Extinction of Animals and Plants

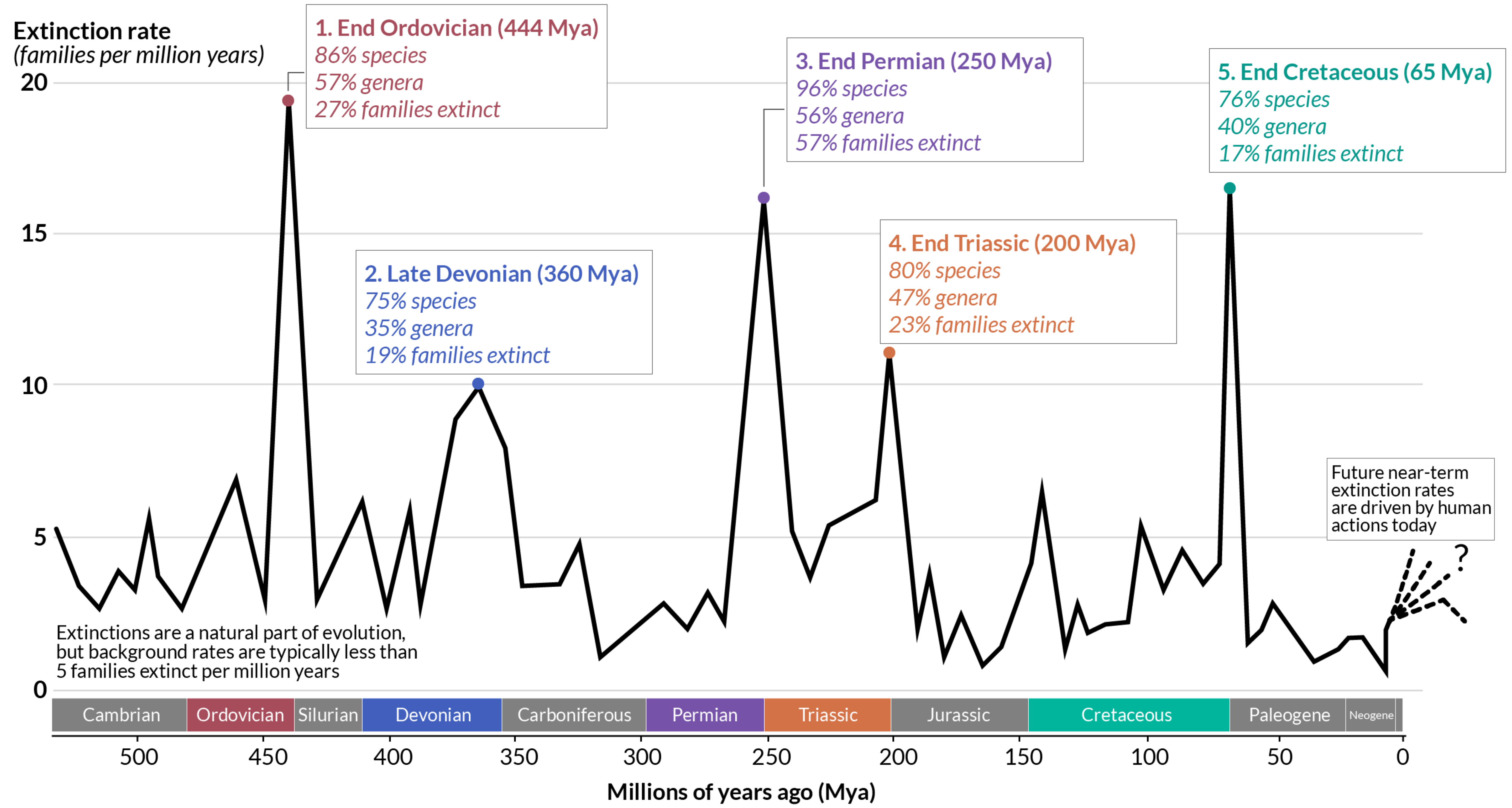
1690 Dodo bird
(predation by introduced pigs/cats)

1768 Stellar’s sea cow
(hunting for fur/oil)

1962 Hawaii chaff flower
(habitat conversion to military installations)

- Extinction is the death of all members of a species
- Currently 2 to 10 million species live on earth
- 99% of all species that lived on earth are extinct

The “big five” mass extinctions



1. End Ordovician (444 Mya)
86% species
57% genera
27% families extinct

2. Late Devonian (360 Mya)
75% species
35% genera
19% families extinct

3. End Permian (250 Mya)
96% species
56% genera
57% families extinct

4. End Triassic (200 Mya)
80% species
47% genera
23% families extinct

5. End Cretaceous (65 Mya)
76% species
40% genera
17% families extinct

Extinctions are a natural part of evolution, but background rates are typically less than 5 families extinct per million years

Future near-term extinction rates are driven by human actions today

Sources: Barnosky et al. (2011); Howard Hughes Medical Institute; McCallum (2015). Vertebrate biodiversity losses point to a sixth mass extinction.
OurWorldinData.org – Research and data to make progress against the world's largest problems.

1. Change in climate & ocean chemistry
2. Rapid and severe global cooling
3. Volcanic activity and global warming
4. Volcanic activity and global warming
5. Asteroid impact in Yucatan/Mexico

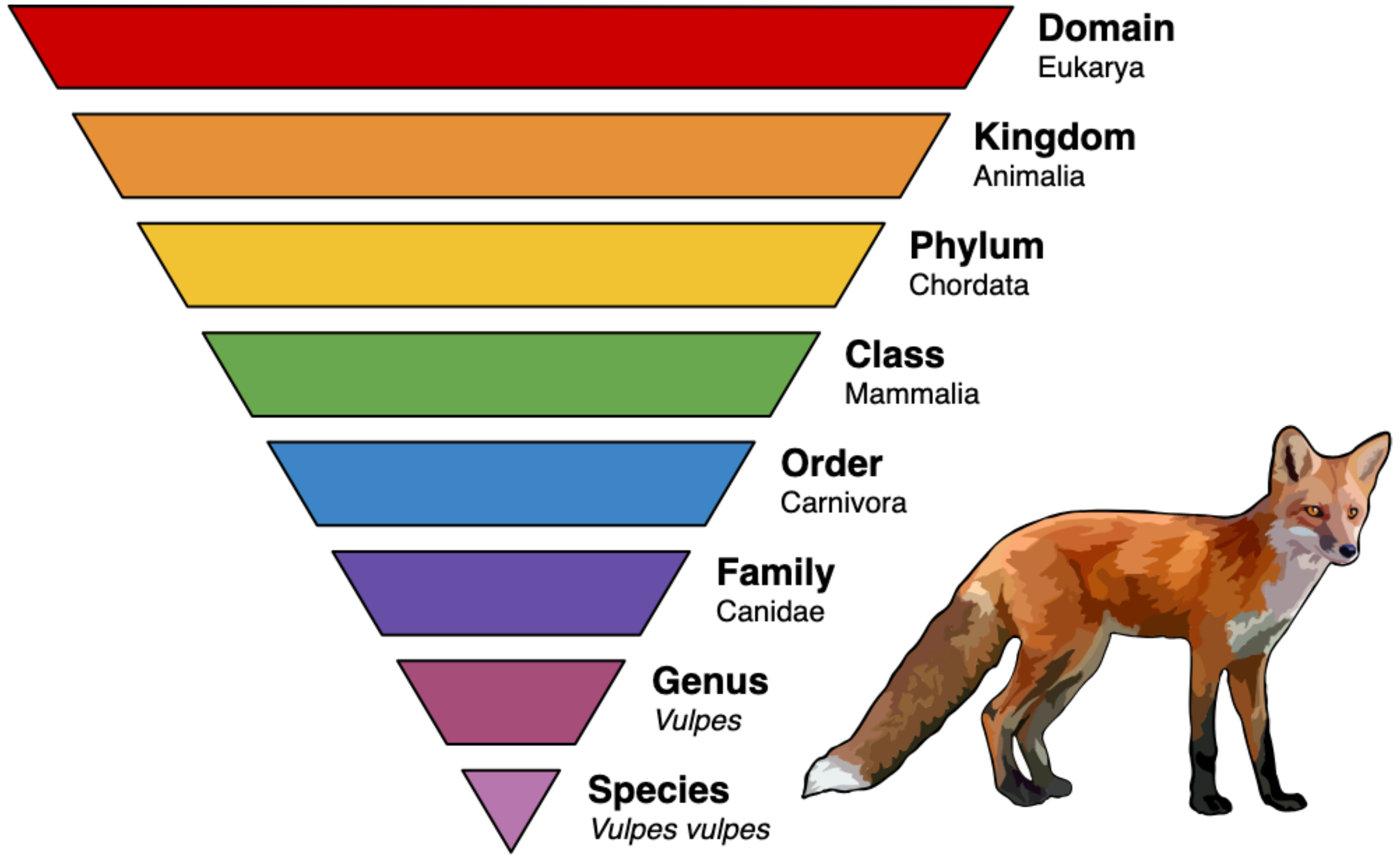
- Mass extinctions occur naturally and periodically over time: 10% of species are lost every 1 million years, 30% every 10 million years, and 65% every 100 million years
- Evolution occurs through the balance of *extinction* and *speciation*

Holocene extinction

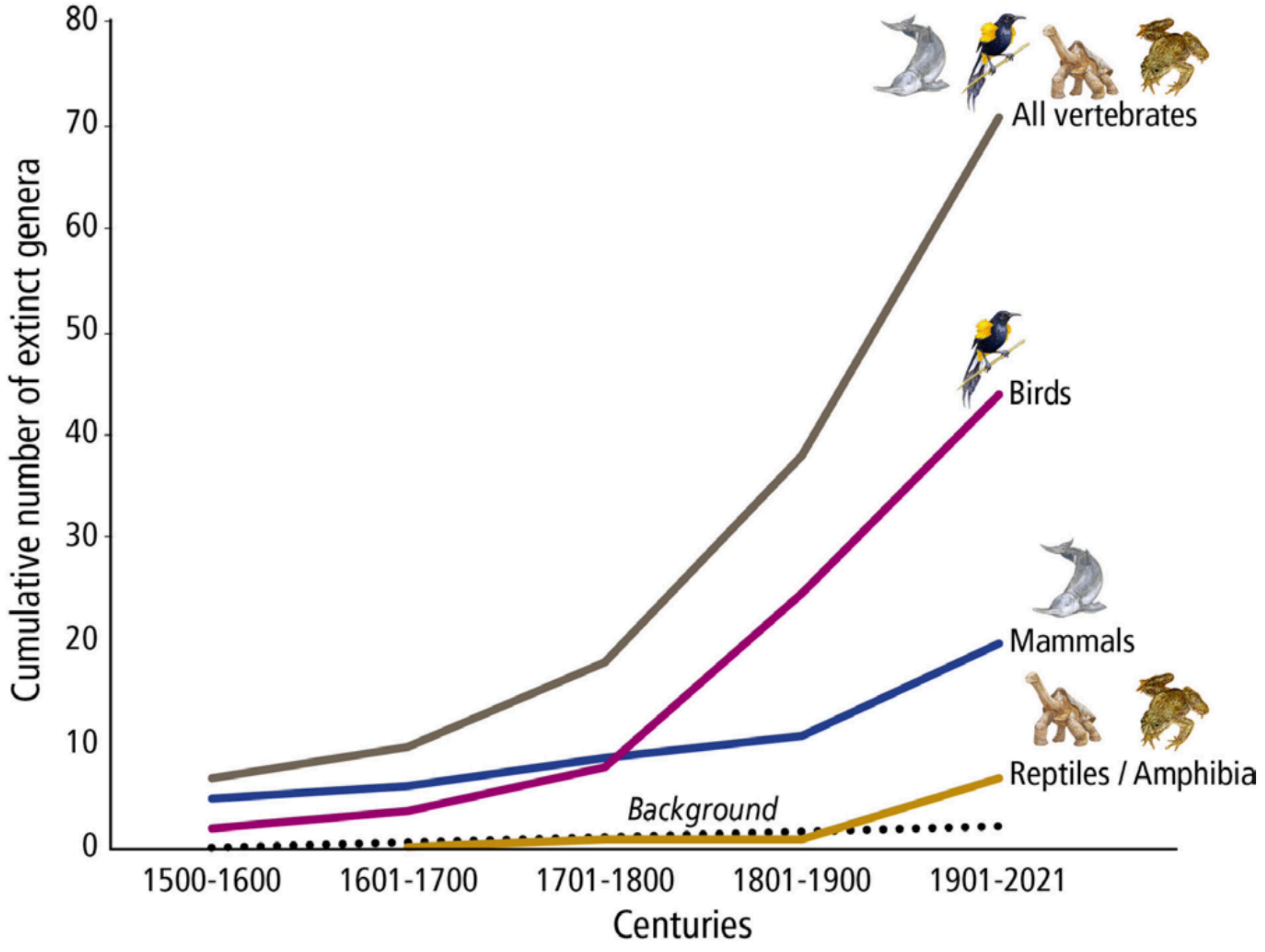
Sixth mass extinction

- Currently ongoing mass extinction caused most likely by human activities (ecocide)
- 2 orders, 10 families, and 73 genera of tetrapods (ie, mammals, birds, reptiles, and amphibians) have gone extinct since 1500 AD
- Background extinction rates are 2 genera per 500 years
- Projected extinctions between 1800 to 2100 would have taken 100,000 years under historical background rates
- Extinction rates >> speciation rates

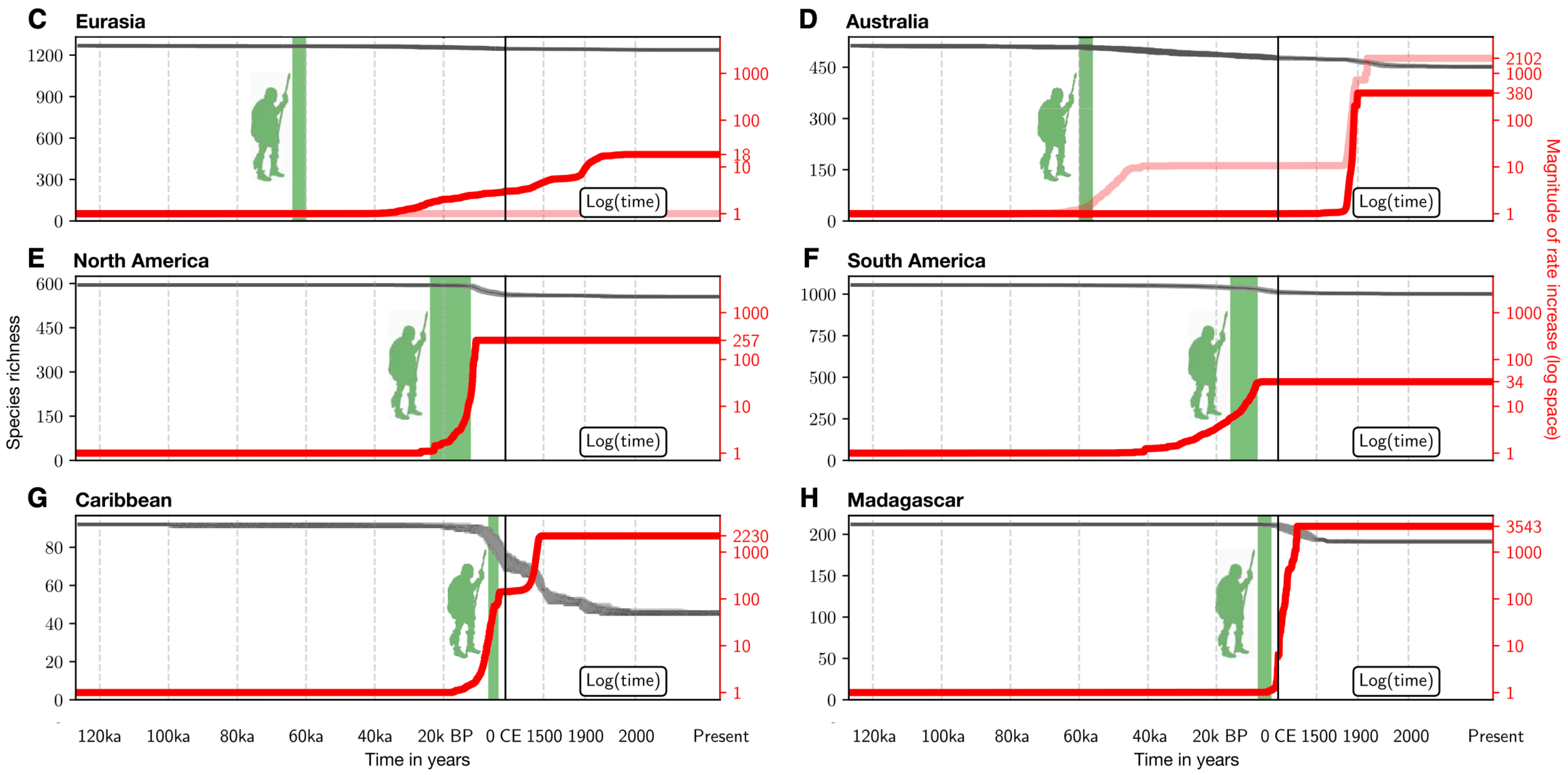
Ceballos & Ehrlich, PNAS 2023



Red fox *(Vulpes vulpes)*



Human presence predicts loss of mammalian diversity



- Humans drive mammal extinctions since the Late Pleistocene (126,000 years ago)
- Human population sizes predict past extinctions with high accuracy
- Past climate changes had a negligible impact on global mammal diversity
- Large increases in extinction rates are expected by 2100 (2nd wave of extinctions)

Andermann et al., Sci. Adv. 2020; 6 : eabb2313

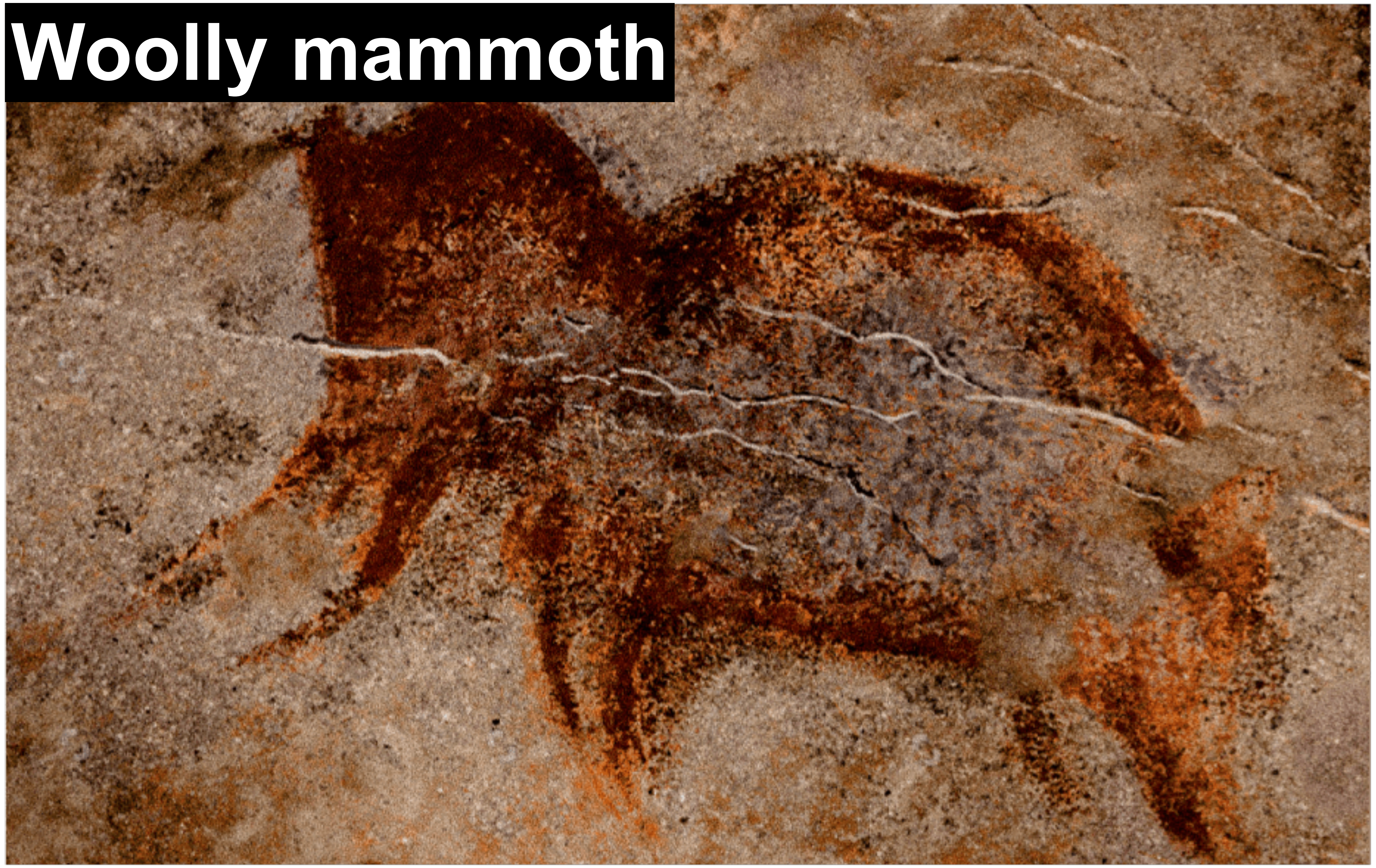
BIO-312 Genomic solutions to sustainable development

École
polytechnique
fédérale
de Lausanne

Ancient genomes

time machines and records for future resurrection

Woolly mammoth

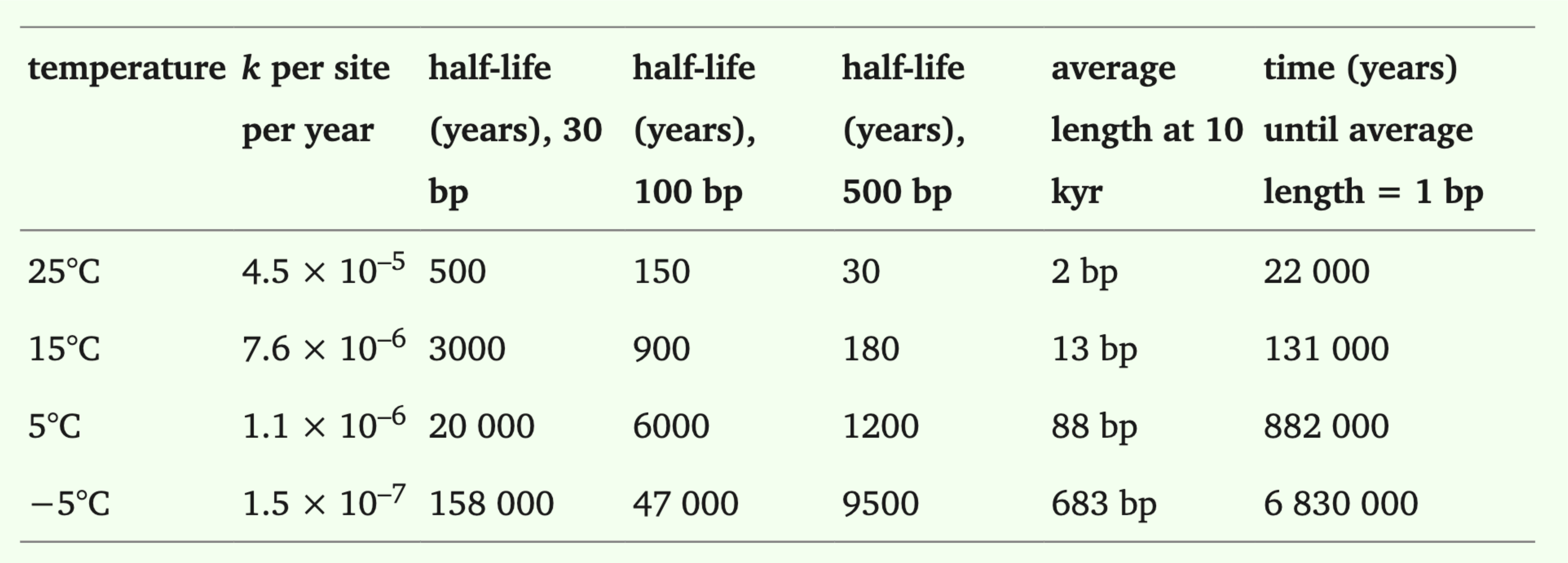


1.6 million year old mammoth DNA

van der Valk et al. *Nature* 2021

The half-life of DNA in bone

- **DNA decay kinetics:** DNA degradation follows an exponential decay model $N(t) = N_0 e^{-\lambda t}$
- **Half-life of DNA:** time required for half of DNA to degrade $t_{1/2} = \frac{\ln(2)}{\lambda}$
- **Temperature-dependent DNA decay:** upper limit >1M years



temperature	k per site per year	half-life (years), 30 bp	half-life (years), 100 bp	half-life (years), 500 bp	average length at 10 kyr	time (years) until average length = 1 bp
25°C	4.5×10^{-5}	500	150	30	2 bp	22 000
15°C	7.6×10^{-6}	3000	900	180	13 bp	131 000
5°C	1.1×10^{-6}	20 000	6000	1200	88 bp	882 000
−5°C	1.5×10^{-7}	158 000	47 000	9500	683 bp	6 830 000

Proc Biol Sci. 2012 Oct 10;279(1748):4724–4733.

Full genome of a horse that lived 780,000 years ago

informs about conservation efforts of endangered wild horses

Genome coverage: 1.1x
DNA fragment size: 77.5 bp

Nature **499**, 74–78 (2013)

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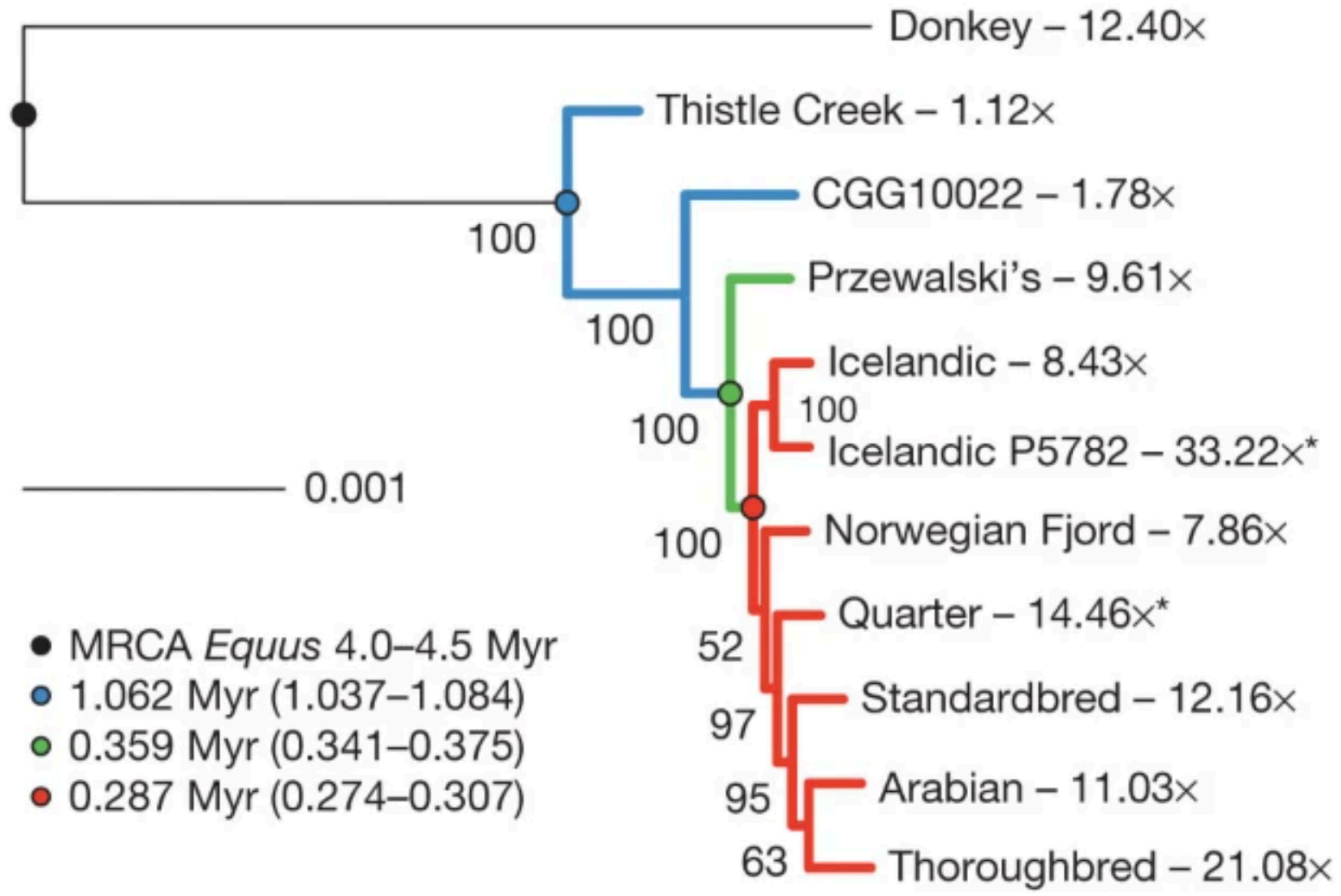

- Ancient horse genome helped to establish phylogenetic relationships within *Equus*
- Horse population sizes fluctuated over past 2 Myrs (periods of climatic change)

Nature **499**, 74–78 (2013)

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informs about conservation efforts of endangered wild horses

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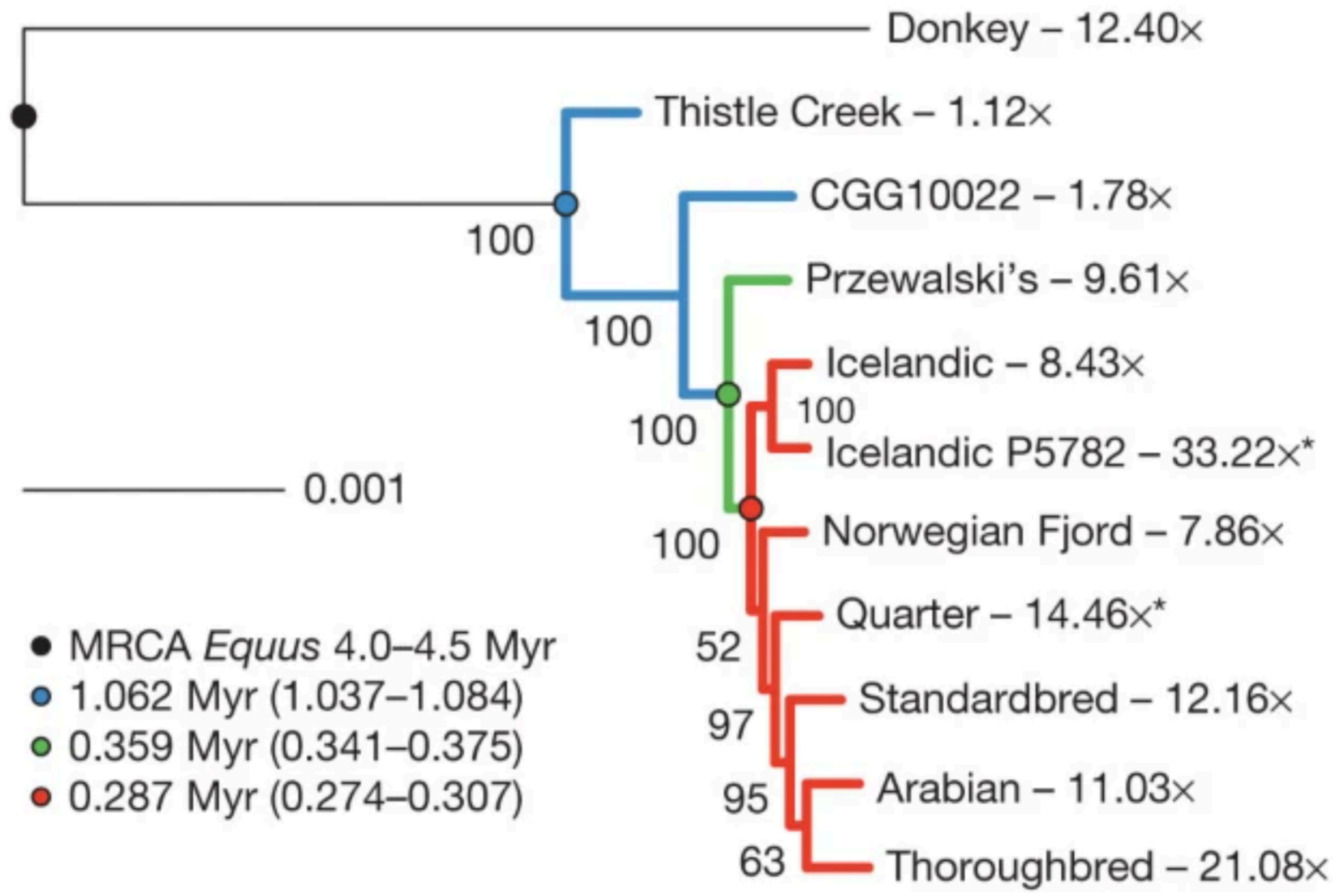
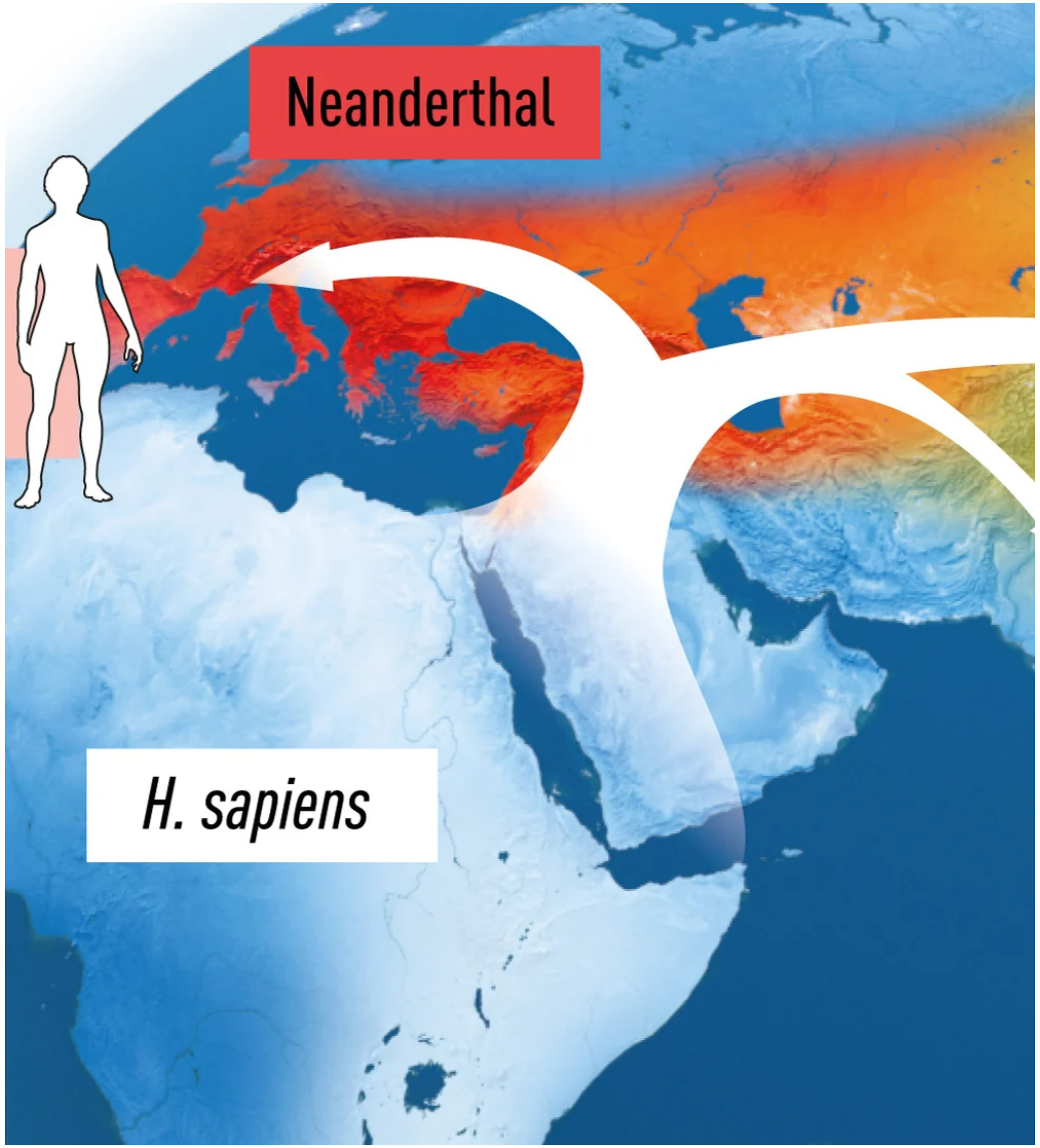


Przewalski's horse
(IUCN Endangered)

- Przewalski's horse: last survivor of wild horses and at some point extinct in the wild
- Przewalski's horses and domestic horses split 340,000 to 431,000 years ago
- Przewalski's and domestic horse genomes show no signs of admixture
- Genetic confirmation that the Przewalski's horse requires strong conservation efforts

Nature **499**, 74–78 (2013)

Neanderthals: a group of extinct hominids that inhabited Europe and Western Asia 300,000 to 40,000 years ago

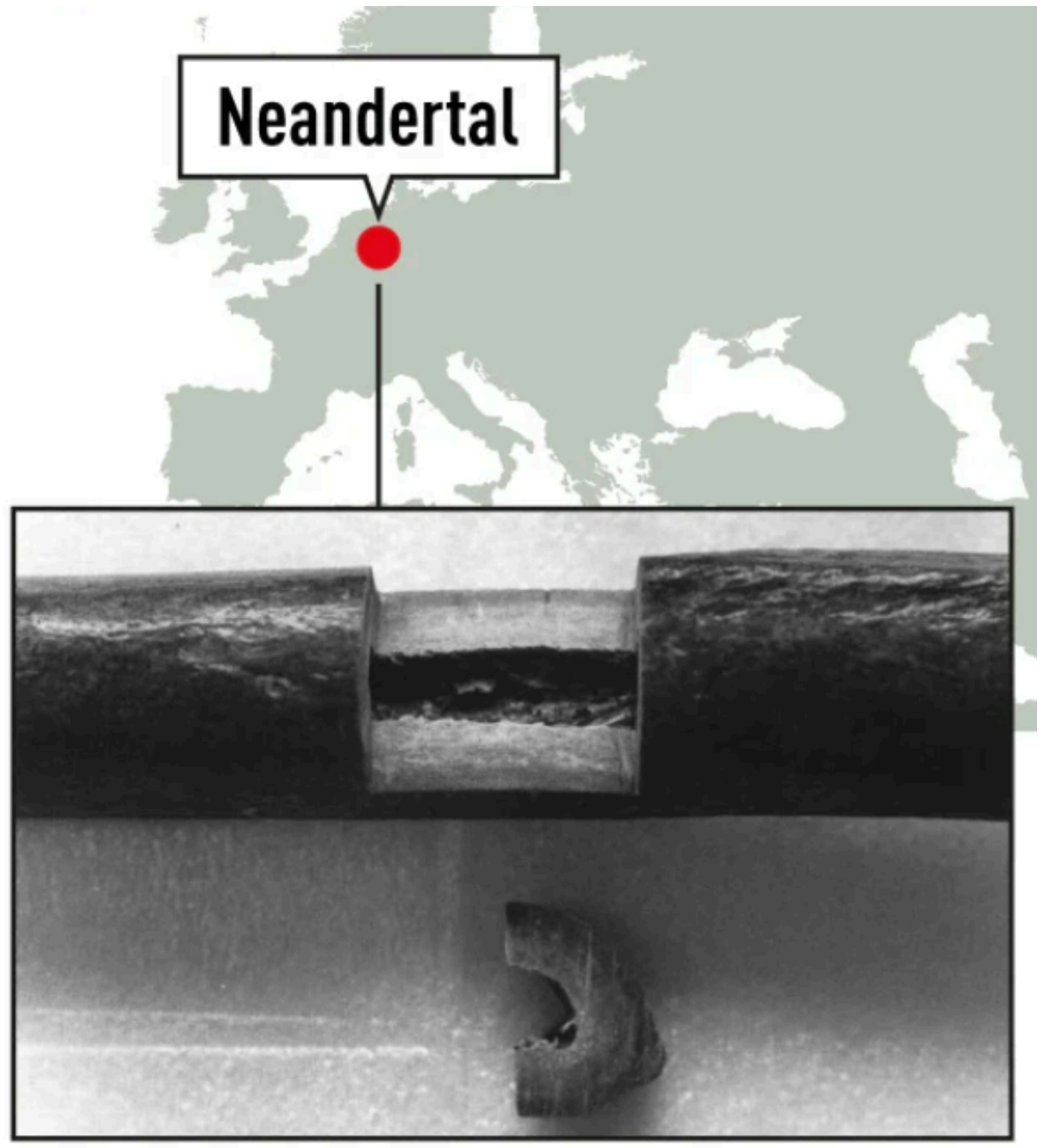


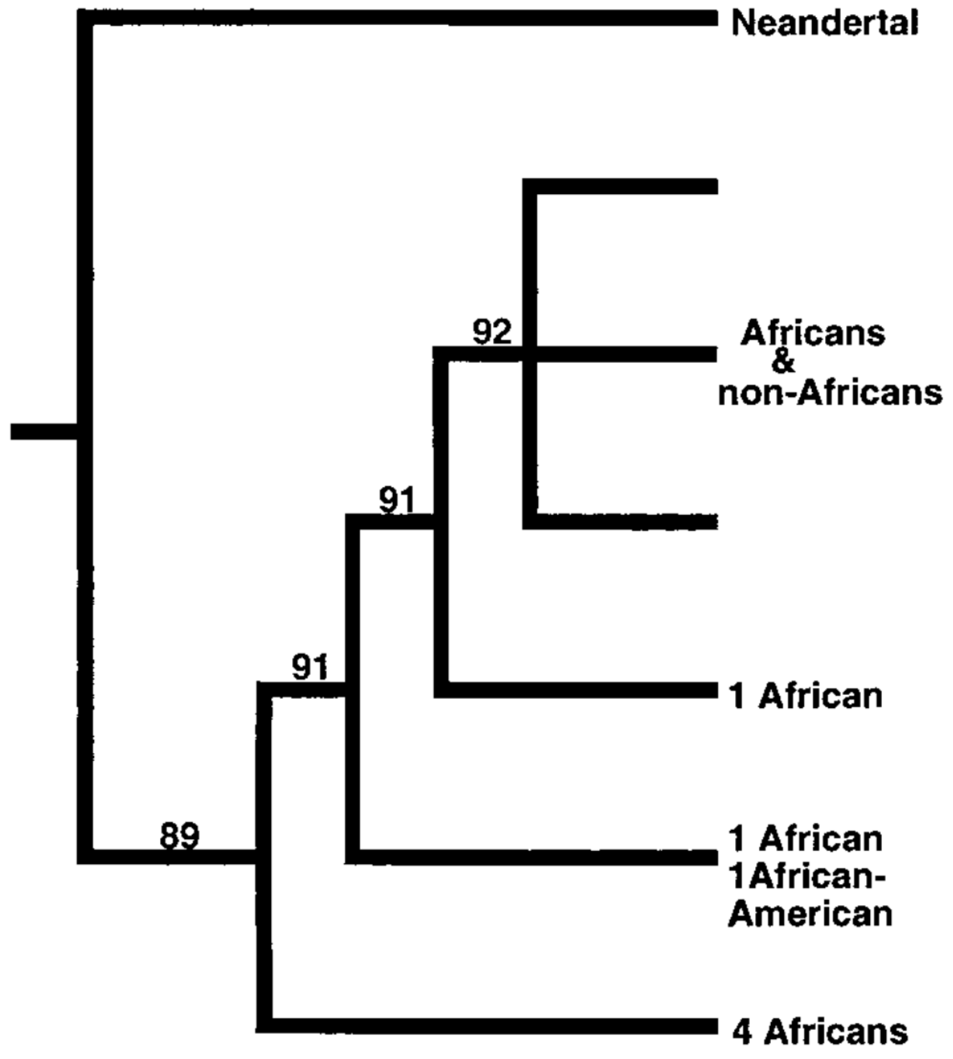
Neanderthals: a group of extinct hominids that inhabited Europe and Western Asia 300,000 to 40,000 years ago

Cell, Vol. 90, 19–30, July 11, 1997, Copyright ©1997 by Cell Press

Neandertal DNA Sequences and the Origin of Modern Humans

Matthias Krings,* Anne Stone,† Ralf W. Schmitz,‡
Heike Krainitzki,§ Mark Stoneking,† and Svante Pääbo*
*Zoological Institute
University of Munich
PO Box 202136
D-80021 Munich
Germany





Neanderthals: a group of extinct hominids that inhabited Europe and Western Asia 300,000 to 40,000 years ago

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Neandertal DNA Sequences and the Origin of Modern Humans

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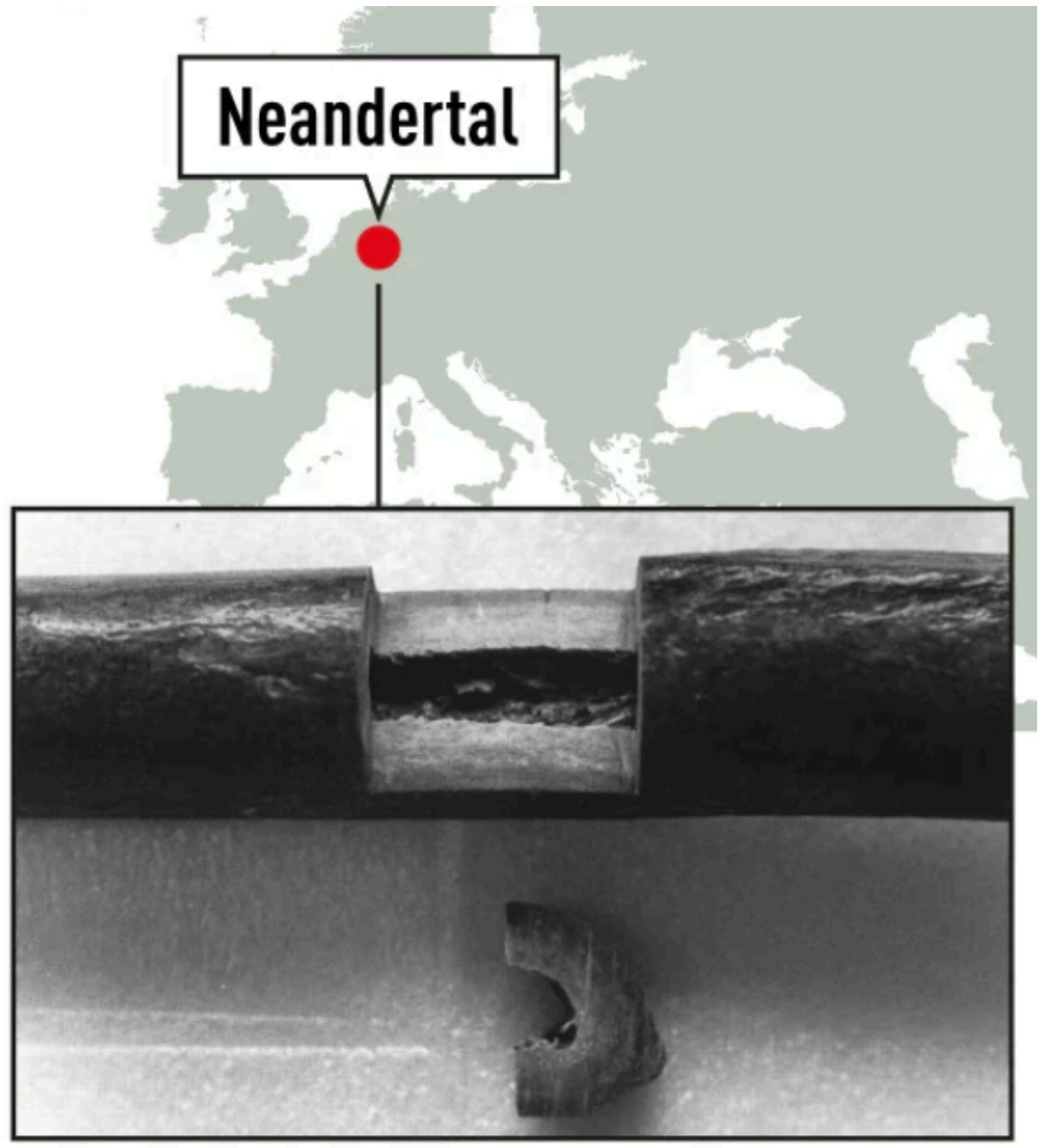
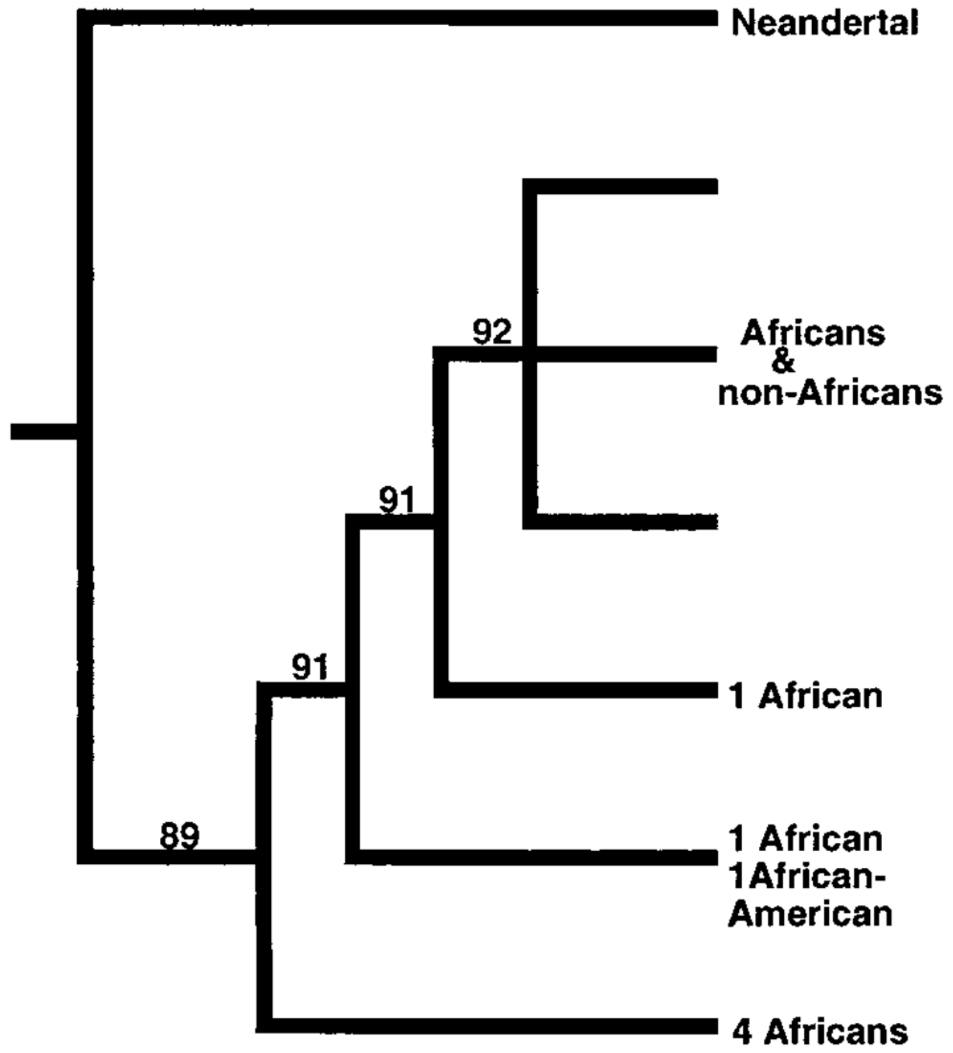
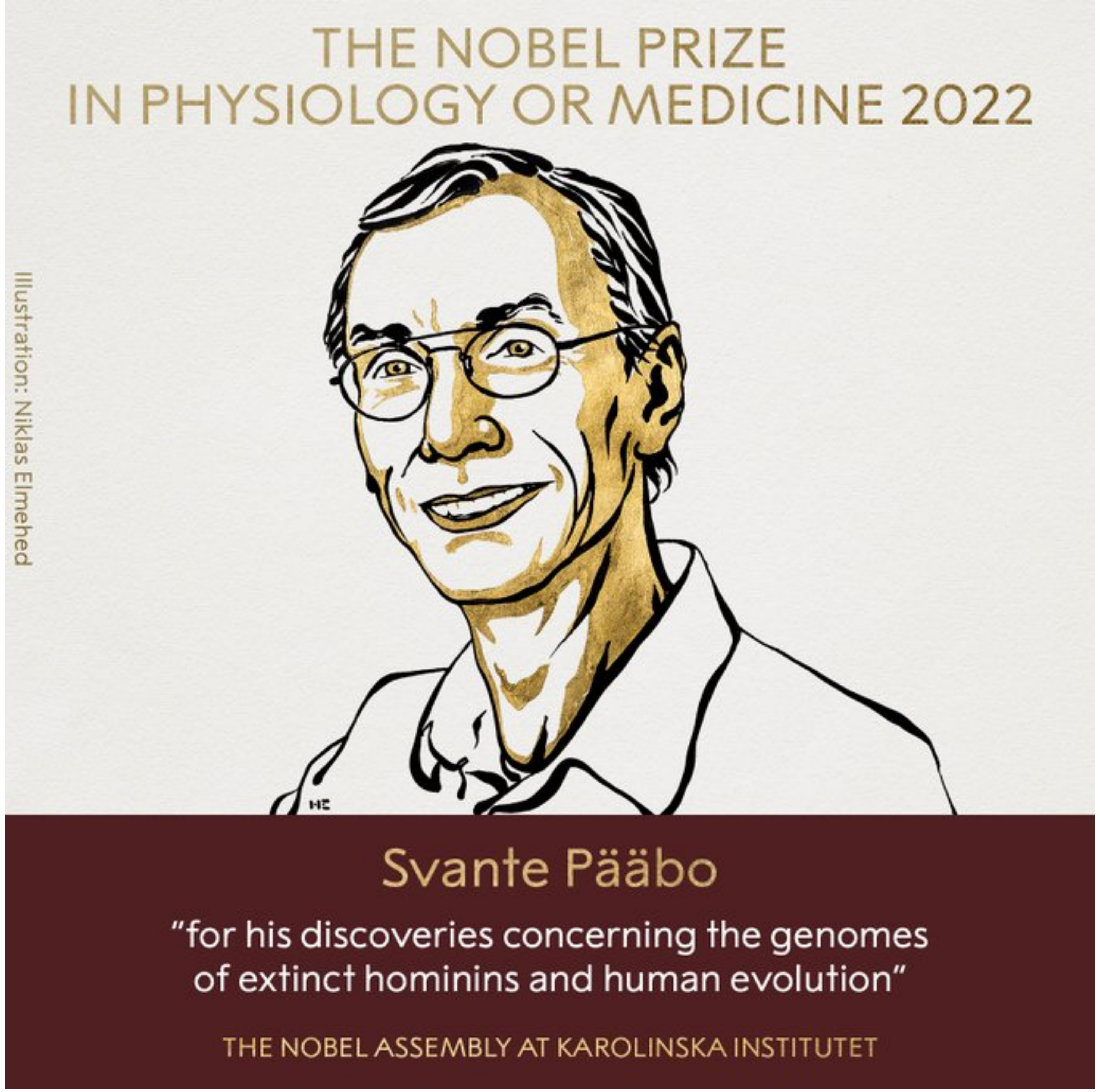






THE NOBEL PRIZE
IN PHYSIOLOGY OR MEDICINE 2022

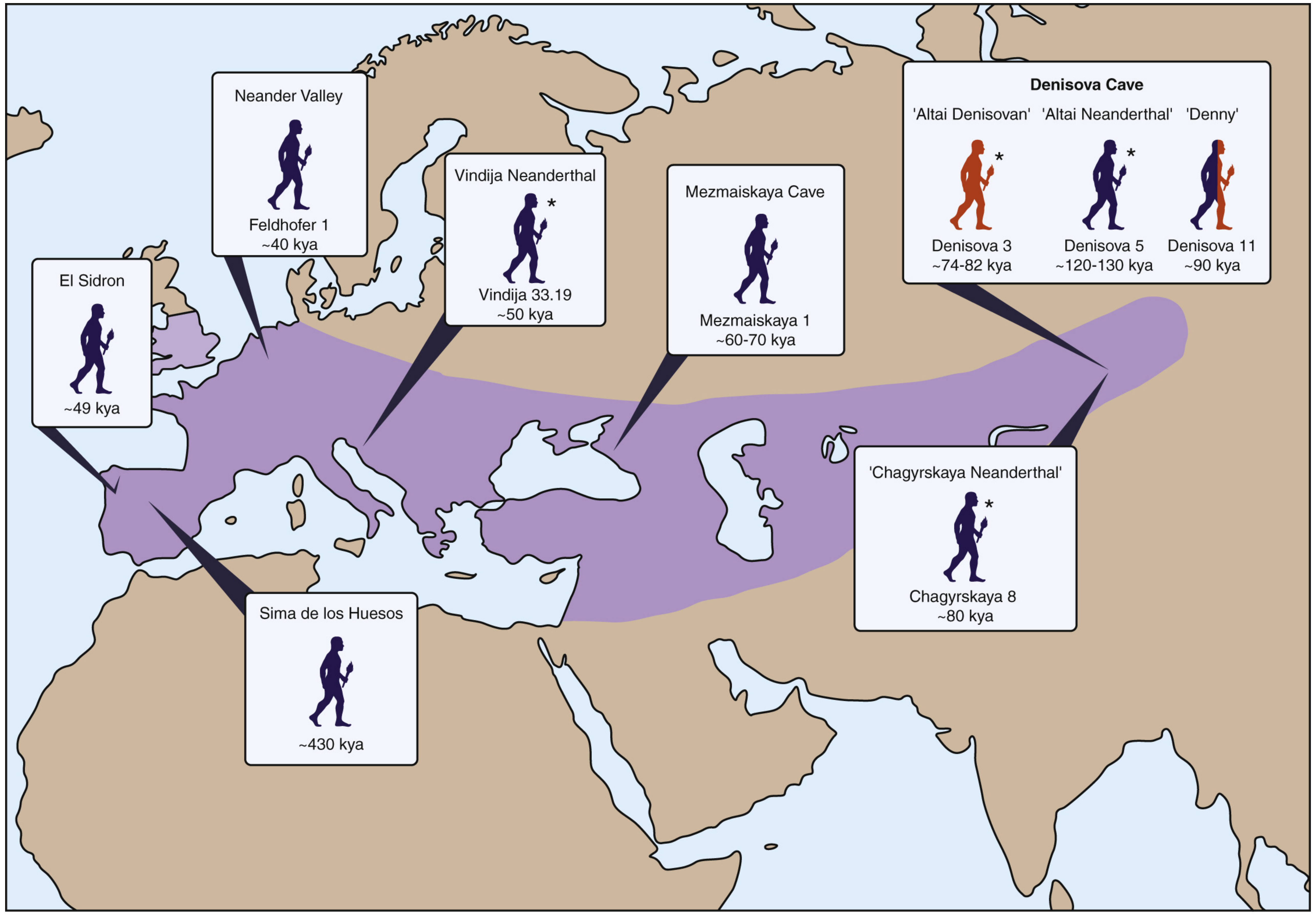
Illustration: Niklas Elmehed

Svante Pääbo

“for his discoveries concerning the genomes of extinct hominins and human evolution”

THE NOBEL ASSEMBLY AT KAROLINSKA INSTITUTET

The era of archaic human genomics



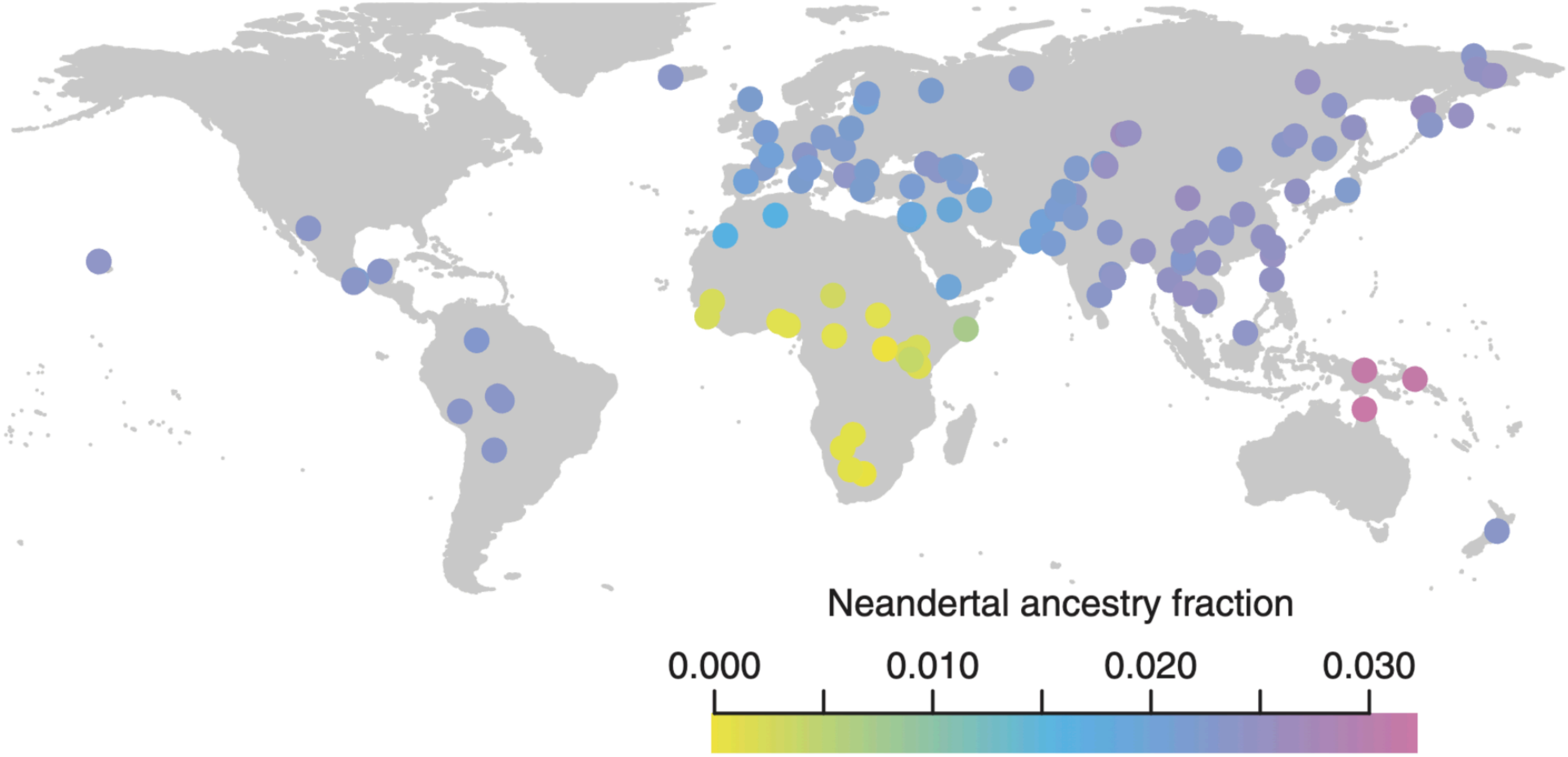
Current Biology

- Neanderthals and modern humans diverged 520,000-630,000 years ago
- Genetic evidence indicates that Neanderthals lived in small, highly inbred, and geographically structured populations
- Early Neanderthals were differentiated into at least two geographic groups (Eastern and Western)
- Western Neanderthal group persisted throughout time and may have migrated and replaced

Current Biology 32, R970–R983 (2022)

Neanderthal DNA in present-day human populations

- Modern humans arrived in Europe more than 45,000 years ago and overlapped for 5,000 years with Neanderthals
- All present-day human populations outside of Africa contain genomes from Neanderthals (1-4%)
- Analysis of modern human and Neanderthal genomes estimated the admixture event to 45,000-49,000 years ago
- Present-day human genomes can reconstruct 35% of the Neanderthal genome



Science 358, 655–658 (2017) Current Biology 32, R970–R983 (2022) Nature 638, 711–717 (2025).

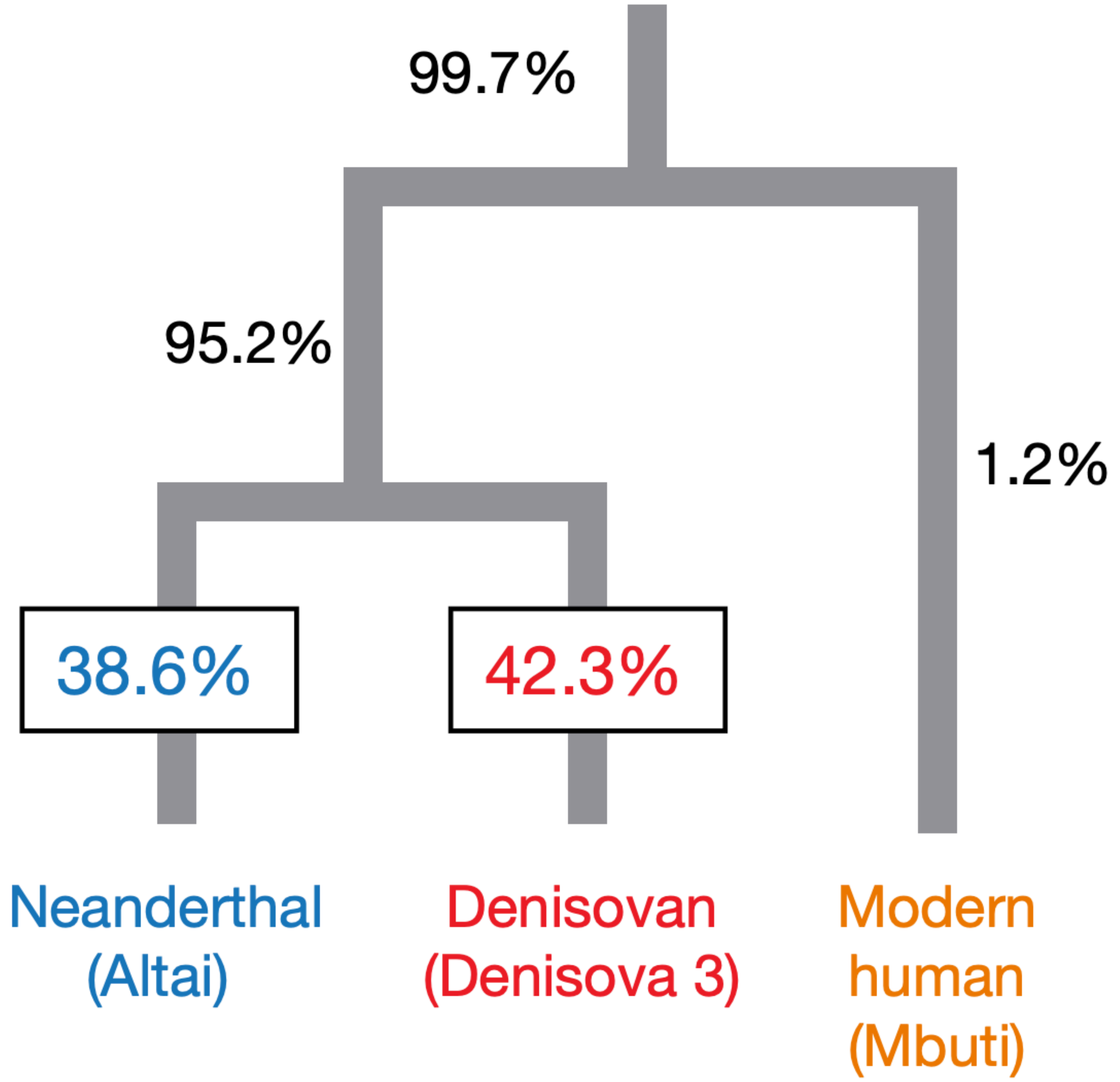
Denisovans

a previously unknown archaic subspecies of modern humans

- Archaic human species discovered in 2010 based on genome sequencing of a finger bone
- Few physical remains have been discovered and most knowledge about Denisovans stems from its genome.
- DNA evidence suggests dark skin/hair/eyes and a Neanderthal-like skeletal features. A key distinction are large molar teeth.

Denisovans, Neanderthals, and modern humans

- Neanderthals and Denisovans separated from each other 390,000 years ago
- Denisovans and Neanderthals are more closely related to each other than to modern humans
- Denisova cave was co-inhabited by Neanderthals during overlapping periods
- A bone fragment revealed an individual “Denisova 11” with a Neanderthal mother and Denisova father
- A modern human “Oase 1” who died 37,000-42,000 years ago had a close Neanderthal relative (6-9% Neanderthaler DNA; 4-6 generations back)
- The Oase population, however, did not contribute significantly to later populations.



Nature. 2015 Jun 22;524(7564):216–219

Nature **561**, 113–116 (2018).

Up to 5% of the genome from people in Southeast Asia is derived from Denisovans

Cell, Volume 177, Issue 4, 1010 - 1021.e32

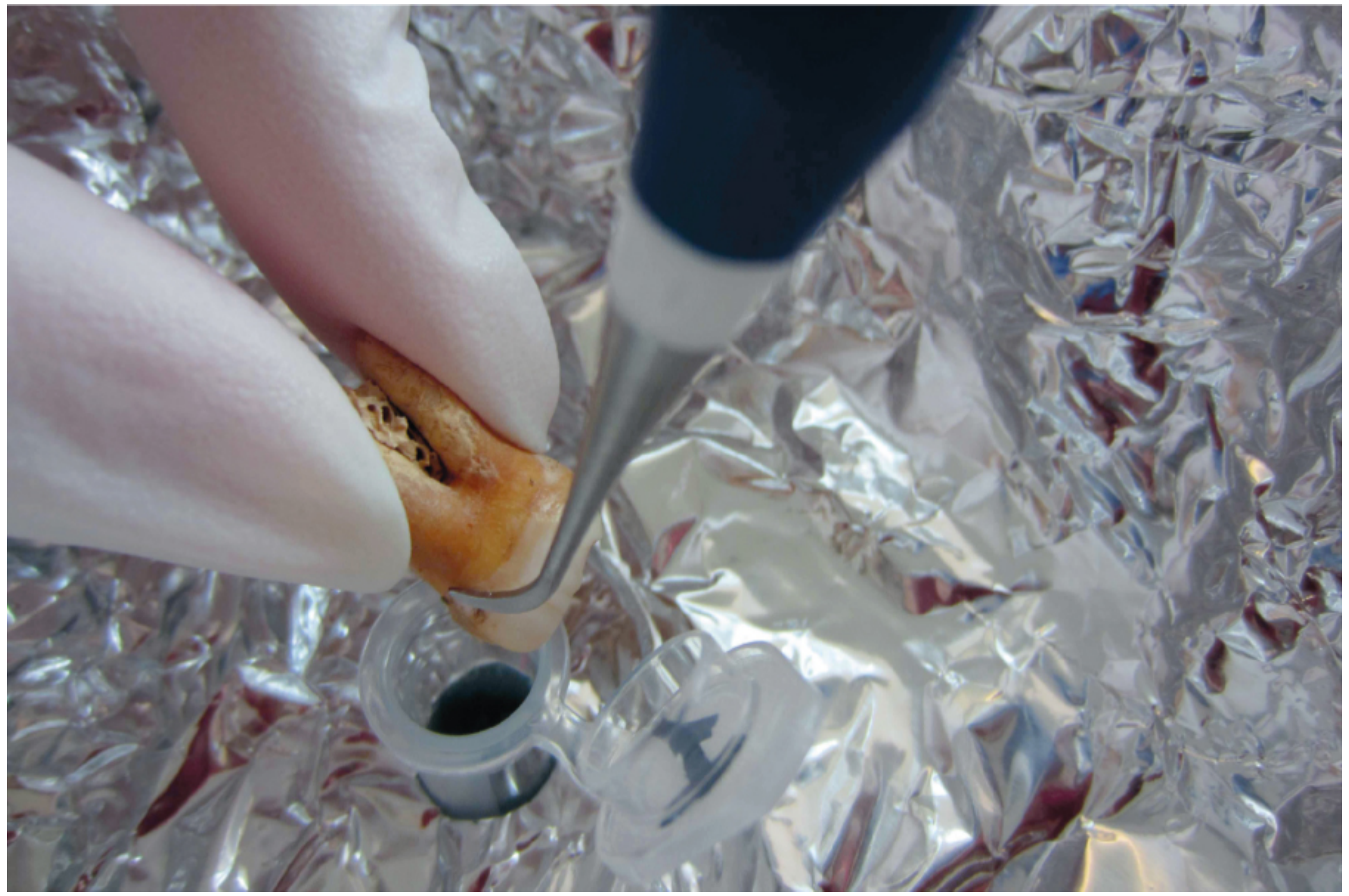
Aeta people. Source: wikipedia

- Modern humans and Denisovans had offspring as early as 14,500 years ago
- Denisovans likely the last surviving archaic human species

Ancient Pathogen Genomics

Using teeth to uncover ancient microbes

C. WARINNER ET AL., NATURE (2014)



DOI: 10.1126/science.342.6164.1303

- Molecular fossil records of ancient pathogens
- Long-time mutation rates and evolution
- Host-pathogen interactions through time

Ancient pathogen genomes

- Yersinia pestis bacterium (bubonic plague)
- Mycobacterium leprae (leprosy)
- Mycobacterium tuberculosis (tuberculosis)
- Treponema pallidum (syphilis)
- Staphylococcus enterica (typhoid fever)
- H. Pylori (gastric ulcer)

nature

THE INTERNATIONAL WEEKLY JOURNAL OF SCIENCE

BLACK DEATH GENOME

Reconstruction from fourteenth-century DNA is close match to modern pathogen PAGES 444, 465 & 506

DWARF PLANETS

MEET PLUTO'S COOLER TWIN

Stellar occultation is chance to observe Eris

PAGES 464 & 493

CLIMATE CHANGE

FOOD SUPPLIES AT RISK

Predicted droughts to cause dust-bowl conditions?

PAGE 450

ATMOSPHERIC SCIENCE

TROUBLE UP NORTH

Arctic ozone hole echoes Antarctic forerunner

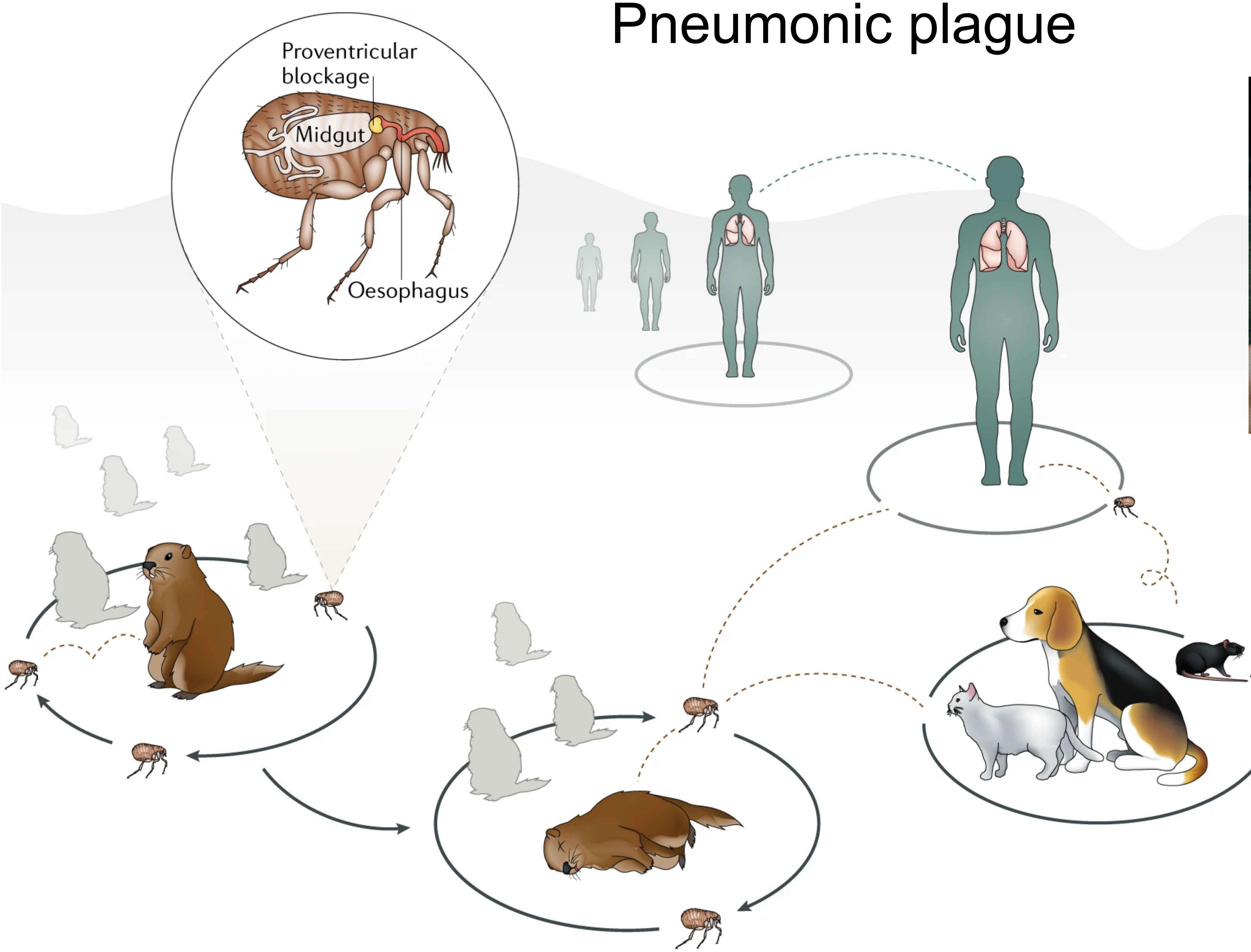
PAGES 462 & 469

NATURE.COM/NATURE

27 October 2011

Vol. 478, No. 7370

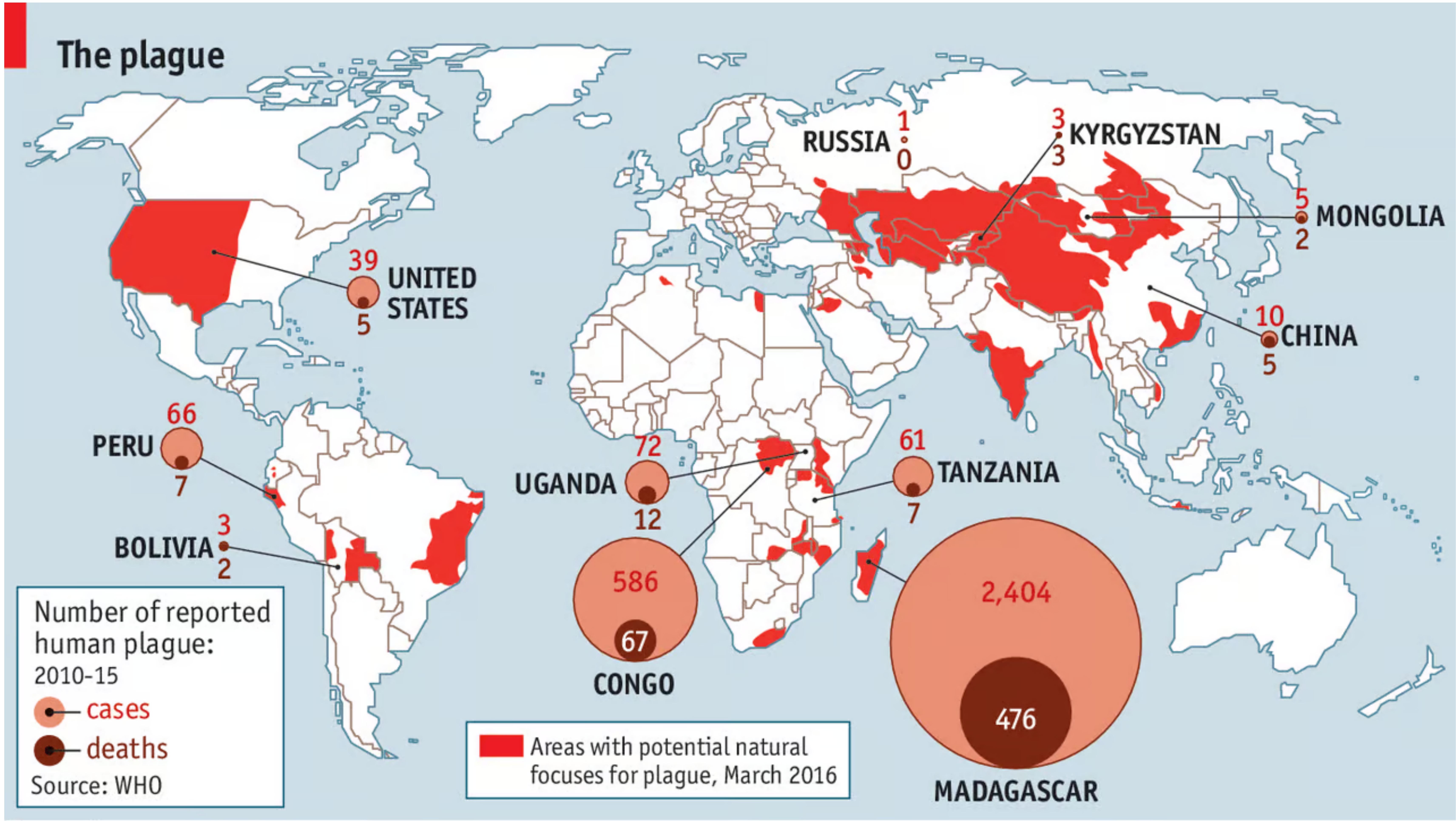
Plague ecology and transmission cycle



Pneumonic plague

Bubonic plague

The return of the plague



Economist.com

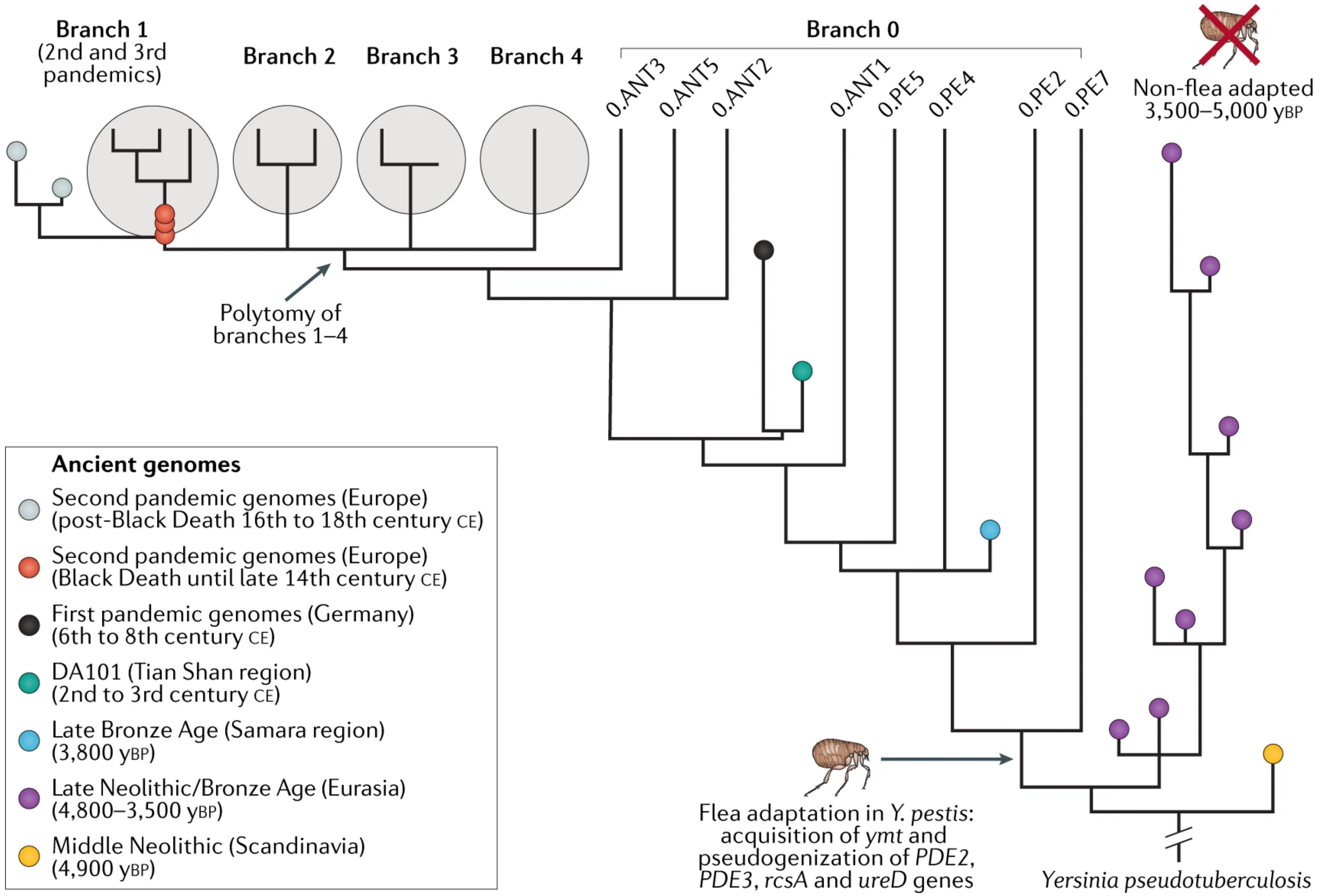
https://www.economist.com/graphic-detail/2017/07/05/the-return-of-the-plague

History of plague

- **1st pandemic plague** (541 to 750): from Egypt to Mediterranean and unto northwest Europe
- **2nd pandemic plague** (1331 to ?1855): from Central Asia to the Mediterranean and Europe (Black Death 1346-1353). Half of Europe's 14th century population died.
- **3rd pandemic plaque** (1855 to ?1960): from Europe back to China to many places around the world (India, USA)

Recent evolutionary history of *Yersinia pestis*

- Branches 1-4 represent 80% of all modern strains of Y. Pestis



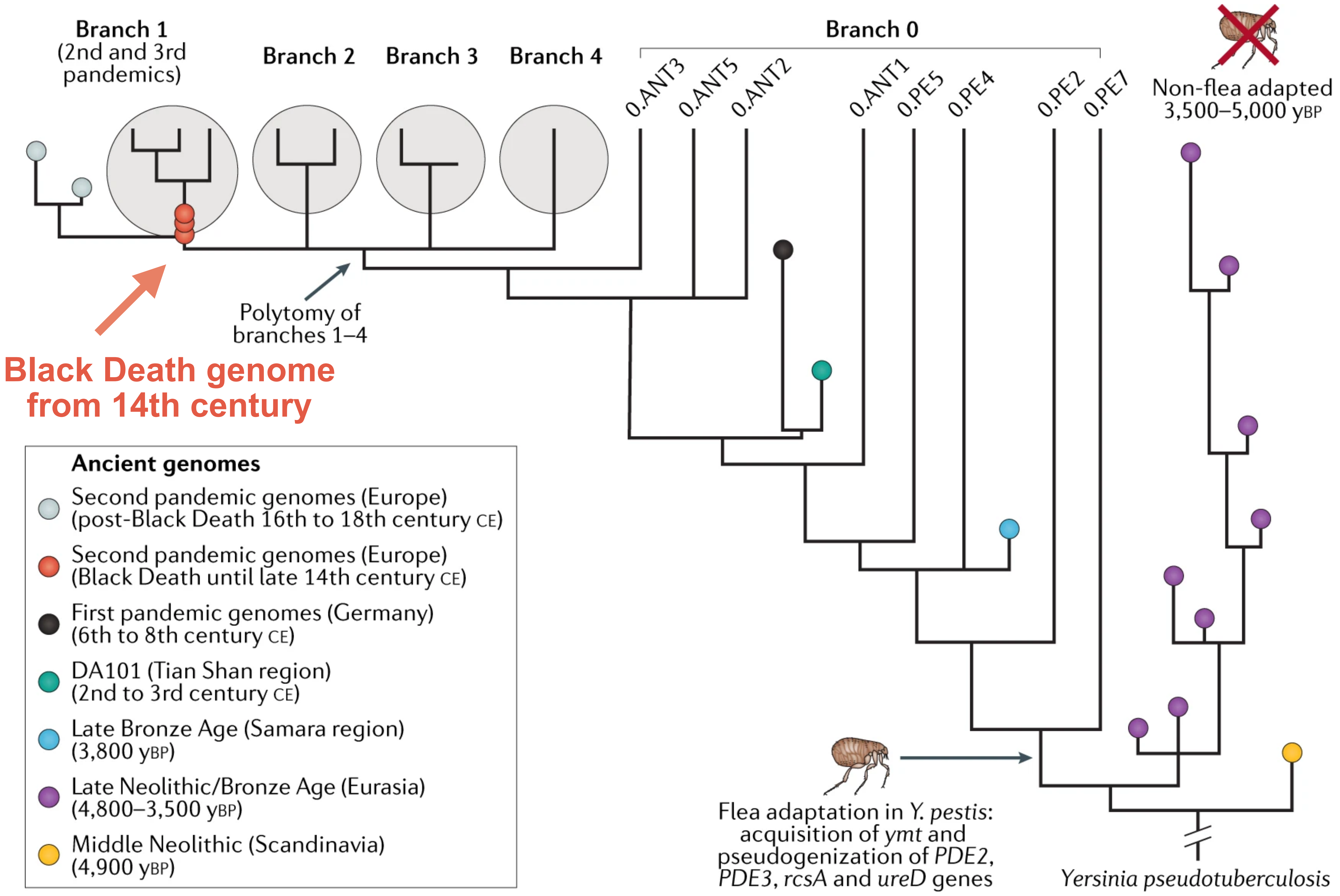
Nature **478**, 506–510 (2011)

Nat Rev Genet **20**, 323–340 (2019).

BIO-312 Genomic solutions to sustainable development

Recent evolutionary history of *Yersinia pestis*

- Branches 1-4 represent 80% of all modern strains of Y. Pestis
- Black Death genome falls onto basis of modern Branch 1-4 genomes and gave rise to the diversity seen today
- 3rd pandemic plague evolved from Black Death in Europe, migrated back to Asia, and spread afterwards worldwide
- Post-Black Death branches evolved in Europe yet became extinct (potentially due to disappearance of black rats)



Ancient genomes

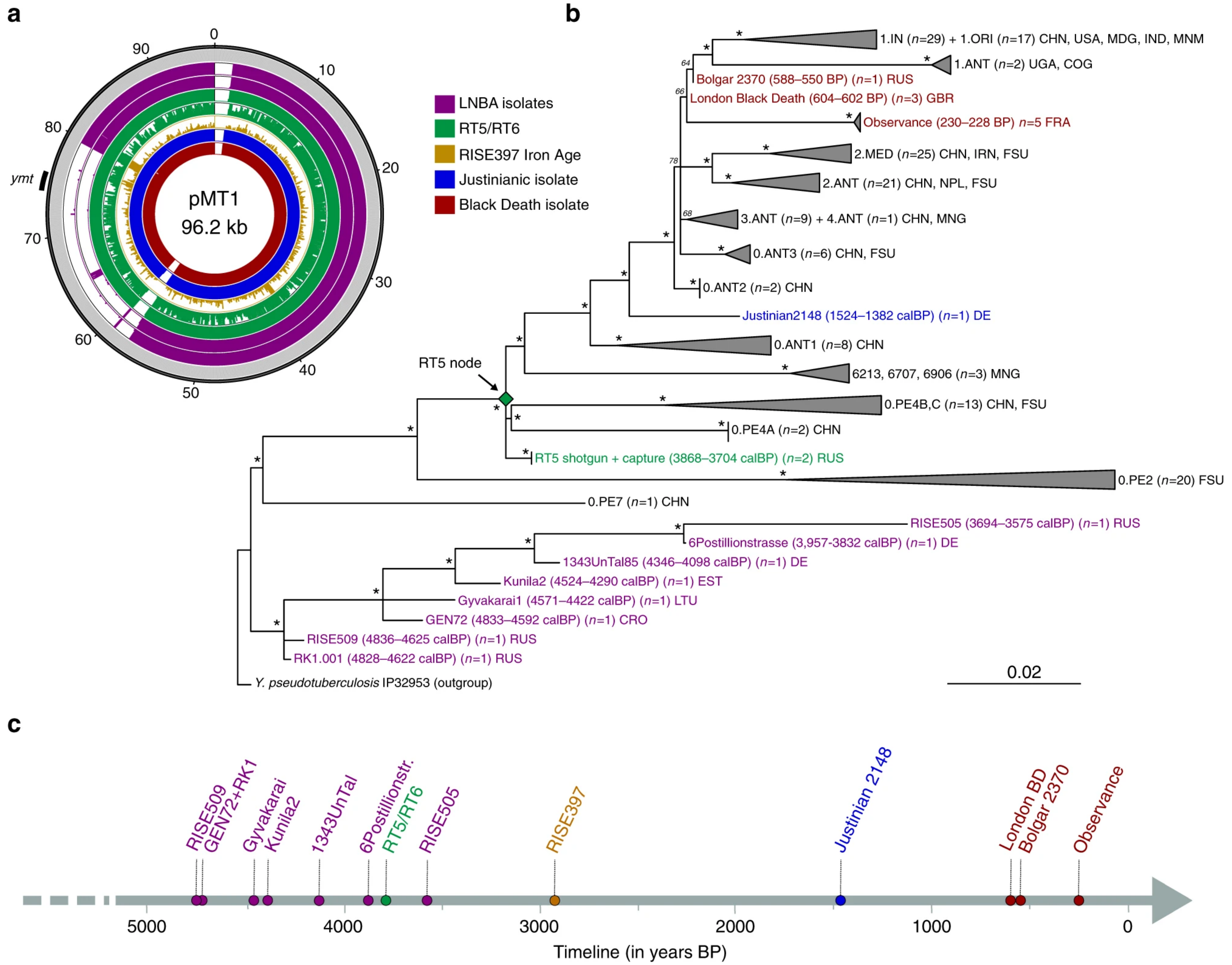
- ⚪ Second pandemic genomes (Europe) (post-Black Death 16th to 18th century CE)
- 🔴 Second pandemic genomes (Europe) (Black Death until late 14th century CE)
- ⚫ First pandemic genomes (Germany) (6th to 8th century CE)
- 🟢 DA101 (Tian Shan region) (2nd to 3rd century CE)
- 🔵 Late Bronze Age (Samara region) (3,800 yBP)
- 🟣 Late Neolithic/Bronze Age (Eurasia) (4,800–3,500 yBP)
- 🟡 Middle Neolithic (Scandinavia) (4,900 yBP)

Nature **478**, 506–510 (2011)

Nat Rev Genet **20**, 323–340 (2019).

Emergence of modern bubonic plague from mid Bronze Age

- Earliest genetic evidence for Y. Pestis infections in humans date back to the Bronze Age period (5000-3500 years ago)
- All modern strains (1st/2nd/3rd pandemic) evolved from ancient Y. Pestis strain 3800 years ago (mid Bronze Age)
- 5,000 years ago Y. Pestis strains were not bubonic, yet 4,000 years later became bubonic



Nat Commun **9**, 2234 (2018).