

# Aplicación de herramientas moleculares en muestras antiguas: oportunidades y desafíos.

Dr. Sebastián Tambusso  
Dra. Federica Moreno

Departamento de Biodiversidad y Genética, Instituto de Investigaciones Biológicas Clemente Estable-MEC

Departamento de Paleontología, Facultad de Ciencias, Universidad de la República

Departamento de Arqueología, Facultad de Humanidades y Ciencias de la Educación- Universidad de la República

**Aplicaciones moleculares para la conservación de fauna nativa del Uruguay.**



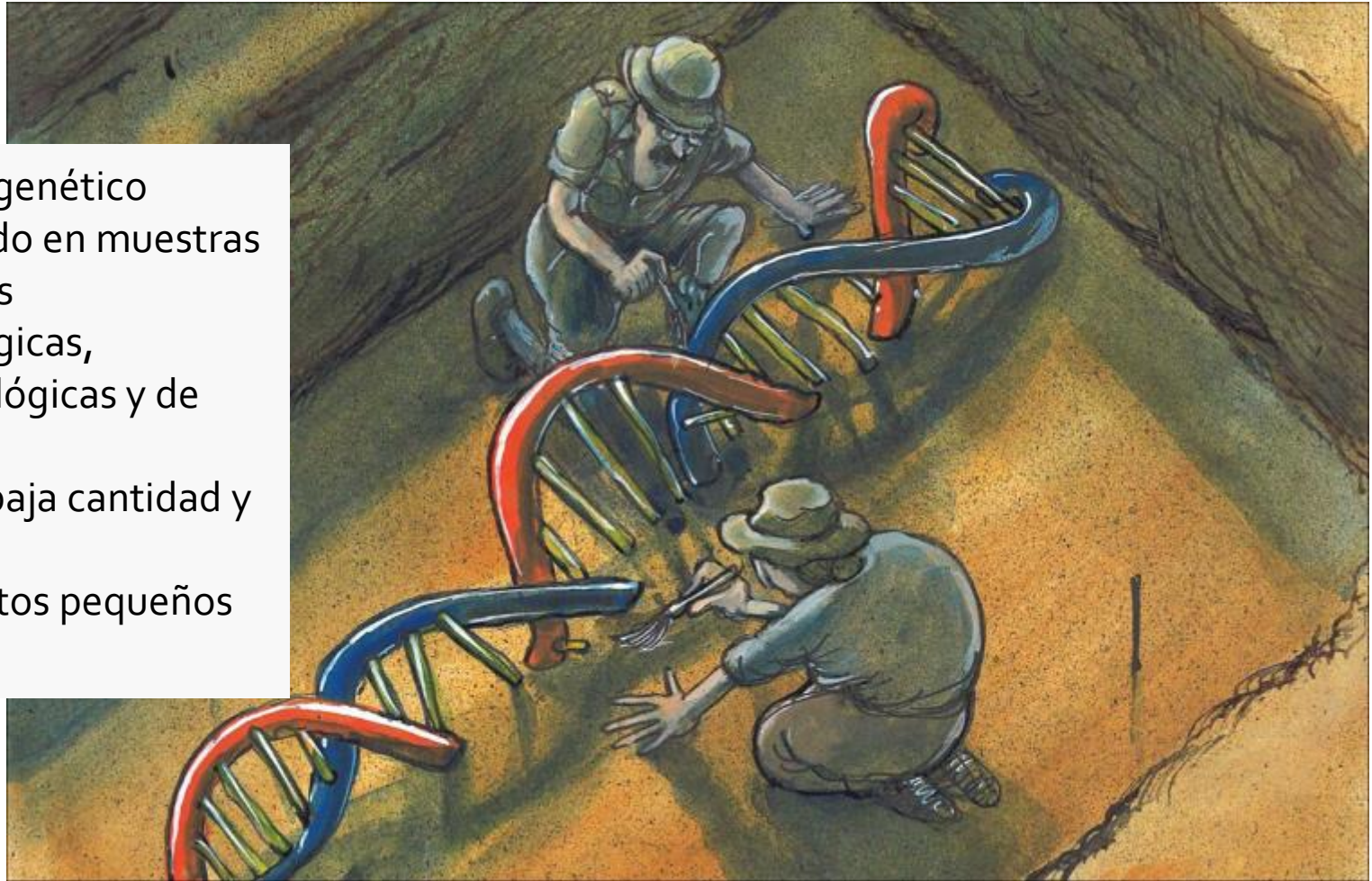
Programa de  
Desarrollo de las  
Ciencias Básicas



Ministerio  
de Educación  
y Cultura

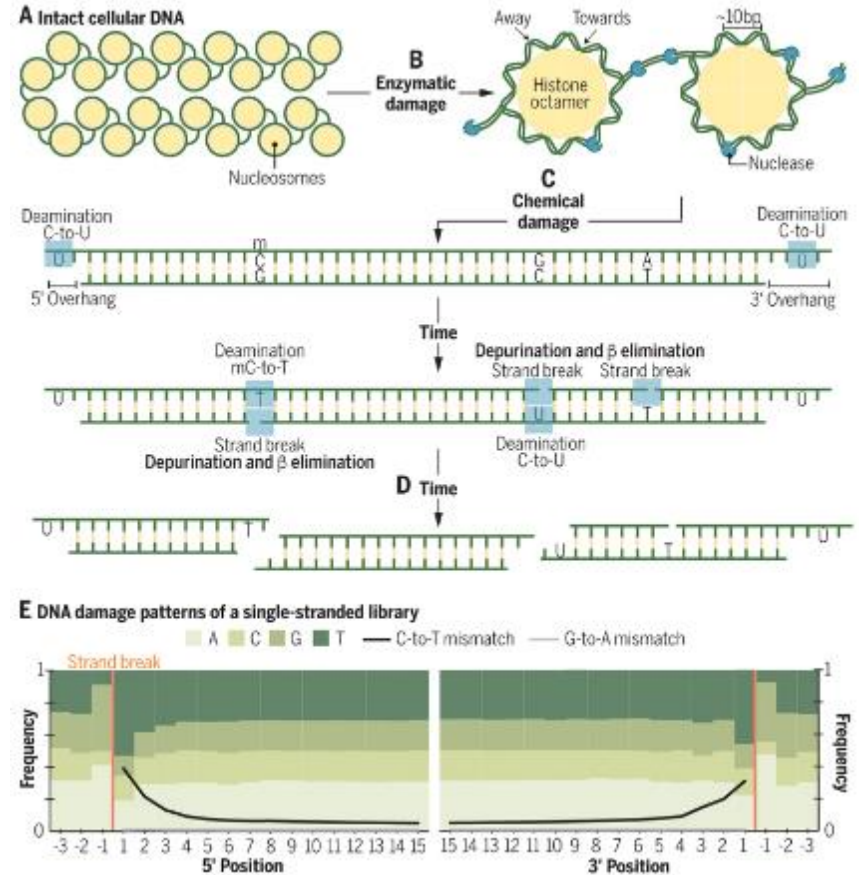


- Material genético preservado en muestras biológicas arqueológicas, paleontológicas y de museos.
- ADN en baja cantidad y calidad.
- Fragmentos pequeños (200pb).



➤ Daño postmortem (PMD):

- Radiación UV. Rompe las cadenas de ADN, modifica su estructura.
- Hidrólisis: el agua descompone las moléculas, rompe las cadenas.
- Oxidación: los radicales libres reaccionan con las bases nitrogenadas, provoca mutaciones y errores en la secuencia.
- Fragmentación: temperatura, fluctuaciones ambientales y actividades biológicas (ej. descomposición).
- Contaminación: ADN moderno de personas, animales o bacterias.



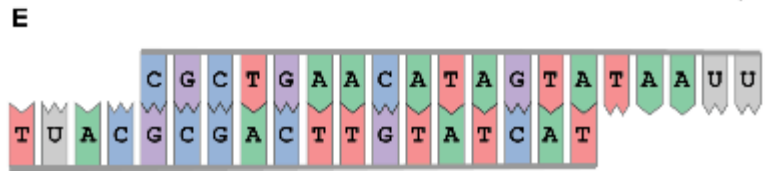
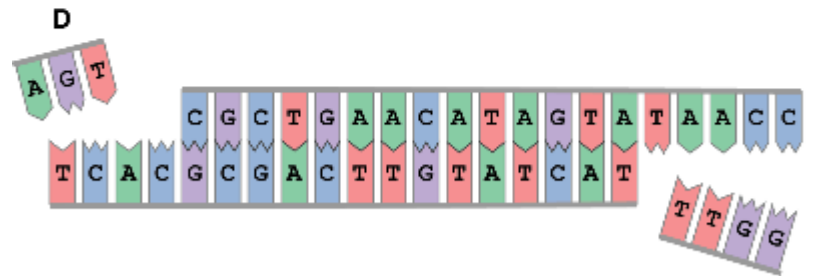
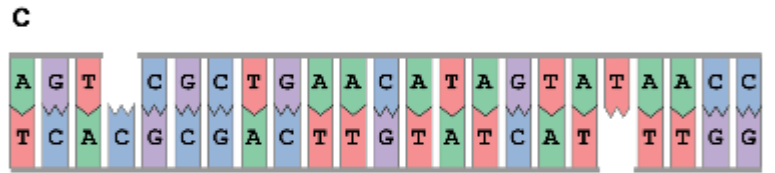
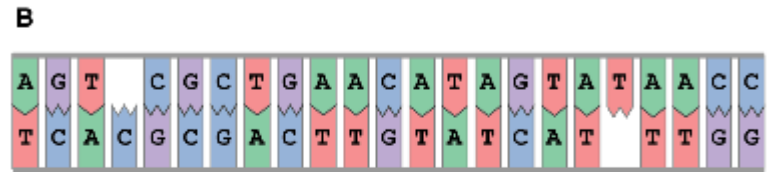
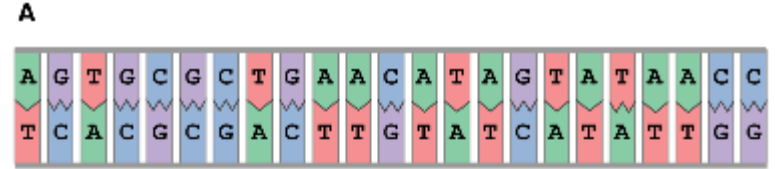
Desaminación: sustitución de C por U (Uracilo) y A por H (Hipoxantina).

Uracilo (U) (ARN) se empareja con adenina (A) en lugar de guanina (G).

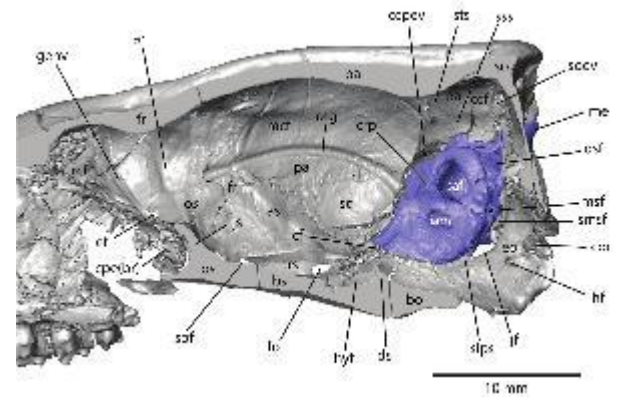
Hipoxantina (H) se empareja con citosina (C) en lugar de timina (T).

Progresión daño: pérdida aleatoria de G y A, por ataque hidrolítico en los sitios sin bases, hay roturas monocatenarias. Se separa la doble hélice y se forman fragmentos con salientes monocatenarios.

Las C en los salientes mutan en uracilos y timinas. La polimerasa interpreta a las dos como timinas, y lo que resulta en un exceso de timinas, particularmente en los extremos de las secuencias.



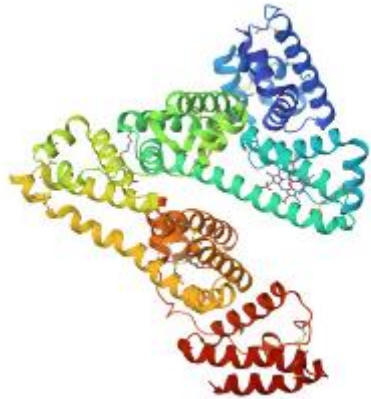
# Tipos de muestras ideales para obtener ADN antiguo



## Mammoth Albumin

ELLEN M. PRAGER, A. C. WILSON, JEROLD M. LOWENSTEIN, AND VINCENT M. SARICH [Authors Info & Affiliations](#)

SCIENCE · 11 Jul 1980 · Vol 209, Issue 4453 · pp. 287-289 · DOI: 10.1126/science.6155699



- 40.000 años
- Anticuerpos de elefante reaccionan con la del mamut
- No muy informativa, pero evidencia la posibilidad de extraer biomoléculas del pasado



# Molecular cloning of Ancient Egyptian mummy DNA

Svante Pääbo

*Nature* 314, 644–645 (1985) | [Cite this article](#)

7474 Accesses | 519 Altmetric | [Metrics](#)



Svante Pääbo



**Fig. 1** Tissue section of skin from the left lower leg of the Berlin mummy used for molecular DNA cloning. Ethidium bromide staining allows the visualization of nucleic acids in the cell nuclei (arrows).

**Methods.** Small tissue samples were rehydrated in an aqueous solution of 1%  $\text{Na}_2\text{CO}_3$  (w/v), 0.5% formalin and 28.5% ethanol<sup>1</sup> for 48 h. Paraffin embedding and sectioning were performed using routine protocols. After deparaffination, the sections were stained in a  $5 \mu\text{g ml}^{-1}$  solution of ethidium bromide in phosphate-buffered saline (PBS) for 30 min, followed by extensive washing in PBS and inspection under a Leitz fluorescence microscope.  $\times 180$ .

- individuo muerto hace 4600 años
- clonación ADN mitocondrial
- restos momificados





## Chloroplast DNA sequence from a Miocene *Magnolia* species

[Edward M. Golenberg](#), [David E. Giannasi](#), [Michael T. Clegg](#), [Charles J. Smiley](#), [Mary Durbin](#), [David Henderson](#) & [Gerard Zurawski](#)

[Nature](#) **344**, 656–658 (1990) | [Cite this article](#)

1096 Accesses | 175 Altmetric | [Metrics](#)



➤ 17-20 Myr

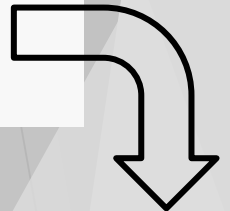
**The New York Times**

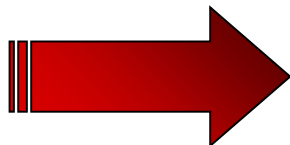
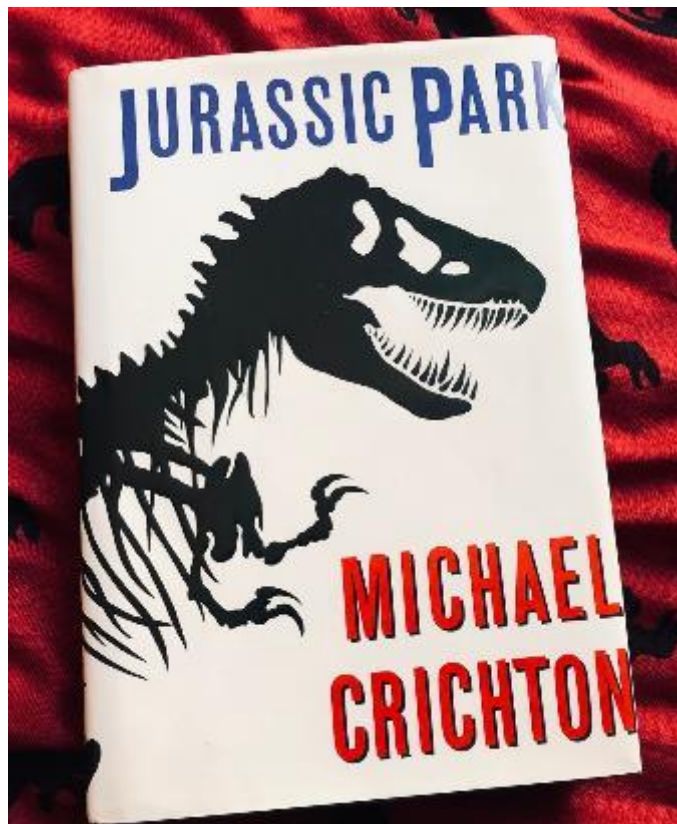
### ***40-Million-Year-Old Yields Oldest Ge***

By Malcolm W. Browne

Sept. 25, 1992

"Sooner or later, we're going to find amber containing some biting insect that filled its stomach with blood from a dinosaur before getting trapped in the resin that eventually turned into amber. The blood may contain actual dinosaur DNA. That will be an exciting discovery."  
Hendrik N. Poinar





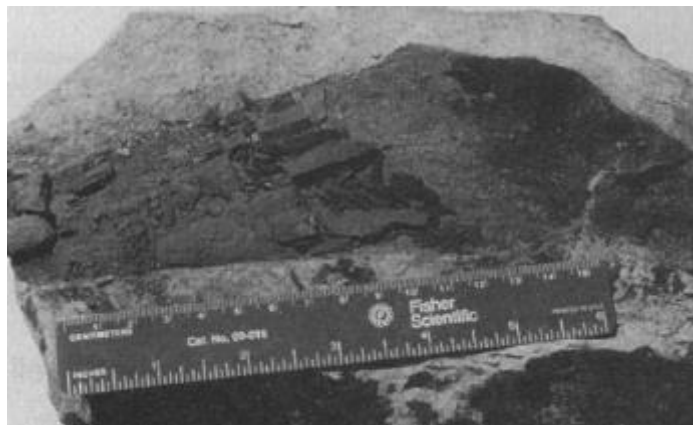
REPORT



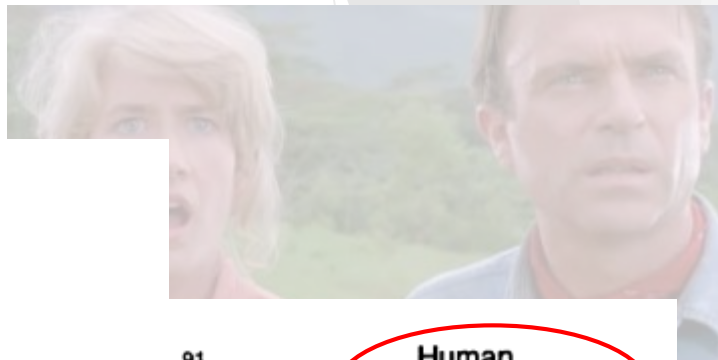
## DNA Sequence from Cretaceous Period Bone Fragments

SCOTT R. WOODWARD, NATHAN J. WEYAND, AND MARK BUNNELL [Authors Info & Affiliations](#)

SCIENCE • 18 Nov 1994 • Vol 266, Issue 5108 • pp. 1229-1232 • DOI:10.1126/science.73973705



	15,627
Consensus	CC CTT GTA TTA TGC ATT CTC ATT GTA TTC GTT ATT GGT GTA CTC GAC ACA TGC (C) AAA
2-37	...A.....G.....T.....A...../
3-37	...G.....T.....G.....T...../
4-37	...G.....T.....G.....T...../
31-44	...T.....G...../
2-61	...C...T...C.....CA.....A.....T...../
2-18	...T.....G...../
20-61	...T...../
5-37	...C...T...A...T...C.....A...C...A...T.....GT...../
6-37	...T...C...G...C...A...T...C...T.....GT...../
Consensus	GAA CAA AGC ATA ATA TTC GAC CCA TTC AGT GAA TTC GTA TGC TGA TTC TTA GTC CCC GAA
2-37	...G...C...C.....T.....A.....T.....
3-37	...C.....A.....S...G...T...A...A...A...G...C...
4-37	...C...C.....G.....T...A...T...A...A...A...A...
31-44	...G.....C.....C.....A.....C.....A...A...C...
2-61	...T.....U.....T.....A.....G...
2-18	...T.....C.....T...A...A...A...
20-61	T.....T.....C.....
5-37	...G...T.....G...C.....T...T...G...C...
6-37	...G...C...A...G...C.....
Consensus	CGT TTT ACA CTC ACA TG
2-37	...TA.....
3-37	...G...
4-37	...
31-44	...A...C
2-61	...T.....
2-18	...
20-61	...

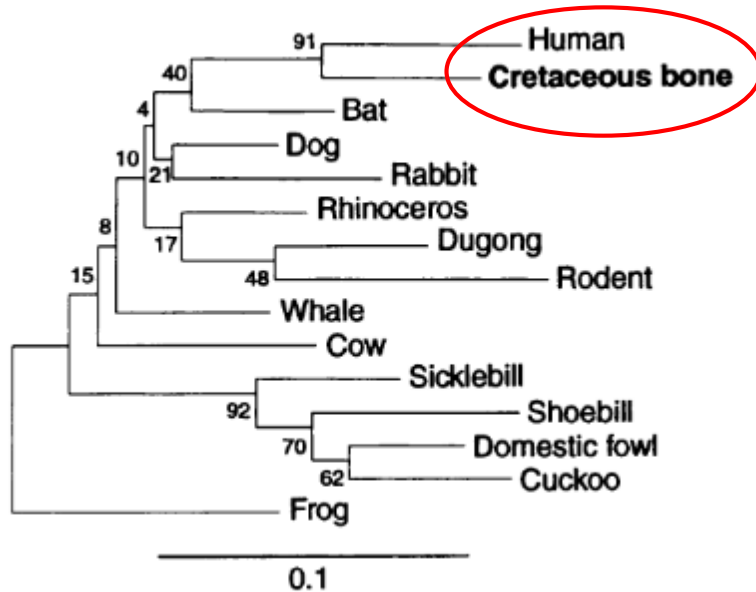
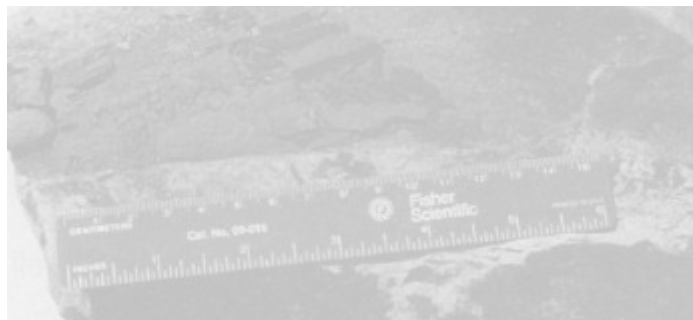


 TECHNICAL COMMENT

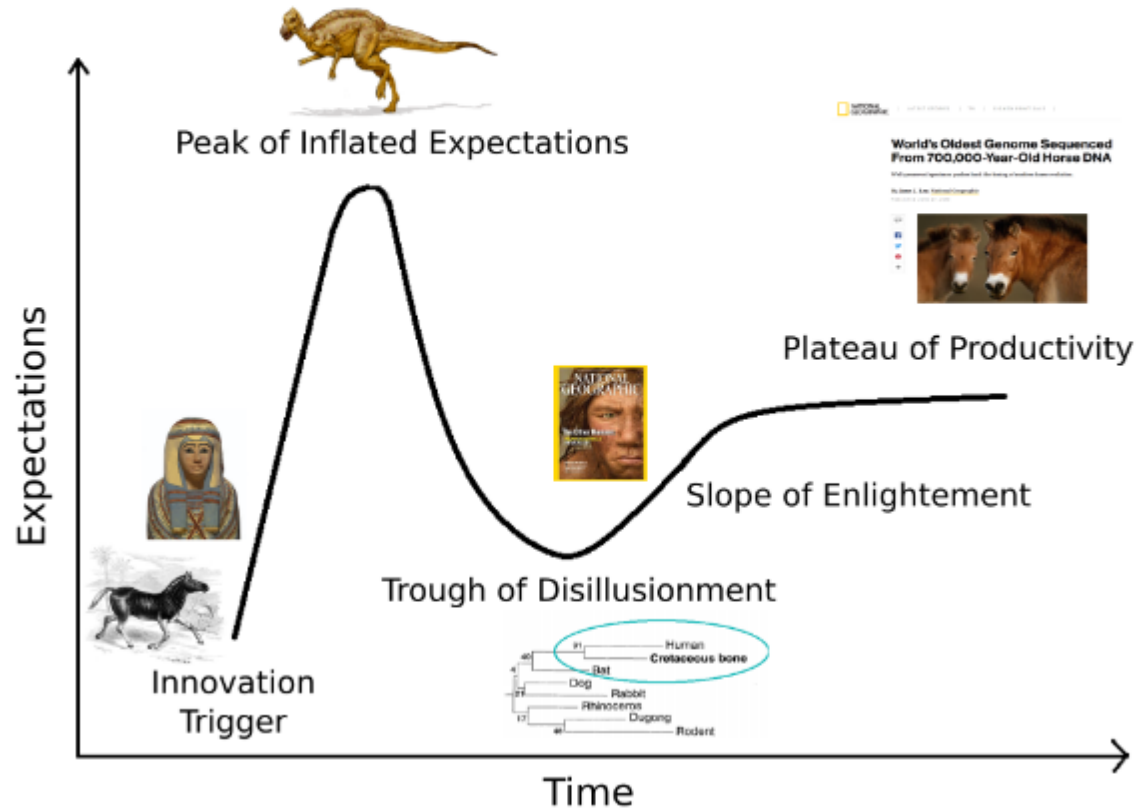
# Detecting Dinosaur DNA

S. BLAIR HEDGES AND MARY H. SCHWEITZER [Authors Info & Affiliations](#)

SCIENCE • 26 May 1995 • Vol 266, Issue 5214 • pp. 1191-1192 • [DOI: 10.1126](#)



# The Hype Cycle of Ancient DNA

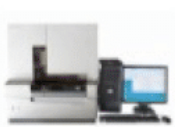


# Evolución de las herramientas de secuenciación de ADN

## First generation

## Second generation (next generation sequencing)

## Third generation



Sanger sequencing  
Maxam and Gilbert  
Sanger chain termination

Infer nucleotide identity using dNTPs,  
then visualize with electrophoresis

500–1,000 bp fragments



454, Solexa,  
Ion Torrent,  
Illumina

High throughput from the  
parallelization of sequencing reactions

~50–500 bp fragments



PacBio  
Oxford Nanopore

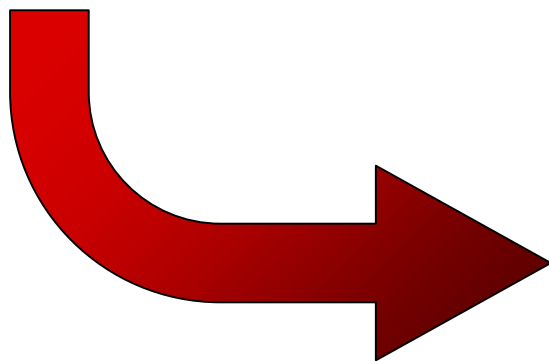
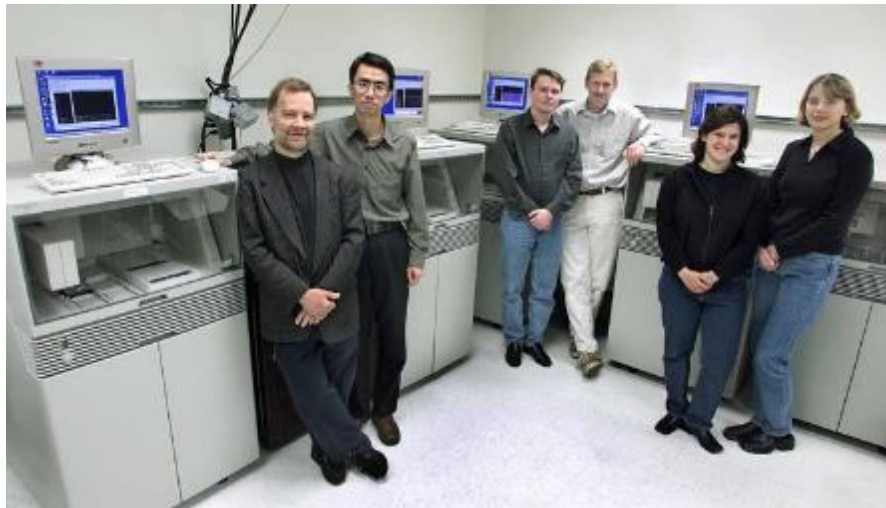
Sequence native DNA in real time  
with single-molecule resolution

Tens of kb fragments, on average

Short-read sequencing

Long-read sequencing

# Proyecto Genoma Humano



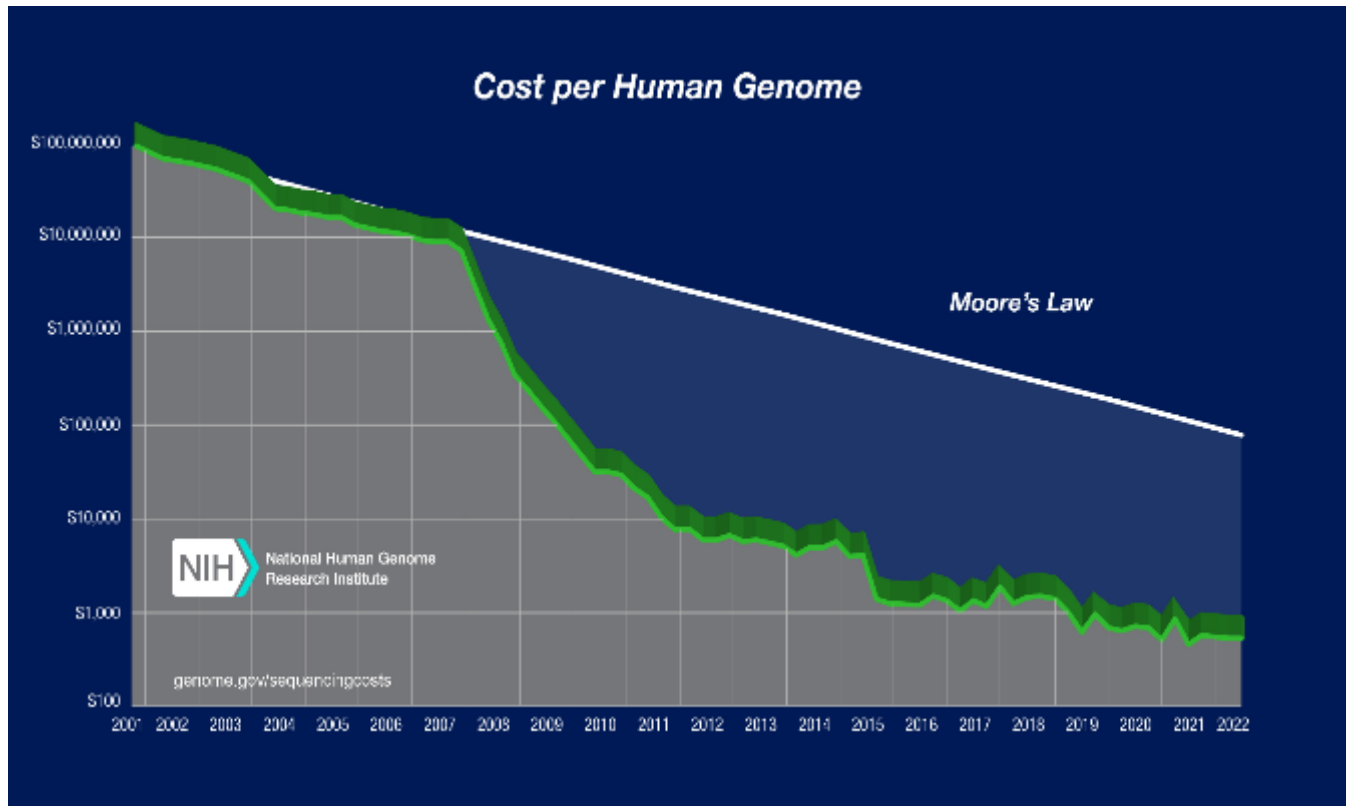


Febrero de 2001



costo total aproximado del proyecto: US\$ 2,7 mil millones

2000: US\$ 300 millones  
2003: US\$ 150 millones  
2006: US\$ 14 millones  
2016: US\$ 1500  
2024: US\$ 500



## AncestryDNA® te ofrece mucho más que tus lugares de origen

La tecnología de ADN te ofrece mucho más que tus lugares de origen. Descubre tu historia familiar y conecta con personas con las que compartes ADN.

¡Mira esto ahora!

### Millones de personas han descubierto algo nuevo. Faltas tú

¡Hazte el prueba de ADN. Identifica a tu gente. Alíate con más de 200 millones de personas. Descubre la posibilidad de conectar con personas con las que compartes ADN.

¡Inclúyete en tus resultados!



Inicio | Mi perfil | Familia | Mis resultados | Tus relaciones | Tus relaciones | Tus relaciones

## VINCULOS FAMILIARES

### ¿QUIERES CONFIRMAR UNA RELACIÓN BIOLÓGICA?

Puede usar los pruebas de ADN para determinar la relación y descartarse de cualquier duda.



#### MATERNIDAD

¿Quieres confirmar si eres la madre biológica de tu hijo? El ADN puede ayudarte a descubrirlo.



#### HERMANDAD COMPLETA

¿Quieres confirmar si eres el hermano biológico de tu hermana? El ADN puede ayudarte a descubrirlo.



#### MEDIA HERMANDAD

¿Quieres confirmar si eres el hermano biológico de tu hermana? El ADN puede ayudarte a descubrirlo.



Descubre la historia de su familia

Comienza tu prueba gratuita

## Sorpréndase a usted mismo

La nueva prueba de ADN de MyHeritage analiza su origen étnico (más), y le dará la posibilidad de conectar con nuevos familiares. Descubre los grupos étnicos de los que eres descendiente de entre 2.114 regiones geográficas, e vive su historia familiar a otro nivel con la prueba de ADN más accesible del mercado.

Conozca más

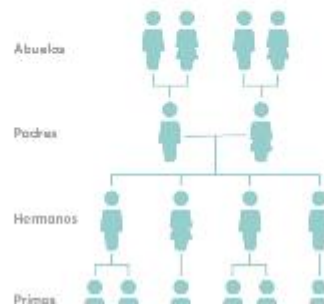
2.114

ORÍGENES ÉTNICOS



Inicio | Resultados | Pruebas de ADN | Familia | Tus relaciones | Tus relaciones | Tus relaciones

### ¿Qué relaciones de parentesco se pueden estudiar mediante el ADN?



¡Inclúyete!

2001



2010



nature &gt; articles &gt; article

Article | [Open access](#) | Published: 11 February 2010

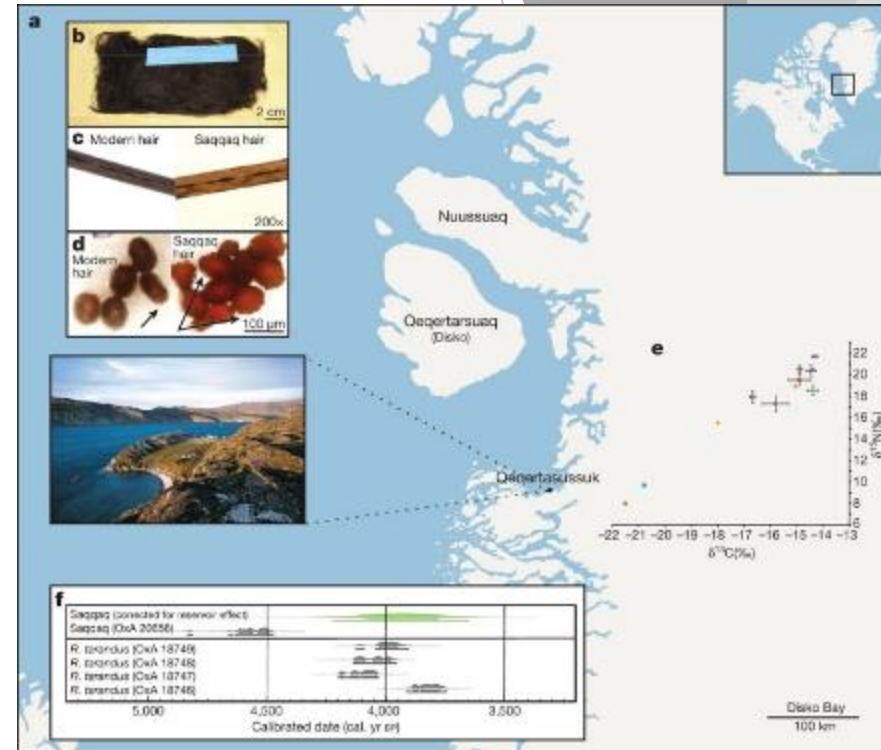
## Ancient human genome sequence of an extinct Palaeo-Eskimo

Morten Rasmussen, Yingrui Li, Stinus Lindgreen, Jakob Skou Pedersen, Anders Albrechtsen, Ida Moltke, Mait Metspalu, Ene Metspalu, Toomas Kivisild, Ramneek Gupta, Marcelo Bertalan, Kasper Nielsen, M. Thomas P. Gilbert, Yong Wang, Maanasa Raghavan, Paula F. Campos, Hanne Munkholm Kamp, Andrew S. Wilson, Andrew Gledhill, Silvana Tridico, Michael Bunce, Eline D. Lorenzen, Jonas Binladen, Xiaosen Guo, ... [Eske Willerslev](#)  [+ Show authors](#)

*Nature* **463**, 757–762 (2010) | [Cite this article](#)

50k Accesses | 590 Altmetric | [Metrics](#)

- ~4.000 yr
- pelo preservado en permafrost
- individuo masculino

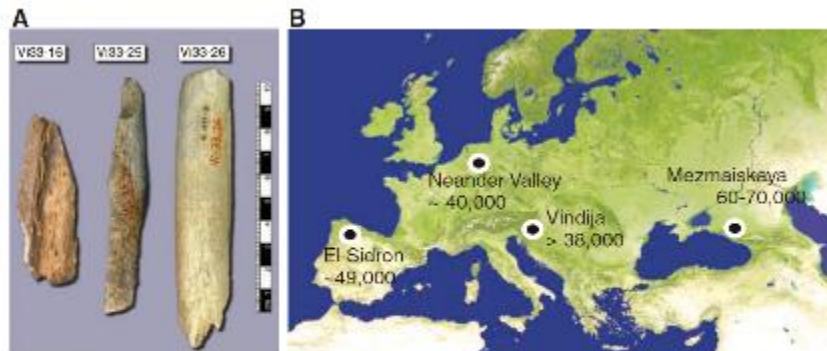


## A Draft Sequence of the Neandertal Genome

RICHARD E. GREEN, JOHANNAS KRAUSE, ADRIAN W. BRIGGS, TOMISLAV MARIC, UDO STENZEL, MARTIN KIRCHER, NICK PATTERSON, HONG LI, WEIWEI ZHAI, MARKUS USIYANG FRITZ, NANCY F. HANSEN, ERIC Y. DIERAND, ANNA-SAPPO MAI ASPINAS, JEFFREY D. JOHNSON, TOMAS MARQUIS-RONTT, CAN AKKAN, KAY PRÖFER, MAI THIAS MEYER, HEINÁN A. BUMBANGI, JEFFREY M. COOK, RICH SCHULZ, AYINUR AKOBU FE III, ANNE BUT THOR, BARBARA HOBEL, BARBARA HOEHNES, MADLEN SIEGEMUND, ANTIJE WEHMANN, CHAD NUSBAUM, ERIC S. LINDER, CARSTEN RISS, NATHANIEL NOVOD, JASON AFFOURTIT, MICHAEL EGHOLM, CHRISTINE VERNA, PAVAO BUDAN, DEJANA BRAJKOVIĆ, ŽELJKO KUČAN, IVAN BUŠIĆ, VLADIMIR B. DORONICHEV, LIUBOV V. SOLOVANOVA, CHARLES LALUEZA-FOX, MARCO DE LA BASILLA, JAVIER FORTEA, ANTONIO ROSAS, RALF W. SCHMITZ, PHILIP L. F. JOHNSON, EVAN E. FICHLER, DANIEL FALUSH, EWAN BIRNEY, JAMES C. MULLIKIN, MONTGOMERY SLATKIN, RASMUS NIJSEN, JANET KILSO, MICHAEL LACHMANN, DAVID REICH, AND SWANT RÄÄNÖ

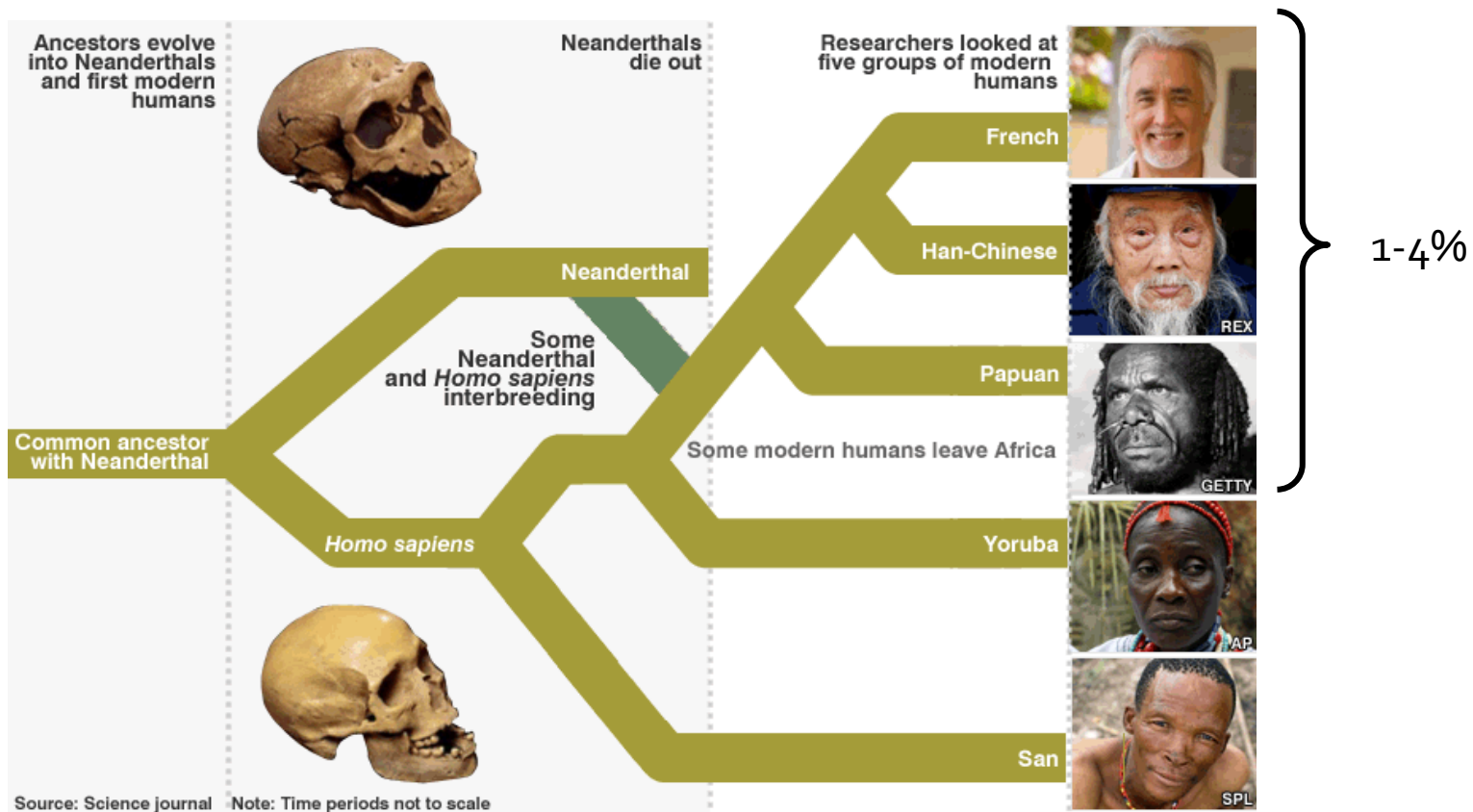
fewer

Authors Info &amp; Affiliations



**Fig. 1.** Samples and sites from which DNA was retrieved. (A) The three bones from Vindija from which Neandertal DNA was sequenced. (B) Map showing the four archaeological sites from which bones were used and their approximate dates (years B.P.).





- el genoma neandertal se parece más al de los humanos modernos de eurasia que a los de áfrica
- **1-4% del genoma de europeos/asiáticos modernos es de origen neandertal**

## An early modern human from Romania with a recent Neanderthal ancestor

[Qiaomei Fu](#), [Mateja Hajdinjak](#), [Qana Teodora Moldovan](#), [Silviu Constantin](#), [Swapan Mallick](#), [Pontus Skoglund](#), [Nick Patterson](#), [Nadin Rohland](#), [Iosif Lazaridis](#), [Birgit Nickel](#), [Bence Viola](#), [Kay Prüter](#), [Matthias Meyer](#), [Janet Kelso](#), [David Reich](#)  & [Svante Pääbo](#) 

*Nature* **524**, 216–219 (2015) | [Cite this article](#)

- 37 - 42 Kyr
- 6-9% de origen neandertal
- ancestro Neandertal 4 a 6 generaciones atrás



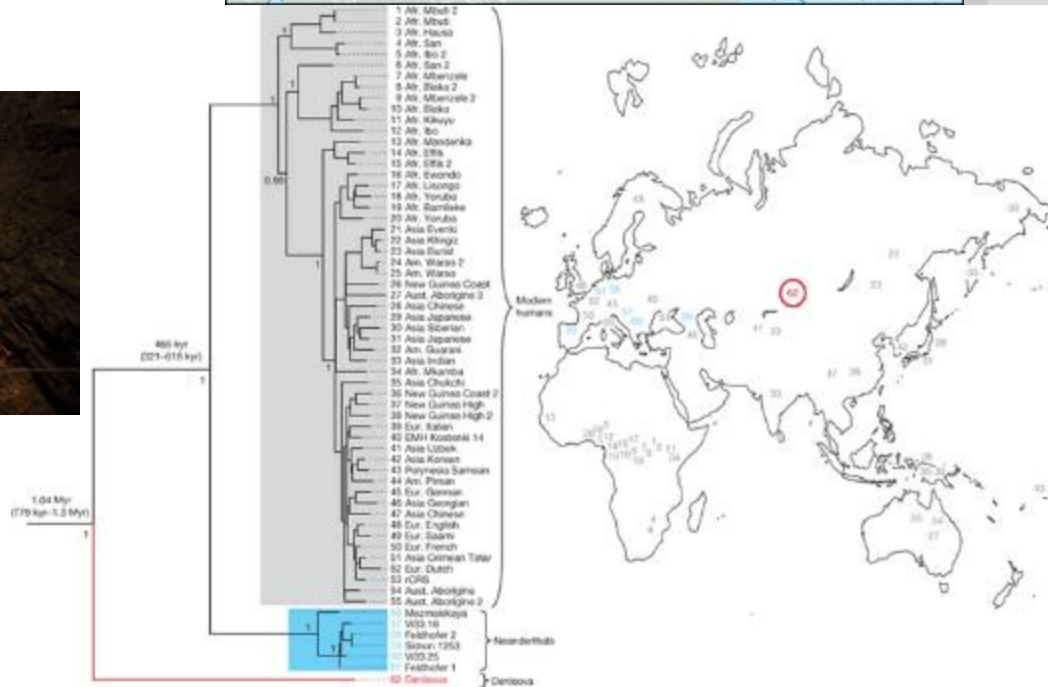


[nature](#) > [letters](#) > articleLetter | [Open access](#) | Published: 24 March 2010

## The complete mitochondrial DNA genome of an unknown hominin from southern Siberia

[Johannes Krause](#) , [Qiaomei Fu](#), [Jeffrey M. Good](#), [Bence Viola](#), [Michael V. Shunkov](#), [Anatoli P. Derevianko](#) & [Svante Pääbo](#)[Nature](#) **464**, 894–897 (2010) | [Cite this article](#)

- Denisova Cave
- 30 a 50 kyr



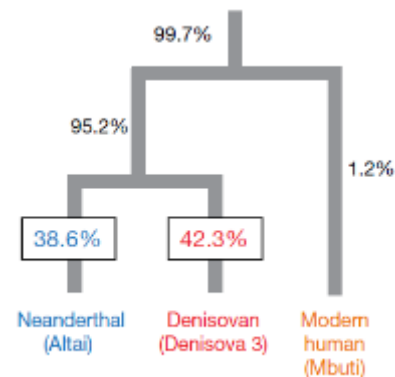
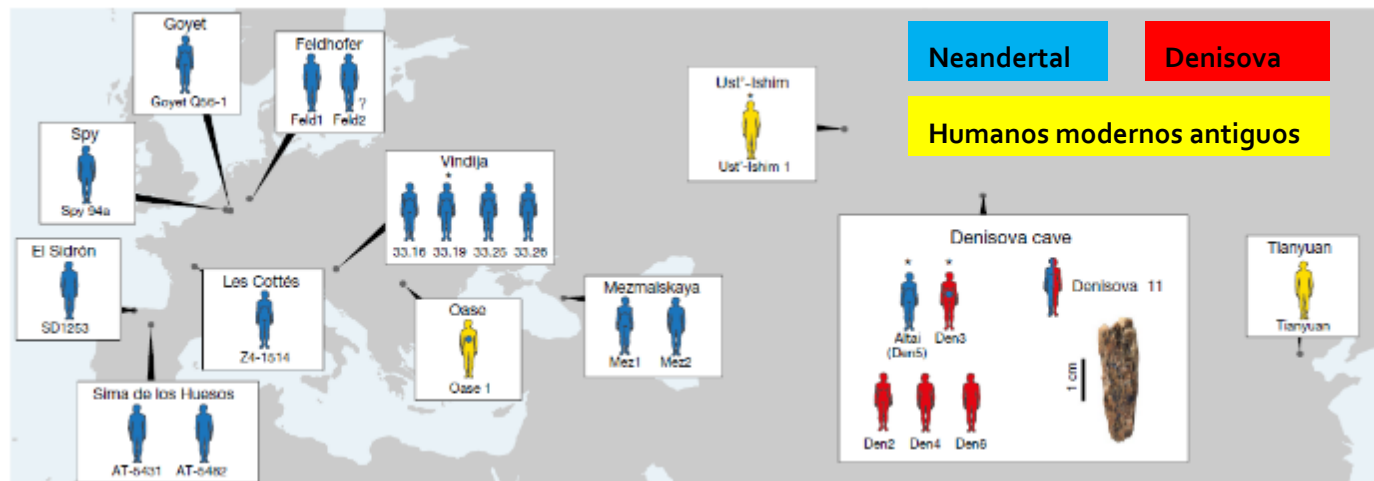
## The genome of the offspring of a Neanderthal mother and a Denisovan father

Viviane Slon , Fabrizio Mafessoni, Benjamin Vernot, Cesare de Filippo, Steffi Grote, Bence Viola, Mateja Hajdinjak, Stéphane Peyrégue, Sarah Nagel, Samantha Brown, Katerina Douka, Tom Higham, Maxim Il, Kozlikin, Michael V. Shunkov, Anatoly P. Derevianko, Janet Kelso, Matthias Meyer, Kay Prüfer & Svante Pääbo 

*Nature* 561, 113–116 (2018) | [Cite this article](#)

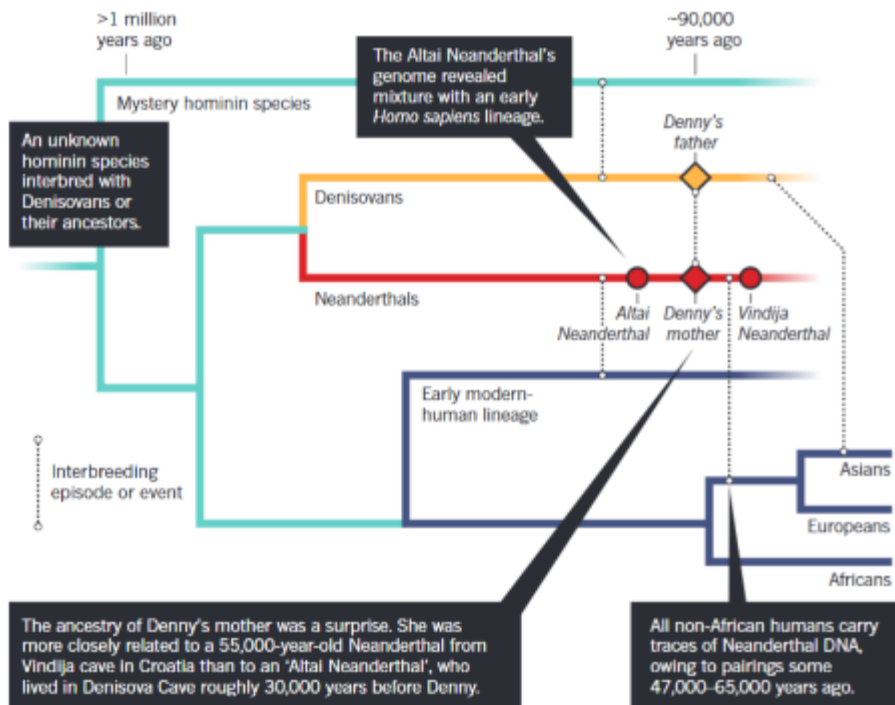


- >50 kyr
- niña de ~13 años



## TANGLED TREE

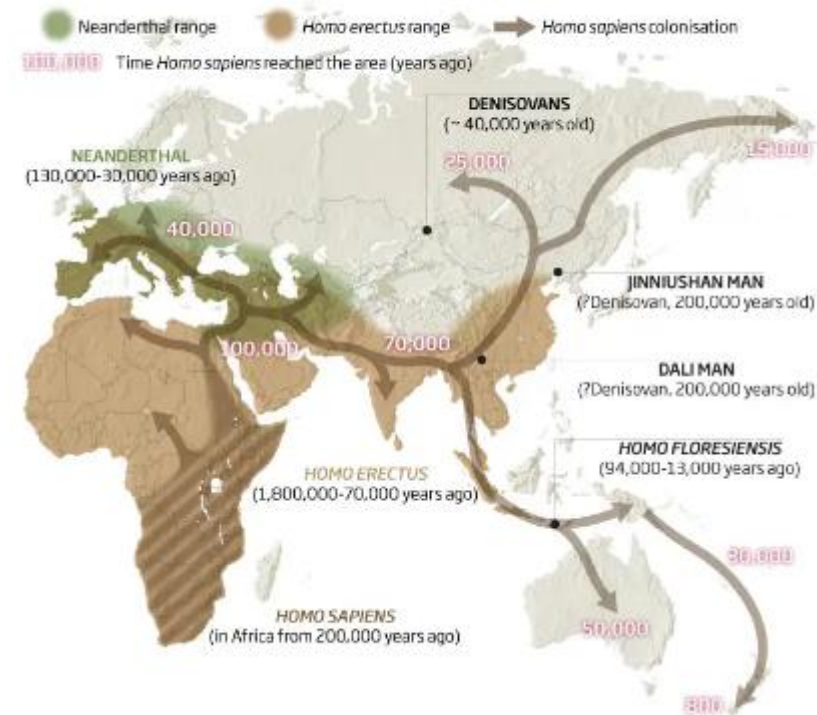
A female born to a Neanderthal mother and Denisovan father roughly 90,000 years ago — nicknamed Denny — is one of many examples of interbreeding between ancient human groups.



## All mixed up

© NewScientist

Genome analysis suggests that after early modern humans left Africa they interbred with Neanderthals in the Middle East around 60,000 years ago and with Denisovans some time before 45,000 years ago



¿Cuál es el límite temporal para extraer ADN antiguo y qué información puede brindarnos?



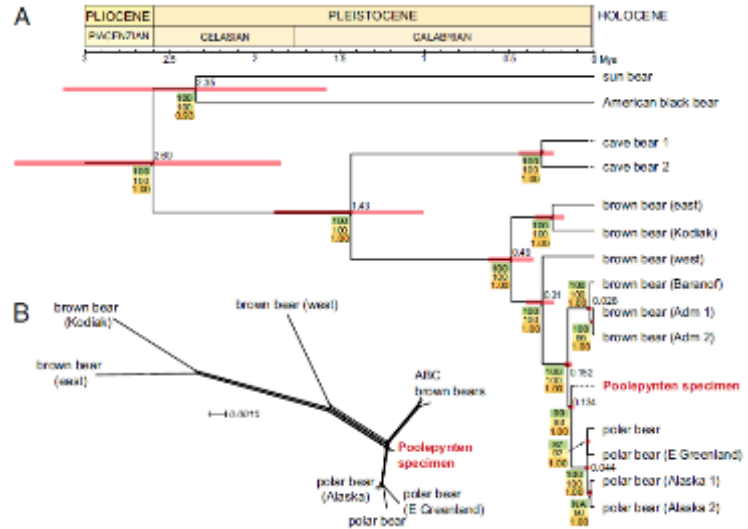
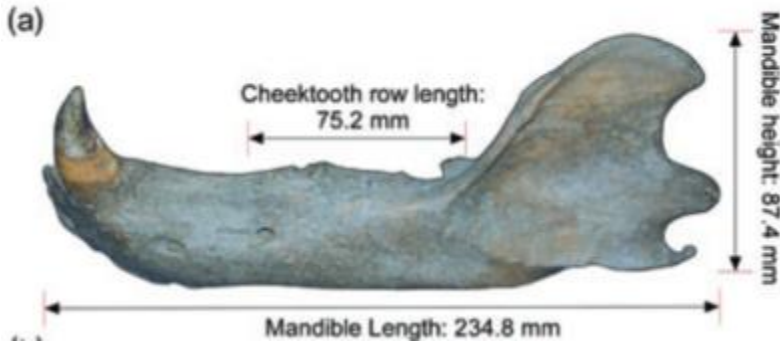
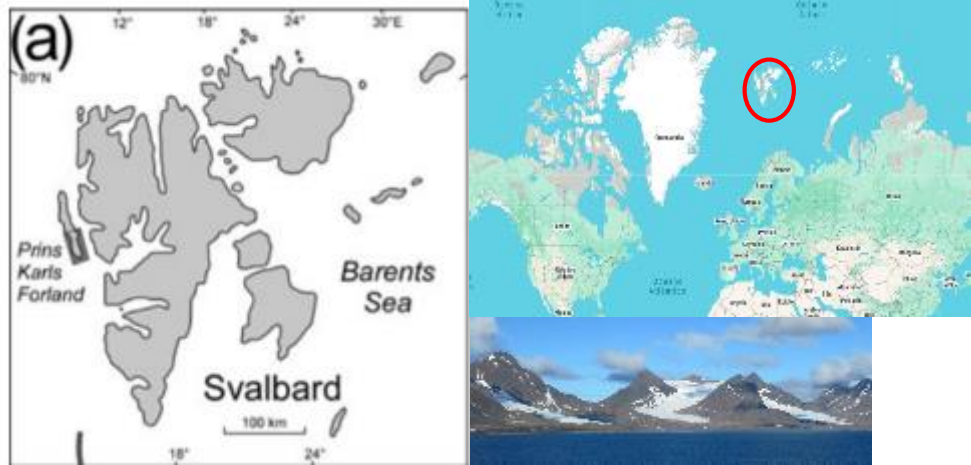
# Complete mitochondrial genome of a Pleistocene jawbone unveils the origin of polar bear

Charlotte Lindqvist, Stephan C. Schuster, Yachou Sun, and Øystein Wiig

Edited by Francisco J. Ayala, University of California, Irvine, CA, and approved January 22, 2010 (received for review December 9, 2009)

March 1, 2010 | 107 (11) 5053-5057 | <https://doi.org/10.1073/pnas.0916266107>

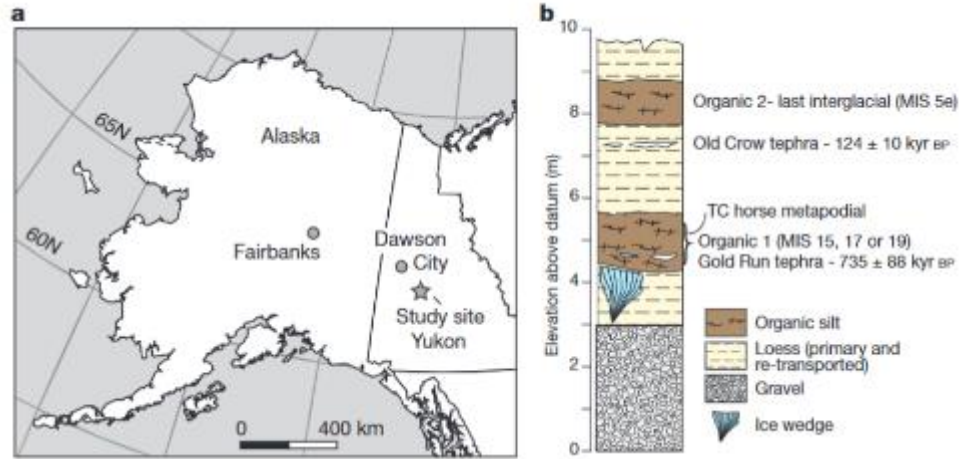
➤ 130,000 a 110,000 yr



## Recalibrating *Equus* evolution using the genome sequence of an early Middle Pleistocene horse

Ludovic Orlando , Aurélien Ginolhac, Guojie Zhang, Duane Froese, Anders Albrechtsen, Mathias Stiller, Mikkel Schubert, Enrico Cappellini, Bent Petersen, Ida Moltke, Philip L. F. Johnson, Matteo Tumagalli, Julia T. Vilstrup, Maanasa Baghavan, Tharfinn Korneliusson, Anna-Sofia Malaspinas, Josef Vogt, Damian Sviderskyj, Christian D. Kelstrup, Jakob Vinther, Andrei Dolanin, Jesper Stenderup, Arvind M. V. Velazquez, James Cahill, ... Eske Willerslev  [+ Show authors](#)

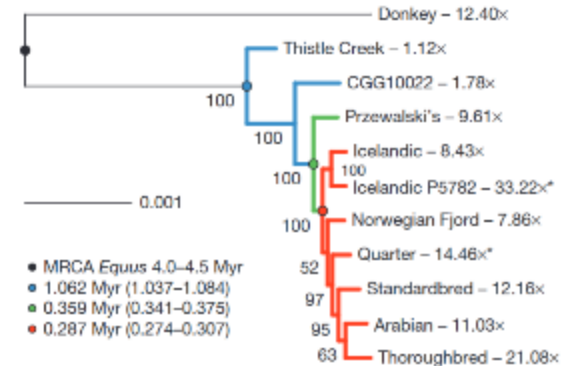
[Nature](#) 499, 74–78 (2013) | [Cite this article](#)



➤ 560 a 780 kyr



Przewalski's horse



# Million-year-old mammoth genomes shatter record for oldest ancient DNA

Permafrost-preserved teeth, up to 1.6 million years old, identify a new kind of mammoth in Siberia.

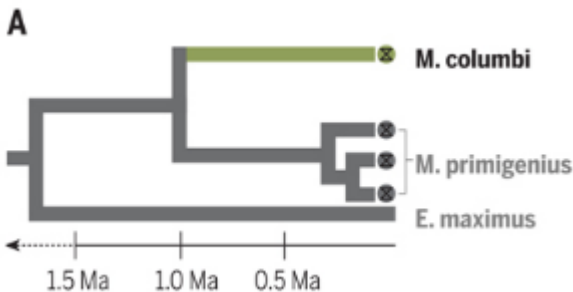


# Million-year-old DNA sheds light on the genomic history of mammoths

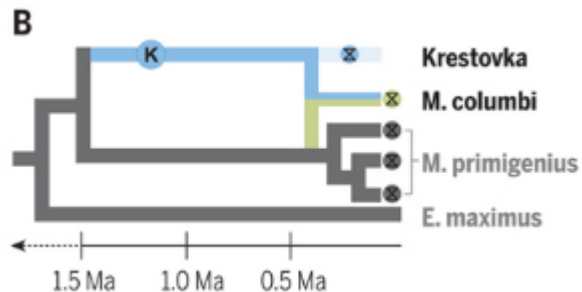
[Jan van der Valk](#) , [Estrella Pechacová](#), [David Díez del Molino](#), [Anders Bergström](#), [Janas Cippenheimer](#), [Stefanie Hartmann](#), [Georgios Xenikoudakis](#), [Jessica A. Thomas](#), [Marianne Dehesque](#), [Ekin Sugliani](#), [Fatma Babur Fider](#), [Jan Barnes](#), [Shanlin Liu](#), [Mohamed Somel](#), [Peter D. Heintzman](#), [Pavel Nikolskiy](#), [Beth Shapiro](#), [Pontus Skoglund](#), [Michael Hofreiter](#), [Adrian M. Lister](#), [Anders Sahlinström](#) & [Lorenzen](#) 

*Nature* 591, 265–269 (2021) [View this article](#)

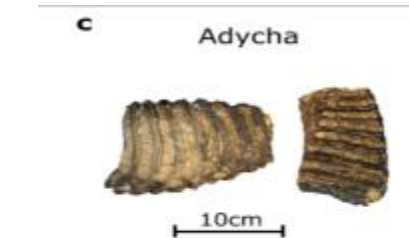
➤ 1,2 a 1,1 Myr



Paleo



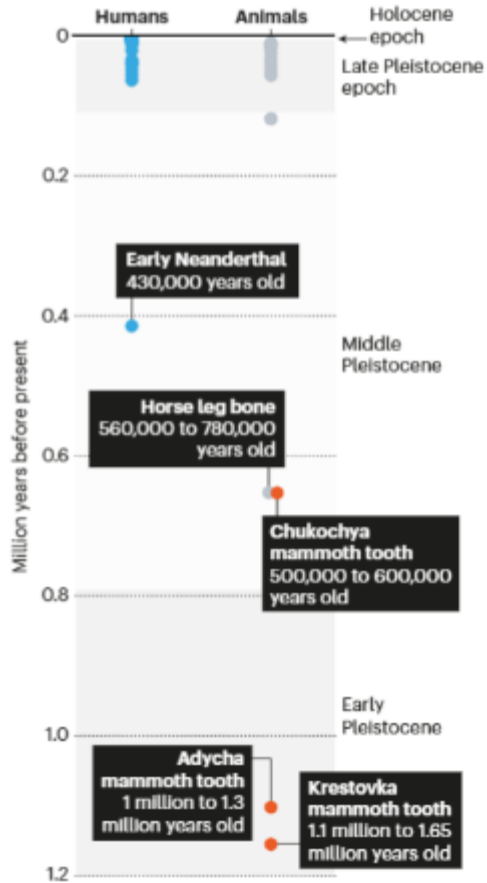
ADN





## ANCIENT GENOMES

Scientists have for the first time sequenced DNA that is more than one million years old — from mammoths. The oldest DNA sequenced previously dates from between 560,000 and 780,000 years ago.



# Complete mitochondrial genome sequence of a Middle Pleistocene cave bear reconstructed from ultrashort DNA fragments

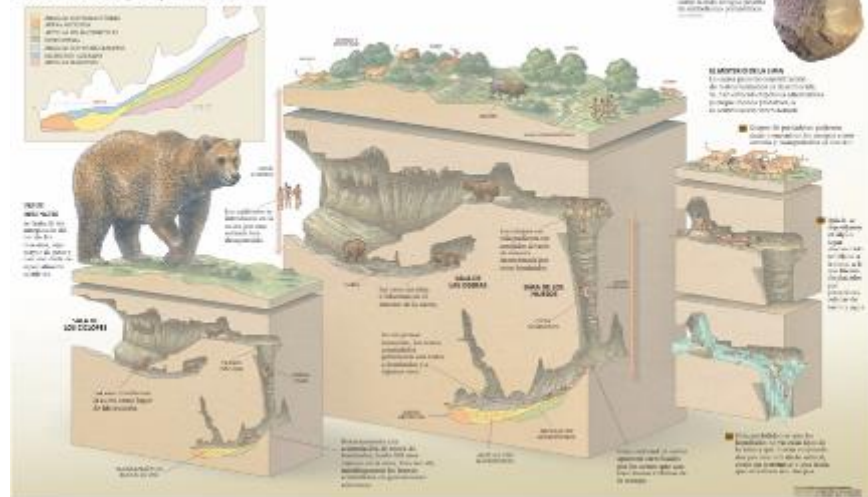
Jesse Delaney, Michael Krause, Isabelle Glöckner, and Matthias Meyer

Contributed by Susana Padua, August 6, 2013 (first for review July 17, 2013)

September 9, 2013 | 110 (39) 15758–15763 | <https://doi.org/10.1073/pnas.1314446110>

## LA SIMA DE LOS HUESOS


La Sima de los Huesos es el nombre de un yacimiento de Cueva Neandertal en una compleja zona de rocas volcánicas. En este sitio se han encontrado restos de los huesos de animales que pertenecen a una colección de fósiles que se cree que son de unos 500.000 años, incluyendo el mayor número de huesos contemporáneos del mundo. La zona expone estratos y estratos de forma paleogeográfica, cada uno de los cuales tiene...



➤ >300.000 yr

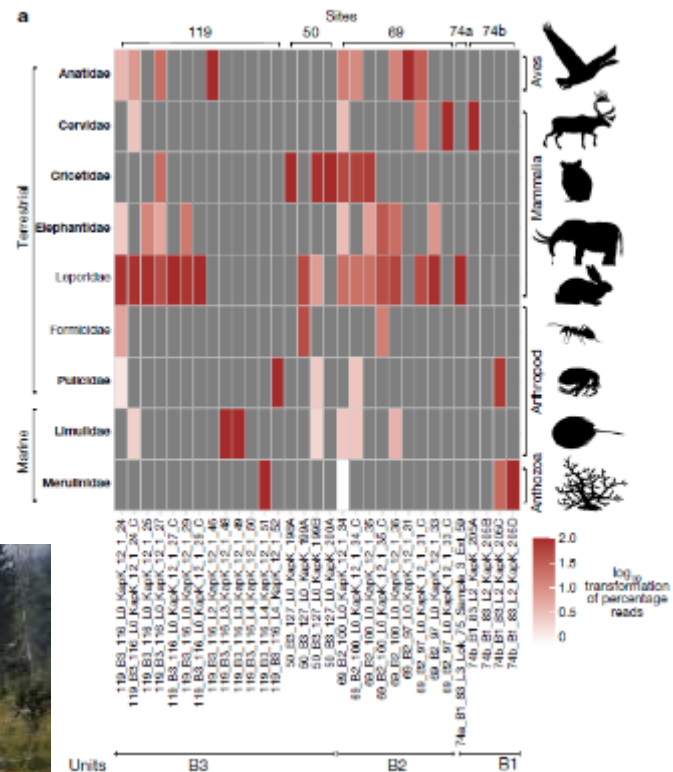
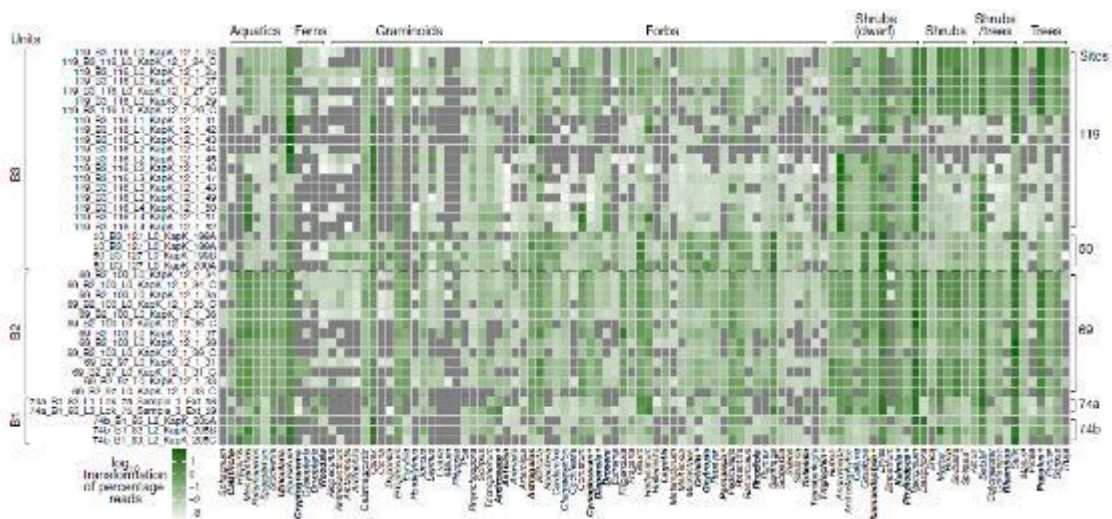
[nature](#) > [articles](#) > [article](#)Article | [Open access](#) | Published: 07 December 2022

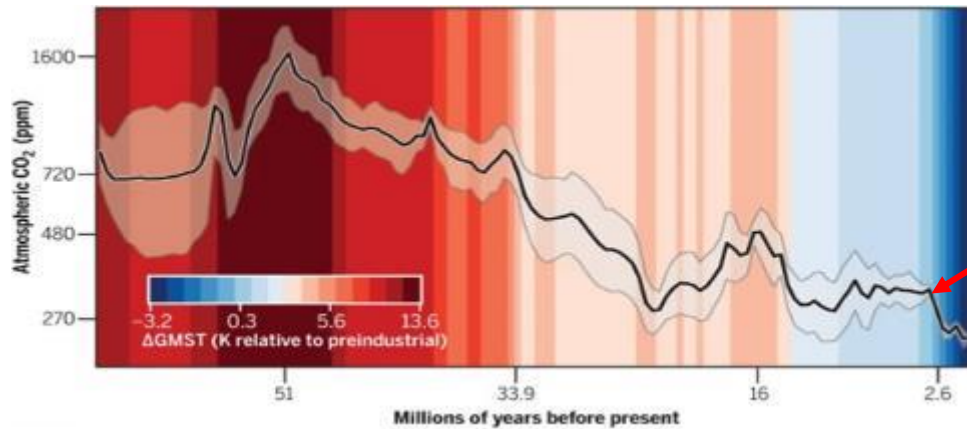
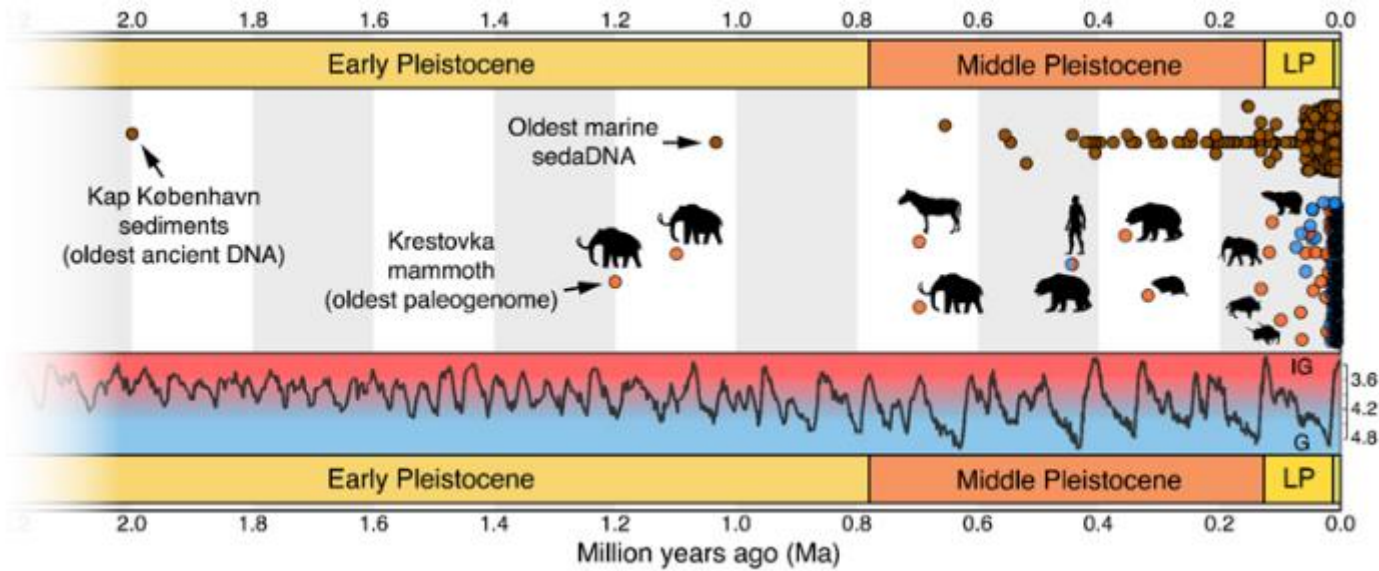
## A 2-million-year-old ecosystem in Greenland uncovered by environmental DNA

[Kurt H. Kjær](#) , [Mikkel Winther Pedersen](#), [Bianca De Sanctis](#), [Binia De Cahsan](#), [Thorfinn S. Kornelussen](#), [Christian S. Michelsen](#), [Karina K. Sand](#), [Stanislav Jelavić](#), [Anthony H. Rutes](#), [Astrid M. A. Schmidt](#), [Kristian K. Kjeldsen](#), [Alexey S. Tesakov](#), [Ian Snowball](#), [John C. Gosse](#), [Inger G. Alsos](#), [Yucheng Wang](#), [Christoph Dockter](#), [Magnus Basimussen](#), [Morten E. Jørgensen](#), [Birgitte Skoldhaug](#), [Ana Prohaska](#), [Jeppie Å. Kristensen](#), [Morten Bjerager](#), [Morten E. Allenroft](#), [PhyloNorway Consortium](#), ... [Eske Willerslev](#)  [+ Show authors](#)

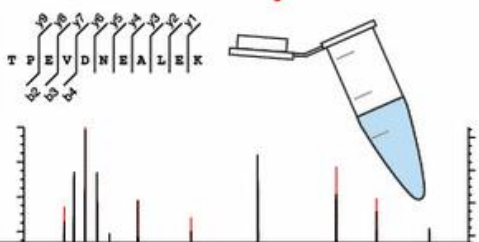
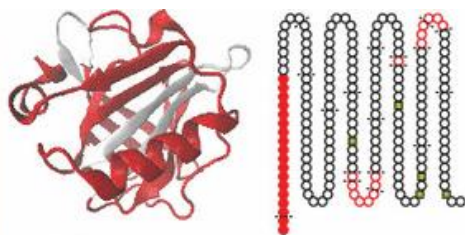
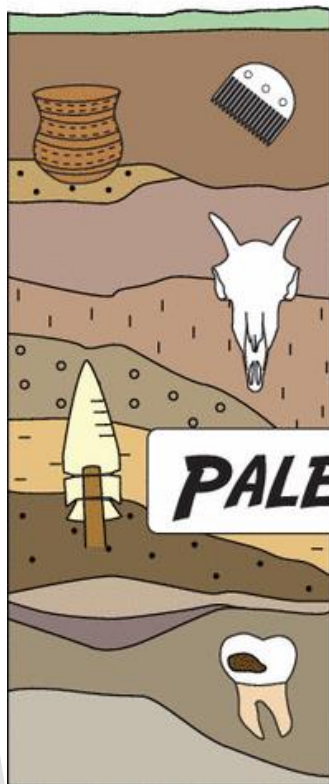
[Nature](#) **612**, 283–291 (2022) | [Cite this article](#)



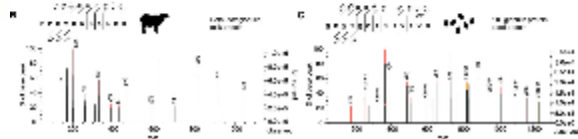
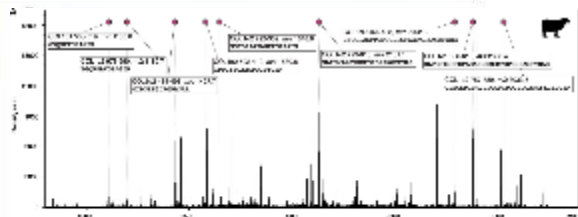




¿límite para el aADN?



# PALEOPROTEOMICS



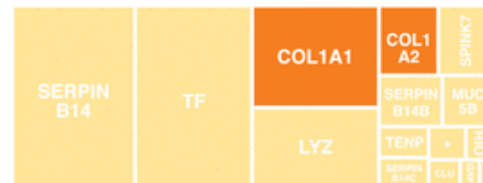
A



B



C



D



Collagen  
Other bone / dentine proteins

Blood  
Immune system  
Milk  
Egg  
Plant  
Other

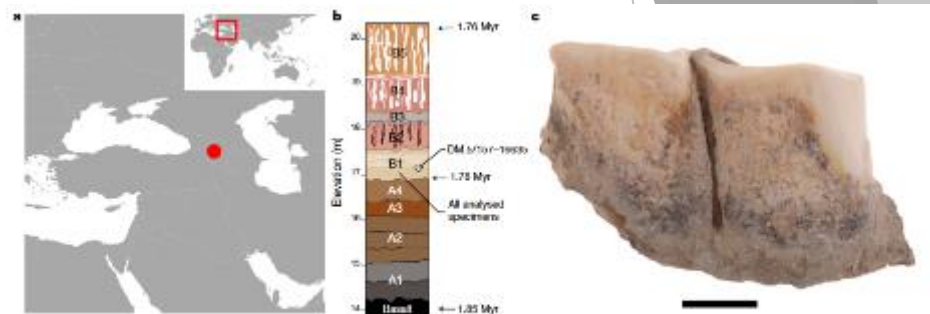
Letter | Published: 11 September 2019

## Early Pleistocene enamel proteome from Dmanisi resolves *Stephanorhinus* phylogeny

Emico Cappellini , Frido Welker, Luca Pandolfi, Jazmin Ramos-Matrigal, Diana Samedova, Patrick L. R  ther, Anna K. Fotakis, David Lyon, J. Victor Moreno-Mayer, Maia Bukharianidze, Rosa Rakownikow, Jessie Christensen, Meghan Mackie, Aur  lien Gimolhas, Reid Ferring, Martha Toppen, Eleftheria Palkopoulou, Mayr B. Dickinson, Thomas W. Stafford Jr, Yvonne L. Chan, Anders G  rberst  m, Scott H. J. O'Sullivan, S. S. Nathan, Peter D. Heintzman, Joshua D. Kapp, Irina Kirillova ... [Eike Willerslev](#)  [+ Show authors](#)

*Nature* 574, 103–107 (2019) | [Cite this article](#)

➤ 1,77 Myr






**Fig. 1** | Location of Dmanisi, stratigraphy, and specimen Dm.5/157-16635. **a**, Location of Dmanisi in the South Caucasus. The base map was generated using public-domain data from [www.naturalearthdata.com](http://www.naturalearthdata.com). **b**, Generalized stratigraphic profile, indicating origin and age of the

analysed specimens. Elevation is referred to the local datum. **c**, Isolated left lower molar (m1 or m2) of *Stephanorhinus* ex gr. *atrascu/handlirsensis* from Dmanisi (labial view). Scale bar, 1 cm.

Research Article

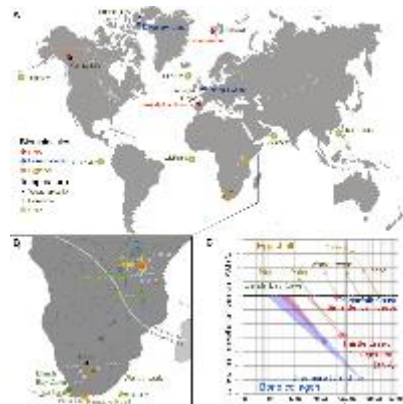
Biochemistry and Chemical Biology, Evolutionary Biology

## Protein sequences bound to mineral surfaces persist into deep time

Beatrice Demarchi , Shaun Hall, Teresa Roncal-Herrero, Collin L. Freeman , Jos Woolley, Molly K. Crisp, Julie Wilson, Anna Fotakis, Roman Fischer ... [Matthew J. Collins](#)  [see all](#)

University of York, United Kingdom; University of Sheffield, United Kingdom; University of Copenhagen, Denmark; University of Oxford, United Kingdom; Bangor University, United Kingdom; Arizona State University, United States; Nelson Mandela Metropolitan University, South Africa; University of Cape Town, South Africa; New York University, United States [see all](#)

Search Q



➤ 3,8 Myr



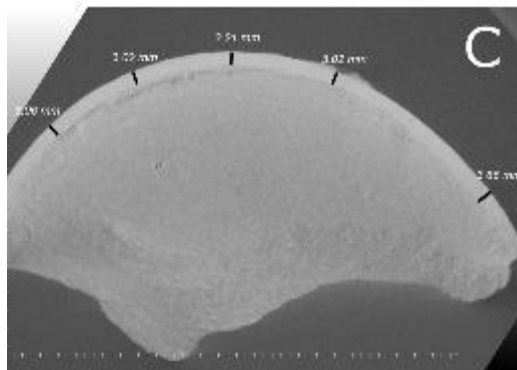
Research Advance

Biochemistry and Chemical Biology, Evolutionary Biology

## Survival of mineral-bour Miocene

Beatrice Demarchi , Meaghan Mackie, Zhiheng Li, Tao I

Department of Life Sciences and Systems Biology, University of  
Medical Sciences, University of Copenhagen, Denmark; The Nov  
Faculty of Health and Medical Sciences, University of Copenhagen;  
Paleoanthropology, Chinese Academy of Sciences, China; McDor  
Cambridge, United Kingdom; Department of Geological Science



>6.5 Myr



HOME > SCIENCE > VOL. 316, NO. 5822 > ANALYSES OF SOFT TISSUE FROM TYRANNOSAURUS REX SUGGEST THE PRESENCE OF PROTEIN

REPORTS



## Analyses of Soft Tissue from *Tyrannosaurus rex* Suggest the Presence of Protein

MARY HIGBY SCHWEITZER, ZHIYONG SUO, RECEP AVCI, JOHN M. ASARA, MARK A. ALLEN, FERNANDO TERAN ARCE, AND JOHN R. HORNER [Authors Info & Affiliations](#)

SCIENCE • 13 Apr 2007 • Vol 316, Issue 5822 • pp. 277-280 • DOI:10.1126/science.1138709

HOME > SCIENCE > VOL. 324, NO. 5927 > BIOMOLECULAR CHARACTERIZATION AND PROTEIN SEQUENCES OF THE CAMPANIAN HADROSAUR B. CANADENSIS

REPORT



## Biomolecular Characterization and Protein Sequences of the Campanian Hadrosaur *B. canadensis*

MARY H. SCHWEITZER, WENXIA ZHENG, CHRIS L. ORGAN, RECEP AVCI, ZHIYONG SUO, LISA M. FREIMARK, VALERIE S. LEBLEU, MICHAEL B. DUNCAN,

MATTHEW G. VANDER HEIDEN, [...] AND JOHN M. ASARA [+6 authors](#) [Authors Info & Affiliations](#)

SCIENCE • 1 May 2009 • Vol 324, Issue 5927 • pp. 626-631 • DOI:10.1126/science.1166069

ARTICLE · Volume 25, Issue 1, 103559, January 21, 2022 · Open Access

Revisiting proboscidean phylogeny and evolution through total evidence and palaeogenetic analyses including *Notiomastodon* ancient DNA

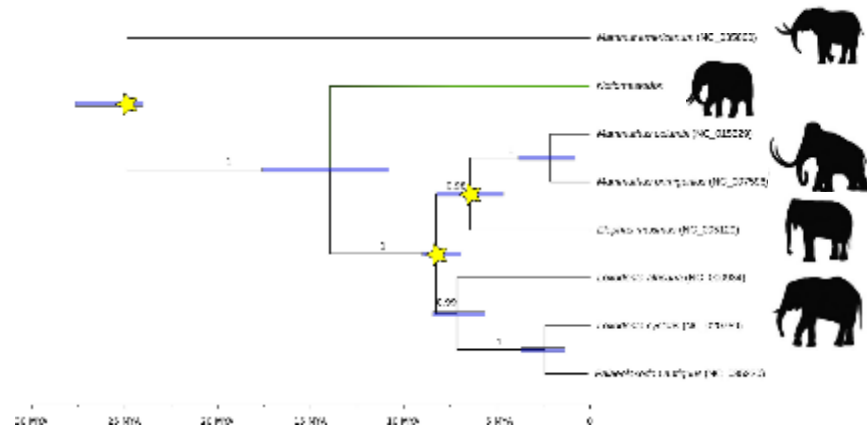
Sina Balca <sup>1,2,8,9,11</sup> ✉ · Luciano Varela <sup>3,4,8</sup> · P. Sebastián Tambusso <sup>3,4</sup> · Johanna L.A. Pajimans <sup>1,10</sup> · Dimila Mothé <sup>5,6</sup> · Thomas W. Stafford, Jr. <sup>7</sup> · Richard A. Fariña <sup>3,4</sup> · Michael Hofreiter <sup>1</sup> Show less



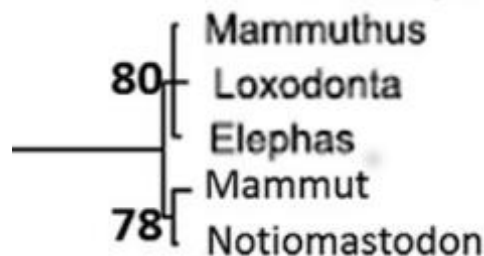
**B**



➤ 27.0 a 30.1 kyr



≠

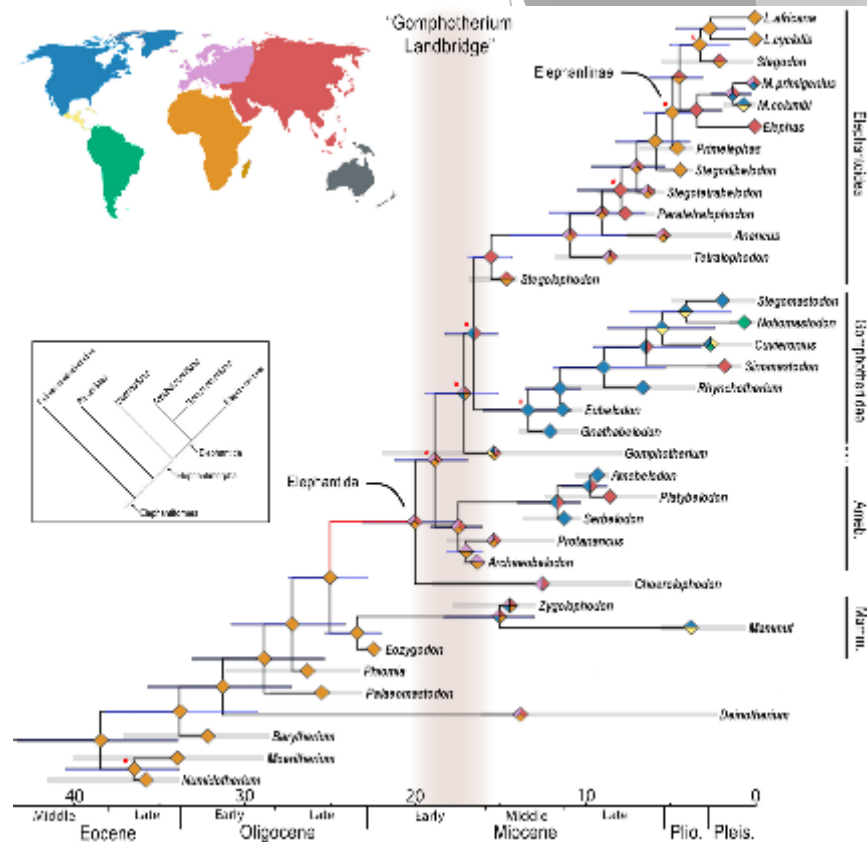


A molecular phylogeny of the extinct South American gomphothere through collagen sequence analysis

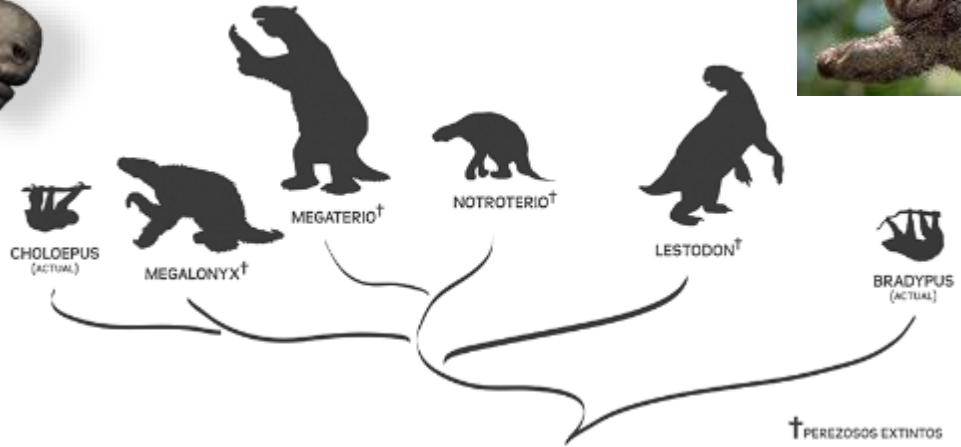
Michael Buckley<sup>1</sup>, J. B. & Omar R. Soto-Rivera<sup>2,3</sup>, Craig Lewellyn<sup>4</sup>, Nuria Garcia<sup>5</sup>, Maria Pina<sup>6</sup>



"Gomphotherium Landbridge"

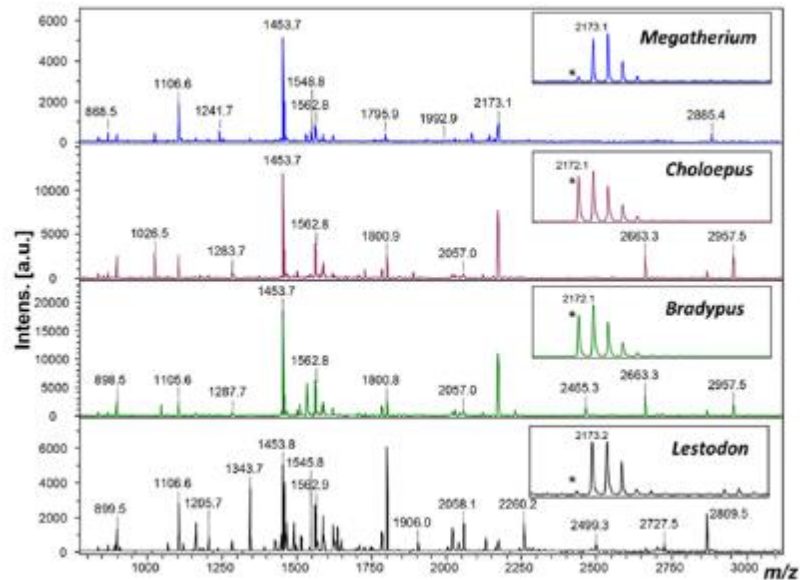


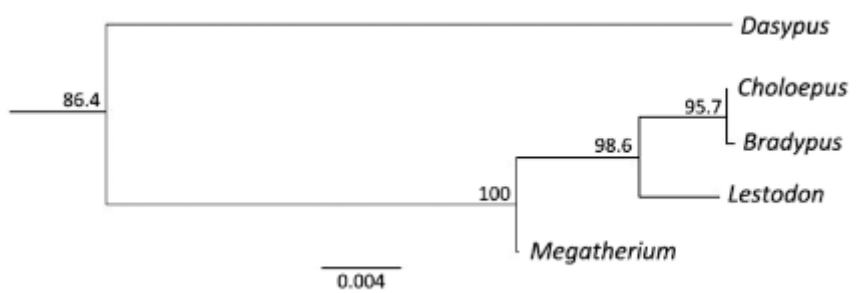
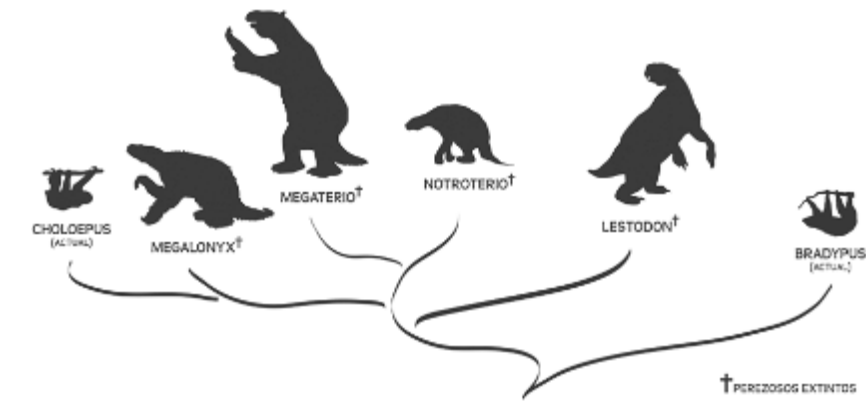
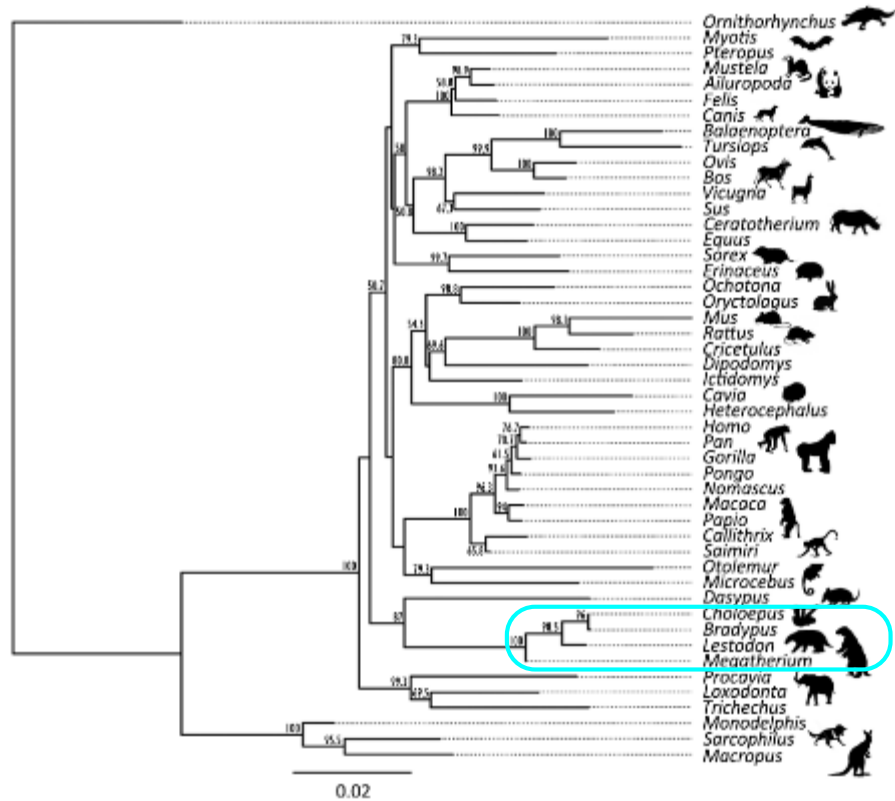
MEGAFAUNA 3D



# Collagen Sequence Analysis of the Extinct Giant Ground Sloths *Lestodon* and *Megatherium*

Michael Buckley<sup>1\*</sup>, Richard A. Farfán<sup>2</sup>, Craig Lawless<sup>3</sup>, P. Sebastián Tambusso<sup>2</sup>, Luciano Varela<sup>2</sup>, Alfredo A. Carlini<sup>4</sup>, Jaime E. Powell<sup>5</sup>, Jorge G. Martínez<sup>6</sup>





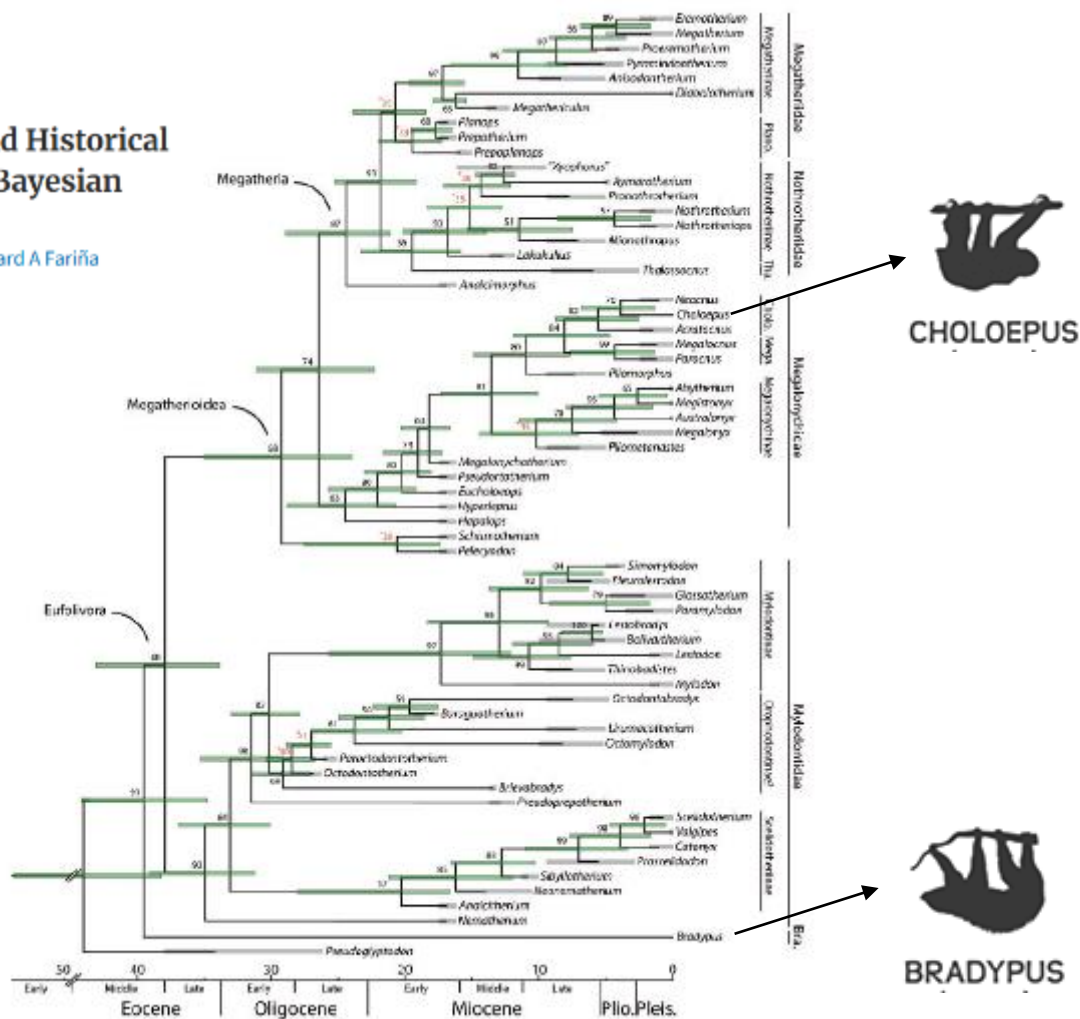
## Phylogeny, Macroevolutionary Trends and Historical Biogeography of Sloths: Insights From a Bayesian Morphological Clock Analysis [Get access >](#)

Luciano Varela , P Sebastián Tambusso, H Gregory McDonald, Richard A Fariña

*Systematic Biology*, Volume 68, Issue 2, March 2019, Pages 204–218,

<https://doi.org/10.1093/sysbio/syy058>

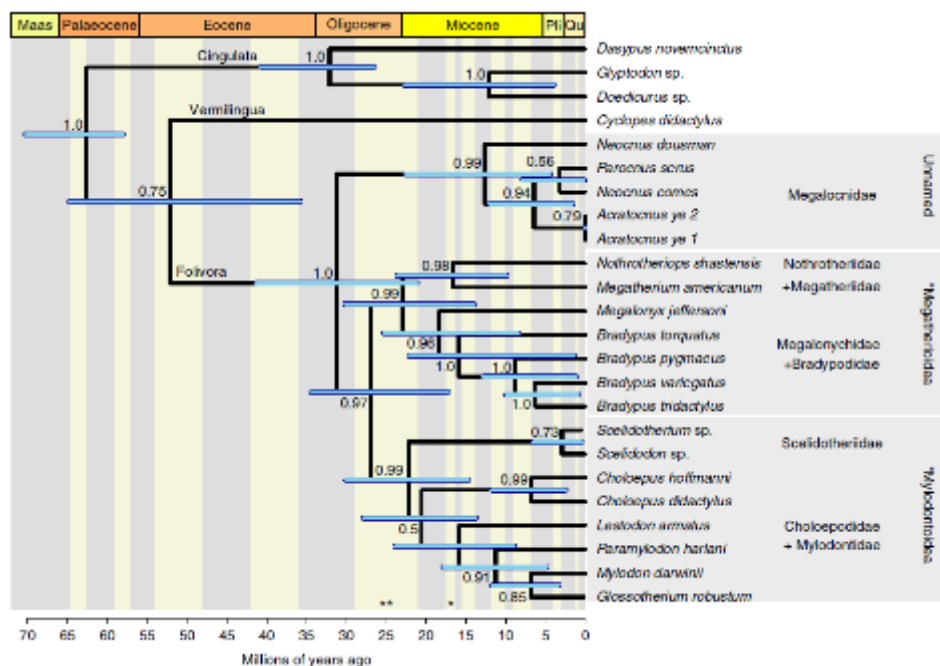
Published: 15 September 2018 [Article history ▾](#)







## Palaeoproteomics resolves sloth relationships

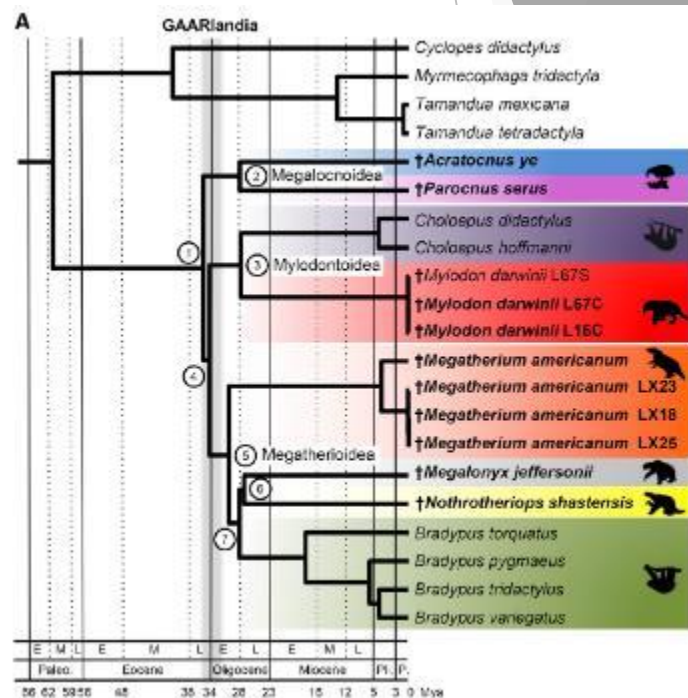
Samantha Preslee, Graham J. Slater, François Pujos, Analia M. Forasiepi, Roman Fischer, Kelly Molloy, Meghan Mackie, Jesper V. Olsen, Alejandro Kramarz, Matteo Lajthorini, Fernando Scaglia, Maximiliano Leciano, José Luis Lamata, John Southon, Robert Ferencs, Jonathan Bloch, Adam Hladik, Fabiana M. Martín, Karolita Salas Gismondi, Marcela Reguera, Christian de Muizon, Alex Greenwood, Brian L. Chait, Kirsty Penkman, **Ross D. E. MacPhee**  [+ Show authors](#)

*Nature Ecology & Evolution* 3, 1121–1130 (2019) | [View this article](#)

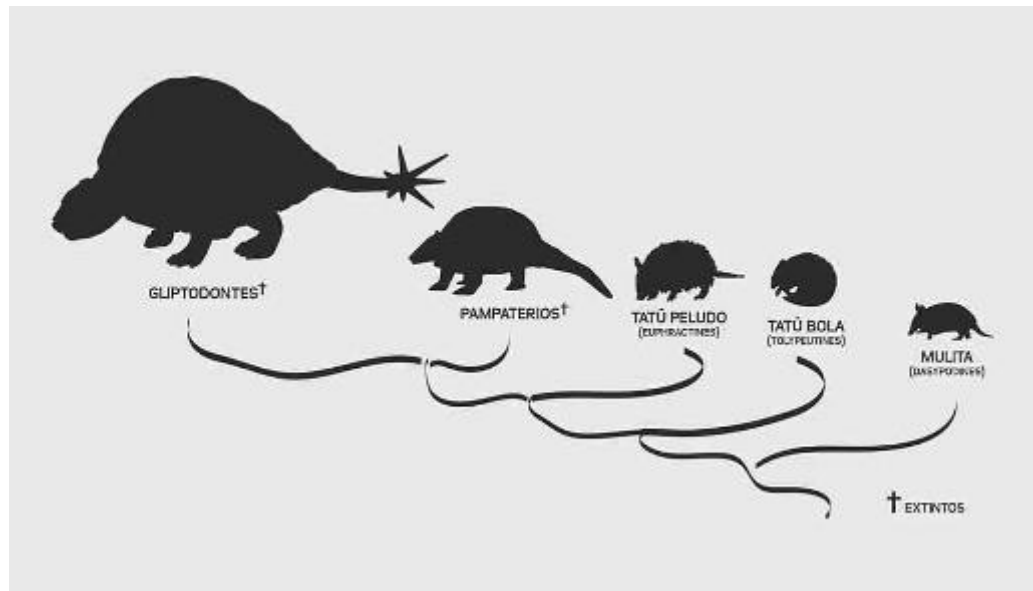


## Ancient Mitogenomes Reveal the Evolutionary History and Biogeography of Sloths

Frédéric Delgado <sup>1,1\*</sup>  <sup>✉</sup>, Mélanie Kuch <sup>2</sup>, Gillian C. Gibb <sup>1,3</sup>  <sup>✉</sup>, Erdem Özdemir <sup>1,3</sup>, Dirk Hackenberger <sup>2</sup>, Paul Szpak <sup>3</sup>, Jorge G. Martínez <sup>4</sup>, Jim I. Mead <sup>1,3</sup> <sup>✉</sup>, H. Gregory McDonald <sup>1</sup>, **Ross D. E. MacPhee**  <sup>✉</sup>, Guillaume Billet <sup>1</sup>, Lionel Heude <sup>1,12</sup>, Henrik N. Poinar <sup>2</sup>  <sup>✉</sup> [Show less](#)



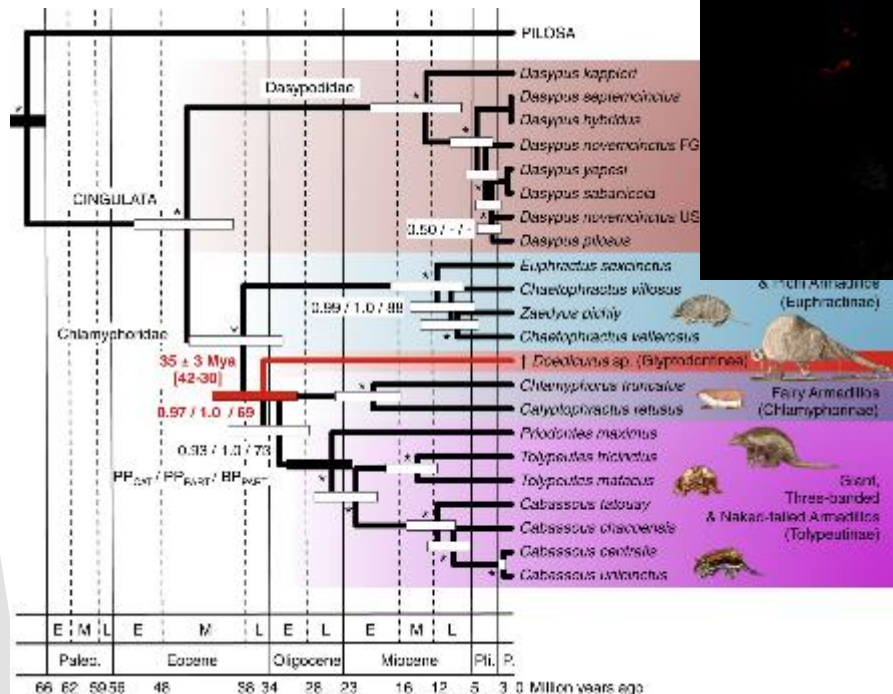




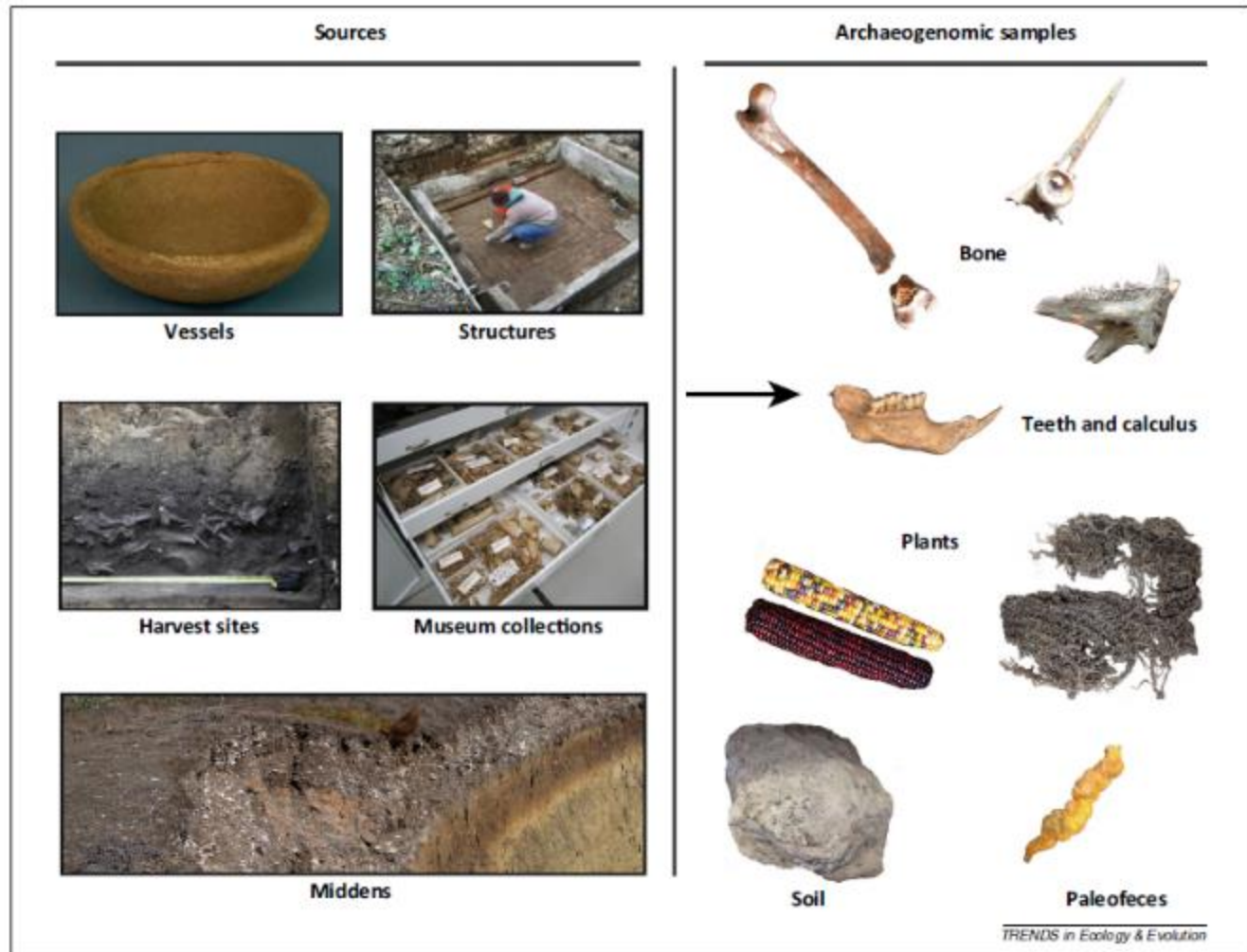
CORRESPONDENCE · Volume 26, Issue 4, PR156-R158, February 22, 2016 · Open Archive

# The phylogenetic affinities of the extinct glyptodont

Frédéric Delsuc<sup>1,2</sup> · Gillian C. Gibb<sup>1,2</sup> · Melanie Kuch<sup>3</sup> · Guillaume Billet<sup>4</sup> · Lionel Hautier<sup>5</sup> · Jean-Marie Rouillard<sup>6</sup> · Juan Carlos Fernicola<sup>7</sup> · Sergio F. Vizcaino<sup>8</sup> · Ross D.E. MacPhee<sup>9</sup>

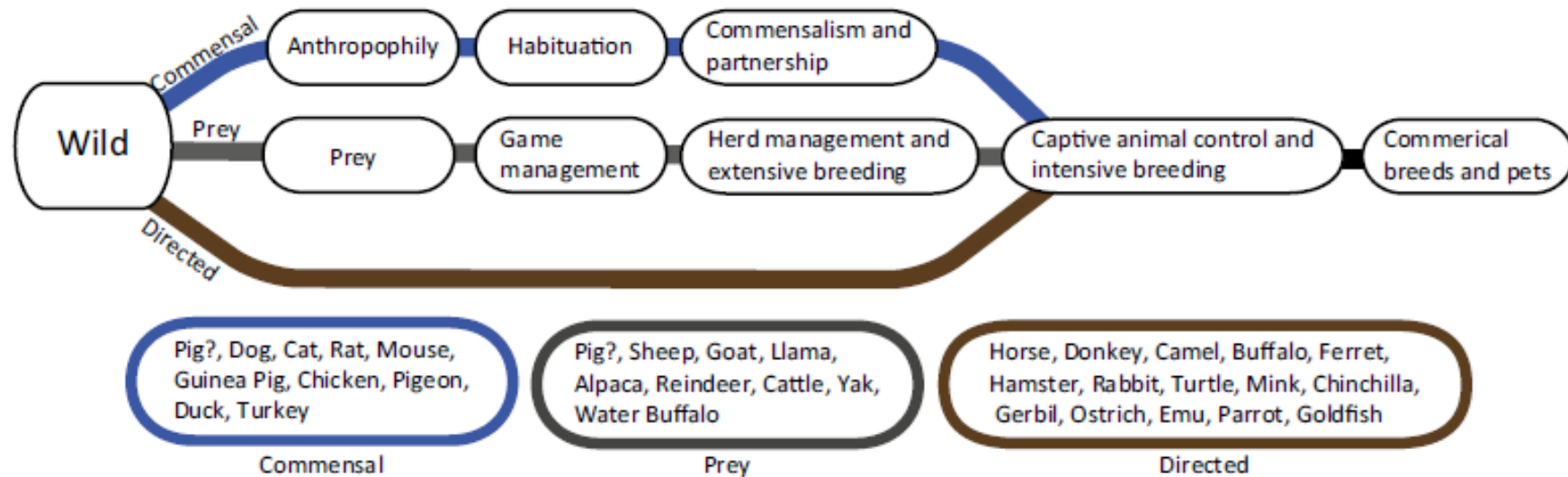


# Arqueogenómica



- Identificación taxonómica y sexual: especies morfológicamente similares.
- Filogenética: diversidad genética, caracterización de poblaciones, fluctuaciones demográficas, flujo genético, sustitución de poblaciones, evolución poblacional, movimientos de población o comercio de animales.
- Caracterización fenotípica: resistencia a enfermedades, producción de leche, selección en base a coloración, pelaje, etc.

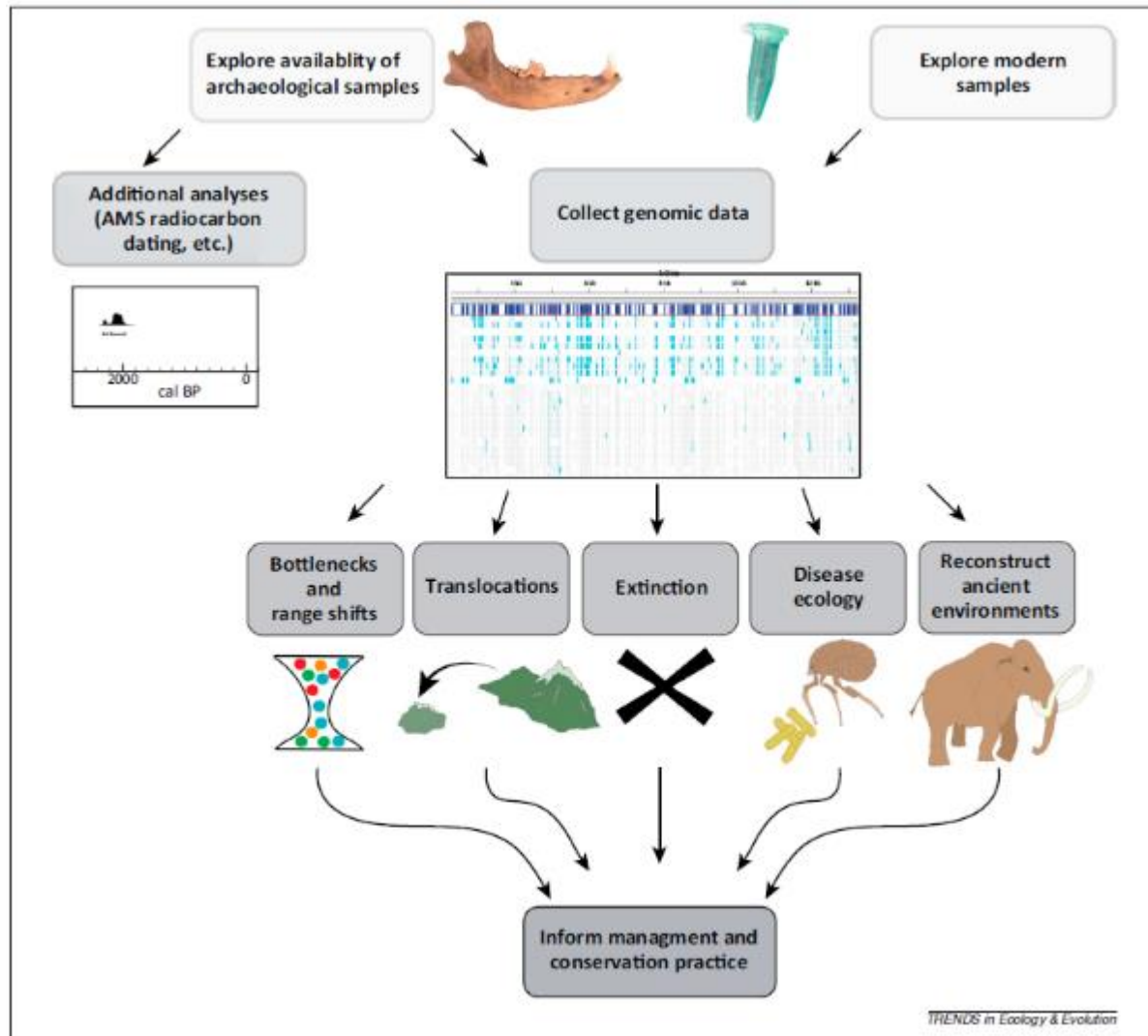
Intensity of human–animal relation



TRENDS in Genetics

**Figure 1.** A representation of the three different pathways [10,11] on top of which the rectangle depicts the increasing degree of human–animal interaction from left to right. The blue, grey, and brown lines represent the commensal, prey, and directed pathways, respectively. Selected domestic animal species by the pathway they may have entered into a domesticated relation with humans are shown in rounded rectangles. These categories are not mutually exclusive, as demonstrated most clearly by pigs. Humans hunted and moved wild boar to Cyprus [77] (among other places), suggesting that pigs went through a prey pathway, but pigs were also domesticated over several millennia at Çayönü Tepesi [13], a process consistent with the commensal pathway.

Usos y aplicaciones del aADN para la conservación de la biodiversidad.





Contents lists available at ScienceDirect

Journal of Archaeological Science: Reports

journal homepage: [www.elsevier.com/locate/jasrep](http://www.elsevier.com/locate/jasrep)



## Use of next-generation molecular tools in archaeological neotropical deer sample analysis



Federica Moreno<sup>a</sup>, Gonzalo Figueiro<sup>b</sup>, Natalia Mannise<sup>c</sup>, Andrés Iriarte<sup>d,e</sup>, Susana González<sup>c,f</sup>, José Mauricio Barbanti Duarte<sup>g</sup>, Mariana Cosse<sup>c,\*</sup>

<sup>a</sup> Programa de Investigación Antropo-Arqueológica, DICYT-MEC, Uruguay

<sup>b</sup> Departamento de Antropología Biológica, FHCE-Udelar, Uruguay

<sup>c</sup> Departamento de Biodiversidad y Genética, IIRCE-MEC, Uruguay

<sup>d</sup> Departamento de Genética, IIRCE-MEC, Uruguay

<sup>e</sup> Departamento de Desarrollo Biotecnológico, Instituto de Higiene, Facultad de Medicina, Udelar, Uruguay

<sup>f</sup> Sección Genética Evolutiva Facultad de Ciencias, Udelar, Uruguay

<sup>g</sup> Núcleo de Pesquisa e Conservação de Cervídeos, Departamento de Zootecnia/Universidade Estadual Paulista Jaboticabal – SP, Brazil

### ARTICLE INFO

#### Article history:

Received 2 May 2016

Received in revised form 3 November 2016

Accepted 3 November 2016

Available online xxxxx

#### Keywords:

Ancient DNA

Cervidae

Deer management

Uruguayan lowlands

### ABSTRACT

Taxonomic identity and genetic variation of three bone samples from a late Holocene earth mound in the eastern Uruguayan lowlands were analyzed. Samples were initially identified by morphology as being from pampas deer (*Ozotoceros bezoarticus*), a middle-sized cervid that occupies open environments forming herds of up to 50 animals. Prehistoric human communities may have developed herd management systems for this species. The aim of this study was to evaluate usefulness of a Next Generation Sequencing (NGS) strategy using pooled samples to explore genetic relationships between specimens. Two mitochondrial D-loop haplotypes were found which surprisingly identifies another deer species (*Mazama gouazoubira*). Our findings confirm that NGS is a powerful tool for taxonomic identification of ancient Uruguayan samples, also indicating that *M. gouazoubira* may be underrepresented in the zooarchaeological record of eastern Uruguay. Finally, since both species have different niches and behaviors it is necessary to formulate new questions in order to understand prehistoric management of Neotropical deer involving larger sample sizes and analysis of other genetic markers.

© 2016 Elsevier Ltd. All rights reserved.



Venado de campo  
(*Ozotoceros bezoarticus*,  
*O.b. uruguayensis*  
*O.b. arerunguaensis*)



Guazubirá  
(*Subulo gouazoubira*)



**Table 1**

Ecological and ethological characteristics of the pampas deer (*O. bezoarticus*) and brown brocket deer (*M. gouazoubira*). Data extracted from Duarte and González (2010).

	Niche	Home range (Km <sup>2</sup> , mean value)	Density (Km <sup>2</sup> , mean value)	Antler	Weight (kg)	Shoulder height (mm)	Group size (individuals)	Diet
Pampas deer	Open grassland	7.3	6	Male, minimum three tines	20–40	600–700	Gregarious 5–17	Mixed grass feeder
Brown brocket deer	Low secondary woodlands and riparian forest	0.3	1.55	Male, single tine	11–25	500–650	Basically solitary	Browser and mostly frugivorous in the wet season

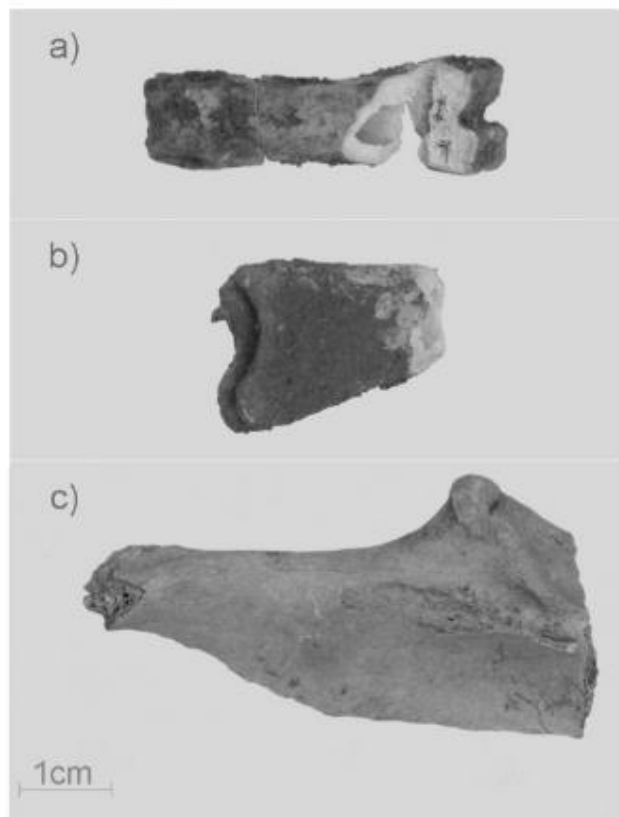


Fig. 2. Three specimens recovered at the site, with a 1 cm scale: a) first phalanx, sample G019; b) second phalanx, sample G016; c) innominate bone, sample G015. Samples were labeled according to the human burial found in the proximity.

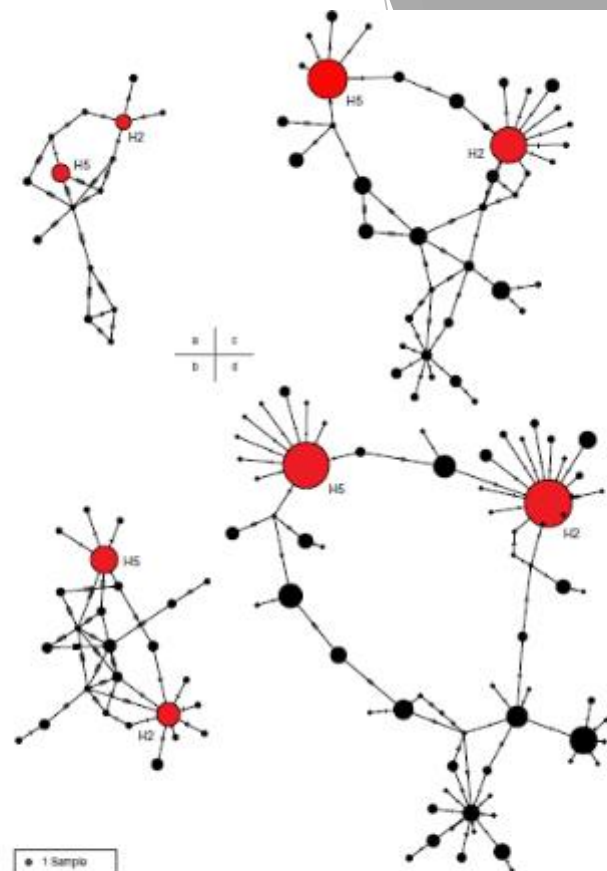


Fig. 3. Median-joining networks (Bandelt et al., 1999) constructed with tcs (Nei, 1999) for each phalanx specimen: a) phalanx score = 30, b) phalanx score = 20, c) phalanx score = 24, d) phalanx score = 22. The size of the circles indicates the frequency of each haplotype in the pooled sample. The crossmatch bars between haplotypes represent nucleotide sequence differences. The haplotypes shown as the most likely based on their frequency and central position in the networks are marked in red. The haplotypes selected for further analysis (H5 and H2) are shown.

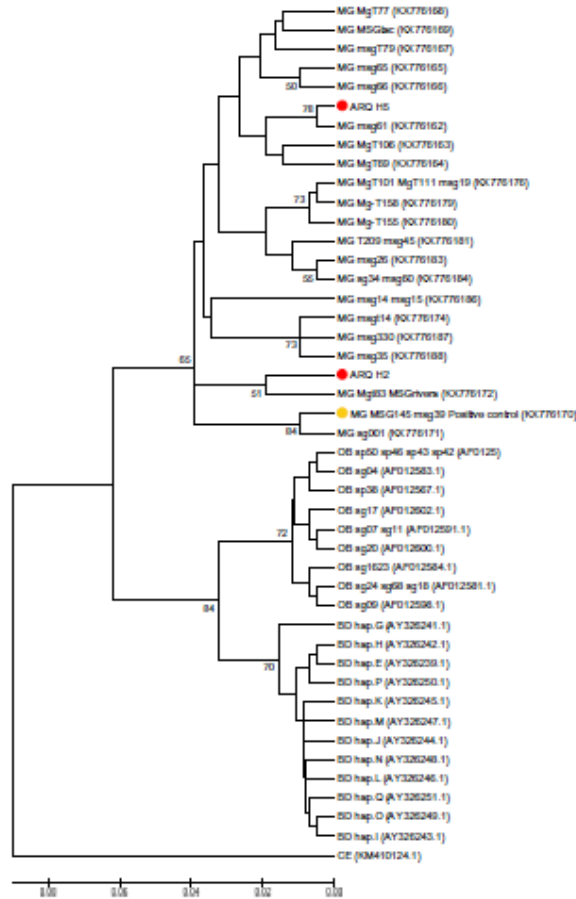


Fig. 4. Phylogenetic tree inferred at neighbor-joining method of the archaeal sequences (●) compared to sequences from those species of archaea found in Uluqayir twenty-year-old geosynthetic haplotype (MG; n = 28), including the positive amplification control (M5 G1-45 (●); n=16). Interspecies haplotype (CIE; n = 15), well-defined bifidobacterium haplotype (BID; a Candidatus Interspecies) were included as an outgroup. Bootstrap values >50 are shown next to the branches and GenBank accession numbers are in parentheses.



#### OPEN ACCESS

##### EDITED BY

Patricia Amavet,  
Facultad de Humanidades y Ciencias (JUNL),  
CONICET, Argentina

##### REVIEWED BY

Brenda Ferrero,  
National Scientific and Technical Research  
Council (CONICET), Argentina  
Solana Tabeni,  
CONICET Mendoza, Argentina

##### \*CORRESPONDENCE

Susana González  
[✉sgonzalez@iibce.edu.uy](mailto:sgonzalez@iibce.edu.uy)

RECEIVED 28 April 2024

ACCEPTED 28 June 2024

PUBLISHED 16 July 2024

##### CITATION

González S, Aristimuño MP and Moreno F  
(2024) New record in Uruguay of the  
marsh deer (*Blastocerus dichotomus*  
Illiger, 1815) redefines its southern  
geographic distribution area.  
*Front. Ecol. Evol.* 12:1424867.  
doi: 10.3389/fevo.2024.1424867

##### COPYRIGHT

© 2024 González, Aristimuño and Moreno

# New record in Uruguay of the marsh deer (*Blastocerus dichotomus* Illiger, 1815) redefines its southern geographic distribution area

Susana González <sup>1,2\*</sup>, María Pía Aristimuño<sup>1</sup>  
and Federica Moreno<sup>1,3</sup>

<sup>1</sup>Instituto de Investigaciones Biológicas Clemente Estable, Ministerio de Educación y Cultura  
(IIBCE-MEC), Montevideo, Uruguay, <sup>2</sup>Deer Specialist Group – International Union for Conservation of  
Nature Species Survival Commission (IUCN), Gland, Switzerland, <sup>3</sup>Facultad de Humanidades y Ciencias  
de la Educación, Universidad de la República, Montevideo, Uruguay

##### KEYWORDS

neotropical deer, mitochondrial DNA, radiocarbon dating, Cervidae, haplotype

- Ciervo más grande de Sudamérica: 80 a 150kg.
- 91-153cm de largo y 110-127cm de altura
- Los machos adultos tienen astas, con 5 puntas de cada lado.
- Pelo marrón rojizo, con la parte de abajo de las patas de color negro.
- Ocupa ambientes inundados: bañados, pantanos.



Lista Roja de Especies  
Amenazadas de la IUCN  
Rojo: distribución histórica.  
Amarillo: distribución actual.  
Destrucción del hábitat.  
En Uruguay habitaba el litoral  
oeste, la región sureste y el norte.  
Extinto desde 1959.

Último individuo avistado en el  
Bañado de Los Indios, Rocha.

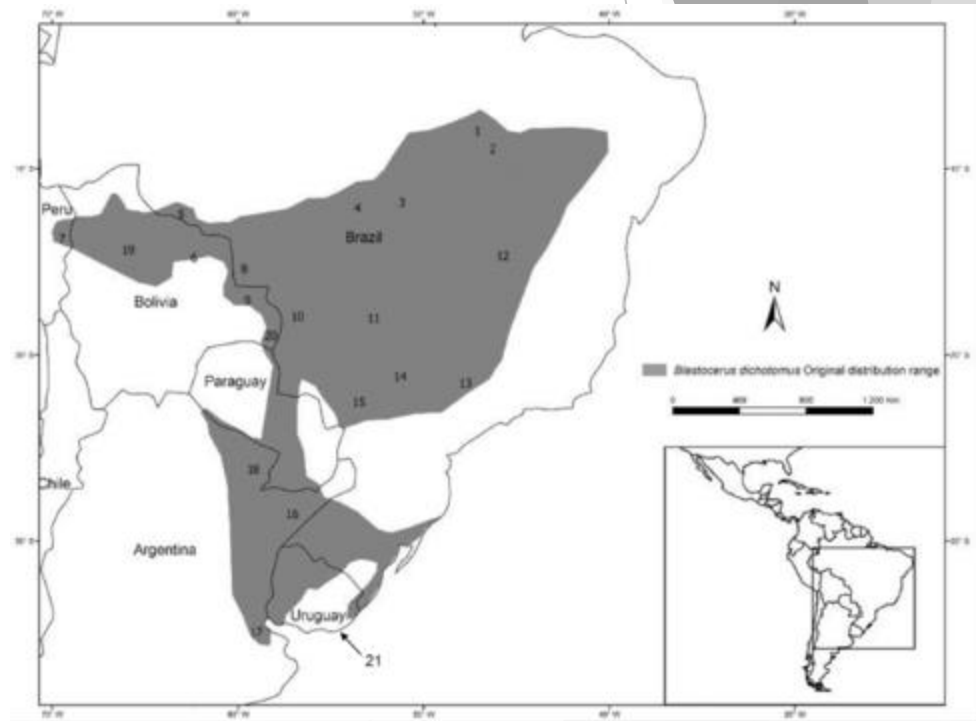


2010

barranca del Arroyo  
Solís Grande

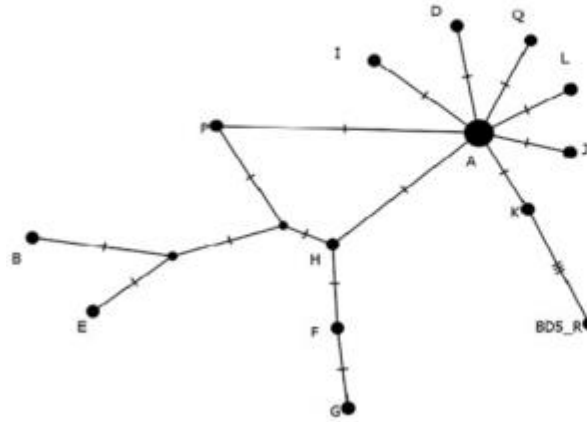


- Fechado radiocarbónico: 294 a AP
- Presencia en Uruguay durante los últimos 3 siglos. Extiende el rango geográfico mejorando el conocimiento de su distribución histórica.





- Se extrajo ADN y se amplificó un fragmento del D-loop (región del adn mitocondrial) de 364 pb.
- Se comparó con haplotipos de Argentina, Bolivia, y Brasil.
- Proximidad con haplotipos de Brasil, con una expansión poblacional desde el haplotipo A (4 mutaciones).



Haplotype	Geographic location	GenBank
A	Brazil	AY326235
B	Argentina	AY326236
C	Brazil	AY326237
D	Argentina	AY326238
E	Argentina	AY326239
F	Argentina	AY326240
G	Argentina	AY326241
H	Brazil	AY326242
I	Brazil	AY326243
J	Brazil	AY326244
K	Brazil	AY326245
L	Brazil	AY326246
M	Brazil	AY326247
N	Bolivia	AY326248
O	Bolivia	AY326249
P	Brazil	AY326250
Q	Brazil	AY326251
R	Uruguay	PP662912

# Qué nos informan en términos de conservación de los cérvidos de Uruguay?

Distribución geográfica en el pasado reciente.

Diversidad genética (cuellos de botella, determinación de unidades de conservación)

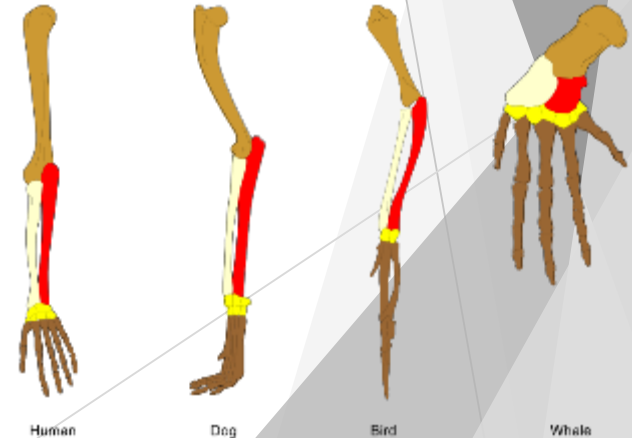
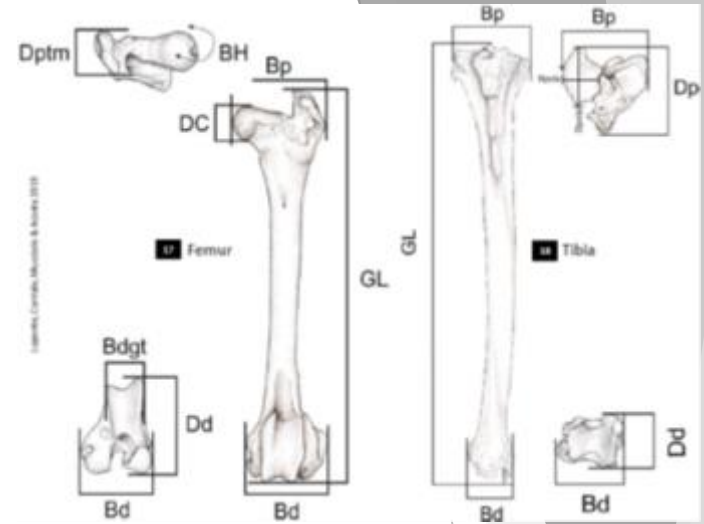
Relaciones filogenéticas con otras poblaciones actuales (y pasadas).

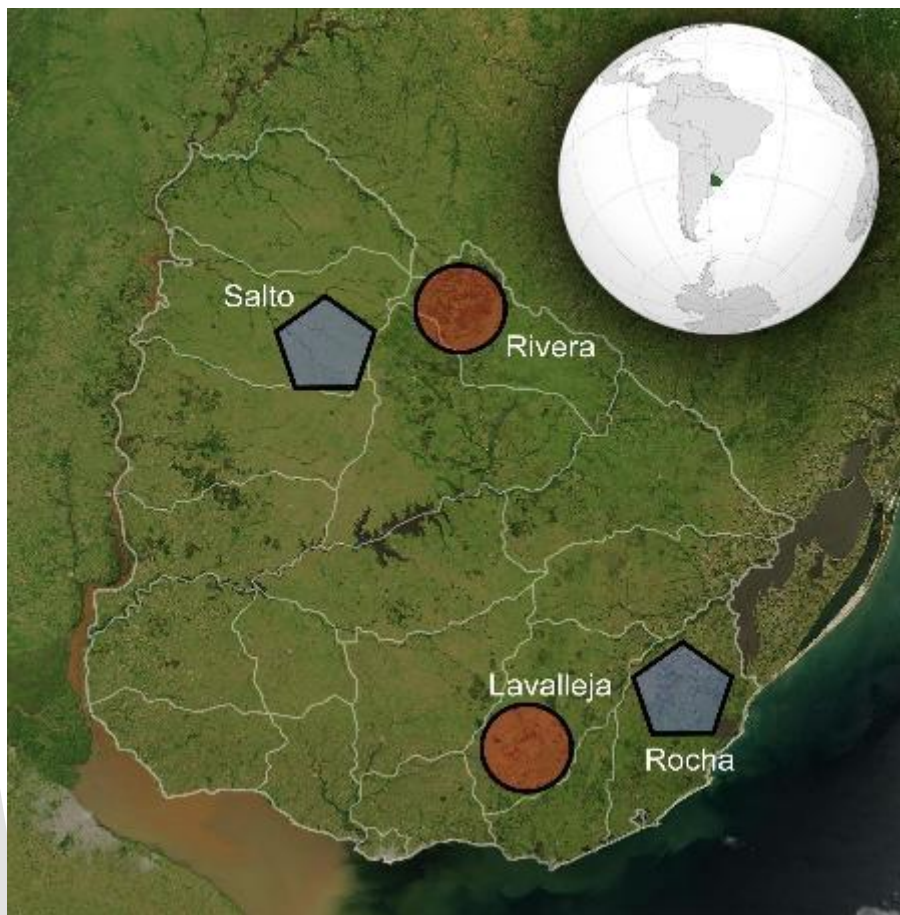
Distribución y conectividad de ambientes en el pasado.

Información para eventuales experiencias de reintroducción.

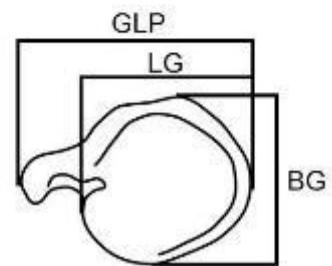
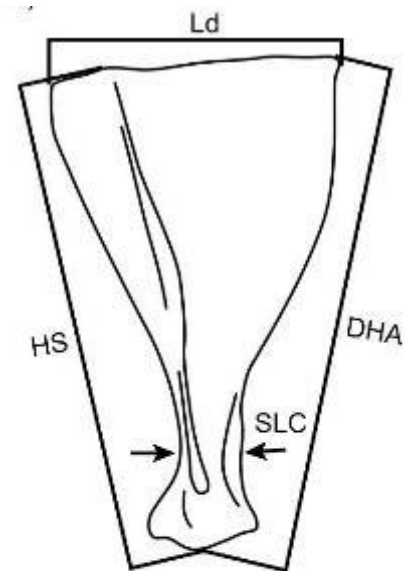
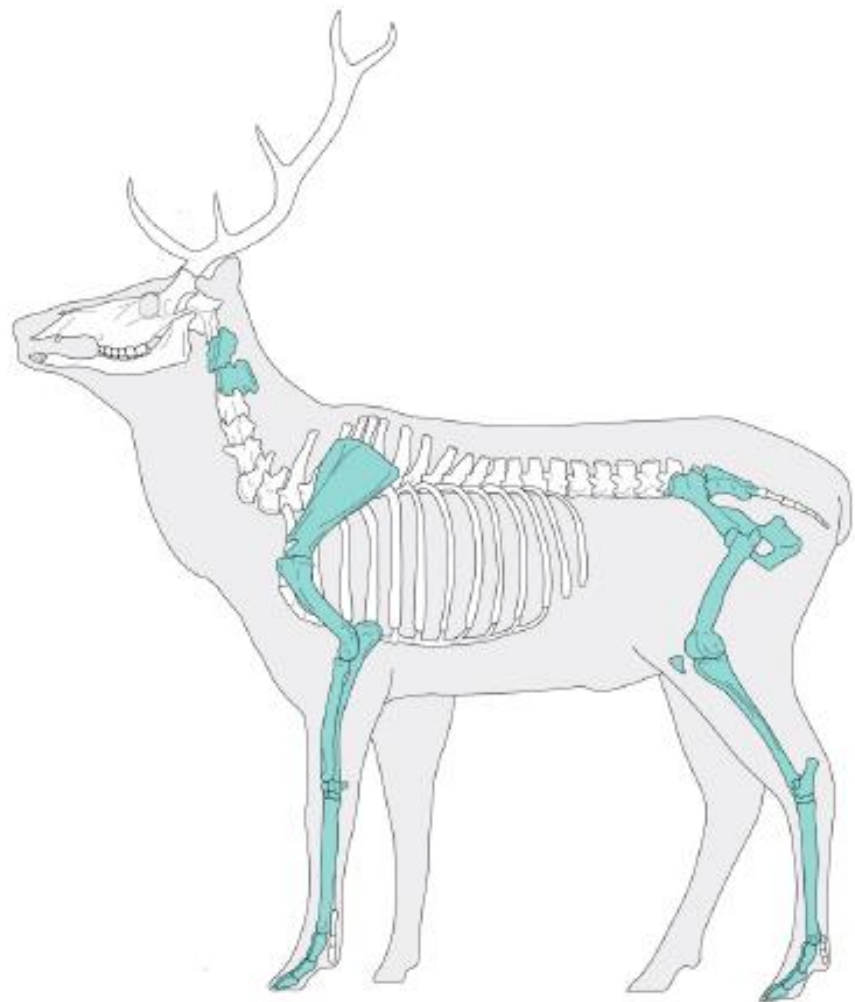
# Abordajes no moleculares

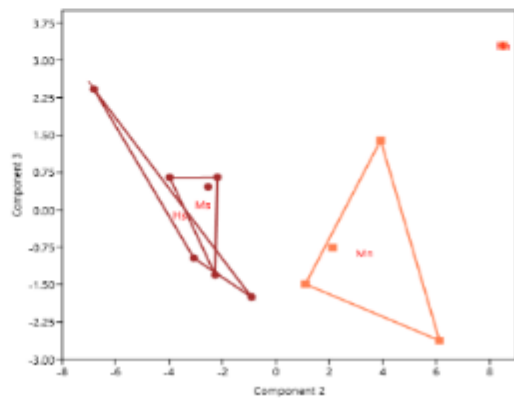
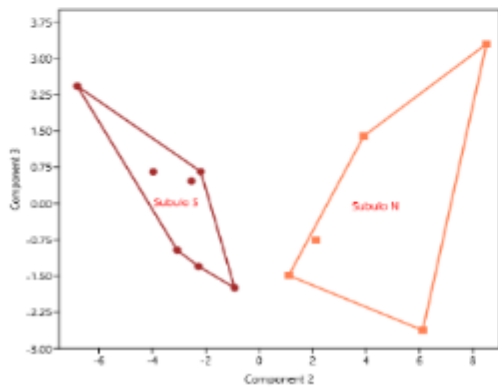
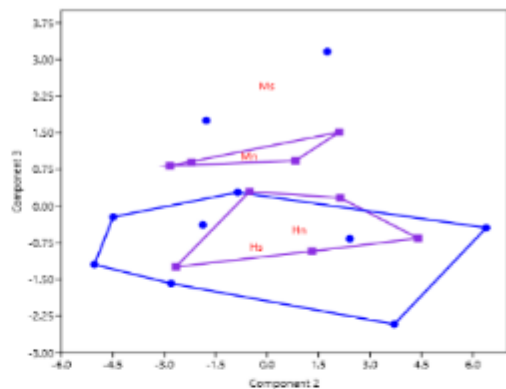
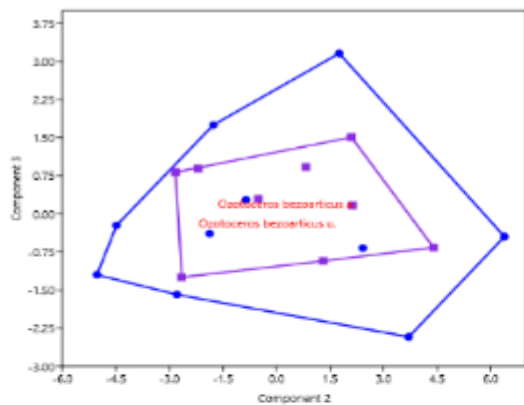
- Similitud postcraneal
- Similitud de tamaño
- Falta de información
- **Biometría**
- **Osteología comparada:** estudio de las semejanzas y diferencias en la osteología de los organismos.





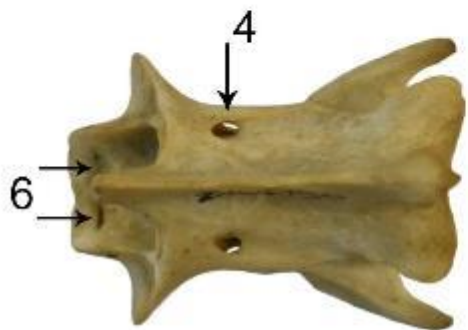
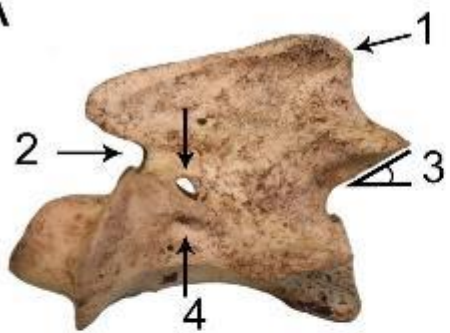
ID	Especie	Procedencia	Sexo	Edad
SG n/n	<i>Subulo gouazoubira</i>	Zoo. Parque Lecoq	no det.	Adulto
SG1019	<i>Subulo gouazoubira</i>	Rivera	M	Adulto joven
ZVCM 1710	<i>Subulo gouazoubira</i>	Zoo. San Carlos	M	Adulto
MNHN 3167	<i>Subulo gouazoubira</i>	no det.	M	Adulto
MNHN 5505	<i>Subulo gouazoubira</i>	no det.	M	Adulto
MNHN 8222	<i>Subulo gouazoubira</i>	Rivera	M	Adulto
MNHN 3068	<i>Subulo gouazoubira</i>	Lavalleja	H	Adulto
MNHN 6409	<i>Subulo gouazoubira</i>	Cabo Polonio	H	Sub adulto
SG1042	<i>Ozotoceros bezoarticus</i>	no det.	no det.	Adulto
SG1039	<i>Ozotoceros bezoarticus</i>	no det.	no det.	Adulto joven
SG1100	<i>Ozotoceros bezoarticus</i>	no det.	no det.	Adulto
SG1000	<i>Ozotoceros bezoarticus</i>	Salto, Arenunguá.	M	Adulto joven
SG 1004	<i>Ozotoceros bezoarticus</i>	Salto, Arenunguá.	no det.	Adulto joven
SG1010	<i>Ozotoceros bezoarticus</i>	Salto, Arenunguá.	M	Adulto
SG1006	<i>Ozotoceros bezoarticus</i>	Salto, Arenunguá.	H	Adulto
SG0017	<i>Ozotoceros bezoarticus</i>	Salto, Arenunguá.	H	Juvenil
ZVCM 1310	<i>Ozotoceros bezoarticus</i>	Salto, Arenunguá.	H	Adulto
SG n/n [1]	<i>Ozotoceros bezoarticus</i>	Rocha, Los Ajos.	M	Adulto joven
SG1070	<i>Ozotoceros bezoarticus</i>	Rocha, Los Ajos.	M	Adulto
SG1089	<i>Ozotoceros bezoarticus</i>	Rocha, Los Ajos.	H	Adulto
SG1088	<i>Ozotoceros bezoarticus</i>	Rocha, Los Ajos.	H	Adulto
SG0140	<i>Ozotoceros bezoarticus</i>	Rocha, Los Ajos.	H	Adulto joven
SG0059	<i>Ozotoceros bezoarticus</i>	Rocha, Los Ajos.	H	Juvenil
SG n/n [2]	<i>Ozotoceros bezoarticus</i>	Rocha, Los Ajos.	H	Adulto
SG1105	<i>Ozotoceros bezoarticus</i>	Rocha, Los Ajos.	H	Adulto
SG0019	<i>Ozotoceros bezoarticus</i>	Rocha, Los Ajos.	M	Adulto
ZVCM 1488	<i>Ozotoceros bezoarticus</i>	Rocha, Los Ajos.	M	Juvenil
ZVCM 1540	<i>Ozotoceros bezoarticus</i>	Rocha, Los Ajos.	H	Adulto
ZVCM 1735	<i>Ozotoceros bezoarticus</i>	Rocha, Los Ajos.	H	Adulto joven



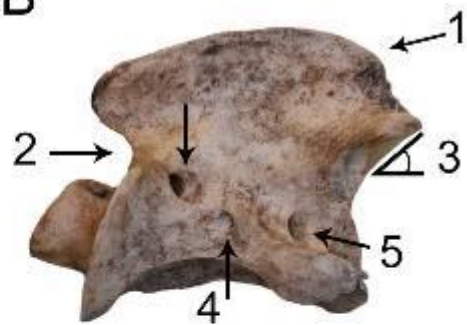


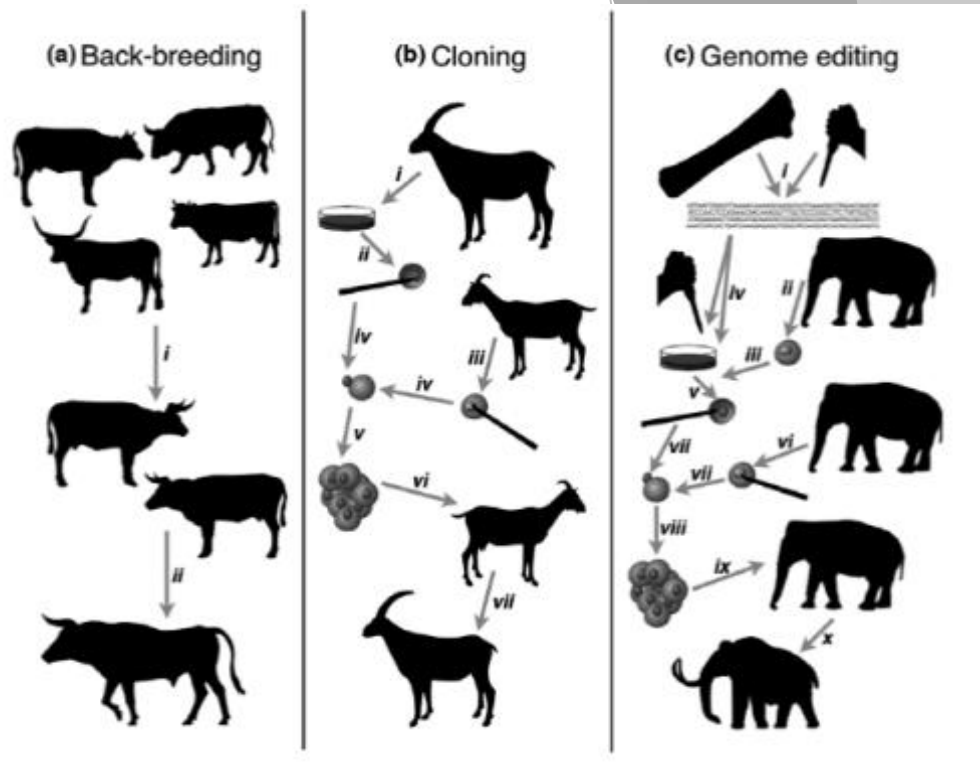
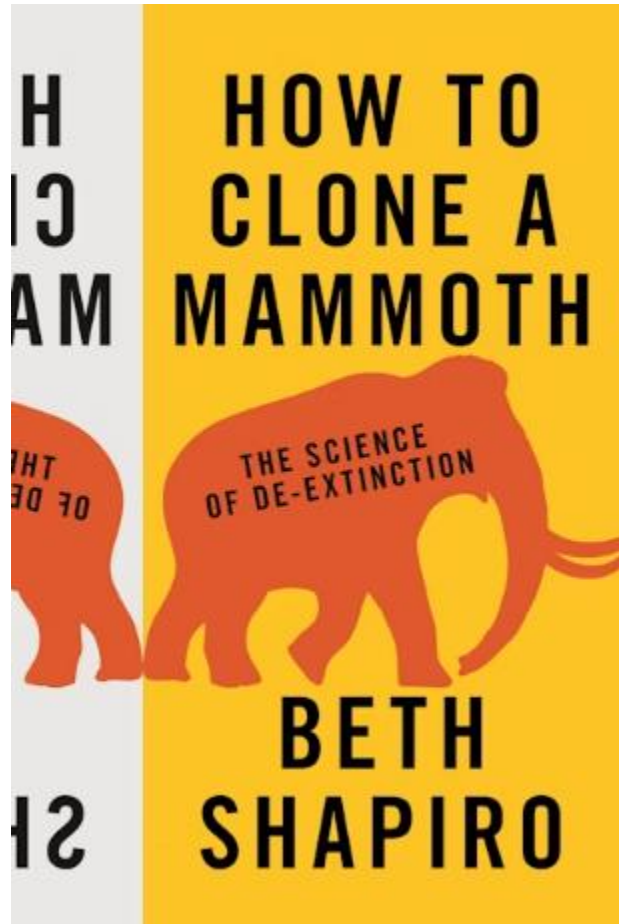


A



B





Proxies



**MODERN CONSERVATION CRISIS**

**GAME CHANGER**

# CLONE A MAMMOTH

An elephant gives birth to an ANIMAL with "mammoth-like traits."



**NOT an EXACT CLONE**  
THAT'S IMPOSSIBLE BUT THE GOAL: CREATE AN ANIMAL

LIVES ACTS LIKE A MAMMOTH

WHAT IS THE POINT?

HOW WOULD THE SCIENCE WORK?

DE-EXTINCTION  
RESURRECTING LOST ECOSYSTEMS

THE SCIENCE OF DE-EXTINCTION

BIOLOGICAL INTERACTIONS

passenger pigeon

dodo

mammoth

ALL EXINCT FOREVER?

by PETER DURAND

www.alphaclump.com

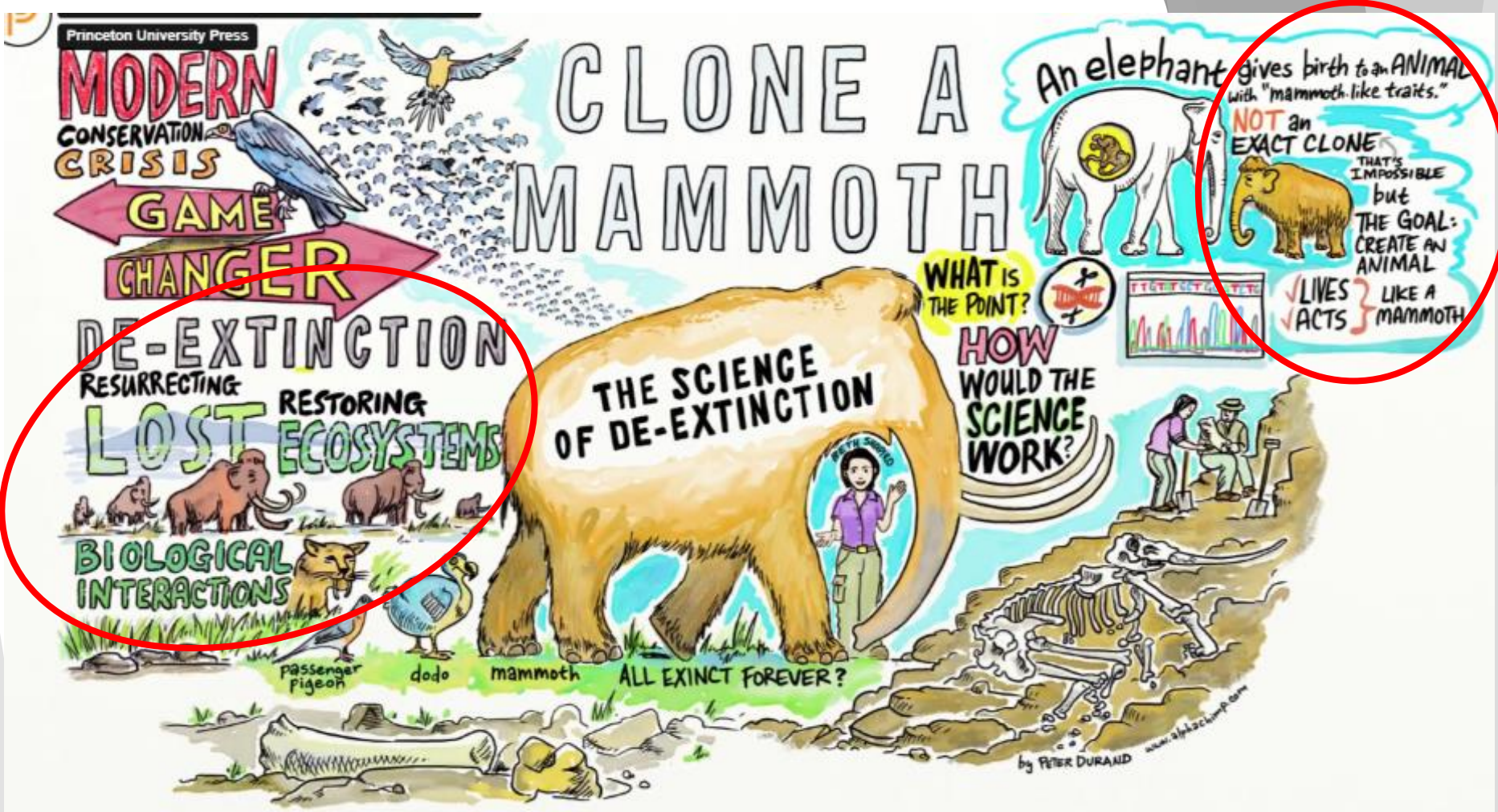


Table 1. List of active de-extinction breeding programs.

Species	Common Name	Extinction Date	De-Extinction Technique	Conservation Category	Template Species	Template Species Conservation Status (IUCN/U.S. ESA)	Organization
<i>Equus quagga quagga</i>	Quagga Zebra	1883 AD	Artificial Selection	Biodiversity	<i>Equus quagga burchelli</i>	Near Threatened/NA	The Quagga Project
<i>Bos taurus primigenius</i>	Aurochs	1627 AD	Backbreeding of Domestic Descendants	Ecosystem engineer (grassland maintenance)	<i>Bos taurus taurus</i>	Not Assessed/NA	Operation Taurus; Taurus Project
<i>Chelonoidis elephantopus</i>	Floreana Island Giant Tortoise	Circa 1850 AD	Hybrid-backbreeding	Ecosystem engineer (megaherbivore)	<i>C. elephantopus</i> × <i>Chelonoidis becki</i> ; <i>C. elephantopus</i> × <i>Chelonoidis hoodensis</i>	becki = vulnerable, hoodensis = critically endangered; U.S. ESA NA to both	Galápagos National Park Service
<i>Ectopistes migratorius</i>	Passenger Pigeon	1914 AD	Precise Hybridization	Ecosystem engineer (forest disturbance/regeneration cycle)	<i>Patagioenas fasciata</i>	Least Concern/Not Listed	Revive & Restore
<i>Mammuthus primigenius</i>	Woolly Mammoth	~3900 yr BP	Precise Hybridization	Ecosystem engineer (megaherbivore, grassland maintenance)	<i>Elephas maximus</i>	Endangered/Endangered	Revive & Restore
<i>Tympanuchus cupido</i>	Heath Hen	1932 AD	Precise Hybridization	Indicator species	<i>Tympanuchus pinnatus</i>	Vulnerable/NA	Revive & Restore
<i>Anomalopteryx didiformis</i> *	Little Bush Moa	15th Century AD	Precise Hybridization	Megaherbivore	<i>Dromaius novaehollandiae</i>	Least Concern/NA	Genetic Rescue Foundation

\* The Genetic Rescue Foundation intends to restore proxies of all nine extinct moa species. The Little Bush Moa is simply the first species with a sequenced genome and serves as a stand in here. AD: anno domini; BP: before present; NA: not applicable.



Colossal Laboratories  
& Biosciences

01 DE-EXTINCTION  
02 SPECIES INDEX

03 CONSERVATION  
04 SCIENCE & TECHNOLOGY

05 A BETTER WORLD  
06 COMPANY

07 LABS  
08 NEWS

INDEX | +

# THE DODO



Colossal Laboratories  
& Biosciences

01 DE-EXTINCTION  
02 SPECIES INDEX

03 CONSERVATION  
04 SCIENCE & TECHNOLOGY

05 A BETTER WORLD  
06 COMPANY

07 LABS  
08 NEWS

INDEX | +

# THYLACINE



Colossal Laboratories  
& Biosciences

01 DE-EXTINCTION  
02 SPECIES INDEX

03 CONSERVATION  
04 SCIENCE & TECHNOLOGY

05 A BETTER WORLD  
06 COMPANY

07 LABS  
08 NEWS

INDEX | +

1 YEAR UP PLAN TO RE-EXTINCT

A MARVEL OF EVOLUTION

Thylacines, Tasmanian wolf or Tasmanian  
demon, mammal was a marsupial  
extinction is a tragedy of human

Colossal determined to give the

1 YEAR UP PLAN TO RE-EXTINCT

# THE MAMMOTH

MAX PREHISTORY THUNDER FORWARD.

WE HAVE THE DNA, THE TECHNOLOGY AND THE LEADING EXPERTS IN THE FIELD.  
NEXT, WE WILL HAVE THE WOOLLY MAMMOTH ALIVE AGAIN.

01 DE-EXTINCTION



## Argumentos a favor de la desextinción

- ✓ **Restauración de ecosistemas:** La reintroducción de especies extintas podría ayudar a recuperar funciones ecológicas perdidas.
- ✓ **Corrección de errores humanos:** Si la extinción fue causada por actividades humanas, la desextinción podría considerarse un acto de reparación.
- ✓ **Avances científicos y tecnológicos:** Impulsa el desarrollo de biotecnología, genética y clonación, lo que podría beneficiar la conservación de especies en peligro.
- ✓ **Mayor conciencia ambiental:** Genera interés público y conciencia sobre la importancia de la conservación.
- ✓ **Potencial uso en medicina y genética:** La investigación genética aplicada a la desextinción podría tener beneficios en otros campos, como la medicina regenerativa.

## Argumentos en contra de la desextinción

- ✗ **Ecosistemas cambiados:** Los ambientes donde vivían estas especies han cambiado, lo que podría hacer imposible su reintegración.
- ✗ **Impacto en la conservación actual:** Podría desviar recursos y atención de la protección de especies en peligro de extinción.
- ✗ **Problemas genéticos y fisiológicos:** Las especies revividas podrían tener problemas de salud debido a la falta de diversidad genética.
- ✗ **Dificultades en la crianza y adaptación:** Criar animales en cautiverio y adaptarlos a la vida silvestre es complejo y puede no ser exitoso.
- ✗ **Riesgos ecológicos desconocidos:** Reintroducir especies puede generar efectos negativos imprevistos en los ecosistemas actuales.

## Debates éticos

- 🗳️ **¿Hasta qué punto es ético?** Modificar la naturaleza mediante ingeniería genética genera dilemas filosóficos y religiosos.
- 🗳️ **¿A quién beneficia realmente la desextinción?** Puede ser más un interés científico, económico o comercial que una solución real para la biodiversidad.
- 🗳️ **¿Cómo evitar que fomente la negligencia ambiental?** Si se normaliza la idea de "revivir" especies, podría disminuir el esfuerzo en la conservación de las actuales.
- 🗳️ **¿Qué derechos tendrían estas especies?** Si se crean organismos artificialmente, ¿qué consideraciones éticas deben tenerse en cuenta para su bienestar?
- 🗳️ **¿Qué papel juegan las comunidades indígenas y locales?** Algunas especies extintas tienen un valor cultural para ciertos pueblos, y su reintroducción podría no ser bien recibida.

**¡¡Gracias!!**

