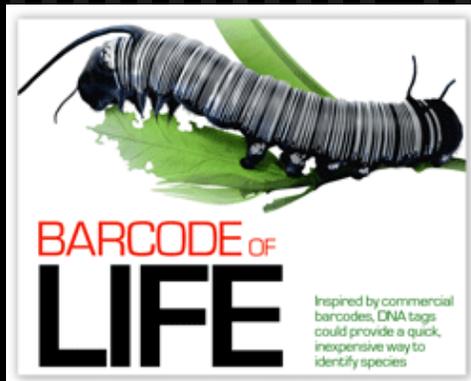
Red Temática del Código de Barras de la Vida en México



Analogía con el código de barras del supermercado



¿Marcador molecular en el ADN que se pueda leer como un código de barras?



http://www.boldsystems.org - BOLD Systems - Sequence Record - Microsoft Internet Explorer

COI5'

Marker : COI5' GenBank Accession :
Last Updated : 2007-10-29 Translation Matrix : Vertebrate Mitochondrial

Sequencing Runs

	Run Date	Direction	Trace File	PCR primers	Seq Primer	Marker	Status
<input type="checkbox"/>	2007-06-20 12:04:59	Reverse	BOM146-07-R1_1.ab1	BirdF1/COIbirdR2	COIbirdR2	COI5'	med qual
<input type="checkbox"/>	2007-06-20 10:17:12	Forward	BOM146-07-F1_1.ab1	BirdF1/COIbirdR2	BirdF1	COI5'	high qual

Nucleotide Sequence

Residues : 651
Comp. A : 173
Comp. G : 102
Comp. C : 208
Comp. T : 168
Ambiguous : 0

CCCTAAGCCTCCTTATCGGAGCAGAAGTAGGCCAACCTGGAGCCCTTCTAGGAGACGATCAAGTTTATAAAGTAG
TTGTCACGGCCATGCTTCTGTAATAATCTTCTCATAGCTATACCAATTATAATCGGAGATTGGAAGACTGAC
TAGTTCCTTAATAATCGGAGCCCTGACATAGCAATCCACGAATAAACACATAAGCTTCTGACTACTCCAC
CATCATTTCTCCTCTACTAGCATCTCCACAGTTGAAGCAGGTGATGGCAGGGCTGAACAGTGTACCTCCAC
TAGCAGGCAACCTAGCTACGCCGGAGCCTCACTGACCTTSCAACTTCTCCCTACATCTAGCCGGTATCTTT
CAATCTAGGGCAATCAATTTTATACAAACAGCAATCAACATGAAACCCCTGCCCTCTCACAAATACCAACC
CCCTATTCTTTGATCGTACTGATCAGTCTCTATTACTTCTATCTCTCCAGTCTCCCTGACAGGAATCA
CAATACTTCTACAGACCGCAACCTTAACACCAATTTCTTGTATCTGCCGGAGGAGGAGCCCGTACTATACC
AACACTTGTTGATTTTGGCCACCAGAACTCATACCTAATCTCTC

Identify Sequence Using : Full Database Species Database Ref Database

Amino Acid Sequence

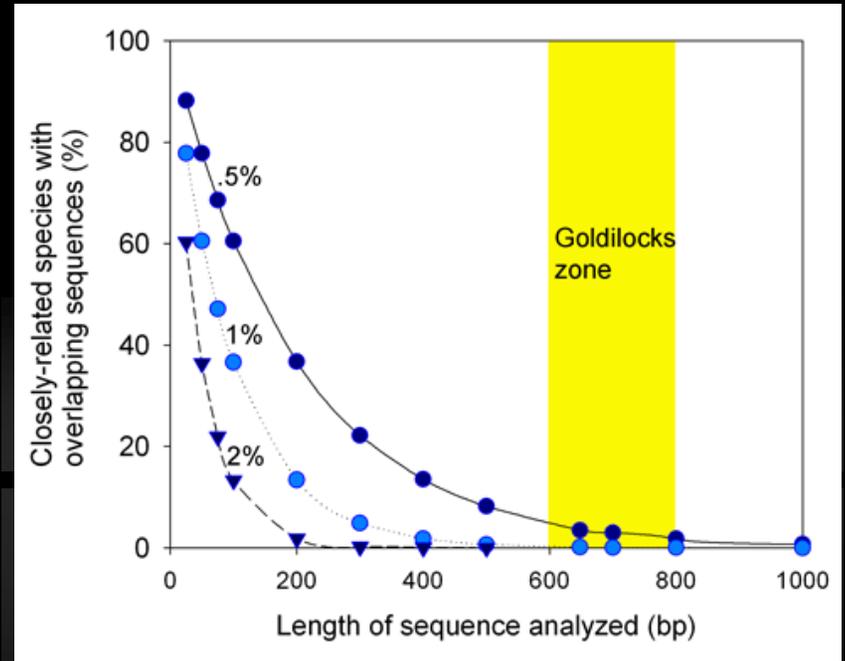
Residues : 233

----->XLSLLRAELGQPGALLGDDQVYNVVVTAHAFVMIFFMVMPEIMIGGFGNWLPLMIGAPD
MAFPRDNNMSFULLPPSFLLLASSTVEACVCTGTVYYPPLAGNLAHAGASVDLAIPLHLGAGISSILGAINFIT
TAINMKPPALSOYQTPLFVWSVLITAVLLLSLPLVLAAGITMILLDRNLMTFFDPAGGGDPVLYQHLFWFFGHP
EVIYLILX

Illustrative Barcode

Se requería:

- ✓ Seleccionar una región del genoma única cuya variabilidad diera información suficiente para la identificación de cualquier especie de eucarionte



Se selecciona y hacen pruebas en un fragmento de 650 pb del gen CO1 mitocondrial

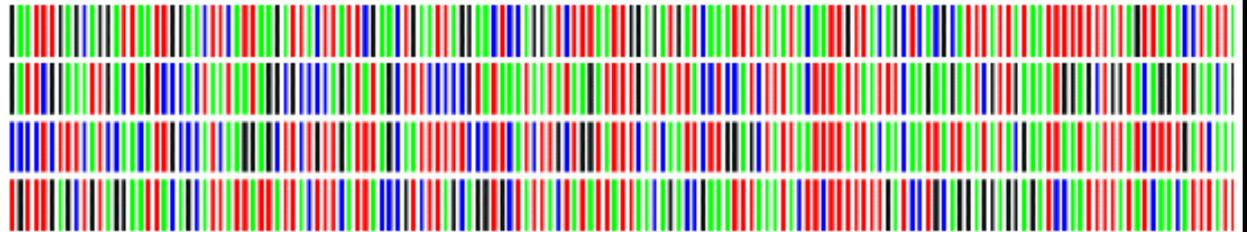
Se propone usar CO1, marcador el ADN mitocondrial ampliamente usado en insectos (para plantas se tiene que usar un par de marcadores diferente)

Biological identifications through DNA barcodes

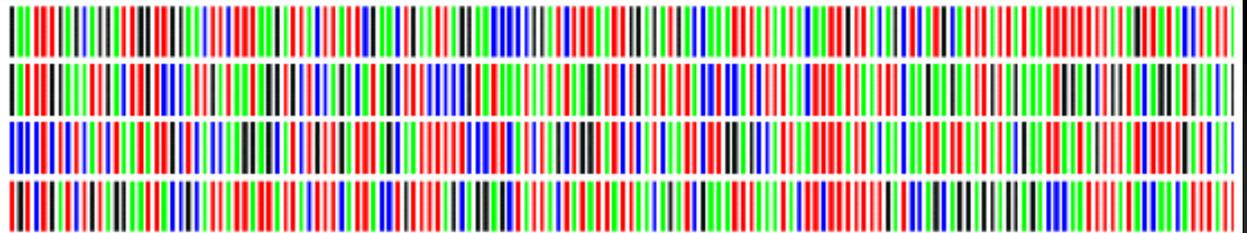
Paul D. N. Hebert*, Alina Cywinska, Shelley L. Ball
and Jeremy R. deWaard

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

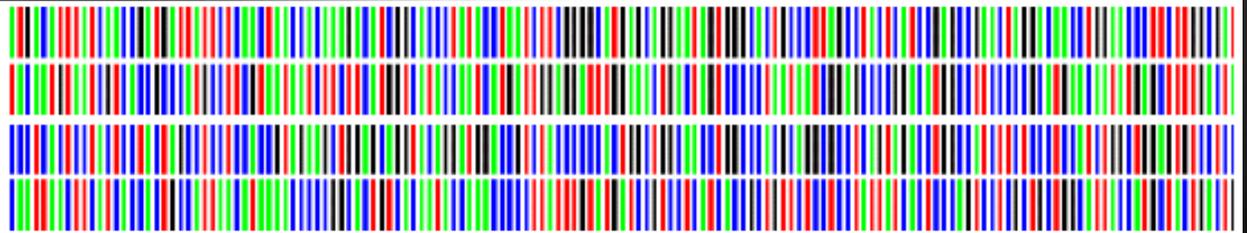
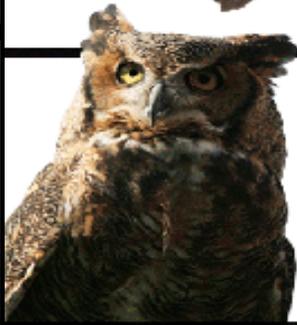
Although much biological research depends upon species diagnoses, taxonomic expertise is collapsing. We are convinced that the sole prospect for a sustainable identification capability lies in the construction of systems that employ DNA sequences as taxon 'barcodes'. We establish that the mitochondrial gene cytochrome *c* oxidase I (COI) can serve as the core of a global bioidentification system for animals. First, we demonstrate that COI profiles, derived from the low-density sampling of higher taxonomic categories, ordinarily assign newly analysed taxa to the appropriate phylum or order. Second, we demonstrate that species-level assignments can be obtained by creating comprehensive COI profiles. A model COI profile, based upon the analysis of a single individual from each of 200 closely allied species of lepidopterans, was 100% successful in correctly identifying subsequent specimens. When fully developed, a COI identification system will provide a reliable, cost-effective and accessible solution to the current problem of species identification. Its assembly will also generate important new insights into the diversification of life and the rules of molecular evolution.



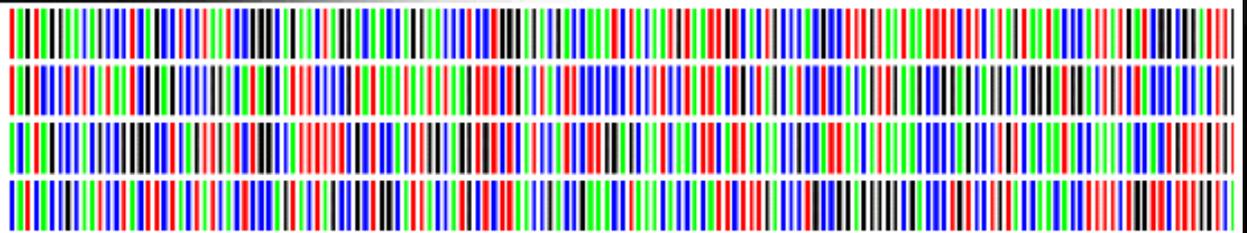
Astraptes fulgerator CELT



Astraptes fulgerator TRIGO



Bubo virginianus



Tyto alba

Se forma un Consorcio para promover y discutir la idea



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Tring

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[News](#)

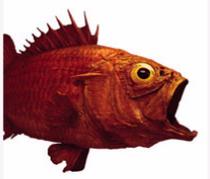
[Archives 2005](#)

First steps to barcode all life

10 February 2005

The first step towards genetically identifying, or barcoding, every species on Earth has been taken at the International Conference for the Barcoding of Life, held on 10 February 2005.

The conference, hosted by the Natural History Museum on behalf of the Consortium for the Barcode of Life (CBOL), brought together many experts in plant and animal taxonomy, forensic sequencing, environmental genomics, information management, and other related fields.



DNA Barcoding:

A New Tool for Identifying Biological Specimens and Managing Species Diversity



BARCODING LIFE

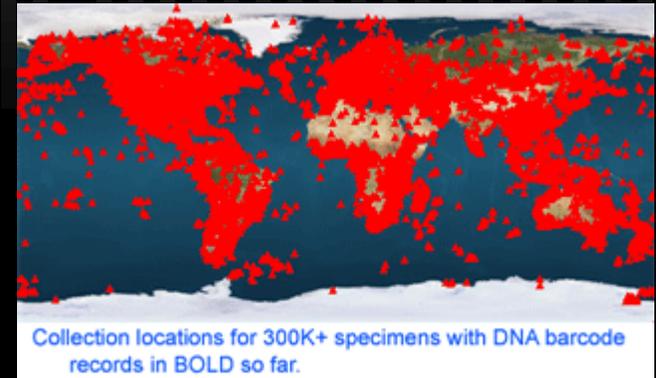
TAKES FLIGHT

ALL BIRDS BARCODING INITIATIVE
Needs and Resources Statement
version 1.1 19 July 2005

Mark Stoeckle, The Rockefeller University



Se identifican a las colecciones de los museos de historia natural como jugadores clave en el proyecto



Se empieza a difundir ampliamente el proyecto en revistas, internet y en la prensa para conseguir la participación de los expertos, el interés de los usuarios y el apoyo de la sociedad



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Feature
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?

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Cover Story
DEMOCRATIZING TAXONOMY



THE TIMES THURSDAY FEBRUARY 10 2005

**Is it a bird?
Is it a plant?
Hang on, I'll
check its
barcode ...**

Scott Miller, of the Smithsonian Institution, unveils plans to catalogue organisms' DNA barcodes

... would be able to drop an insect from the garden into the device and identify the species immediately.

When the organism is snatched, as with an insect or small plant, it could be placed into the device whole before DNA is extracted and tested. For larger species, a hair or a few drops of blood could be used instead.

The ambitious project, which was announced yesterday at a conference at the Natural History Museum in London, will begin with initiatives to barcode the world's species of fish, of which there are estimated to be 23,000, and birds, which are estimated to number 10,000. A parallel project is embarking on the more difficult task of bar-

coding plants, starting with flora native to Costa Rica.

Genetic barcodes are short sequences of DNA, taken from a portion of a single gene that vary sufficiently between species to provide a snapshot of its genome as a whole. Differences in this short sequence are unique to a single species in 98 per cent of cases, and in the remaining 2 per cent the differences can narrow identification to two or three close relatives.

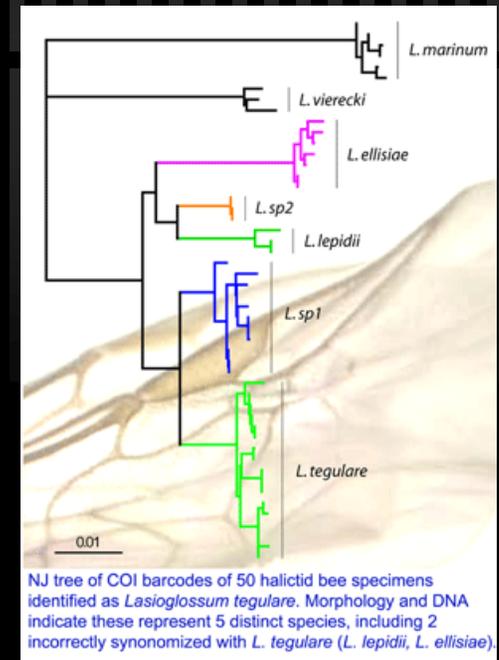
This provides a quick and powerful means of recognising species that often look so similar that even the eye of a specialist struggles to tell them apart. At present, difficult specifications rely on sending specimens to an expert for

detailed analysis, a process that can take up to a year.

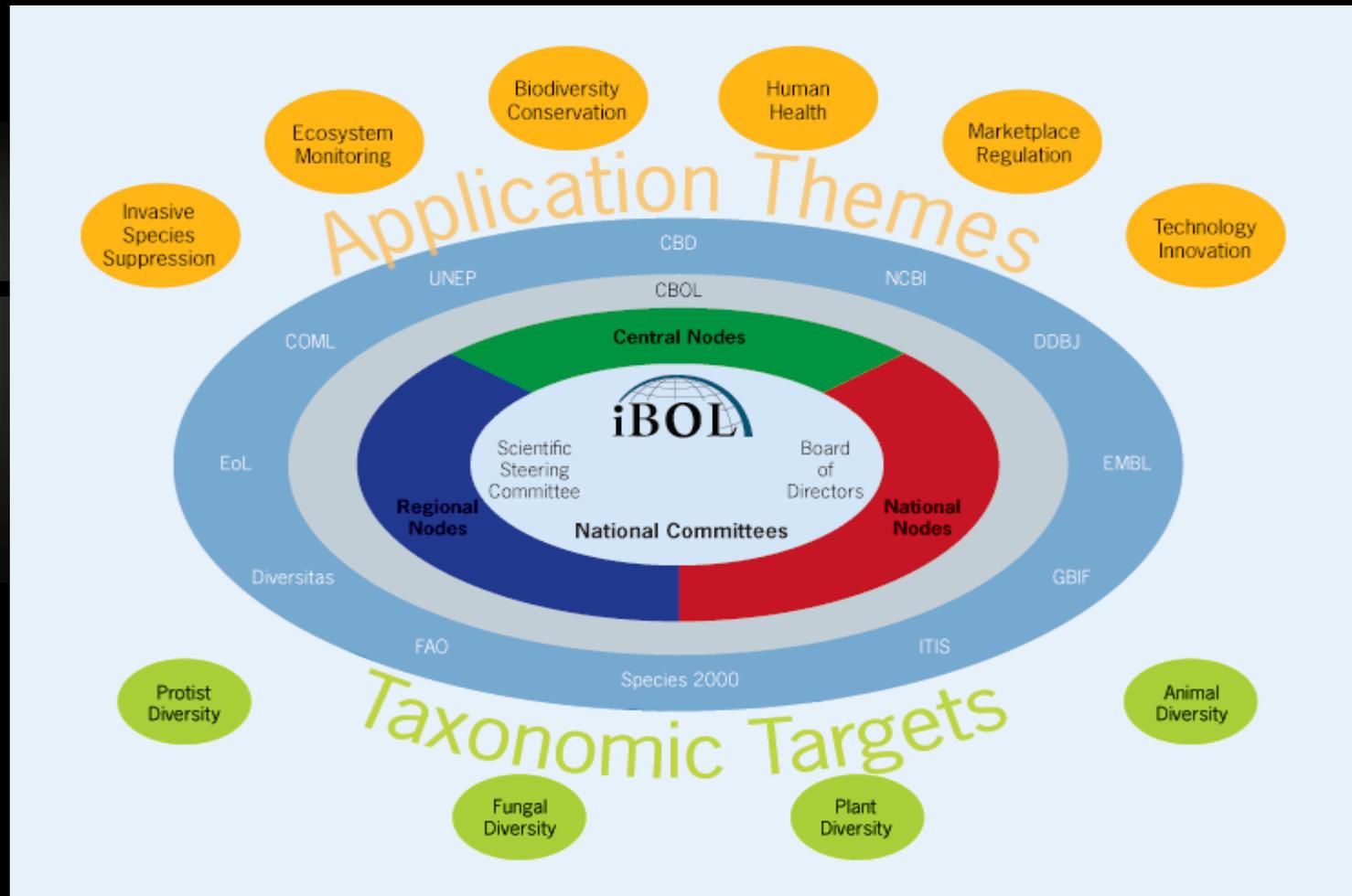
Richard Lane, the director of science at the Natural History Museum, said that the resource will preserve a record of world biodiversity and help scientists to determine how quickly species are disappearing.

"If we don't know what species we have, how can we know what we're losing, and take practical steps to stem the loss of the world's plants and animals?" Dr Lane asked.

Paul Hackett, of the University of Guelph in Ontario, Canada, one of the project's chief architects, said that a barcode costs about £3 to produce at present, but is likely to cost less in future.



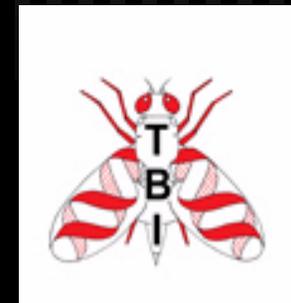
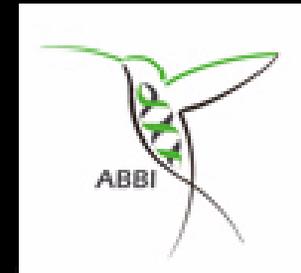
Se requiere construir una amplia alianza científica internacional para ensamblar una amplia base de datos para consulta de los códigos de barras de la vida



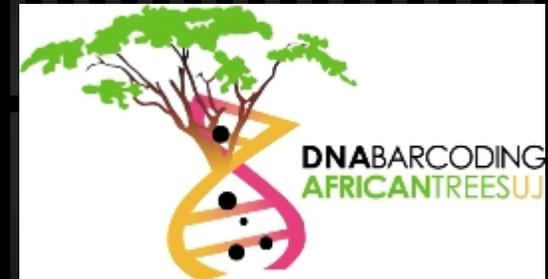
Se inician y están en marcha varias campañas,



por grupo taxonómico:



y por región geográfica:



Se pretenden desarrollos tecnológicos que ayuden a la identificación cuasi-instantánea *in situ* mediante la consulta remota a la base de datos

BARCODE OF LIFE DATA SYSTEMS
 Advancing species identification and discovery through the analysis of short, standardized gene regions

SEARCH

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Published Projects | Taxonomy Browser | Request an Account | Identify Specimen | Introductory Tutorial | Documentation | Citation

The Barcode of Life Data Systems (BOLD) is an online workbench that aids collection, management, analysis, and use of DNA barcodes. It consists of 3 components (MAS, IDS, and ECS) that each address the needs of various groups in the barcoding community.

MANAGEMENT & ANALYSIS

BOLD-MAS provides a repository for barcode records coupled with analytical tools. It serves as an online workbench for the DNA barcode community.

Username
 Password
[Request a new user account](#)

IDENTIFICATION ENGINE

BOLD-IDS provides a species identification tool that accepts DNA sequences from the barcode region and returns a taxonomic assignment to the species level when possible.

EXTERNAL CONNECTIVITY

BOLD-ECS provides web developers and bioinformaticians the ability to build tools and workflows that can be integrated with the BOLD framework. We welcome the addition of new analytical modules.

BARCODE COUNTS

Formally Described Species With Barcodes	50,559
Total Barcode Records	536,377
Source	Breakdown
GenBank	68,087
Canadian Centre	428,767
Others	39,523

SYSTEM UPDATES

Sept-23-2008 - **Merging Private Data with Public Projects (MAS)**
 The Project List page now displays all public projects as a distinct part of a user's access list. Users can view, merge, and analyze this data along with their own.

Aug-8-2008 - **Performance Upgrade (MAS)**
 The BOLD data access modules have been upgraded to be more efficient and caching mechanisms have been integrated to improve user experience.

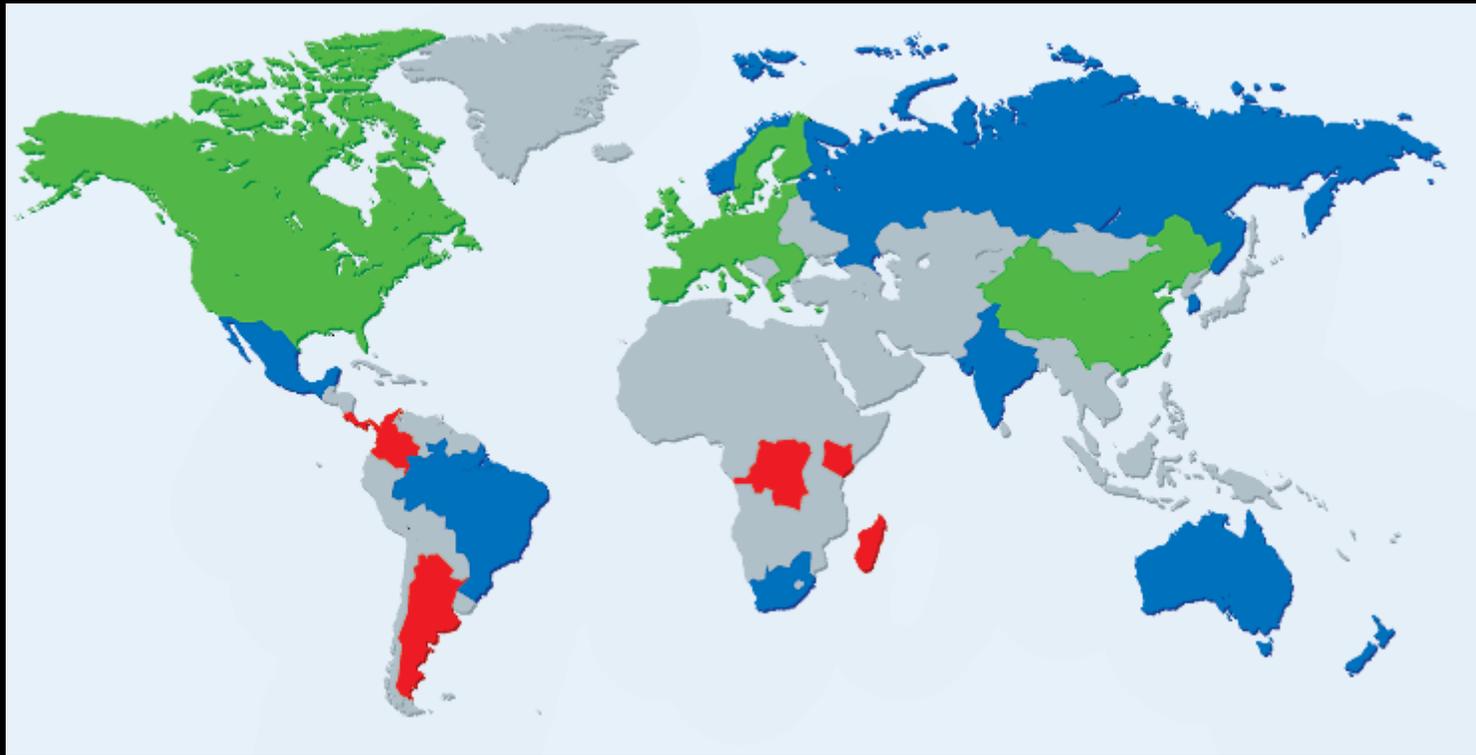
Apr-30-2008 - **Primer Registry Interface (MAS)**
 A primer registry is now available from both the Project List page and the Project Console. The registry allows users to access and get information on all publicly available primers. A new form has been added to allow users to modify and maintain their own registered primers.

Mar-2-2008 - **BOLD Integration with LIMS (MAS)**
 BOLD users that make use of our standard Laboratory Information Management System (LIMS) now have access to LIMS progress reports and audit trails directly from the specimen page of a record. Gel electrophoresis images are also available for each sample through this interface.

Jan-12-2007 - **Support for ITS Marker (MAS & IDS)**
 BOLD now supports the storage and limited analysis of records utilizing ITS as a barcode marker. Selection of ITS as the primary marker when instantiating a project activates features specific to non-coding markers. A separate ID engine has been incorporated into BOLD to support the identification of ITS barcode markers. BLAST is utilized to generate a list of high scoring matches to query sequences. Due the difficulty in aligning ITS, treeing of results have been deactivated for this pipeline.



En 2008, México decide subir su nivel de participación de nodo nacional a nodo regional



Con el apoyo de CONACYT se forma el Comité de la Red Temática del Código de Barras de la Vida en México (MEXBOL)

Instituciones participantes inicialmente:

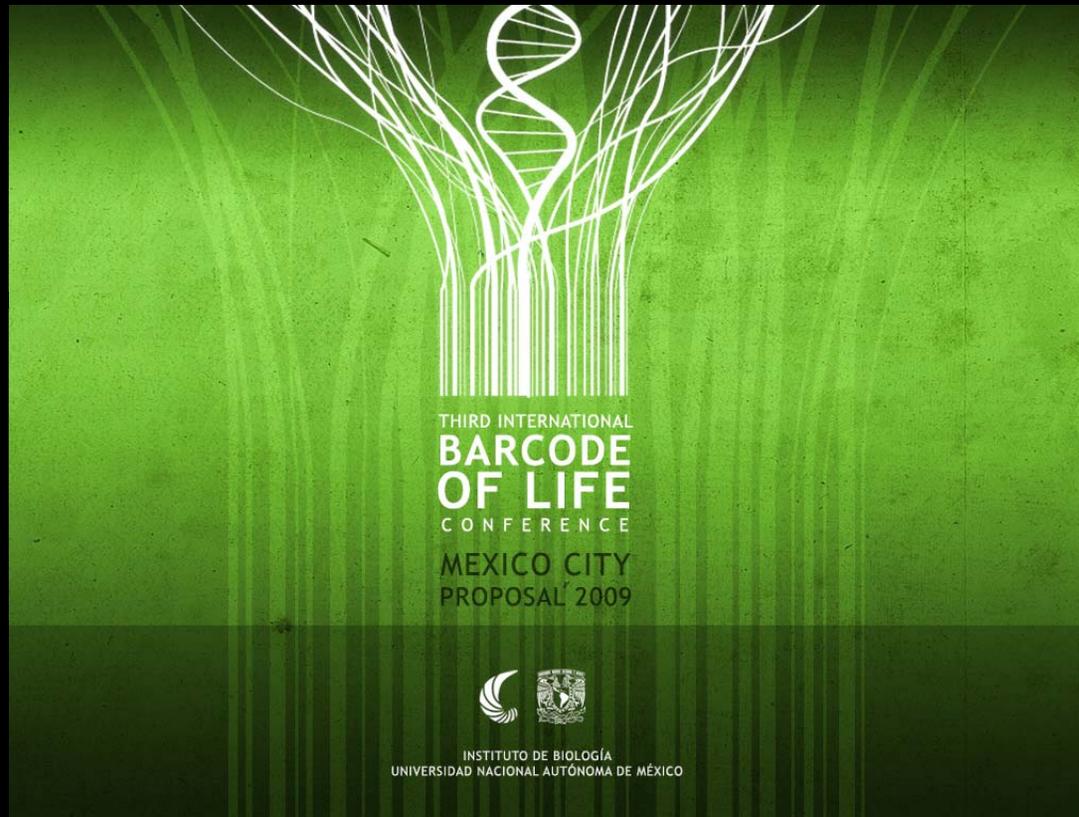


El plan de trabajo actual incluye eventos para el lanzamiento de la Red:

- Simposio, 2 de marzo, Auditorio UNIVERSUM
- Talleres de especialistas y estudiantes en cada sede académica: 3-10 marzo

y el inicio del montaje de 3 laboratorios de servicio

Adicionalmente, el Instituto de Biología presentó una propuesta para traer la sede de la 3ª Conferencia Internacional a México



El Código de Barras de la Vida en México

Simposio de Presentación de la Red Temática del CONACYT



Lunes 2 de marzo, 4:30 pm
Auditorio del Museo UNIVERSUM
Circuito Cultural de Ciudad Universitaria
México, D.F.
canal.dgscu.unam.mx/

Programa

- 4:30 Palabras de bienvenida**
Dra. Tila María Pérez Ortiz
Directora del Instituto de Biología de la UNAM
- 4:40 Presentación de las Redes Temáticas del CONACYT**
Dr. José Antonio de la Peña
Director Adjunto de Desarrollo Científico y Académico, CONACYT
- 4:55 Conferencia Inaugural**
Dr. José Sarukhán Kermez
Coordinador Nacional de la Comisión Nacional para el Conocimiento y Uso de la Biodiversidad
- 5:40 Red Temática del Código de Barras de la Vida en México (MEXBOL)**
Dr. Manuel Elías
El Colegio de la Frontera Sur
Dra. Patricia Escalante
Instituto de Biología de la UNAM
Dr. Sergio Ticul Álvarez Castañeda
Centro de Investigaciones Biológicas del Noroeste
Ing. Raúl Jiménez Rosenberg
Director General de Bioinformática de la Comisión Nacional para el Conocimiento y Uso de la Biodiversidad
- 6:25 Conferencia del Sector Empresarial**
Dr. Jorge Paniagua
Laboratorios Silanes
- 6:45 Conferencia de Clausura**
Dr. Paul Hebert
Universidad de Guelph, Canadá
- 7:30 Brindis**

Talleres en los nodos académicos de la Red Temática MEXBOL

Martes 3 de marzo

Taller en la sede del IBUNAM
Auditorio del Jardín Botánico
del Instituto de Biología de la UNAM

5-6 de marzo

Taller en la sede del Centro de Investigaciones Biológicas del Noroeste (CIBNOR)
La Paz, Baja California Sur

9 - 10 de marzo

Taller en la sede de El Colegio de la Frontera Sur (ECOSUR), Chetumal, Quintana Roo



Informes:
E-mail: tilmatura@ibiologia.unam.mx

Diseño: B.G. Julio César Herrera Rojas, Fotografía: Dr. Carmelo Sánchez Hernández





EL C Ó D I G O D E B A R R A S D E L A V I D A - M É X I C O



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