

Colecciones de tejidos y ADN

isabel.rey@csic.es



Colecciones de tejidos y ADN

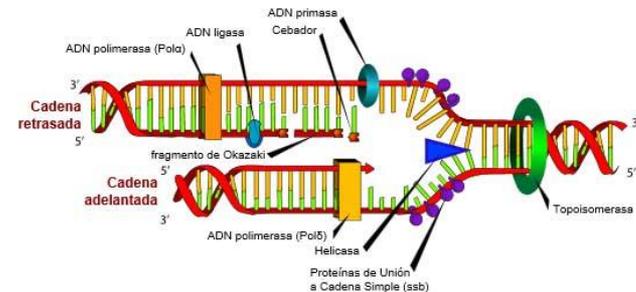
En la década de los 70 estuvieron disponibles las herramientas necesarias para cortar, pegar y copiar el ADN

Enzimas de restricción

Enzimas de ligado

Clonación

Métodos para descifrar la secuencia de nucleótidos del ADN



GILBERT & MAXAM, 1973, 1977; SANGER & COULSON, 1975; SANGER *ET AL.*, 1977

Colecciones de tejidos y ADN

El ADN es molécula donde radica la información de cada individuo y donde se almacenan las diferencias o cambios (mutaciones) que provocan la variabilidad y las diferencias específicas

Uso extensivo para estudios

Taxonomía (<http://www.barcodeoflife.org/>)

Filogenia (<http://tolweb.org/tree/>)

Microevolución y macroevolución

Genética de poblaciones



Búsqueda de componentes bioactivos naturales localizados en plantas y animales con interés para la biotecnología

Colecciones de tejidos y ADN

Durante los últimos cuarenta años del siglo pasado han aparecido un tipo de “nuevas colecciones”, denominadas de forma genérica **biobancos, colecciones de tejidos, bancos de germoplasma, bancos de recursos genéticos, biorrepositorios**, etc

Todos estos términos se han empleado tanto en ciencias biológicas como en disciplinas médicas y esto ha provocado cierta confusión entre los propios investigadores y en la sociedad en general.

Colecciones de tejidos y ADN

A priori, todas se consideran bajo un mismo paraguas porque conservan **tejidos y moléculas orgánicas o inorgánicas básicamente congeladas**; pero su finalidad y espectro de posibilidades puede ser muy diferente

Desde un biobanco de sangre de cordón umbilical hasta uno de muestras ambientales cuya finalidad es localizar contaminantes químicos

Colecciones de tejidos y ADN

Importancia

Crecimiento muy rápido

Los laboratorios se quedan sin espacio

Almacenado en condiciones no optimas

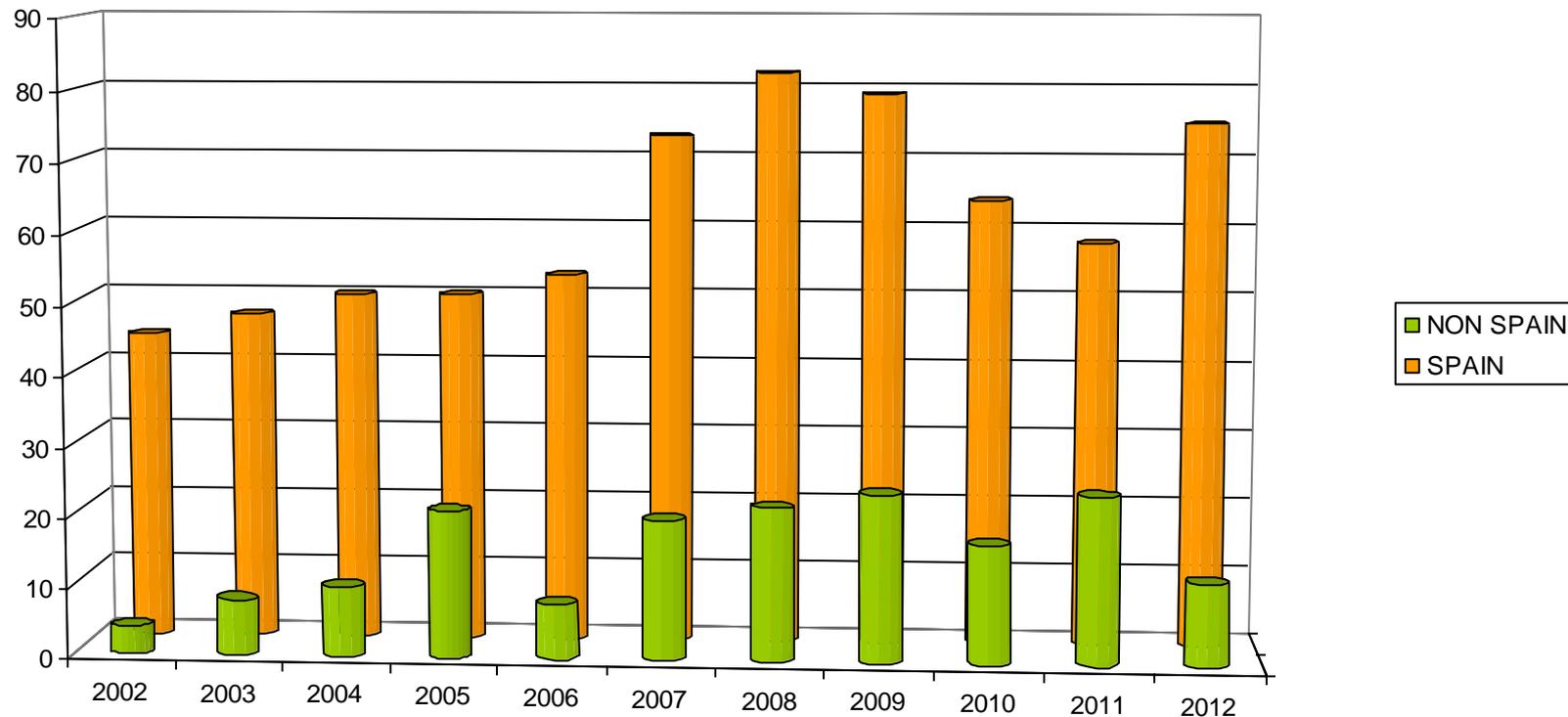
Documentación variable - disociación

Dispersos a través de la institución

Gestionado por investigadores individuales

Sin estrategia de conservación a largo plazo

Colecciones de tejidos y ADN



Colecciones de tejidos y ADN

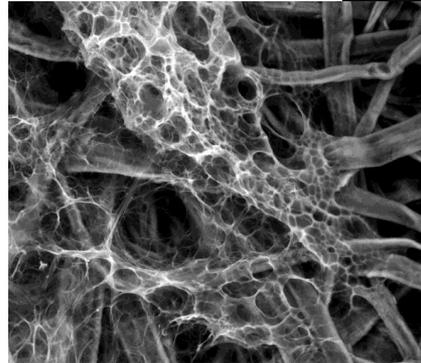
- The Cryogenic Collection The Museum of Comparative Zoology (MCZ) at Harvard University 1973
- MVZ Tissue Collection, Museum of Vertebrate Zoology. University of California, Berkeley 1973
- South Australian Biological Tissue Collection (ABTC) 1979
- Colección de Tejidos y ADN, MNCN 2000
- The Ambrose Monell Collection for Molecular and Microbial Research, AMNH 2001
- Molecular and Frozen Tissues, NHM London 2011

Colecciones de tejidos y ADN

- En la actualidad se conocen alrededor de 100 instituciones con colecciones de tejidos y ADN exclusivamente de biodiversidad.



La colección de Tejidos y ADN del MNCN



HV Spot WD VacMode 100.0µm
25.0 kV 6.0 7.5 mm Low vacuum ADN-Calamar-01



MÉTODOS DE CONSERVACIÓN

SECO	Tarjetas FTA	Tejido / ADN
	Silica gel	Tejido
	Liofilizados	Tejido / ADN
FLUIDO	Alcohol etílico 96-70%	Tejido
	Tampón DMSO o EDTA	Tejido
CONGELADO	-80° C, -20° C	Tejido / ADN



MÉTODOS DE CONSERVACIÓN

SECO	Tarjetas FTA	Tejido / ADN
	Silica gel	Tejido
	Liofilizados	Tejido / ADN
FLUIDO	Alcohol etílico 96-70%	Tejido
	Tampón DMSO o EDTA	Tejido
CONGELADO	-80° C, -20° C	Tejido / ADN

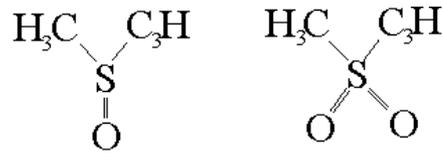


MÉTODOS DE CONSERVACIÓN

SECO	Tarjetas FTA	Tejido / ADN
	Silica gel	Tejido
	Liofilizados	Tejido / ADN
FLUIDO	Alcohol etílico 96-70%	Tejido
	Tampón salino con DMSO	Tejido
CONGELADO	-80° C, -20° C	Tejido / ADN



DMSO



DIMETHYL SULFOXIDE



SEUTIN G., WHITE B.N., BOAG P.T. Preservation of avian blood and tissue samples for DNA analyses. *Canadian Journal of Zoology* (1991) 69:82–90

HUMASON, GRETCHEN L. 1997 *Humason's Animal Tissue Techniques*

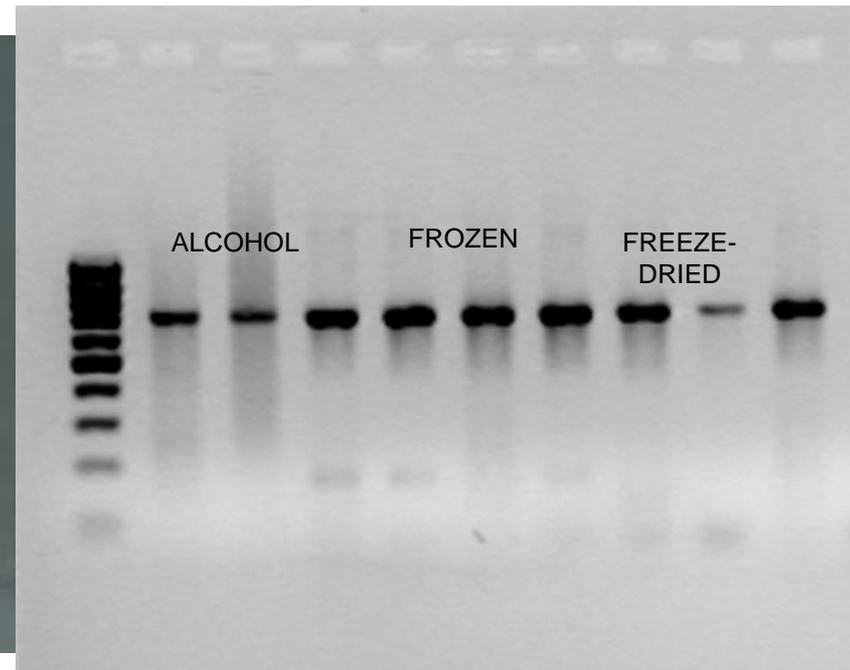
MÉTODOS DE CONSERVACIÓN

SECO	Tarjetas FTA	Tejido / ADN
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FLUIDO	Alcohol etílico 96-70%	Tejido
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CONGELADO	-80° C, -20° C	Tejido / ADN



MÉTODOS DE CONSERVACIÓN

SECO	Tarjetas FTA	Tejido / ADN
	Silica gel	Tejido
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FLUIDO	Alcohol etílico 96-70%	Tejido
	Tampón salino con DMSO	Tejido
CONGELADO	-80° C, -20° C	Tejido / ADN



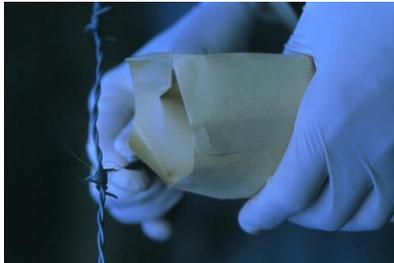
ORIGEN DE LOS FONDOS

Proyectos de investigación

Centros de recuperación de fauna

Zoológicos y acuarios

Decomisados

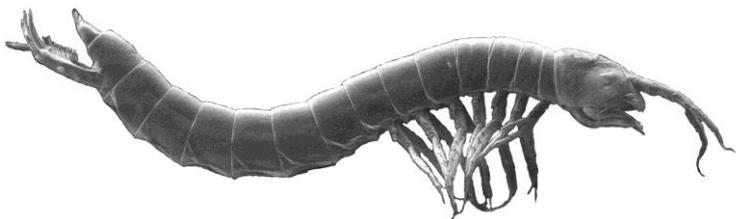


ORIGEN DE LOS FONDOS

Colecciones clásicas

Conservados en fluidos

Especímenes en seco



Quaternary International 179-200 (2008)

CATÁLOGO DE LAS MUESTRAS DE FAUNA DE LA COMUNIDAD DE MADRID CONSERVADAS EN LA COLECCIÓN DE TEJIDOS Y ADN DEL MUSEO NACIONAL DE CIENCIAS NATURALES

I. Rey* y B. A. Dorda**

Contribución to Zoology, 71 (1) 123-129 (2005)
© 2005 Academic Publishing Inc. The Hong Kong

A note on the systematic position of the Bathynellacea (Crustacea, Malacostraca) using molecular evidence

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Keywords: Systematics, Crustacea, Malacostraca, Bathynellacea, 16S rDNA.

Abstract

Molecular data for the mt 16S rDNA gene fragment of a bathynellacean is here presented for the first time and used to analyze the relationships of the group.

lar, it usually homogeneous amongst the specialists. The traditional way of working is to use the latest information or the latest hypothesis published in order to select those views that are going to be compared. However, it must be universal that where there is more than one taxonomist working on a group there will not be a single hypothesis or interpretation of the group's descent. How big or small are these inter- and intra-specific differences and does it not invalidate this universal law.

The group known as "Bathynellacea" (Serban, 1972) is a good example of the above. First discovered by Vojvodsky (1822), their systematic position has been a problem since then. They were considered an "aberrant" member of Malacostraca (Calkins, 1909). Although nobody knows what "aberrant" members in evolution are, the term generally implies organisms that do not fit well into our limited reconstructed ground patterns. Other authors have designated them as simplified taxa (see Schminke, 1981). However, the morphological taxonomist that most deeply studied the internal and external morphology of the Bathynellacea, Eugene Serban, never joined the Bathynellacea with the Sycoraxia, but proposed a more radical model of relationships (Serban, 1970, 1972): the order Bathynellacea in his scheme would belong to the superorder Podophthalmea Serban, 1970 under the infra-class Eumalacostraca Serban, 1972. True Sycoraxia, on the other hand, would be placed by Serban under a different infra-class, the Ammonostraca.

In this paper we present the first nucleotide data for a bathynellacean species and we discuss the results of an analysis of the mt 16S rDNA data for the other malacostracans.

Introduction

In museums and taxonomic collections, water mites (Acari: Parasitengona, Hydrachnida) are usually, but not always, mounted on microscope slides or preserved in Koenig's fluid (a mixture of acetic acid, glycerine and water; Barr 1973; Smith et al. 2001). Microscope slides are the preferred method, but very commonly the "liquid collection" is larger. Alcohol can be used to preserve most Acari, but this medium is unsuitable for Hydrachnida, leaving specimens in poor condition for dissection and mounting on slides. Formal is even worse. A little used fixative, Angster's fluid (mixture of water, chromic acid and acetic acid) can be used for whole benthic samples (Valdecasas and Battaglia 1999) for water mites separated from such samples. It is particularly useful during field work since it can be concentrated, making it easier to transport. Preserving mites frozen in water is also a possibility.

To date, molecular research on the Hydrachnida (Otto and Wilson 1999; Söder et al. 2001) has been performed with fresh material. No trials on the feasibility of extracting and sequencing DNA from mites preserved in the above fixatives have been performed. The aim of the present work was to determine the suitability of Koenig's fluid, Angster's fluid, alcohol and frozen water in this respect.

Estimotool and Applied Anatomy, 34: 19-21, 2004.
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Traditional water mite fixatives and their compatibility with later DNA studies

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¹Museo Nacional de Ciencias Naturales (MNCN), Depto. de Colecciones, C/ José Gutiérrez Abascal 2, 28002 Madrid, Spain; ²Museo Nacional de Ciencias Naturales (MNCN), Depto. Biodiversidad y Biología Evolutiva, C/ José Gutiérrez Abascal 2, 28002 Madrid, Spain; ³Author's address determined at time of printing; ⁴Museo Nacional de Ciencias Naturales (MNCN), Depto. de Colecciones, C/ José Gutiérrez Abascal 2, 28002 Madrid, Spain; ⁵Author for correspondence: e-mail: valdecasas@mncn.csic.es

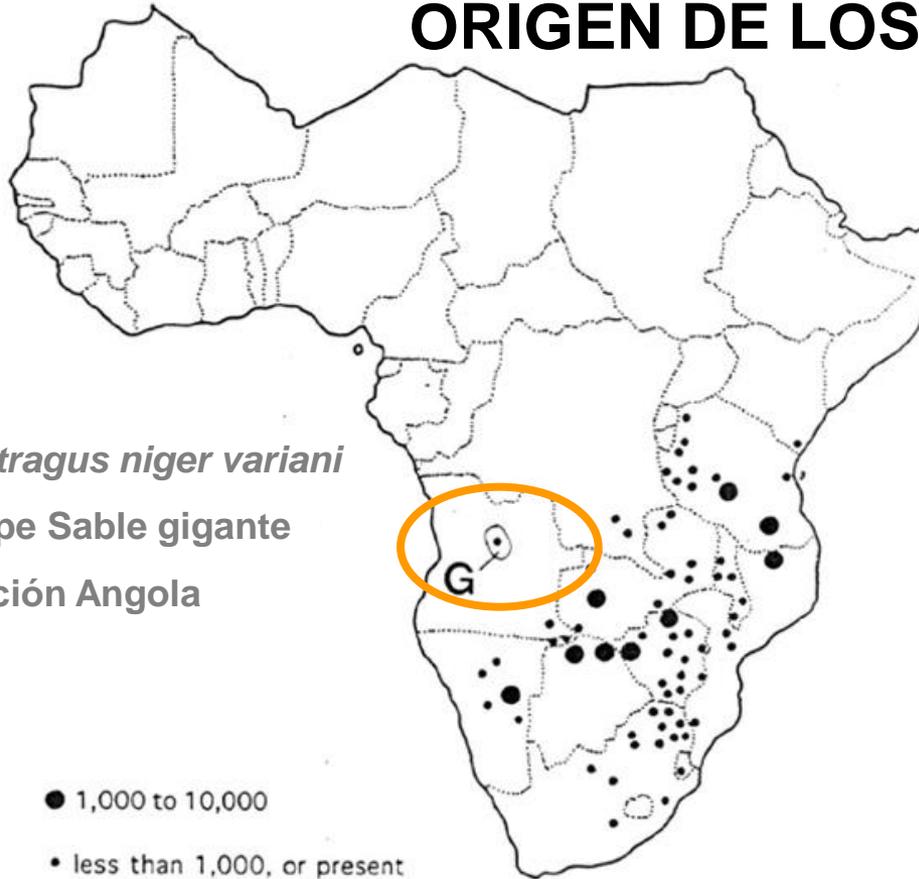
Key words: 16S, Angster's fluid, Cal, Hydrachnida, Koenig's fluid

Abstract. This work compares formal water, 70% alcohol, Koenig's and Angster's fluid as preservation media for water mites in terms of their eventual facilitation of DNA extraction and preservation. The time the mites spent in the fixative ranged between 1 week and 24 years. Two nucleotide markers were amplified: 16S ribosomal DNA and Cal mitochondrial DNA. DNA was extractable and could be sequenced from specimens fixed in all the above media, although this was generally more difficult as time progressed. In the light of the known characteristics of these media, the results suggest Angster's fluid to be the most practical, especially on long expeditions.

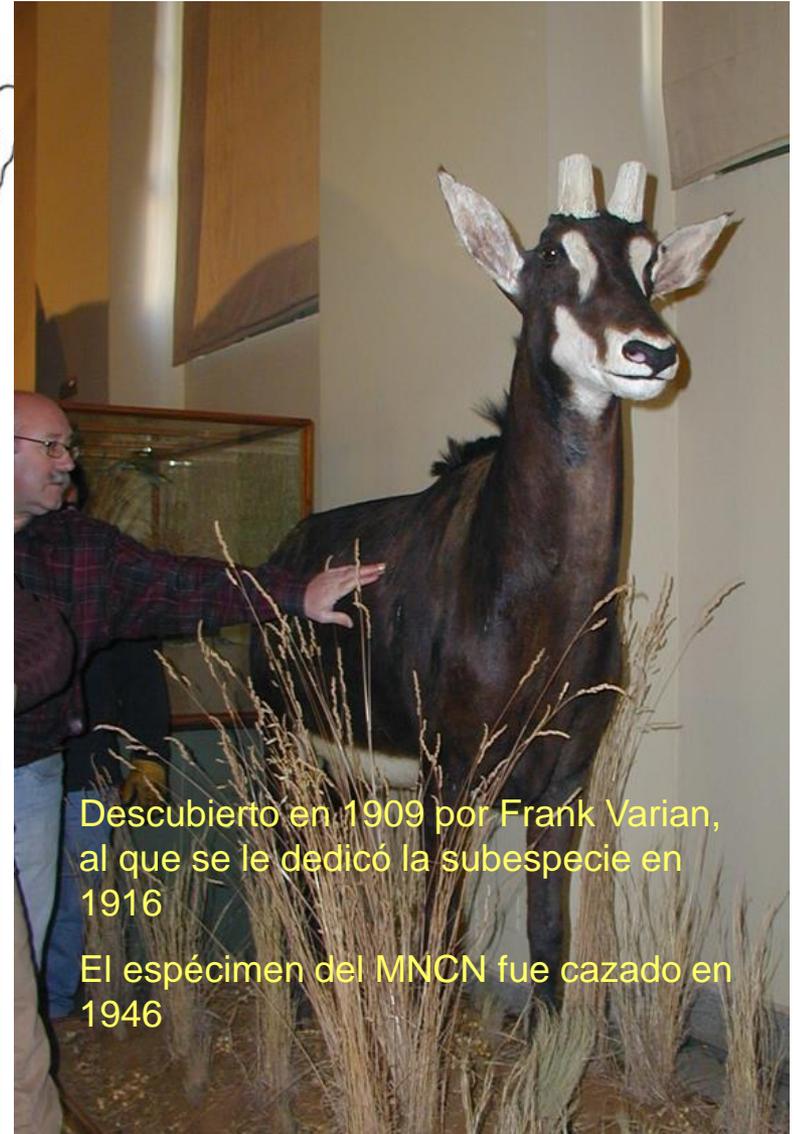
7/1/2002 HV Spot Mag WD Det
1:00:02 PM 20.0 kV 5.0 352x10.3 mm LFD 1.0mm

ORIGEN DE LOS FONDOS

Hippotragus niger variani
Antílope Sable gigante
Población Angola



Colecciones clásicas



Descubierto en 1909 por Frank Varian,
al que se le dedicó la subespecie en
1916

El espécimen del MNHN fue cazado en
1946

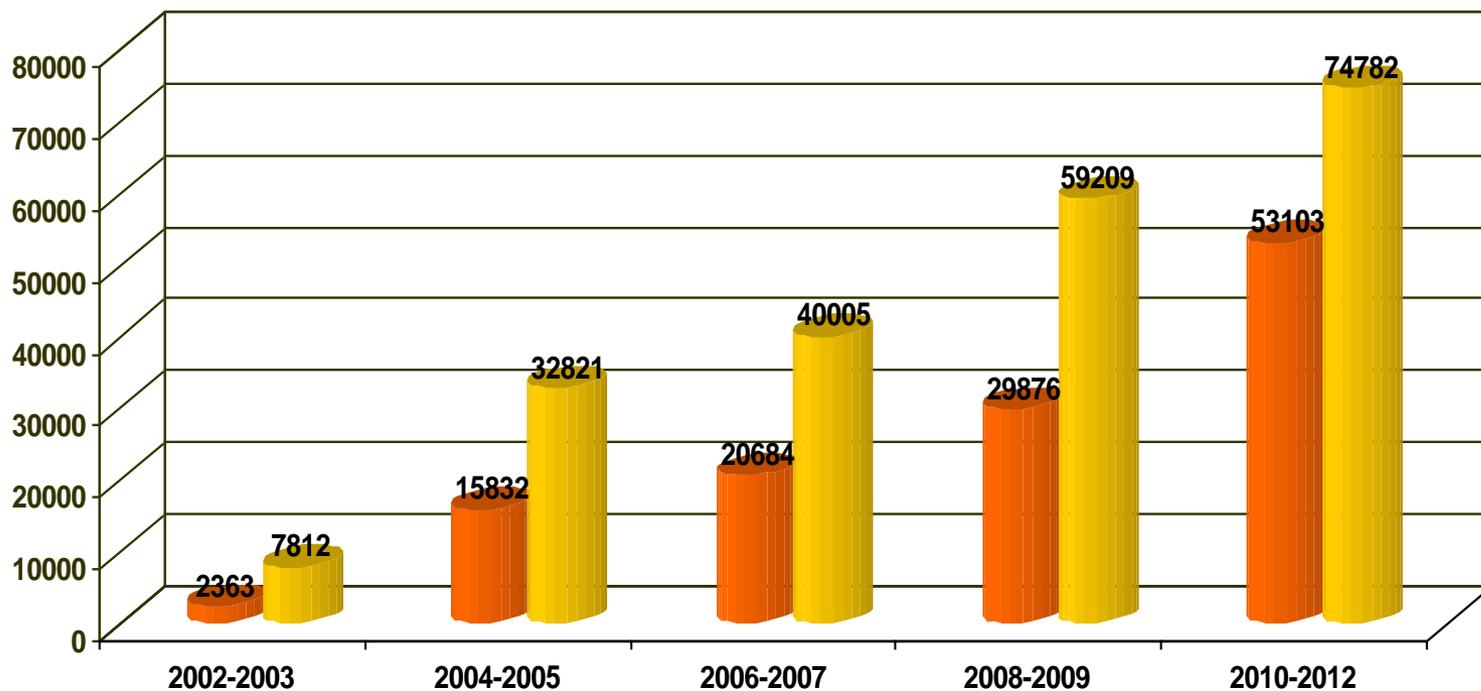
ORIGEN DE LOS FONDOS

Colecciones clásicas



Cymbiola aulica (Sowerby I, 1825)





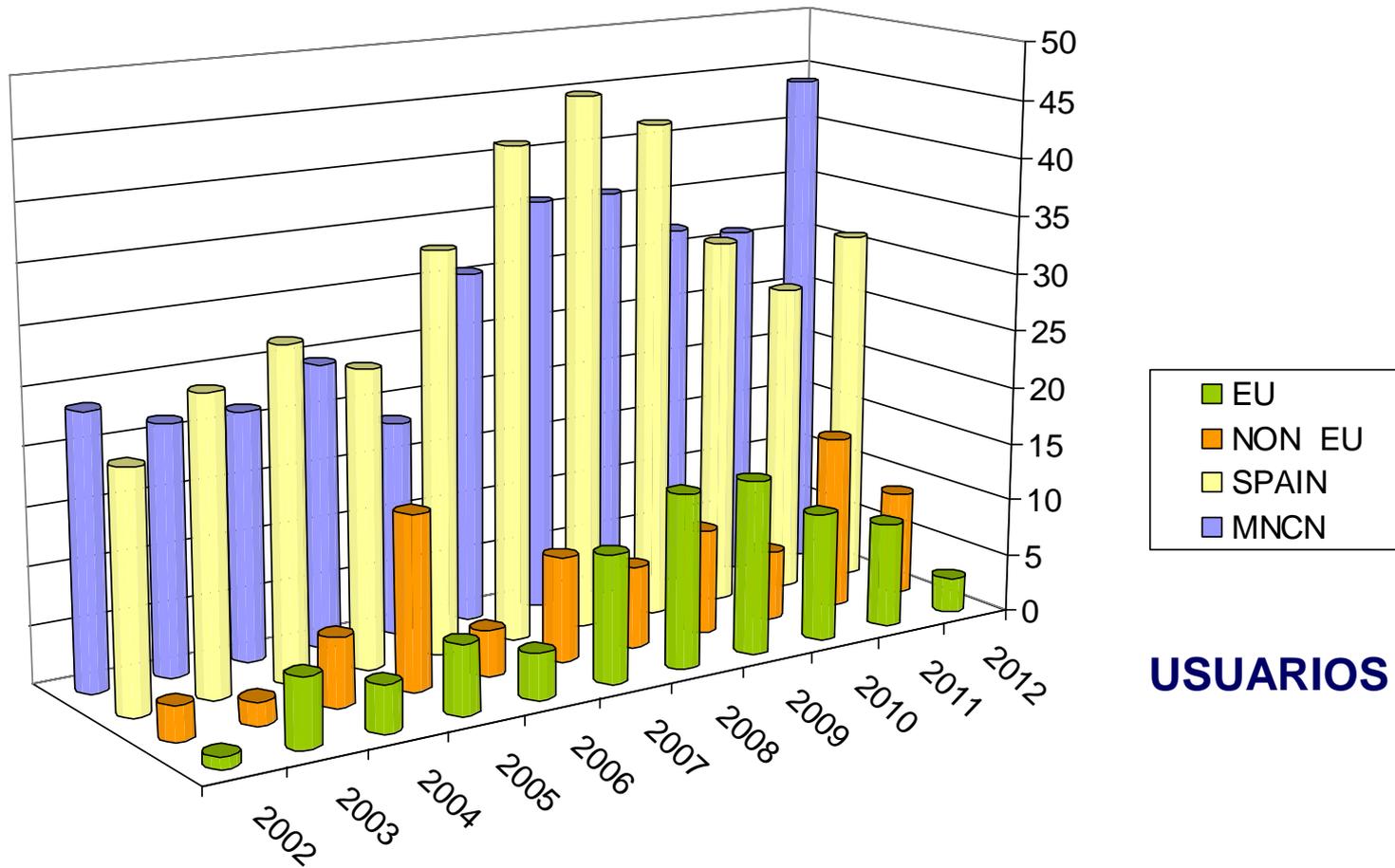
Especímenes 57.220

Muestras 85.523

Tipos 132

Especies 4.900

12.445 especímenes, están disponibles en www.gbif.es



USUARIOS

Especímenes prestados 10.500

Search across databases

MNCN

GO

Clear

Help

- Result counts displayed in gray indicate one or more terms not found

217



PubMed: biomedical literature citations and abstracts



none



Books: online books



none



OMIM: online Mendelian Inheritance in Man

70



PubMed Central: free, full text journal articles

3



Site Search: NCBI web and FTP sites

7935



Nucleotide: Core subset of nucleotide sequence records



none



dbGaP: genotype and phenotype

none



EST: Expressed Sequence Tag records



none



UniGene: gene-oriented clusters of transcript sequences

none



GSS: Genome Survey Sequence records



none



CDD: conserved protein domain database

5763



Protein: sequence database



none



Clone: integrated data for clone resources

none



Genome: whole genome sequences



none



UniSTS: markers and mapping data

none



Structure: three-dimensional macromolecular structures



275



PopSet: population study data sets

none



Taxonomy: organisms in GenBank



GEO DataSets: expression and molecular abundance profiles

none



SNP: short genetic variations



none



Epigenomics: Epigenetic maps and data sets

none



dbVar: Genomic structural variation



none



PubChem BioAssay: bioactivity screens of chemical substances

52



Gene: gene-centered information



none



PubChem Compound: unique small molecule chemical structures

none



SRA: Sequence Read Archive



none



PubChem Substance: deposited chemical substance records

none



BioSystems: Pathways and systems of interacting molecules



none



Protein Clusters: a collection of related protein sequences

none



HomoloGene: eukaryotic homology groups



none



OMIA: online Mendelian Inheritance in Animals

none



Probe: sequence-specific reagents



none



Go to PopSet Results Page

El número de catálogo de la colección es un número de resguardo o *voucher number* que se le asigna a un fragmento de tejido o al contenido genómico de un espécimen



ADN



Colectión de Tejidos y ADN

Especie:

Filum: Clase: Orden: Familia:

Localidad:

Provincia: País:

Coordenadas:

Datos del colector

Nombre: País:

N° col.: N° tejido/ADN: Fecha captura:

Procedencia:

Referencias: Instrucción:

Observaciones: Estado:

N° de extracciones: Fecha de extracción: Etiqueta:

Historial de préstamos: Informada: Estado:

Ubicación:

Nº orden	Tipo de tejido	Sala	Ubicación	Puerta	Balda	Rack	Capón	Caja	Posición
14429	ADN	1	Complejo 02		A	2	A	1	15
14430									

Registro: de 1

Fitze et al. BMC Evolutionary Biology 2011, 11:347
<http://www.biomedcentral.com/1471-2148/11/347>



RESEARCH ARTICLE

Open Access

Integrative analyses of speciation and divergence in *Psammodromus hispanicus* (Squamata: Lacertidae)

Patrick S. Fitze^{1,2,3,4*}, Virginia González-Jimena^{2,3}, Luis M. San-José^{2,3}, Diego San Mauro⁵, Pedro Aragón¹, Teresa Suárez⁶ and Rafael Zardoya²

Abstract

Background: Genetic, phenotypic and ecological divergence within a lineage is the result of past and ongoing evolutionary processes, which lead ultimately to diversification and speciation. Integrative analyses allow linking diversification to geological, climatic, and ecological events, and thus disentangling the relative importance of different evolutionary drivers in generating and maintaining current species richness.

Results: Here, we use phylogenetic, phenotypic, geographic, and environmental data to investigate diversification in the Spanish sand racer (*Psammodromus hispanicus*). Phylogenetic, molecular clock dating, and phenotypic analyses show that *P. hispanicus* consists of three lineages. One lineage from Western Spain diverged 8.3 (2.9-14.7) Mya from the ancestor of *Psammodromus hispanicus edwardsianus* and *P. hispanicus hispanicus* Central lineage. The latter diverged 4.8 (1.5-8.7) Mya. Molecular clock dating, together with population genetic analyses, indicate that the three lineages experienced northward range expansions from southern Iberian refugia during Pleistocene glacial periods. Ecological niche modelling shows that suitable habitat of the Western lineage and *P. h. edwardsianus* overlap over vast areas, but that a barrier may hinder dispersal and genetic mixing of populations of both lineages. *P. h. hispanicus* Central lineage inhabits an ecological niche that overlaps marginally with the other two lineages.

Conclusions: Our results provide evidence for divergence in allopatry and niche conservatism between the Western lineage and the ancestor of *P. h. edwardsianus* and *P. h. hispanicus* Central lineage, whereas they suggest that niche divergence is involved in the origin of the latter two lineages. Both processes were temporally separated and may be responsible for the here documented genetic and phenotypic diversity of *P. hispanicus*. The temporal pattern is in line with those proposed for other animal lineages. It suggests that geographic isolation and vicariance played an important role in the early diversification of the group, and that lineage diversification was further amplified through ecological divergence.

Background

Species diversity emerges from the combination of both past and ongoing evolutionary and ecological processes driving speciation [1-3]. However, it is challenging to determine the relative contributions of historical and ecological factors in causing genetic differentiation [4]. The traditional classification of modes of speciation (allopatric, peripatric, parapatric, and sympatric) within

a spatial context [5,6] is currently revisited in the light of recent studies that integrate phylogenetic, ecological, and geographical data [3,7,8]. In the last decade, evolutionary biologists have focused on discerning the mechanisms leading to reproductive isolation, and the field has witnessed major advances in determining the relative contribution of historical geographic barriers to diversification thanks to the possibility of linking geological and phylogenetic data [9]. In contrast, the elucidation of the contribution to diversification of ecologically-based divergent selection due to environmental differences has been hindered until recently by

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 Full list of author information is available at the end of the article



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region shown

size view

this sequence

ST

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Sequence Features

is Sequence

Change region shown

Customize view

Analyze this sequence

Run BLAST

Pick Primers

Highlight Sequence Features

Find in this Sequence

Related information

Related Sequences

Full text in PMC

PopSet

PubMed

Taxonomy

Recent activity

- Psammodromus edwardsianus locus 17 genomic sequence
- Psammodromus edwardsianus suppressor of SWI 1-like gene
- Psammodromus edwardsianus NADH dehydrogenase subunit
- Microthya sp. MICHN DNA 284 (proteome:leocottin (prot))
- MICHN DNA 2011 (51)

PopSet

PopSet

Limits Advanced

Search

Help

Display Settings: PopSet

Send to:

Vejdovskybathynella cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial.

PopSet: 321271096

GenBank FASTA

Go to:

Study Details

Undisclosed Taxonomic Diversity of Bathynellacea (Malacostraca:Syncarida) in the Iberian Peninsula Revealed by Molecular Data

Camacho,A.I., Dorda,B.A. and Rey,I.
(2012) J. Crust. Biol. 32:(5)816-826

Go to:

Sequences in this data set

- [HQ596574.1](#) Vejdoskybathynella sp. ABI 2010b bio-material MNCN:DNA:29524 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
- [HQ596572.1](#) Vejdoskybathynella sp. ABI 2010c bio-material MNCN:DNA:29487 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
- [HQ596570.1](#) Vejdoskybathynella edelweiss bio-material MNCN:DNA:29414 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
- [HQ596568.1](#) Vejdoskybathynella edelweiss bio-material MNCN:DNA:29543 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
- [HQ596566.1](#) Vejdoskybathynella edelweiss bio-material MNCN:DNA:29479 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
- [HQ596564.1](#) Vejdoskybathynella edelweiss bio-material MNCN:DNA:29415 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
- [HQ596573.1](#) Vejdoskybathynella sp. ABI 2010a bio-material MNCN:DNA:29523 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
- [HQ596571.1](#) Vejdoskybathynella edelweiss bio-material MNCN:DNA:29440 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
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- [HQ596567.1](#) Vejdoskybathynella edelweiss bio-material MNCN:DNA:29482 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
- [HQ596564.1](#) Vejdoskybathynella edelweiss bio-material MNCN:DNA:29415 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
- [HQ596563.1](#) Vejdoskybathynella edelweiss bio-material MNCN:DNA:29366 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial

Analyze this data set

Run BLAST alignment

Related information

Nucleotide

Protein

Taxonomy

Recent activity

Turn Off Clear

- Vejdoskybathynella cytochrome oxidase subunit I (COI) gene, partial cds; mitoc PopSet
- Neobatrachia 16S ribosomal RNA gene, partial sequence; mitochondrial. PopSet
- Proctoporus 12S ribosomal RNA gene, partial sequence; mitochondrial. PopSet
- MNCN (275) PopSet
- MNCN (52) Gene

See more...

You are here: NCBI > DNA & RNA > PopSet

Write to the Help Desk

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Genetic Testing Registry

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Research at NCBI

NCBI Handbook

Especie: *Eugaster spinulosa* (Johannson, 1763) CITES

Filum: Arthropoda Clase: Insecta Orden: Orthoptera Familia: Tettigoniidae

Localidad: Colinas Jbilet. Carretera de Marrakech a Casablanca

Provincia: País: Marruecos

Coordenadas: N 31° 49' 08" / W 007° 58' 30.3"

Datos del colector
R. Márquez, J.F. Beltrán Gala, H. El Mouden, A. Fattah

N° col.: Eug 2 N° tejido/ADN: Fecha captura: 1/05/2009

Procedencia: R. Márquez

Referencias:

Observaciones: **CÓDIGO FONOTECA 9015, 9019, 9020, 9021, 9022, 9025**
527 m. de altitud

N° de entrada: 31/2009 Fecha de entrada: 2/06/2009

Historial de préstamo:

Ubicación:

N° orden	Tipo de tejido	Ubicación	Balda	Rack	Cajón	Caja	Posición
7283		Congelador 01	C	6	A	3	32
7283		Congelador 01	C	6	A	3	33

N° de orden: 7283

N° otra colección: MNCN:ENT 73569

Sexo: Macho Edad:

Extracción ADN: [ADN]:

Fecha: Tipo:

Extraído por:

Informatizado por: Beatriz Alvarez Julio 2009

Volcado CBIF: Fecha:

Acceso: Libre

Cerrar ficha

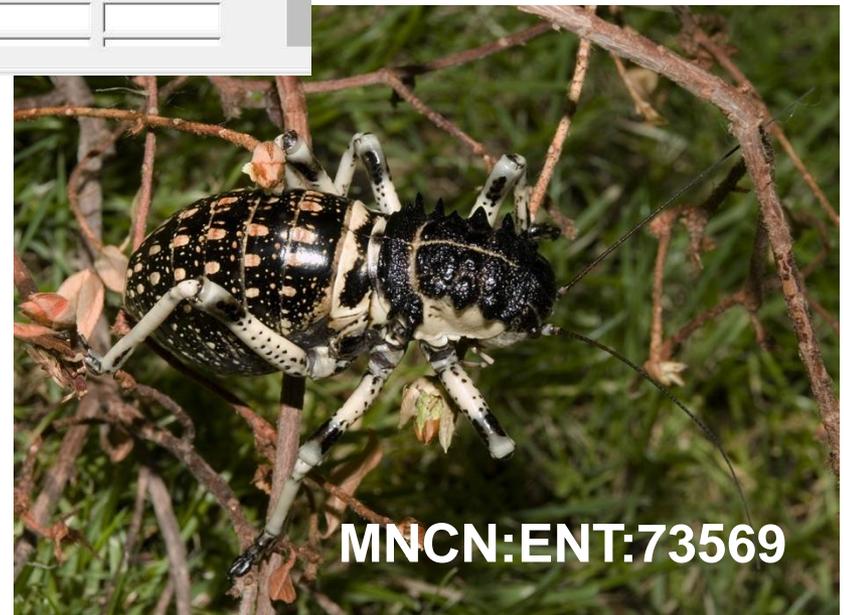
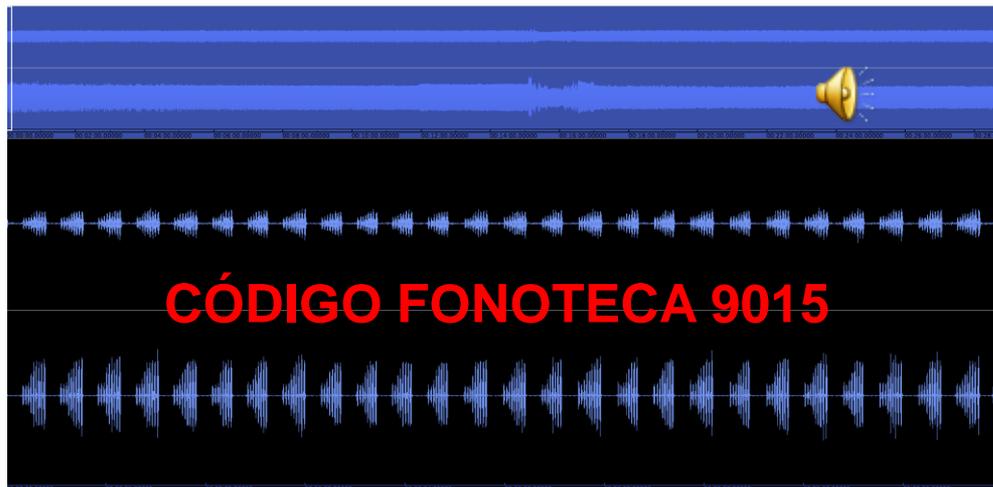
Duplicar registro

GenBank Accession Numbers:

Voucher Number: 7283

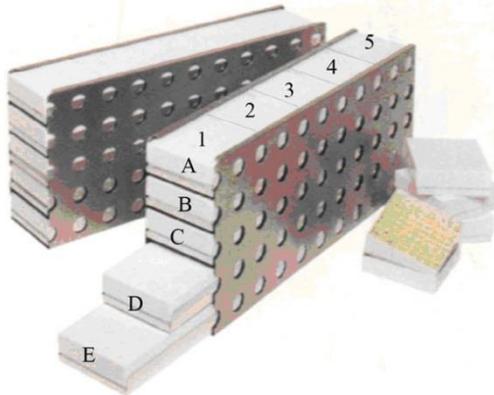
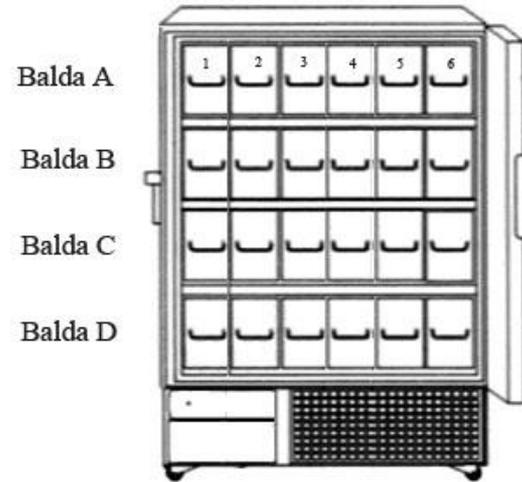
registro: 7043 de 55472

MNCN:ADN:7283



Congeladores: muestras de tejido y ADN congelado

- Baldas (A -D)
- Racks (1-6)
- Cajones (A -E)
- Cajas (1-5)







Laboratorio de Identificación Molecular

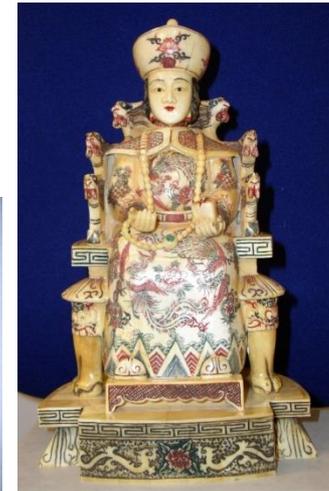
Determinación del sexo (aves y mamíferos)

Identificación de especies (ADN mitocondrial)

Identificación individual y paternidades (microsatélites)

ADN antiguo

Investigación sobre conservación preventiva



Muestras frescas

Manchas de sangre

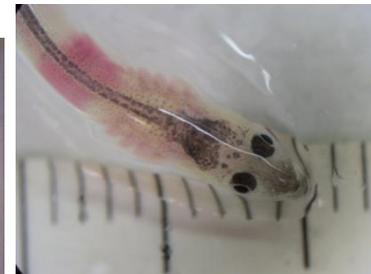
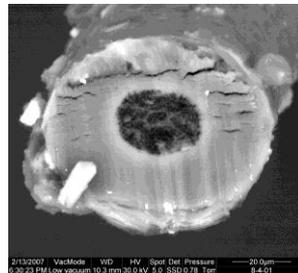
Plumas

Pelo

Hueso / Marfil

Piel

Madera



ADN antiguo

“Cultura Moche”



Falange (1400 a 1500 años AD) “Huaca del Sol y Luna”







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