

El papel de las colecciones de historia natural en los estudios moleculares

María P. Martín

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Método Científico

Mycol Progress (2010) 9:585–596
DOI 10.1007/s11557-010-0666-5

ORIGINAL ARTICLE

Morphological and molecular studies of *Hyphodermella* in the Western Mediterranean area

M. Teresa Telleria · Margarita Dueñas · Ireneia Melo ·
María P. Martín

Mycologia, 102(6), 2010, pp. 1426–1436. DOI: 10.3852/09-242
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A re-evaluation of *Hypochnicium* (Polyporales) based on morphological and molecular characters

doi:10.5598/mafungus.2013.04.01.03

IMA FUNGUS · VOLUME 4 · NO 1: 21–28

Molecular analyses confirm *Brevicellicium* in *Trechisporales*

M. Teresa Telleria¹, Ireneia Melo², Margarita Dueñas¹, Karl-Henrik Larsson³, and María P. Paz Martín¹

¹Real Jardín Botánico (RJB-CSIC), Plaza de Murillo 2, 28014 Madrid, Spain; corresponding author e-mail: telleria@rjb.csic.es

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³Natural History Museum, University of Oslo, P.O. Box 1172 Blindern, 0318 Oslo, Norway



Método Científico

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Contact Information :

Contact Person : Dr. Margarita Dueñas, Curator of Cryptogams

E-mail : mduenas@rjb.csic.es

Phone : [34] 91/ 420 3017.

Fax : [34] 91/ 420 0157.

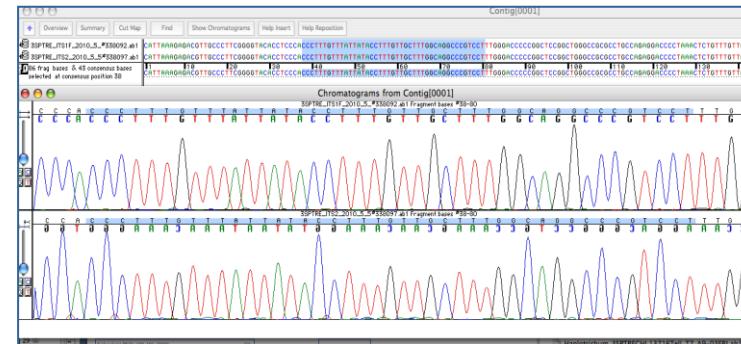
URL :



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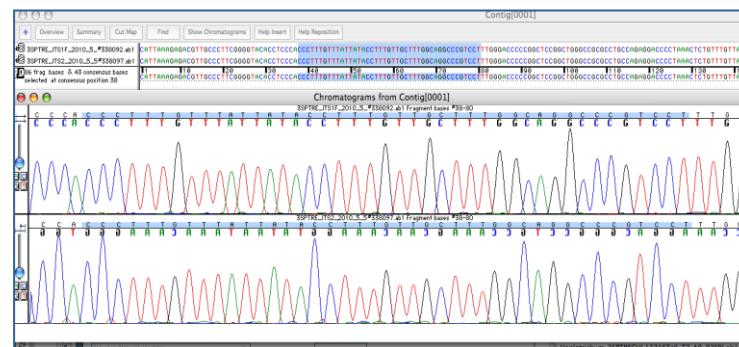


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Barcoding of Life

Método Científico



Especie 1

?

Especie 2

GGATGGTATCGTGGCTCCGGTGTGCGCGTGTCAAGGTGAAGATATCATCATCGGCAAGACTGCGCCGATTGATCAAGAGAACCGAGATCTGGGTACCAAGGAC
GGATGGTATCGTGGCTCCGGTGTGCGCGTGTCAAGGTGAAGATATCATCATCGGCAAGACTGCGCCGATTGATCAAGAGAACCGAGATCTGGGTACCAAGGAC
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pero, se ¿pueden verificar todos los estudios moleculares publicados?

2008

Molecular Phylogenetics and Evolution 48 (2008) 369–371



Contents lists available at ScienceDirect

Molecular Phylogenetics and Evolution

journal homepage: www.elsevier.com/locate/ympev



Short Communication

Phylogenies without roots? A plea for the use of vouchers in molecular phylogenetic studies

F. Pleijel^{a,*}, U. Jondelius^b, E. Norlinder^a, A. Nygren^c, B. Oxelman^d, C. Schander^{e,f}, P. Sundberg^c, M. Thollesson^g

^a Department of Marine Ecology, Tjärnö Marine Biological Laboratory, Göteborg University, SE-452 96 Strömstad, Sweden

^b Department of Invertebrate Zoology, Swedish Museum of Natural History, Box 50007, SE-104 05 Stockholm, Sweden

^c Department of Zoology, Göteborg University, Box 463, SE-405 30 Göteborg, Sweden

^d Department of Plant and Environmental Sciences, Göteborg University, Box 461, SE-405 30 Göteborg, Sweden

^e Department of Biology, University of Bergen, Postbox 7800, NO-5020 Bergen, Norway

^f Centre for Geobiology, University of Bergen, Allegatan 41, 5007 Bergen, Norway

^g Department of Evolution, Genomics and Systematics, Evolutionary Biology Centre, Uppsala University, Norbyvägen 18C, SE-752 36 Uppsala, Sweden

by individual identification numbers. Of 205 relevant papers published that year, 46% included designated vouchers, either since the studies were based on already deposited specimens, or because specimens were newly deposited for the purpose. Consequently, for 54% of the studies there were no specified vouchers, meaning that more than half of the studies were published without any possibility for other systematists to assess the origin of the data.

205 artículos
2006

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205 artículos
2006

46 % ejemplares testigo

54 % sin ejemplares testigo

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museums or other institutions. Furthermore, at GenBank there is currently no dedicated field for specification of vouchers. Without

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Mol Phylogenet Evol. Author manuscript; available in PMC 2010 October 1.

Published in final edited form as:

Mol Phylogenet Evol. 2009 October ; 53(1): 357–358. doi:10.1016/j.ympev.2009.04.016.

Comments on the paper by : vouching for GenBank^{Pleijel et al. (2008)}

Scott Federhen, Carol Hotton, and Ilene Mizrachi

NCBI, NLM, NIH, 8600 Rockville Pike, Bethesda MD, USA

Scott Federhen: federhen@ncbi.nlm.nih.gov; Carol Hotton: ; Ilene Mizrachi:



museums or other institutions. Furthermore, at GenBank there is currently no dedicated field for specification of vouchers. Without



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Mol Phylogenet Evol. Author manuscript; available in PMC 2010 October 1.

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Scott Federhen: federhen@ncbi.nlm.nih.gov; Carol Hotton: ; Ilene Mizrachi:



/specimen_voucher
/strain
/tissue_type

1998

museums or other institutions. Furthermore, at GenBank there is currently no dedicated field for specification of vouchers. Without

Nucleotide

Nucleotide

Limits Advanced

Display Settings: GenBank

Send to

Rhizopogon roseolus strain BCC-MPM 1511 5.8S ribosomal RNA gene, partial sequence; and internal transcribed spacer 2, complete sequence

GenBank: AF115840.1

FASTA Graphics

Go to: ▾

LOCUS AF115840 338 bp DNA linear PLN 24-AUG-1999
DEFINITION Rhizopogon roseolus strain BCC-MPM 1511 5.8S ribosomal RNA gene, partial sequence; and internal transcribed spacer 2, complete sequence.
ACCESSION AF115840
VERSION AF115840.1 GI:5762292
KEYWORDS .
SOURCE Rhizopogon roseolus
ORGANISM Rhizopogon roseolus
Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina;
Agaricomycetes; Agaricomycetidae; Boletales; Suillineae;
Rhizopogonaceae; Rhizopogon.
REFERENCE 1 (bases 1 to 338)
AUTHORS Johannesson,H. and Martin,M.P.
TITLE Cladistic analysis of European species of Rhizopogon (Basidiomycotina) based on morphological and molecular characters
JOURNAL Mycotaxon 71, 267-283 (1999)
REFERENCE 2 (bases 1 to 338)
AUTHORS Johannesson,H. and Martin,M.P.
TITLE Direct Submission
JOURNAL Submitted (22-DEC-1998) Biol. Vegetal (Botanica), Fac. Biologia, Univ. Barcelona, Avda. Diagonal 645, Barcelona 08028, Spain
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121 gtgggggtcg ccggagacta ggactttcg tcttgactc gggcttc taaaatgcatc
181 ggcttgcgtt cgactttcg aattgcgcga caagggttc ggcgtgataa tgatgcgcgt
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301 gagagaaaaac gtcctcccta ttgactttt acctcaaa
//

Nucleotide

Nucleotide

Limits Advanced

Display Settings: GenBank

Send to

Rhizopogon roseolus strain BCC-MPM 1511 5.8S ribosomal RNA gene, partial sequence; and internal transcribed spacer 2, complete sequence

GenBank: AF115840.1

FASTA Graphics

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LOCUS AF115840 338 bp DNA linear PLN 24-AUG-1999
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 ACCESSION AF115840
 VERSION AF115840.1 GI:5762292
 KEYWORDS .
 SOURCE Rhizopogon roseolus
 ORGANISM Rhizopogon roseolus
 Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Boletales; Suillineae; Rhizopogonaceae; Rhizopogon.
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 JOURNAL Mycotaxon 71, 267-283 (1999)

| | |
|-----------|--|
| REFERENCE | 2 (bases 1 to 338) |
| AUTHORS | Johannesson, H. and Martin, M.P. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (22-DEC-1998) Biol. Vegetal (Botanica), Fac. Biologia, Univ. Barcelona, Avda. Diagonal 645, Barcelona 08028, Spain |
| FEATURES | Location/Qualifiers |
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| misc | |
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//

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Protein

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Mar 20, 2014

NCBI staff will attend the 2014 ACMG Annual Clinical Genetics Meeting

NCBI requests feedback on proposed

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AF230891 – GQuery: Global Cross-database NCBI search – NCBI

http://www.ncbi.nlm.nih.gov/gquery/?term=AF230891

Nucleotide BLAST Apple Yahoo! Google Maps YouTube Wikipedia Noticias Populares

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GQuery
NCBI Global Cross-database Search

Search NCBI databases

AF230891

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(none) PubMed Central: full-text journal articles
(none) NLM Catalog: books, journals and more in the NLM Collections

(none) MeSH: ontology used for PubMed indexing
(none) Books: books and reports
(none) Site Search: NCBI web and FTP site index

Health

(none) PubMed Health: clinical effectiveness, disease and drug reports
(none) MedGen: medical genetics literature and links
(none) GTR: genetic testing registry
(none) dbGaP: genotype/phenotype interaction studies

(none) ClinVar: human variations of clinical significance
(none) OMIM: online mendelian inheritance in man
(none) OMIA: online mendelian inheritance in animals

Organisms

(none) Taxonomy: taxonomic classification and nomenclature catalog

Nucleotide Sequences

1 Nucleotide: DNA and RNA sequences

(none) GSS: genome survey sequences
(none) EST: expressed sequence tag sequences

(none) SRA: high-throughput DNA and RNA sequence read archive
(none) PopSet: sequence sets from phylogenetic and population studies
(none) Probe: sequence-based probes and primers

Genomes

(none) Genome: genome sequencing projects by organism

(none) dbVar: genome structural variation studies

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Nucleotide Nucleotide Search Help

Display Settings: GenBank Send to: Change region shown

Macowanites ammophilus MA-Fungi 40137 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence

GenBank: AF230891.1

FASTA Graphics

Go to: ▾

LOCUS AF230891 612 bp DNA linear PLN 05-MAR-2002

DEFINITION Macowanites ammophilus MA-Fungi 40137 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.

ACCESSION AF230891

VERSION AF230891.1 GI:929519

KEYWORDS .

SOURCE Macowanites ammophilus

ORGANISM Macowanites ammophilus Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Russulales; Russulaceae; Macowanites.

REFERENCE 1 (bases 1 to 612)

AUTHORS Calonge,F.D. and Martin,M.P.

TITLE Morphological and molecular data on the taxonomy of Gymnomycetes, Martelia and Zelleromyces (Russulales)

JOURNAL Mycotaxon 76, 9-15 (2000)

REFERENCE 2 (bases 1 to 612)

AUTHORS Martin,M.P. and Calonge,F.D.

TITLE Direct Submission

JOURNAL Submitted (03-FEB-2000) Micologia, Real Jardin Botanico, C.S.I.C., Plaza de Murillo 2, Madrid 28014, Spain

FEATURES Location/Qualifiers

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misc RNA 6..215 /product="internal transcribed spacer 1"

rRNA 216..370 /product="5.8S ribosomal RNA"

misc RNA 371..>612 /product="internal transcribed spacer 2"

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61 tgctttcaca cacaatccat ctcacccttt tggcatgac cgccgtggggg tcccttttag
121 ctatctca aacccatctt cactttttta caacacaccc ctttaatacc aatatctaca

Customize view Analyze this sequence

Run BLAST Pick Primers Highlight Sequence Features Find in this Sequence

LinkOut to external resources SH224416.06FU [UNITE] Herbarium, Real Jardin Botanico-CSIC, Madrid [Herbarium, Real Jardin Botanico]

Related information Related Sequences Taxonomy

Recent activity Turn Off Clear Macowanites ammophilus MA-Fungi 40137 18S ribosomal RNA gene, partial sequence Nucleotide See more...

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LinkOut ... 19.2.2003 ... /specimen voucher Herbarium MA (MA-Fungi)

NCBI Taxonomy Browser

Search for as lock

Display 3 levels using filter: none

Macowanites ammophilus

Taxonomy ID: 132181
Inherited blast name: basidiomycetes
Rank: species
Genetic code: [Translation table 1 \(Standard\)](#)
Mitochondrial genetic code: [Translation table 4 \(Mold Mitochondrial; Protozoan Mitochondrial; Coelenterate Mitochondrial; Mycoplasma; Spiroplasma\)](#)
Other names:
synonym: **Gymnomyces ammophilus**

[Lineage \(full\)](#)
[cellular organisms](#); [Eukaryota](#); [Opisthokonta](#); [Fungi](#); [Dikarya](#); [Basidiomycota](#); [Agaricomycotina](#); [Agaricomycetes](#); [Agaricomycetes incertae sedis](#); [Russulales](#); [Russulaceae](#); [Macowanites](#)

Comments and References:

Calonge, F.D. & J.M. Vidal.
Vidal J.M., Calonge F.D., Martin M.P. Macowanites ammophilus, Russulales, a new combination based on new evidence. (Unpublished). Calonge, F.D. & J.M. Vidal. (1999)- "Gymnomyces ammophilus Vidal & Calonge; sp. nov. found in Portugal".- Bol. Soc. Micol. Madrid 24: 65-70.

External Information Resources (NCBI LinkOut)

| LinkOut | Subject | LinkOut Provider |
|---|---------------------------|--|
| search GBIF | taxonomy/phylogenetic | Global Biodiversity Information Facility |
| MA-Fungi 40132 | culture/stock collections | Herbarium, Real Jardin Botanico-CSIC, Madrid |
| MA-Fungi 40137 | culture/stock collections | |
| Gymnomyces ammophilus J.M. Vidal & Calonge 1999 | taxonomy/phylogenetic | Index Fungorum |
| Macowanites ammophilus (J.M. Vidal & Calonge) J.M. Vidal & Calonge 2002 | taxonomy/phylogenetic | |
| Gymnomyces ammophilus J.M. Vidal & Calonge | taxonomy/phylogenetic | MycoBank |
| Macowanites ammophilus (J.M. Vidal & Calonge) J.M. Vidal & Calonge | taxonomy/phylogenetic | |

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To see LinkOut links in this lineage click [here](#).

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Noticias
Adquisiciones
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por F. Pando

Resultados

Volver al formulario de búsqueda
Back to the query form

Gymnomycetes ammophilus J.M. Vidal & Calonge

1

Det. F.D.Calonge

Macowanites ammophilus (Vidal & Calonge) Vidal & Calonge



2

Det. F.D.Calonge (04 -200)

PRT, BAI: Alcácer do Sal
bajo Halimium halimifolium

J.M. Vidal

27-mar-1998

MA-Fungi 40137 GenBank Acc. No. AF230891

- [GenBank Acc. No. AF230891](#) -

Nombre aceptado en el Herbario : Macowanites ammophilus (Vidal & Calonge) Vidal & Calonge

NCBI/NLM/NIH/....

21.03.2014 ... Biological Repositories Colecciones de Historia Natural

ftp://ftp.ncbi.nih.gov/pub/taxonomy/coll_dump.txt



The screenshot shows a Mac OS X Finder window with the title bar "ftp://ftp.ncbi.nih.gov/pub/taxonomy/coll_dump.txt". The window lists numerous entries from the file, each consisting of a two-letter code followed by a character (s, c, or b) and a descriptive name. The names represent various biological collections and institutions.

| | | |
|------------|----|--|
| A | s | Arnold Arboretum, Harvard University |
| AA | s | Ministry of Science, Academy of Sciences |
| AAH | s | Arnold Arboretum, Harvard University |
| AAPI | s | Plant Industry Laboratory |
| AAR | s | Reliquae Aaronsohniae |
| AARI | s | Anatolian Agricultural Research Institute |
| AAS | s | British Antarctic Survey |
| AAU | s | University of Aarhus, Institute of Biological Sciences |
| AAU<ETH> | s | Addis Ababa University, Department of Biology |
| AAU<ETH>:A | s | Addis Ababa University, Department of Biology, Amphibian collection |
| AAUB | s | Anhui Agricultural University, Department of Basic Courses |
| AAUF | s | Anhui Agricultural University, Forest Utilization Faculty |
| ABB | c | Asian Bacterial Bank |
| ABD | s | University of Aberdeen, Plant and Soil Science Department |
| ABDAM | s | Aberdeen Art Gallery and Museum |
| ABDC | s | Aba Institute for Drug Control |
| ABDF | s | University of Aberdeen, Forestry Department |
| ABDH | s | United Arab Emirates University, Department of Biology |
| ABDM | s | Marischal College, University of Aberdeen |
| ABFM | s | The Barnes Foundation Arboretum |
| ABH | s | Universidad de Alicante, Centro Iberoamericano de la Biodiversidad (CIBIO) |
| ABI | s | Centre ORSTOM d'Adiopodoume |
| ABKMI | c | Department of Applied Biology, Faculty of science |
| ABL | s | Adviesbureau voor Bryologie en Lichenologie |
| ABN | s | Radley College |
| ABO | s | Aboyn Castle |
| ABRC | b | Arabidopsis Biological Resource Center |
| ABRIICC | c | ABRIICC Agricultural Biotechnology Research Institute of Iran Culture collection |
| ABRN | s | Centre for Ecology and Hydrology |
| ABS<UK> | sc | University of Wales, Botany Department |
| ABS<USA> | s | Archbold Biological Station |
| ABSH | s | Southern Illinois University, Department of Plant Biology |
| ABSL | s | University of Minnesota, American Bryological and Lichenological Society |
| ABSM | s | Duke University, Botany Department |
| ABT | s | Laboratoire de Biologie Vegetale et d'Ecologie Forestiere |
| ABTC | s | Australian Biological Tissue Collection, South Australian Museum |
| ABU<NGA> | s | Ahmadu Bello University Herbarium |
| AC | s | Amherst College |
| ACA | s | Agricultural University of Athens |
| ACA-DC | c | Greek Coordinated Collections of Microorganisms |

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21.01.2014 ... Base de datos taxonomia ... Colecciones Tipo

<http://www.ncbi.nlm.nih.gov/news/01-21-2014-sequence-by-type/>

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Taxonomy database now shows type material, sequences from type specimens and strains now labeled in Entrez

Tuesday, January 21, 2014

The naming, classification and identification of organisms traditionally relies on the concept of type material, which defines the representative examples ("name-bearing") of a species. For larger organisms, the type material is often a preserved specimen in a museum drawer, but the type concept also extends to type bacterial strains as cultures deposited in a culture collection. Of course, modern taxonomy also relies on molecular sequence information to define species. In many cases, sequence information is available for type specimens and strains. Accordingly, the NCBI has started to curate type material from the Taxonomy database, and are using this data to label sequences from type specimens or strains in the sequence databases. The figure below shows type material as it appears in the NCBI taxonomy entry and a sequence record for the recently described African monkey species, *Cercopithecus lomamiensis*.

Cercopithecus lomamiensis

Taxonomy ID: 1191211
Genbank common name: lesula
Inherited blast name: primates
Rank: species
Genetic code: Translation table 1 (Standard)
Mitochondrial genetic code: Translation table 2 (Vertebrate Mitochondrial)
Other names:
synonym: Cercopithecus sp. ASB-2012
authority: Cercopithecus lomamiensis Hart et al. 2012

type material: YPM MAM 14192
type material: YPM MAM 14191
type material: YPM MAM 14189
type material: YPM MAM 14080
type material: YPM 14192
type material: YPM 14191
type material: YPM 14189
type material: YPM 14080

| Entrez records | |
|----------------|--------------|
| Database name | Direct links |
| Nucleotide | 8 |
| Protein | 4 |
| PubMed Central | 1 |
| Taxonomy | 1 |

LOCUS JN106060 4688 bp DNA linear PRI 05
DEFINITION Cercopithecus lomamiensis isolate ME408 X chromosome inter
region genomic sequence.
ACCESSION JN106060
VERSION JN106060.1 GI:387865320
KEYWORDS .
SOURCE Cercopithecus lomamiensis (lesula)
ORGANISM Cercopithecus lomamiensis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhin
Catarrhini; Cercopithecididae; Cercopithecinae; Cercopithecus
REFERENCE 1 (bases 1 to 4688)
AUTHORS Hart,J.A., Detwiler,K.M., Gilbert,C.C., Burrell,A.S., Full
Bartshu,M., Hause,M., Numan,M., Saito,M., and Mank,J.

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Archives Year: 2014

Jan Feb Mar Apr
May Jun Jul Aug
Sep Oct Nov Dec

Archives prior to July, 2012

Fungi RefSeqITS database

Robbertse et al. 2014. Finding needles in haystacks: linking scientific names, reference specimens and molecular data for Fungi (en fase de publicación).

- Seleccionado y revisado secuencias ITS nrDNA (barcoding de hongos) depositadas en NCBI obtenidas de **especímenes tipo**.

Especie 1, T

?

Especie 2, T

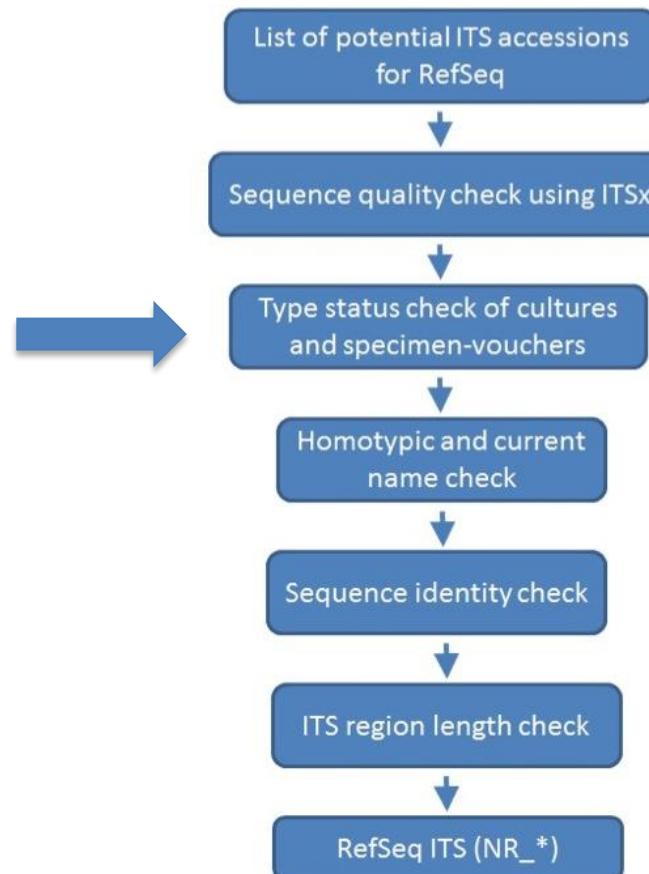


Fungi RefSeqITS database

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- Seleccionado y revisado secuencias ITS nrDNA (barcoding de hongos) depositadas en NCBI obtenidas de **especímenes tipo**.
- Proponemos el protocolo para verificar estas secuencias e incluirlas en la RefSeqITS database: **RefSeq ITS (NR_*)**.

Figure 1. Workflow of the ITS verification for RefSeq ITS database.



Fungi RefSeqITS database

Robbertse et al. 2014. Finding needles in haystacks: linking scientific names, reference specimens and molecular data for Fungi (en fase de publicación).

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- Proponemos el protocolo para verificar estas secuencias e incluirlas en la RefSeqITS database: [RefSeq ITS \(NR_*\)](#).
- Implementamos la identificación automática de secuencias de hongos a través de distintas herramientas on line (cibertaxonomía).

The screenshot shows the BLAST® Basic Local Alignment Search Tool interface. At the top, there's a navigation bar with 'Home', 'Recent Results', 'Saved Strategies', and 'Help' buttons. Below the navigation bar, it says 'NCBI/ BLAST Home' and 'BLAST finds regions of similarity between biological sequences'. A 'New' button is highlighted, followed by 'DELTA-BLAST, a more sensitive protein-protein search' and a 'Go' button. The main area is titled 'BLAST Assembled RefSeq Genomes' and asks 'Choose a species genome to search, or [list all genomic BLAST databases](#)'. There are two columns of species listed with checkboxes:

| Species | Species |
|--|---|
| <input type="checkbox"/> Human | <input type="checkbox"/> <i>Oryza sativa</i> |
| <input type="checkbox"/> Mouse | <input type="checkbox"/> <i>Bos taurus</i> |
| <input type="checkbox"/> Rat | <input type="checkbox"/> <i>Danio rerio</i> |
| <input type="checkbox"/> <i>Arabidopsis thaliana</i> | <input type="checkbox"/> <i>Drosophila melanogaster</i> |
| | <input type="checkbox"/> <i>Gallus gallus</i> |
| | <input type="checkbox"/> <i>Pan troglodytes</i> |
| | <input type="checkbox"/> <i>Microbes</i> |
| | <input type="checkbox"/> <i>Apis mellifera</i> |

Fungi RefSeqITS database

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The collage consists of four panels:

- Top Left:** A screenshot of the Broad Institute's Fusarium Comparative Database. It shows a search interface with a sidebar for 'Fusarium' and various image thumbnails related to the genus.
- Top Right:** A screenshot of MycoBank, the International Mycological Association's Fungal Databases and Nomenclature and Species Banks. It features a large image of a red mushroom and links for 'Home', 'Search', 'Login', and 'Identifications'.
- Bottom Left:** A screenshot of the CBS-KNAW Fungal Biodiversity Centre website. It displays a blue background image of fungi and navigation links like 'Home', 'Strain catalog', 'Other databases', 'Cart', 'Strain deposit form', 'Regular', 'Identifications', 'Help', and 'Contact us'.
- Bottom Right:** A screenshot of the SGD (Saccharomyces Genome Database) showing a fluorescence microscopy image of yeast cells with green and orange spots, labeled 'Localization of active Rps in a wild type strain'.

Bottom Center: A screenshot of the BLAST Basic Local Alignment Search Tool. It shows a search interface for 'BLAST zebra fish genome' and a link to 'DELTABLAST'. A sidebar lists 'BLAST Assembled RefSeq Genomes' for species like Human, Mouse, Rat, Arabidopsis thaliana, Oryza sativa, Bos taurus, Danio rerio, Drosophila melanogaster, Gallus gallus, Pan troglodytes, Microbes, and Apis mellifera.

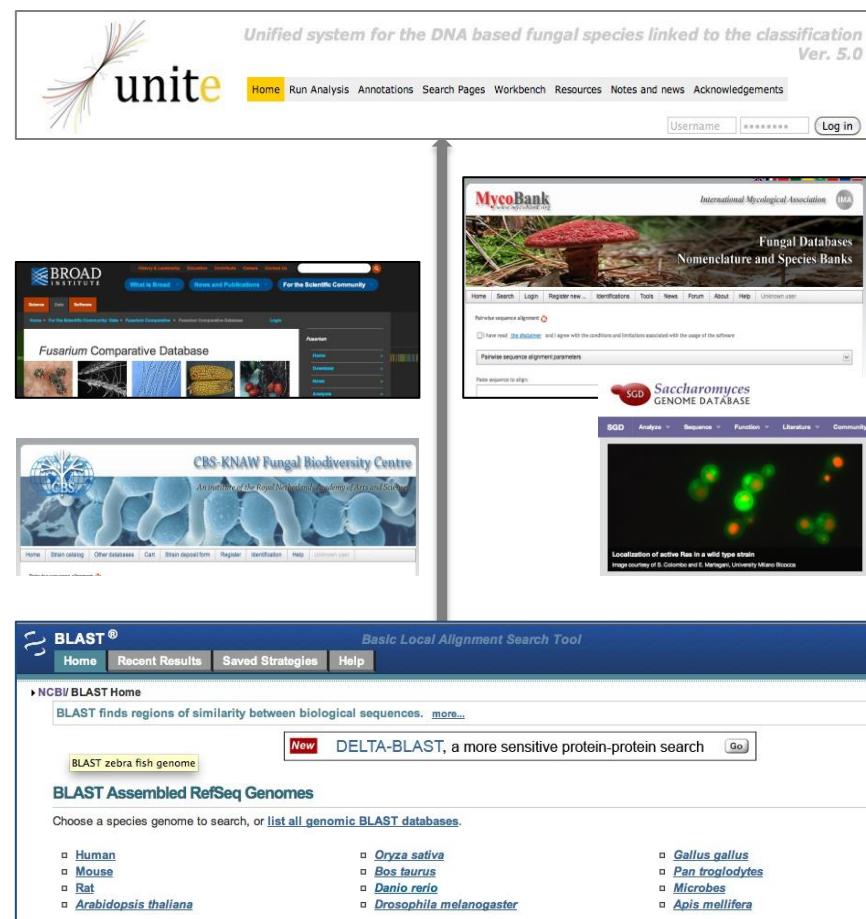
Fungi RefSeqITS database

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- Implementamos la identificación automática de secuencias de hongos a través de distintas herramientas on line (cibertaxonomía).



¿Identificación automática?

NEWS AND VIEWS

OPINION

Towards a unified paradigm for sequence-based identification of fungi

URMAS KÖLJALG,^{1,2} R. HENRIK NILSSON,³ KESSY ABARENKOVA,² LEHO TEDERSOO,² ANDY F. S. TAYLOR,^{4,5} MOHAMMAD BAHRAM,¹ SCOTT T. BATES,⁶ THOMAS D. BRUNS,⁷ JOHAN BENGTSSON-PALME,⁸ TONY M. CALLAGHAN,⁹ BRIAN DOUGLAS,¹⁰ TIIA DRENKHAN,¹⁰ URSULA EBERHARDT,¹¹ MARGARITA GRUÑEA,¹² TINE GREBENC,¹³ GARETH W. GRIFFITH,⁹ MARTIN HARTMANN,^{14,15} PAUL M. KIRK,¹⁶ PETR KOHOUT,^{1,17} ELLEN LARSSON,³ BJÖRN D. LINDHOLM,¹⁸ ROBERT LÜCKING,¹⁹ MARÍA P. MARTÍN,¹² P. BRANDON MATHENY,²⁰ NHU H. NGUYEN,⁷ TUULA NISKANEN,²¹ JANE OJA,² KABIR G. PEAY,²² URSULA PEINTNER,²³ MARKO PETERSON,¹ KADRI PÖLDMAA,¹ LAURI SAAG,¹ IRIJA SAAR,¹ ARTHUR SCHÜBLER,²⁴ JAMES A. SCOTT,²⁵ CAROLINA SENÉS,²⁶ MATTHEW E. SMITH,²⁶ AVE SUJJA,^{1,2} D. LEE TAYLOR,²⁷ M. TERESA TELLERIA,¹² MICHAEL WEISS²⁸ and KARL-HENRIK LARSSON²⁹

¹Institute of Ecology and Earth Sciences, University of Tartu, Lai 40, Tartu 51005, Estonia; ²National History Museum, University of Tartu, Vanemuise 46, Tartu 51014, Estonia;

³Department of Biological and Environmental Sciences, University of Gothenburg, Box 461, Göteborg SE-40530, Sweden; ⁴The James Hutton Institute, Cragside, Aberdeen, AB15 8QH, UK; ⁵Institute of Biological and Environmental Sciences, University of Aberdeen, Cruckshank Building, St Machar Drive, Aberdeen AB24 3UU, UK; ⁶Cooperative Institute for Research in Environmental Sciences, University of Colorado, Boulder, CO 80309, USA; ⁷Department of Plant and Microbial Biology, University of California, Berkeley, CA 94720, USA;

⁸Department of Neuroscience and Physiology, The Sahlgrenska Academy, University of Gothenburg, Box 434, Göteborg SE-40530, Sweden; ⁹Institute of Biological, Environmental and Rural Sciences, Aberystwyth University, Cefn Bryn Building, Aberystwyth SY23 3DD, UK; ¹⁰Institute of Forestry and Rural Engineering, Estonian University of Life Sciences, Fr. R. Kreutzwald 5, Tartu 51014, Estonia; ¹¹Naturkunde Stuttgart, Abt. Botanik, Rosenstein 1, Stuttgart D-70191, Germany; ¹²Departamento de Micología, Real Jardín Botánico (IJB-CSIC), Plaza de Maríllo 1, Madrid 28014, Spain;

¹³Department of Forest Physiology and Genetics, Slovenian

Forestry Institute, Vecna pot 2, Ljubljana SI-1000, Slovenia; ¹⁴Forest Soils and Biogeochemistry, Swiss Federal Research Institute WSL, CH-8903 Birmensdorf, Switzerland; ¹⁵Molecular Ecology, Agroscope Reckenholz-Tänikon Research Station ART, CH-8046 Zurich, Switzerland; ¹⁶Mycology Section, Jodrell Laboratory, Royal Botanic Gardens Kew, Surrey TW9 3DS, UK; ¹⁷Institute of Botany, Academy of Science of the Czech Republic, Průhonice CZ-252 43, Czech Republic; ¹⁸Department of Forest Mycology and Plant Pathology, Swedish University of Agricultural Sciences, Box 7026, Uppsala SE-75007, Sweden; ¹⁹Science and Education, Integrative Research and Collections (Botany), The Field Museum, 1400 South Lake Shore Drive, Chicago, IL 60605-2496, USA; ²⁰Department of Ecology and Evolutionary Biology, University of Tennessee, Hasler Biology Building 332, Knoxville, TN 37996-1610, USA; ²¹Plant Biology, Department of Biosciences, University of Helsinki, P.O. Box 56, Helsinki FI-00014, Finland; ²²Department of Biology, Stanford University, Stanford, CA 94305, USA; ²³Institute of Microbiology, University Innsbruck, Technikerstr. 25, Innsbruck 6020, Austria; ²⁴Genetics, Department Biology, Ludwig-Maximilians-University, Grosshaderner Str. 4, Martinsried, Munich 82152, Germany; ²⁵Dalla Lana School of Public Health, University of Toronto, 223 College Street, Toronto, ON MST 1R4, Canada; ²⁶Department of Plant Pathology, University of Florida, Gainesville, FL 32611-0680, USA; ²⁷Department of Biology, University of New Mexico, MSC03 2020, Albuquerque, NM 87131-0001, USA; ²⁸Department of Biology, University of Tübingen, Auf der Morgenstelle 5, Tübingen D-72076, Germany; ²⁹Natural History Museum, University of Oslo, P.O. Box 1172 Blindern, Oslo 0318, Norway

Abstract

The nuclear ribosomal internal transcribed spacer (ITS) region is the formal fungal barcode and in most cases the marker of choice for the exploration of fungal diversity in environmental samples. Two problems are particularly acute in the pursuit of satisfactory taxonomic assignment of newly generated ITS sequences: (i) the lack of an inclusive, reliable public reference data set and (ii) the lack of means to refer to fungal species, for which no Latin name is available in a standardized stable way. Here, we report on progress in these regards through further development of the UNITE database (<http://unite.ut.ee>) for molecular identification of fungi. All fungal species represented by at least two ITS sequences in the international nucleotide sequence databases are now given a unique, stable name of the accession number type (e.g. *Hymenoscyphus pseudoulmibus* | GU586904).

Correspondence: Urmas Kõlalg, Fax: +372 7376380;
E-mail: urmas.kolalg@ut.ee

✓ “Species Hypothesis”

✓ Secuencias de referencia

Unified system for the DNA based fungal species linked to the classification
Ver. 5.0



Current version: 5.0; Release date: 18.12.2012 (read more)

Number of UNITE fungal Species Hypotheses: 52 481 (based on 98% threshold value, see also SH statistics below)

Number of fungal ITS sequences in current version (UNITE+INSd): 352 622

UNITE provides unified way how you delimit, identify, communicate and work with DNA based Species Hypotheses (SH). All SHs are connected to the taxon name and classification. Read **Kõlalg et al. 2013** paper for the description of the system.

What is Species Hypothesis?

Species Hypothesis – any species level group of individuals that share a given set of observed characters. [Read more](#)



Click to enlarge

What are reference and representative sequences?

Reference sequence (RefS) – serves as a name anchor for the Species Hypothesis and is chosen by the expert. [Read more](#)



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UNITE Community

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[UNITE list](#)

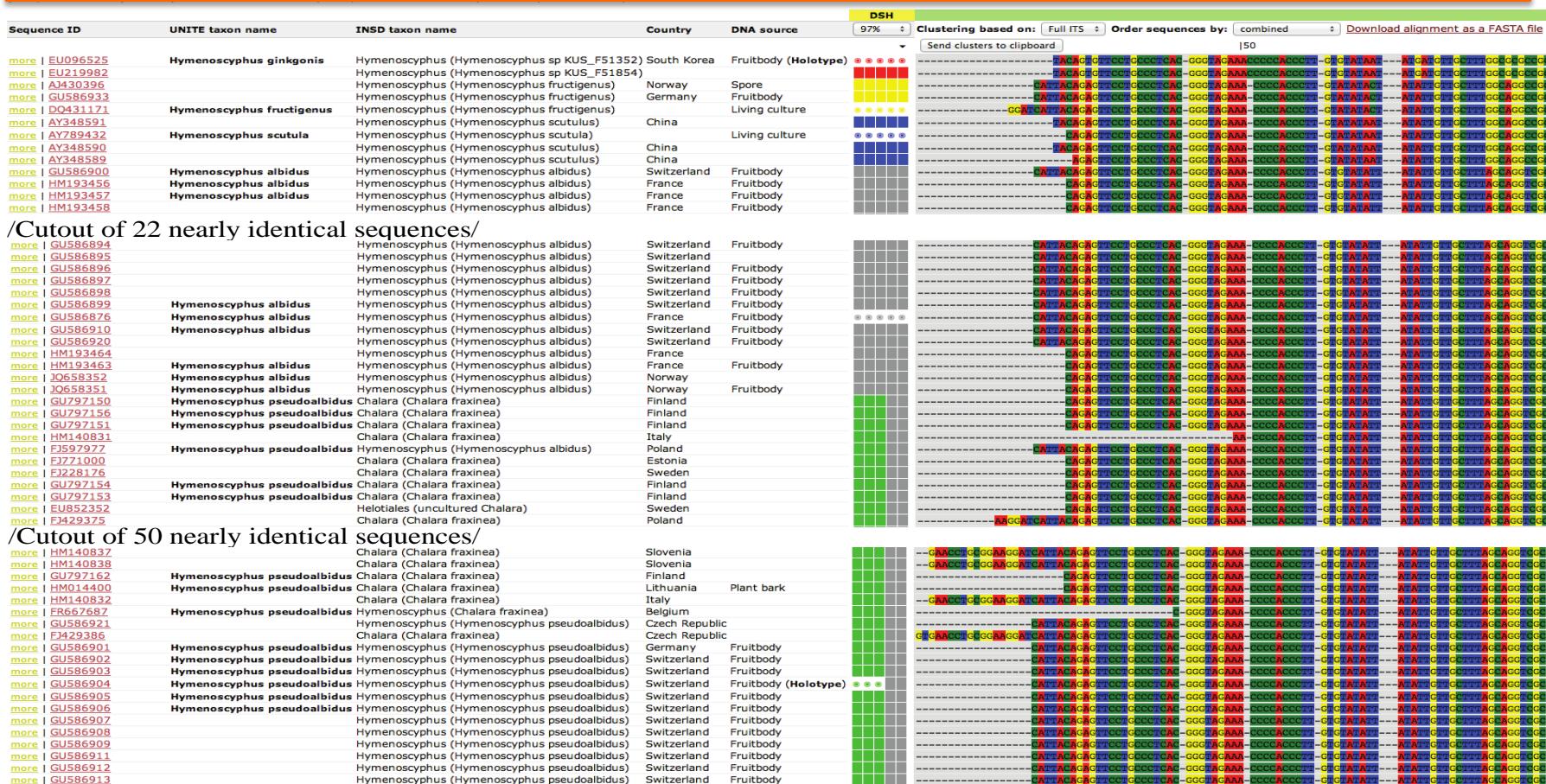
News

Oct. 14, 2013 UNITE homepage updated: Unified system for the DNA based fungal species (ver. 5.0) released.

Species Hypotheses statistics (ver 5.0)

Dos subniveles de agrupamiento para definir Unidades Taxonómicas Operacionales, OTUs (97%, 97.5%, 98%, 98.5%, 99%):

1. Nivel género/subgénero
2. Nivel específico – “Species Hypothesis” SH



Cada cluster tiene un código único *Hymenoscyphus/UCL5_005639* 172 sec

SH

97% 99%



DSH

| Sequence ID | UNITE taxon name | INSD taxon name | Country | DNA source | 97% Clustering based on: Full ITS Order sequences by: combined Download alignment as a FASTA file |
|-----------------|----------------------------------|---|-------------|----------------------|---|
| more EU096525 | <i>Hymenoscyphus ginkgonis</i> | Hymenoscyphus (Hymenoscyphus sp KUS_F51352) South Korea | | Fruitbody (Holotype) | Send clusters to clipboard 150 |
| more EU219982 | | Hymenoscyphus (Hymenoscyphus sp KUS_F51854) | | | |
| more AJ430396 | | Hymenoscyphus (Hymenoscyphus fructigenus) | Norway | Spore | |
| more GU586933 | | Hymenoscyphus (Hymenoscyphus fructigenus) | Germany | Fruitbody | |
| more DQ431171 | <i>Hymenoscyphus fructigenus</i> | Hymenoscyphus (Hymenoscyphus fructigenus) | | Living culture | |
| more AY348591 | | Hymenoscyphus (Hymenoscyphus scutulus) | China | | |
| more AY789432 | <i>Hymenoscyphus scutula</i> | Hymenoscyphus (Hymenoscyphus scutulus) | China | Living culture | |
| more AY348590 | | Hymenoscyphus (Hymenoscyphus scutulus) | China | | |
| more AY348589 | | Hymenoscyphus (Hymenoscyphus scutulus) | Switzerland | Fruitbody | |
| more GU586900 | <i>Hymenoscyphus albidus</i> | Hymenoscyphus (Hymenoscyphus albidus) | France | Fruitbody | |
| more HM193456 | <i>Hymenoscyphus albidus</i> | Hymenoscyphus (Hymenoscyphus albidus) | France | Fruitbody | |
| more HM193457 | <i>Hymenoscyphus albidus</i> | Hymenoscyphus (Hymenoscyphus albidus) | France | Fruitbody | |
| more HM193458 | | Hymenoscyphus (Hymenoscyphus albidus) | | | |

/Cutout of 22 nearly identical sequences/

| | | | | | |
|-----------------|------------------------------|---------------------------------------|-------------|-----------|--|
| more GU586894 | | Hymenoscyphus (Hymenoscyphus albidus) | Switzerland | Fruitbody | |
| more GU586895 | | Hymenoscyphus (Hymenoscyphus albidus) | Switzerland | Fruitbody | |
| more GU586896 | | Hymenoscyphus (Hymenoscyphus albidus) | Switzerland | Fruitbody | |
| more GU586897 | | Hymenoscyphus (Hymenoscyphus albidus) | Switzerland | Fruitbody | |
| more GU586898 | | Hymenoscyphus (Hymenoscyphus albidus) | Switzerland | Fruitbody | |
| more GU586899 | <i>Hymenoscyphus albidus</i> | Hymenoscyphus (Hymenoscyphus albidus) | Switzerland | Fruitbody | |
| more GU586876 | <i>Hymenoscyphus albidus</i> | Hymenoscyphus (Hymenoscyphus albidus) | France | Fruitbody | |
| more GU586910 | <i>Hymenoscyphus albidus</i> | Hymenoscyphus (Hymenoscyphus albidus) | Switzerland | Fruitbody | |
| more GU586920 | | Hymenoscyphus (Hymenoscyphus albidus) | Switzerland | Fruitbody | |
| more HM193464 | | Hymenoscyphus (Hymenoscyphus albidus) | France | | |
| more HM193463 | <i>Hymenoscyphus albidus</i> | Hymenoscyphus (Hymenoscyphus albidus) | France | Fruitbody | |
| more JO658352 | <i>Hymenoscyphus albidus</i> | Hymenoscyphus (Hymenoscyphus albidus) | Norway | | |
| more JO658351 | <i>Hymenoscyphus albidus</i> | Hymenoscyphus (Hymenoscyphus albidus) | Norway | Fruitbody | |
| more GU797150 | | Chalara (Chalara fraxinea) | Finland | | |
| more GU797156 | | Chalara (Chalara fraxinea) | Finland | | |
| more GU797151 | | Chalara (Chalara fraxinea) | Finland | | |
| more HM140831 | | Chalara (Chalara fraxinea) | Italy | | |
| more FJ597977 | | Hymenoscyphus (Hymenoscyphus albidus) | Poland | | |
| more FJ771000 | | Chalara (Chalara fraxinea) | Estonia | | |
| more FJ228176 | | Chalara (Chalara fraxinea) | Sweden | | |
| more GU797154 | | Chalara (Chalara fraxinea) | Finland | | |
| more GU797153 | | Chalara (Chalara fraxinea) | Finland | | |
| more EU852352 | | Helotiales (uncultured Chalara) | Sweden | | |
| more FJ429375 | | Chalara (Chalara fraxinea) | Poland | | |

/Cutout of 50 nearly identical sequences/

| | | | | | |
|-----------------|------------------------------------|---|----------------|------------|--|
| more HM140837 | | Chalara (Chalara fraxinea) | Slovenia | | |
| more HM140838 | | Chalara (Chalara fraxinea) | Slovenia | | |
| more GU797162 | <i>Hymenoscyphus pseudoalbidus</i> | Chalara (Chalara fraxinea) | Finland | | |
| more HM014400 | <i>Hymenoscyphus pseudoalbidus</i> | Chalara (Chalara fraxinea) | Lithuania | Plant bark | |
| more HM140832 | | Chalara (Chalara fraxinea) | Italy | | |
| more FR667687 | <i>Hymenoscyphus pseudoalbidus</i> | Hymenoscyphus (Chalara fraxinea) | Belgium | | |
| more GU586921 | | Hymenoscyphus (Hymenoscyphus pseudoalbidus) | Czech Republic | | |
| more FJ429386 | | Chalara (Chalara fraxinea) | Czech Republic | | |
| more GU586901 | | Hymenoscyphus (Hymenoscyphus pseudoalbidus) | Germany | Fruitbody | |
| more GU586902 | | Hymenoscyphus (Hymenoscyphus pseudoalbidus) | Switzerland | Fruitbody | |
| more GU586903 | <i>Hymenoscyphus pseudoalbidus</i> | Hymenoscyphus (Hymenoscyphus pseudoalbidus) | Switzerland | Fruitbody | |
| more GU586904 | | Hymenoscyphus (Hymenoscyphus pseudoalbidus) | Switzerland | Fruitbody | |
| more GU586905 | | Hymenoscyphus (Hymenoscyphus pseudoalbidus) | Switzerland | Fruitbody | |
| more GU586906 | | Hymenoscyphus (Hymenoscyphus pseudoalbidus) | Switzerland | Fruitbody | |
| more GU586907 | | Hymenoscyphus (Hymenoscyphus pseudoalbidus) | Switzerland | Fruitbody | |
| more GU586908 | | Hymenoscyphus (Hymenoscyphus pseudoalbidus) | Switzerland | Fruitbody | |
| more GU586909 | | Hymenoscyphus (Hymenoscyphus pseudoalbidus) | Switzerland | Fruitbody | |
| more GU586910 | | Hymenoscyphus (Hymenoscyphus pseudoalbidus) | Switzerland | Fruitbody | |
| more GU586911 | | Hymenoscyphus (Hymenoscyphus pseudoalbidus) | Switzerland | Fruitbody | |
| more GU586912 | | Hymenoscyphus (Hymenoscyphus pseudoalbidus) | Switzerland | Fruitbody | |
| more GU586913 | | Hymenoscyphus (Hymenoscyphus pseudoalbidus) | Switzerland | Fruitbody | |

/Cutout of 43 sequences/

*Hymenoscyphus
pseudoalbidus/GU586904/SH13*

37810510

| Secuencias | Nº |
|--------------------|---------|
| Secuencias ITS | 350.000 |
| Bien identificadas | 130.000 |
| Mal identificadas | 35.000 |
| Sin identificación | 175.000 |

| Valor umbral similitud | Nº SH |
|------------------------|-------|
| 97 % | 44537 |
| 97.5 % | 48007 |
| 98 % | 52481 |
| 98.5 % | 58594 |
| 99 % | 68938 |



| Valor umbral | |
|--------------------------------|--------|
| 98.5 % | |
| “Species Hypothesis” | 52.481 |
| Phyllum (División) conocido | 41.094 |
| Phyllum (División) desconocido | 11.387 |



iBOL | Terrestrial
Biosurveillance

Lepidoptera barcode of life

progress

BARCODE

specimens barcoded: **514387**

species barcoded: **22183**

unnamed barcode clusters: **18086**

Progress Reports

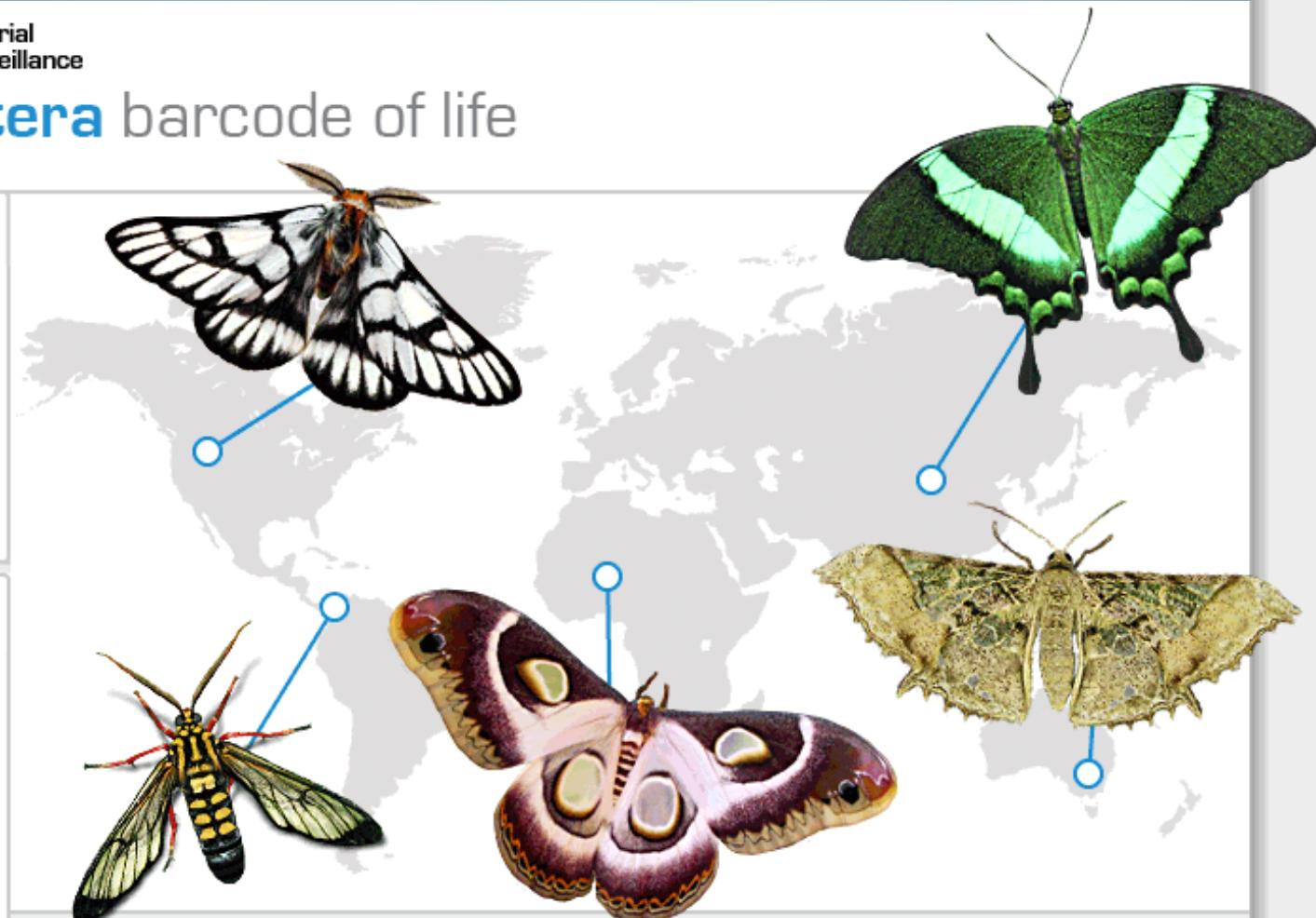
Research

Leadership Team

Campaigns

Publications

Get Involved!



OTHER TERRESTRIAL BIO-SURVEILLANCE
CAMPAIGNS:

TERMITIDAE
Termites

FORMICIDAE
Ants

LUMBRICIDAE
Earthworms



iBOL WORKING GROUP | 1.1 VERTEBRATES

Fish barcode of life (FISH-BOL)

INTERNATIONAL
BARCODE
OF LIFE



progress

specimens barcoded: **96425**

species barcoded: **10267**

unnamed barcode
clusters found: **2029**

[Progress Reports](#)



RELATED BARCODING CAMPAIGNS:

MAMMALiBOL
iBOL WG 1.1

MARINEBOL
iBOL WG 1.8

[The Blog](#)[The Partners](#)[The Team](#)[The Project](#)

[Species Checklist](#) | [MarBOL Progress Report](#) | [CAML Progress Report](#) | [Protocols](#) | [Upcoming Meetings](#) | [Spring 2009 Workshops](#)

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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.

progress

specimens barcoded

37182

species barcoded

6199

[View detailed progress reports](#)

 **iBOL** | Vertebrates

Mammalia barcode of life

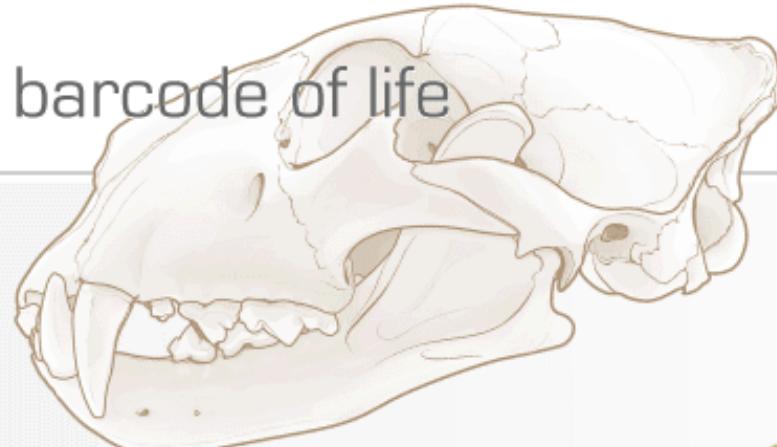
progress BARCODED

specimens barcoded: **19862**

species barcoded: **858**

unnamed barcode clusters found: **305**







OTHER VERTEBRATE CAMPAIGNS:

 **AMPHIBIA**
Amphibians

 **REPTILIA**
Reptiles

Welcome to the Mammal Barcode of Life campaign website 

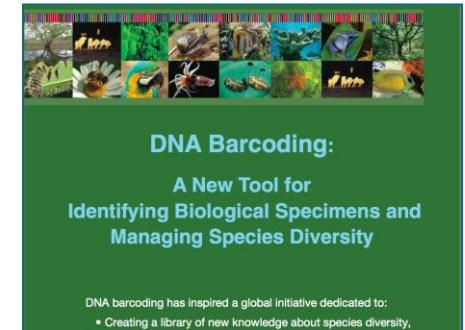
Colecciones Historia Natural vs Estudios moleculares

✓ Fundamentales en trabajos de revisión de grupos taxonómicos.

- Delimitar las especies.

- Descubrir y describir nuevas especies.

- Especies crípticas.



Filogenia

Biogeografía

Conservación

Relaciones patógeno-hospedante

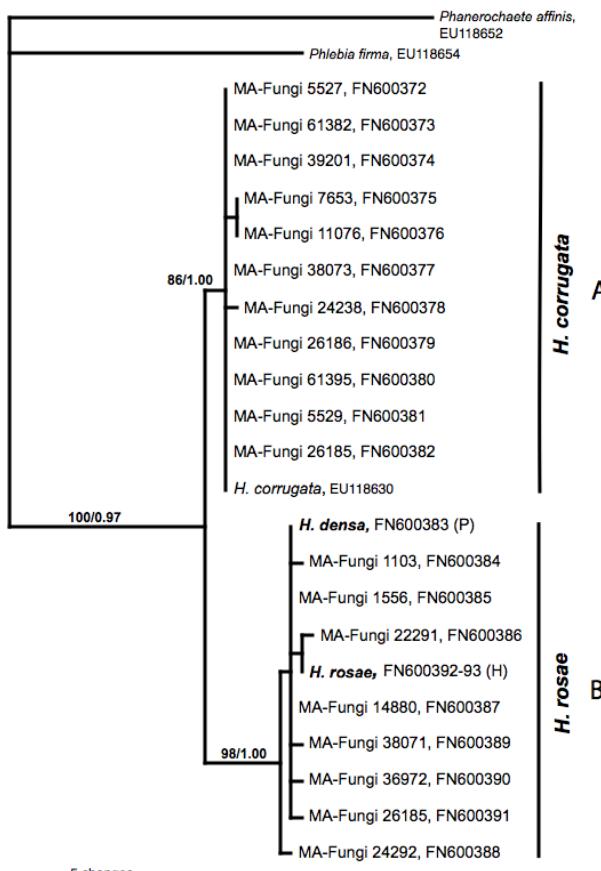
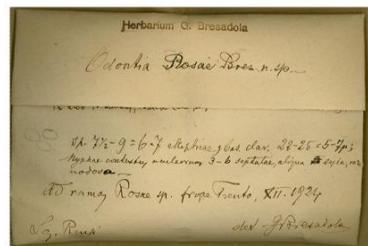
Hyphodermella (Fungi, Agaricomycotina)

Mycol Progress (2010) 9:585–596
DOI 10.1007/s11557-010-0666-5

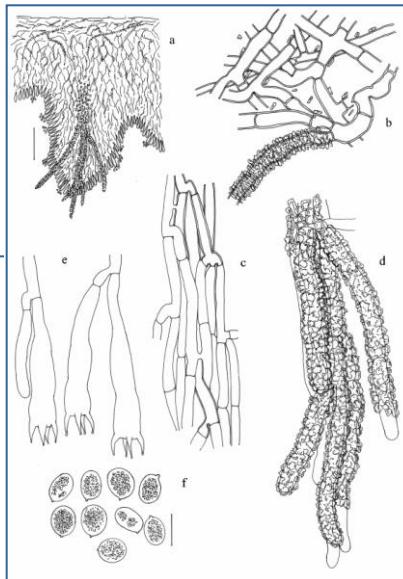
ORIGINAL ARTICLE

Morphological and molecular studies of *Hyphodermella* in the Western Mediterranean area

M. Teresa Tellería · Margarita Dueñas · Ireneia Melo ·
María P. Martín

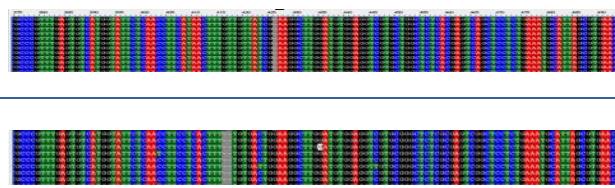
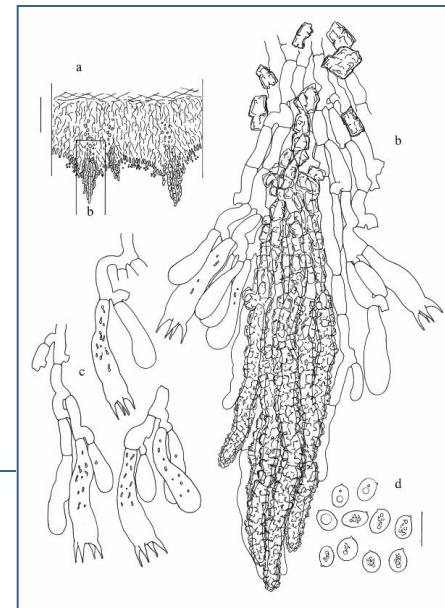


H. corrugata



H. rosae Type 1928

H. rosae



Hypochnicium (Fungi, Agaricomycotina)

M. Teresa Tellería¹
 Margarita Durán²
¹Departamento de Micología, Real Jardín Botánico,
 CSIC, Plaza de Murillo, 2. 28014 Madrid, Spain

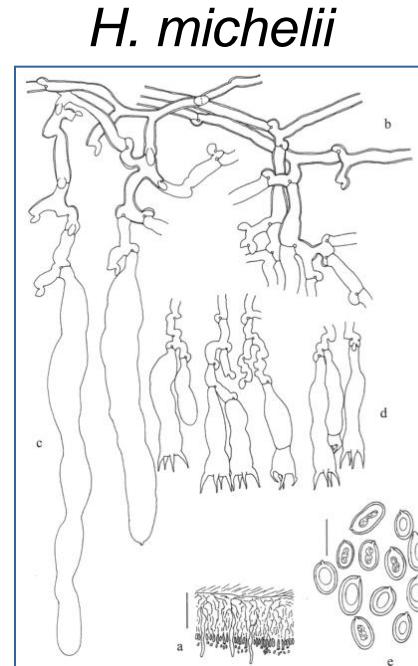
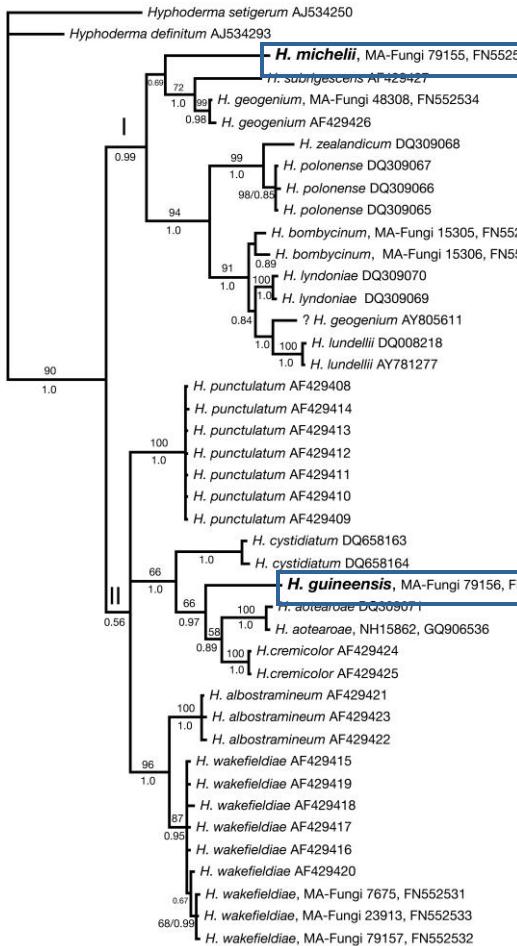
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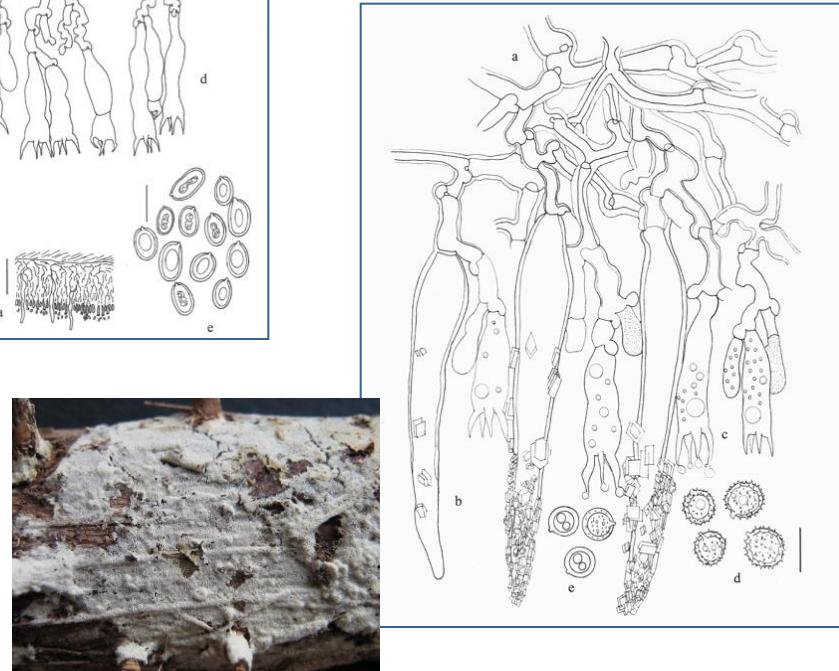
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Mycologia, 102(6), 2010, pp. 1426–1436. DOI: 10.3852/09-242
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A re-evaluation of *Hypochnicium* (Polyporales) based on morphological and molecular characters



H. guineensis



Astraeus (Fungi, Agaricomycotina, O. Boletales)

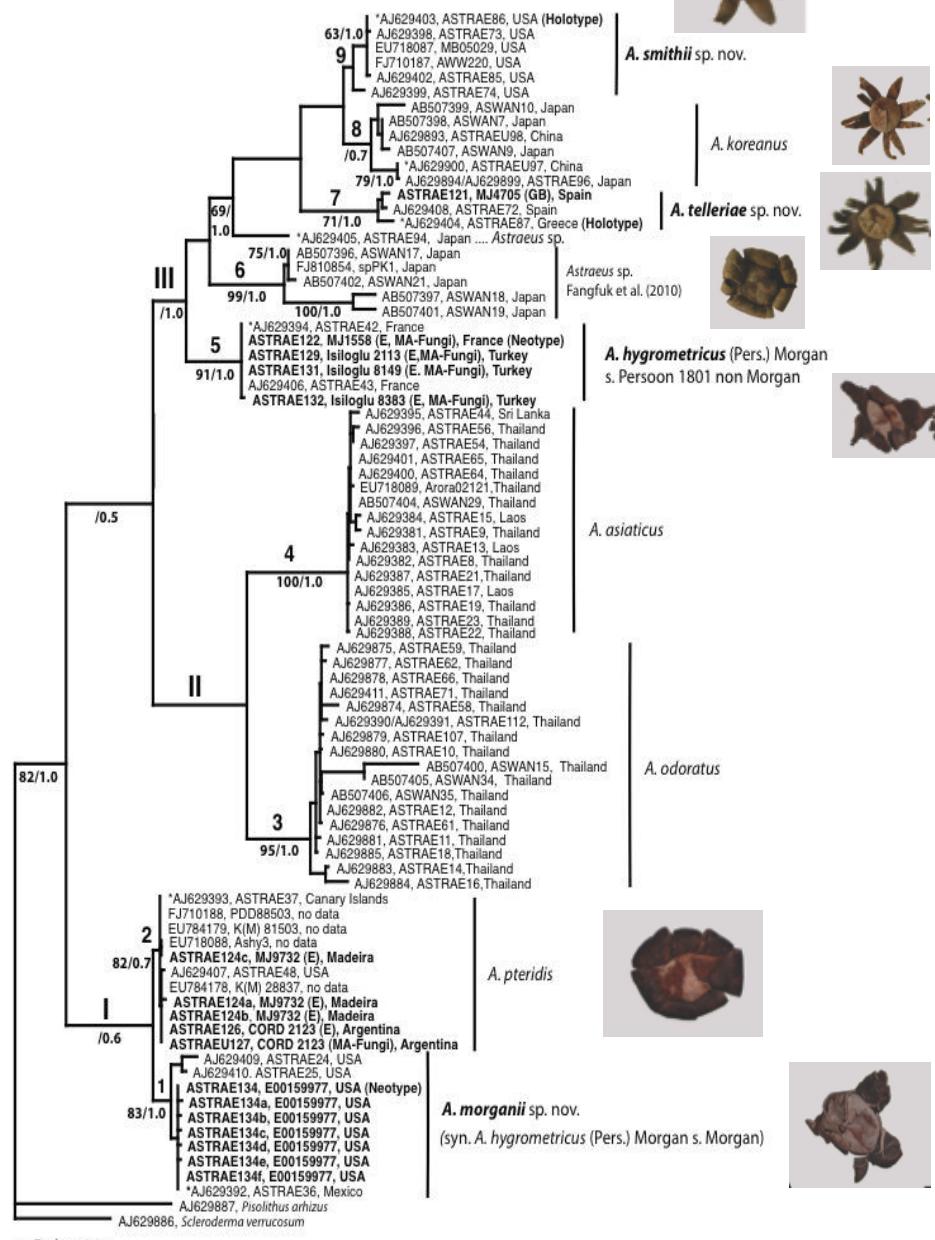
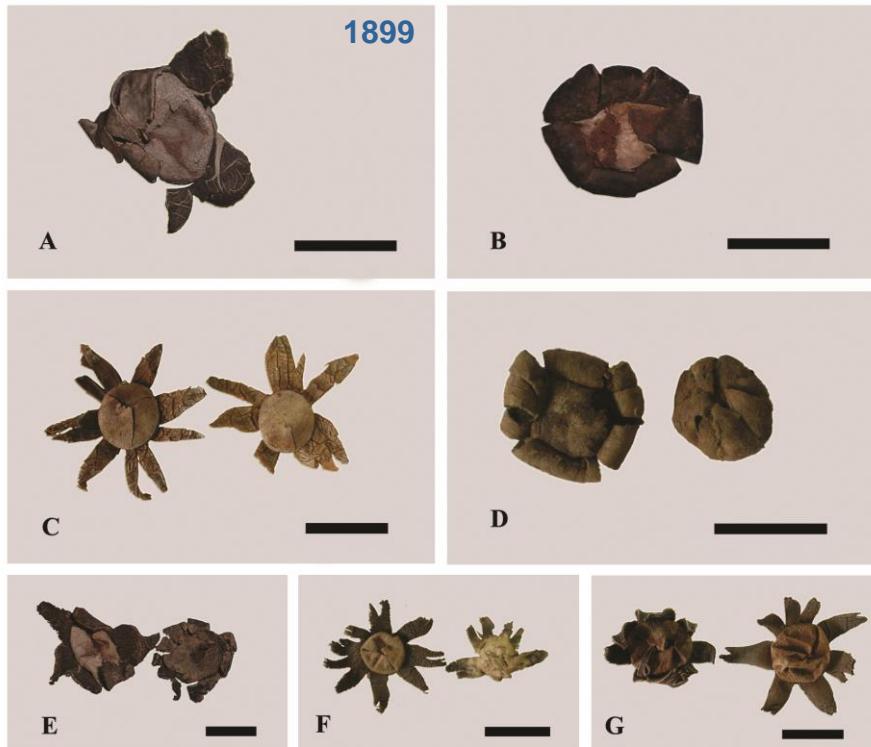
Astraeus: hidden dimensions

Cherdchai Phosri¹, Maria P. Martin², and Roy Watling³

¹Division of Science, Faculty of Liberal Arts and Science, Nakhon Phanom University, 167 Naratchakouy Sub-District, Muang District, Nakhon Phanom, 48000, Thailand

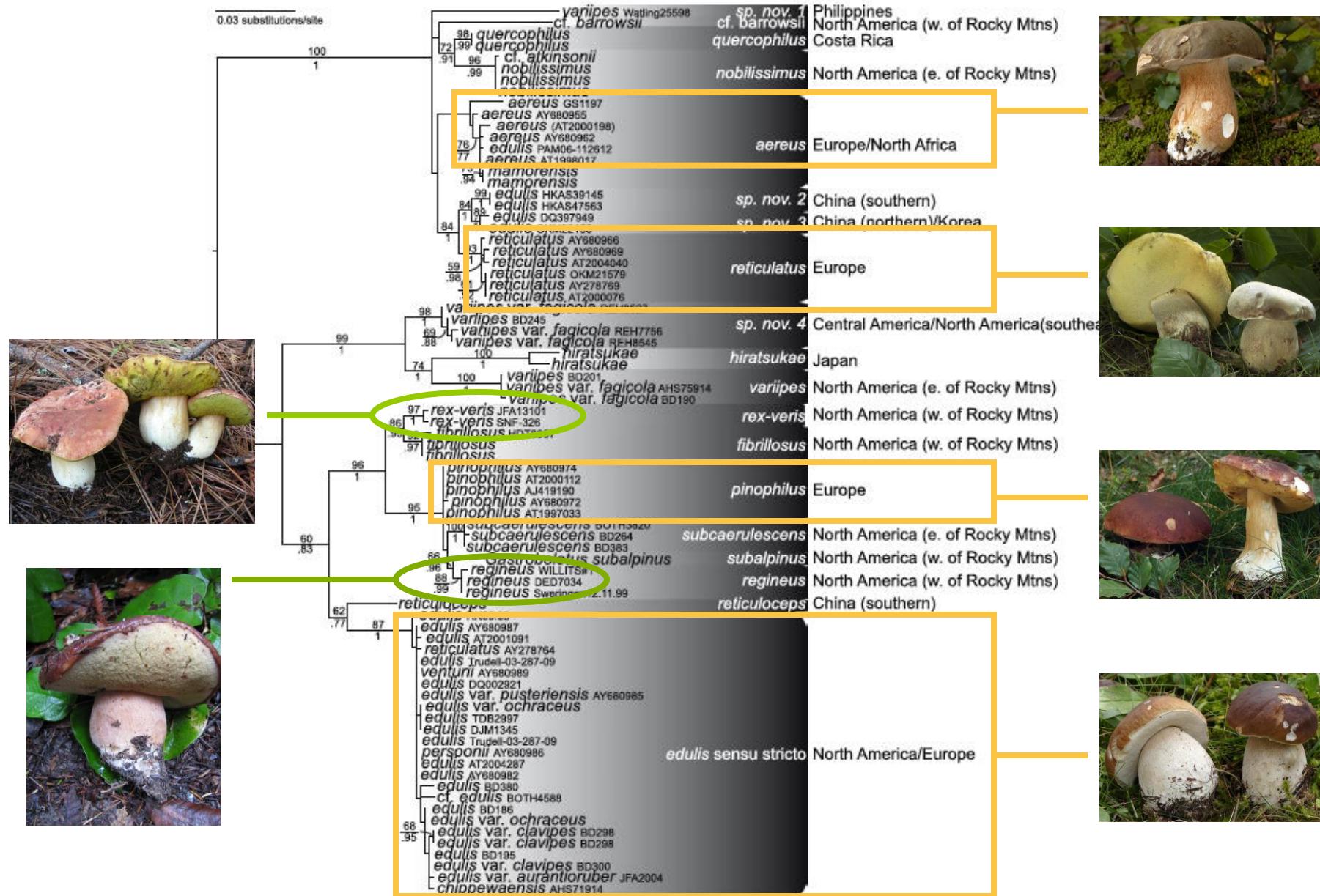
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³Caledonian Mycological Enterprises, 26 Blinkbonny Avenue, Edinburgh EH4 3HU, UK



- 5 changes

***Boletus* (Fungi, Agaricomycotina, O. Boletales)**



Cuscuta (F. Convolvulaceae)

Systematic Botany (2007), 32(4): pp. 899–916
© Copyright 2007 by the American Society of Plant Taxonomists

Phylogeny of *Cuscuta* subgenus *Cuscuta* (Convolvulaceae) Based on nrDNA ITS and Chloroplast *trnL* Intron Sequences

MIGUEL A. GARCÍA¹ and MARÍA P. MARTÍN

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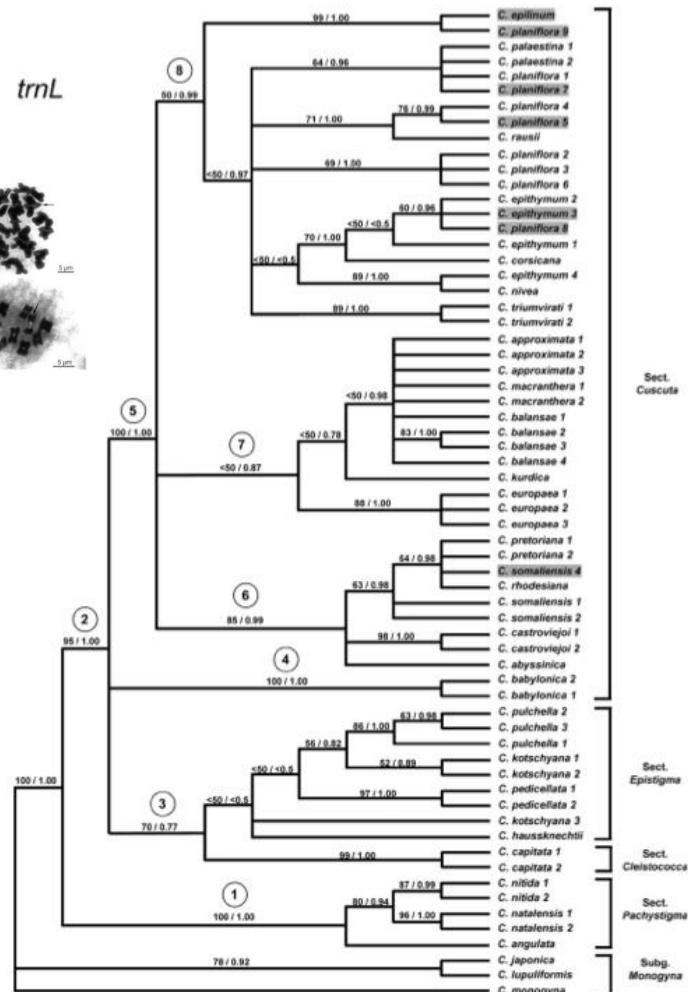


FIG. 1. Strict consensus of 564 equally parsimonious trees obtained from the analysis of the *trnL* intron sequences. Numbers above branches are bootstrap support/Bayesian posterior probability. Major clades are labeled with numbers inside circles and referred to in the text. Accessions showing topological incongruence with the ITS consensus trees in clades with moderate or high support are shaded. *Cuscuta approximata* subsp. *macrantha* and *C. epithymum* subsp. *corsicana* are labeled as *C. macrantha* and *C. corsicana*, respectively.

Plumularia (Animalia, O. Cnidaria)

Molecular Phylogenetics and Evolution 76 (2014) 1–9

Contents lists available at ScienceDirect



Molecular Phylogenetics and Evolution

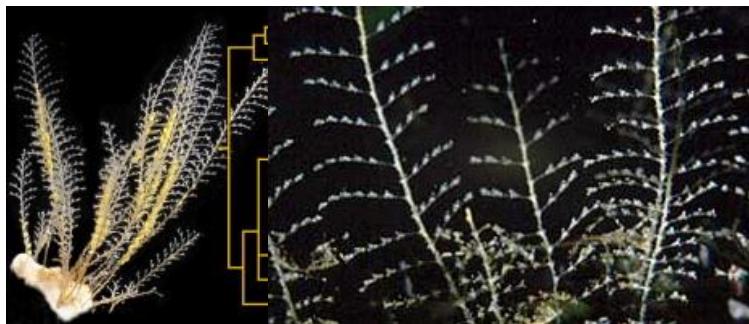
journal homepage: www.elsevier.com/locate/ympev



High genetic diversity in the hydroid *Plumularia setacea*: A multitude of cryptic species or extensive population subdivision?

Peter Schuchert

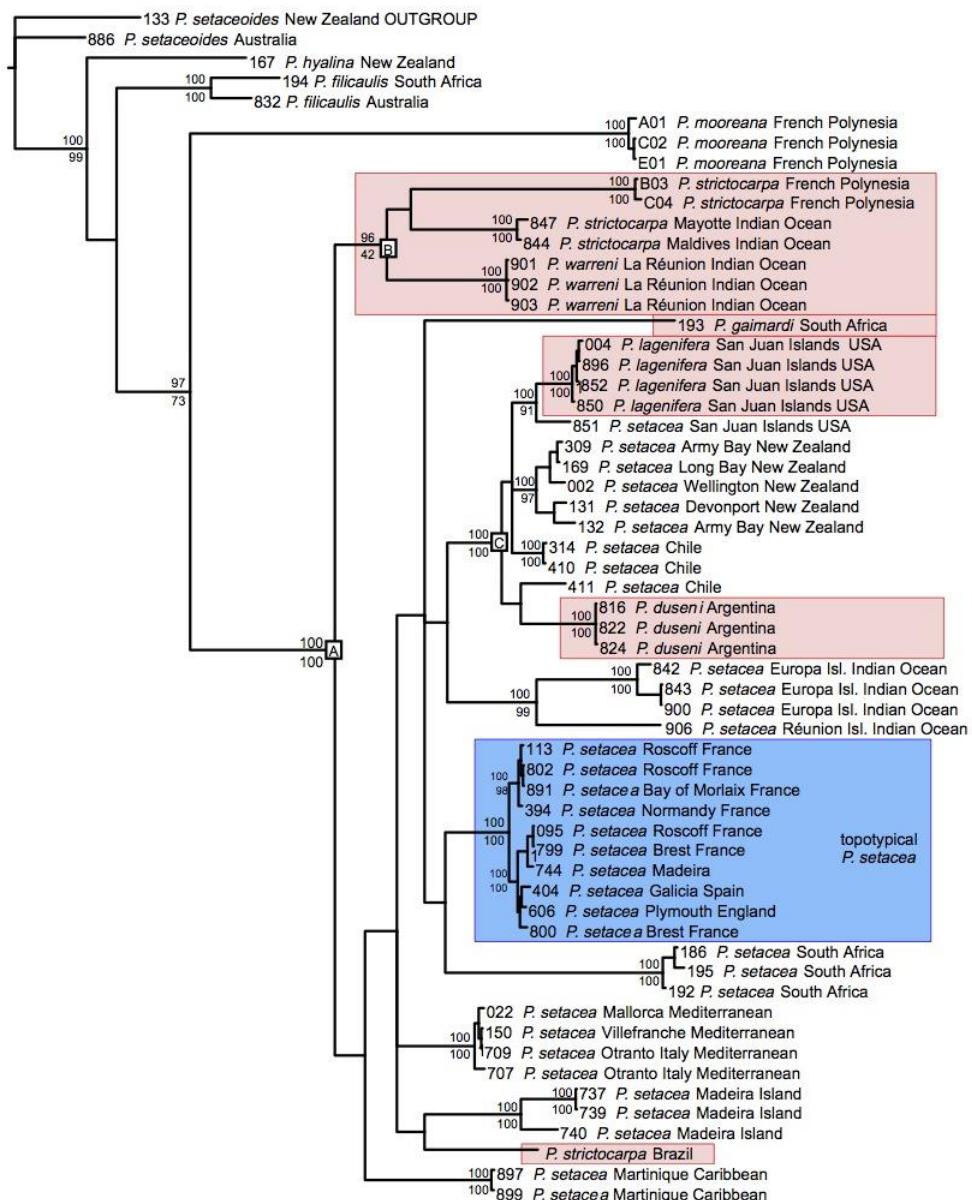
Natural History Museum of Geneva, Route de Malagnou 1, CH-1208 Geneva, Switzerland



2. Material and methods

2.1. Collection and identification of samples

Plumularia colonies were collected at various localities as given in Table 1. Identifications were made based on morphological characters using Millard (1975), Cornelius (1995), and other studies cited in Schuchert (2013a, 2013b), therefore using a morphotype species concept. One to three plumes per sample were preserved in 95% ethanol and kept at -20°C . *Plumularia gaimardi* has previously been identified as *P. cf. lagenifera* in Leclère et al. (2009; 16S sequence Genbank number FJ550491), but following Schuchert (2013a) the identification of this specimen had to be revised.

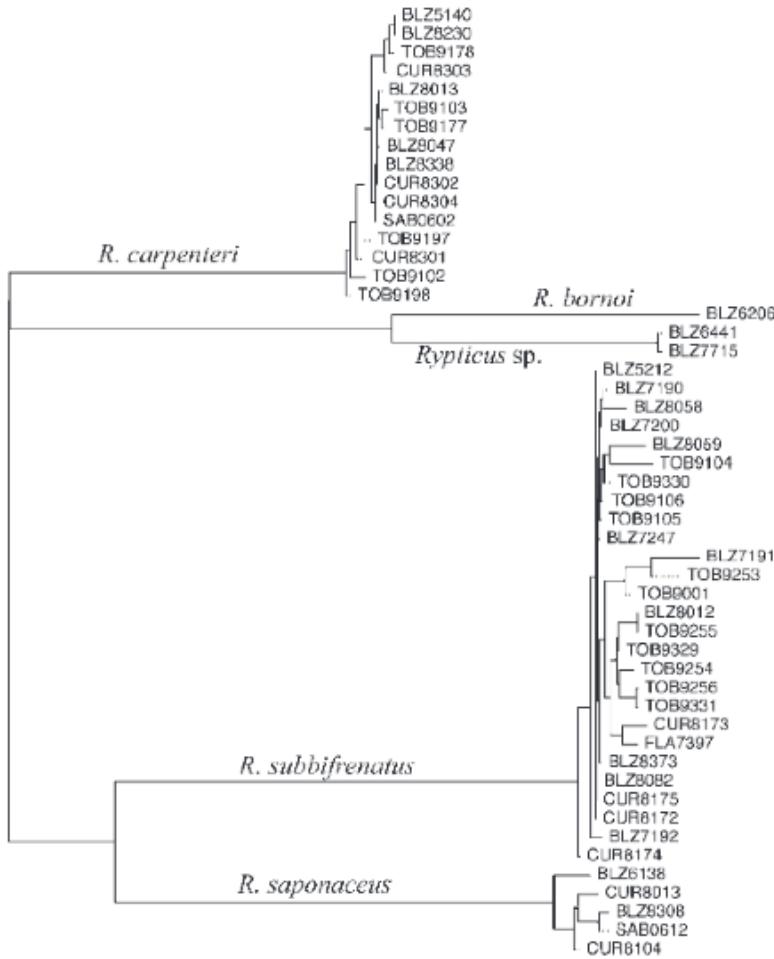


Rypticus (Animalia, O. Perciformes)

Copeia 2012, No. 1, 23–36

A New Species of Soapfish (Teleostei: Serranidae: *Rypticus*), with Redescription of *R. subbifrenatus* and Comments on the Use of DNA Barcoding in Systematic Studies

Carole C. Baldwin¹ and Lee A. Weigt²



Baldwin and Weigt—New western Atlantic species of *Rypticus*

27

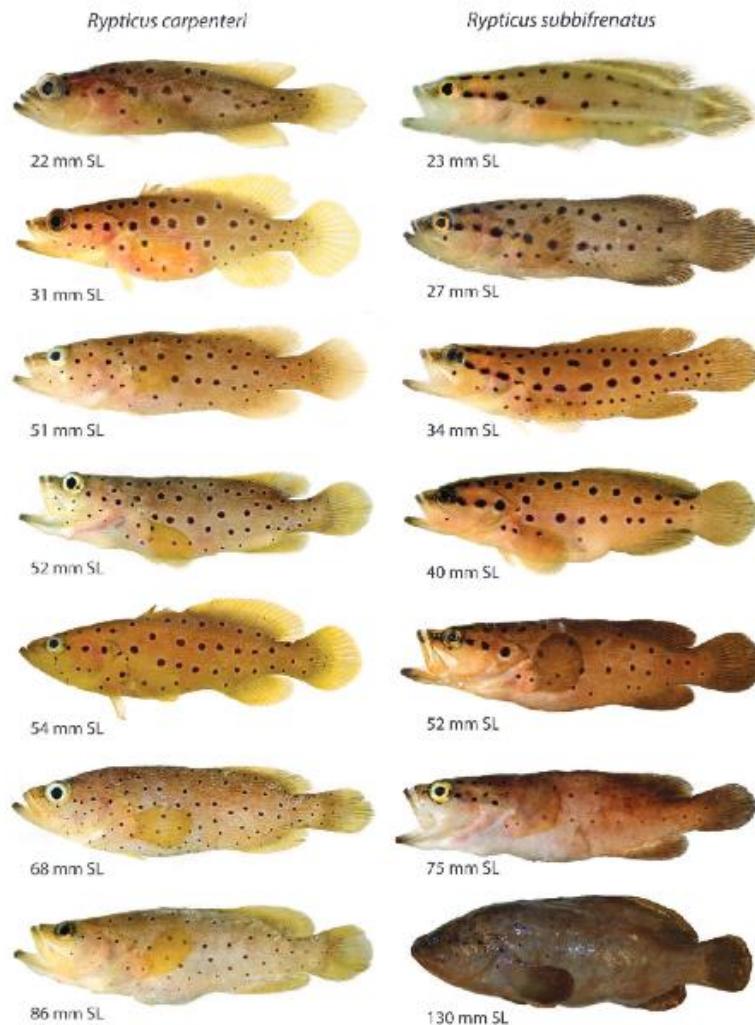
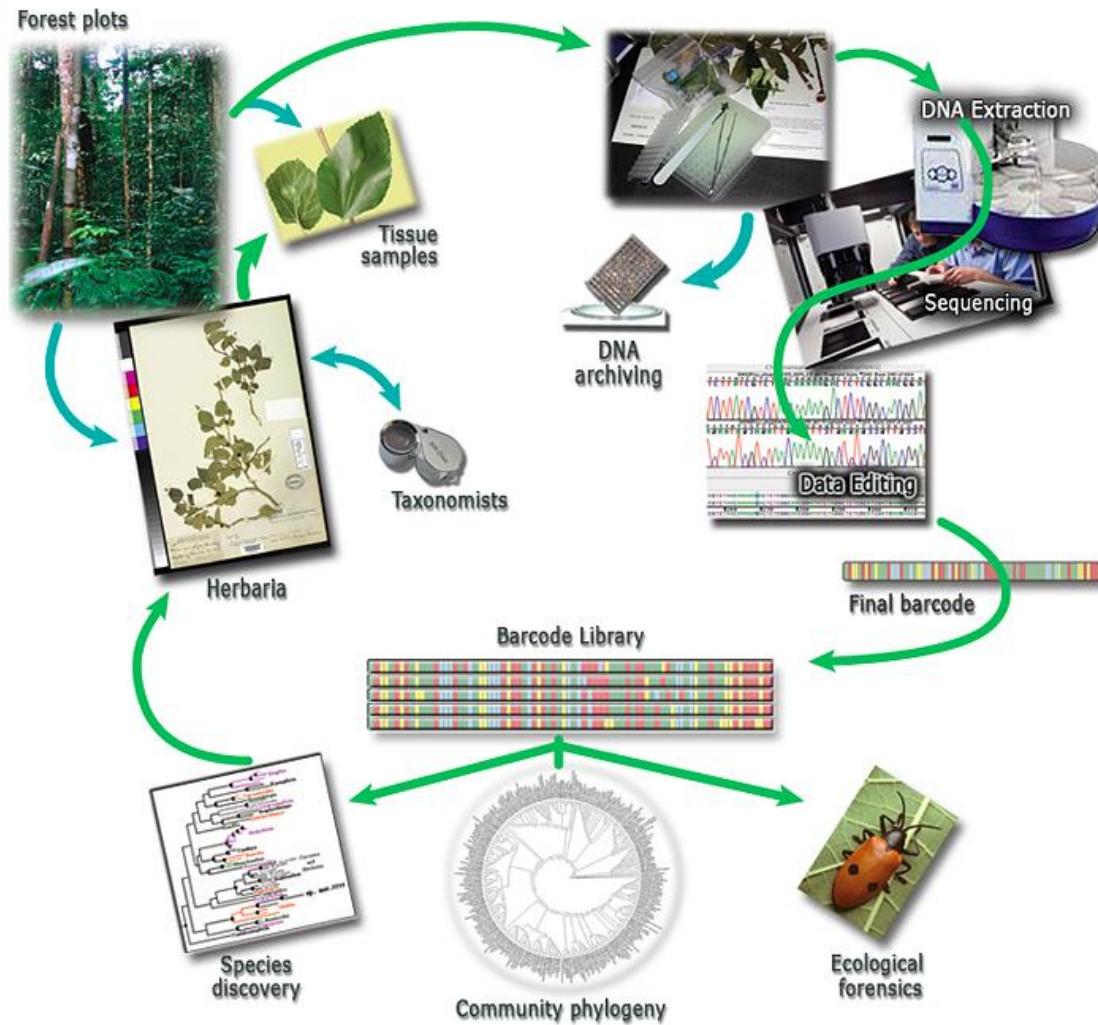
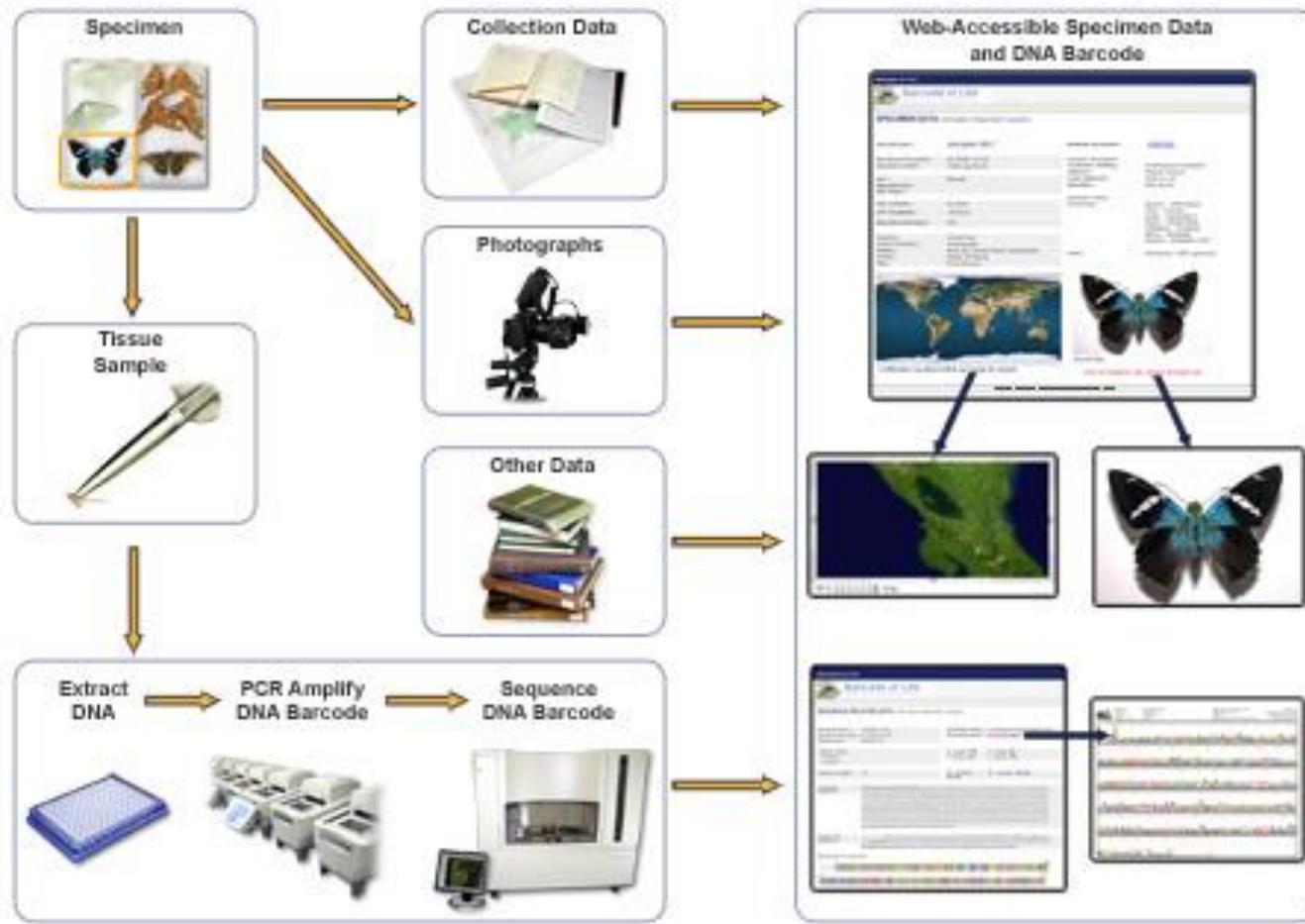


Fig. 4. Comparisons of color patterns between *Rypticus carpenteri*, new species, and *Rypticus subbifrenatus*. Left column, top to bottom: USNM 401043, DNA number CUR 8304; USNM 401040, DNA number BLZ 8230; USNM 401294, DNA number BLZ 5140 (photo by J. Mounts); USNM 401044, DNA number TOB 9103; USNM 387946, holotype (photo by J. Williams); USNM 401297, DNA number TOB 9197; USNM 401046, DNA number TOB 9178. Right column, top to bottom: USNM 401279, DNA number BAH 10090; USNM 401265, DNA number TOB 9256; USNM 401274, DNA number BLZ 5212 (photo by J. Mounts); USNM 401245, DNA number BLZ 7190 (photo by J. Mounts); USNM 401262, DNA number TOB 9106; USNM 401037, DNA number BLZ 8059; DNA number FLA 7397 (no voucher).

El papel de las colecciones de historia natural en los estudios moleculares



El papel de las colecciones de historia natural en los estudios moleculares



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