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*

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Fine-scale phylogenetic architecture of a complex bacterial community

Silvia G. Acinas¹*, Vanja Klepac-Ceraj¹*, Dana E. Hunt¹,
Chanathip Pharino¹, Ivica Ceraj², Daniel L. Distel³ & Martin F. Polz¹
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‡
Welcome to NCBI

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A portal to clinical genetics resources with detailed information about genetic tests and laboratories.
Códigos de barras de ADN: Contexto histórico

$cox1 \rightarrow$ código de barras en animales
Códigos de barras de ADN:
Definición
“Identificador Universal”
Utilización de una región génica Estándar
Códigos de barras de ADN:
Definición

“Identificador Universal”

Variabilidad intraespecífica < Variabilidad interespecífica
El ADN como herramienta taxonómica

Catálogo morfológico de especies

Catálogo molecular de especies

** Identificar especies previamente descritas

** Descubrir nuevas especies
Catálogo de códigos de barras de ADN
Global access to knowledge about life on Earth
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
Divergencia del 2% para diferenciar entre las especies

El gen *cox1* ha permitido una identificación acertada de >95% de las especies de pájaros (*Hebert et al.* 2003, 2004)
KEYNOTE ARTICLE

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

DANIEL H. JANZEN¹, WINNIE HALLWACHS¹, PATRICK BLANDIN², JOHN M. BURNS², 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 Hallwachs⁸

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...Otras aplicaciones del código de barras ADN
Identification of poisonous plants by DNA barcoding approach

Ilaria Bruni · Fabrizio De Mattia · Andrea Galimberti · Gabrielle Galasso · Errico Banti · Maurizio Casiraghi · Massimo Labra

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Abstract The plant exposures are one of the most frequent poisonings reported to control poisons 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 (trnL-trnF, rps16 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 assessment 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 trnL-trnF agreement with CBOL Plant Working Group matK as the best marker, because trnL-trnF problems in sequences sizes and alignments. Relevant observation, we also propose the c matK with a nuclear marker such as At103 to hybrid form parental species. In conclusion, the claim that DNA barcoding is a powerful tool plant identifications.

Keywords DNA barcoding · Poisonous plant · trnL-trnF · At103 · sqd1

Introduction

The human diet includes a lot of domesticates (for instance Hordeum vulgare L., Zea mays L., etc.) derived from an evolutionary people-plants interactions, leading to plants cultivar easy cultivation and deterioration.

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 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 common adulterants and substitutes are also listed. This database provides a web-based platform for storage.

Applications on taxonomy and identification

Taxonomy

Aplicaciones del código de barras ADN


Utilización de Minibarcodes y metabarcoding
Neotropical Bats: Estimating Species Diversity with DNA Barcodes

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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 to estimate past evolutionary processes. Despite numerous past demonstrations of the efficiency and potential for using DNA barcodes with Neotropical bats (order Chiroptera). This represents one group and is certainly the largest to date for land vertebrates. Geographic distances and across extraordinarily diverse geographic regions making them easily recognizable. Intraspecific diversity in the region was high (11.79%) with respect to birds, though comparable to other lineages identified which may suggest interspecific divergence were not good predictors of the investigation using complementary molecular technique data. Our analysis provides strong support for the continuing investigation of bats.

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 mean: 3.29% R, 2.19–6.52%) and likely low divergence. In contrast, three genera contained a species pair or triad that lacked barcode divergence, which is indicative of young taxa or taxonomic over-splitting.

Conclusions/Significance: Although incomplete, this barcode library already provides a valuable tool for the ornamental fish industry, opening a realm of applications linked to species 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. Holmes¹, Dirk Steinke¹, Robert D. Ward¹,²

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METHODOLOGY ARTICLE

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

Sara Botti, Elisabetta Giuffrè

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 methodologies to detect mitochondrial DNA polymorphisms in complex matrices such as foods. The reported
Barcoding bushmeat: molecular identification of Central African and South American harvested vertebrates

Mitchell J. Eaton · Greta L. Meyers · Samia Qasim · Kalahatogou · Martin Schaffner
** Identificar especies previamente descritas
** Descubrir nuevas especies
Catálogo de códigos de barras de ADN

Especimen
Datos colecta
Muestra tejido
Fotografía
ADN
Amplificación PCR
Secuenciación
Códigos de barras de ADN (secuencias + cromatogramas)
Iniciativas internacionales

CBOL

Bee-BOL

All Birds Barcoding Initiative

FISH-BOL

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. Sonet¹, F. C. Breman², G. Lenglet³, M. Louette⁴, G. Montañés³, Z. T. Nagy¹, J. van Houdt², & E. Verheyen³
Project Description: DNA Barcodes of Bird Species in the National Museum of Natural History, Smithsonian Institution, USA

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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).
Butterflies, moths get barcode treatment

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

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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*
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Gent, Belgium

Workflow,
Importancia de enlazar la muestra con las secuencias y los datos geográficos.....
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.
...iBOL Colombia!
...iBOL Colombia!