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Palaeoproteomics gives new insight into early southern African pastoralism

Louise Le Meillour, Séverine Zirah, Antoine Zazzo, Sophie Cersoy, Florent Détroit, Emma Imalwa, Matthieu Lebon, Alma Nankela, Olivier Tombret, David Pleurdeau & Joséphine Lesur

Scientific Reports **10**, Article number: 14427 (2020) | Cite this article

Sci Adv. 2021 Jan; 7(3): eabb9314.
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Ancient protein analysis in archaeology

Jessica Hendy[1,2]

Article | Published: 25 November 2021

The earliest Denisovans and their cultural adaptation

Samantha Brown, Diyendo Massilani, Maxim B. Kozlikin, Michael V. Shunkov, Anatoly P. Derevianko, Alexander Stoessel, Blair Jope-Street, Matthias Meyer, Janet Kelso, Svante Pääbo, Thomas Higham & Katerina Douka

Nature Ecology & Evolution **6**, 28–35 (2022) | Cite this article

Species identification of ivory and bone museum objects using minimally invasive proteomics

CATHERINE GILBERT, VACLAV KRUPICKA, FRANCESCA GALLUZZI, ALEKSANDRA POPOWICH, KATELL BATHANY, STÉPHANE CLAVEROL, JULIE ARSLANOGLU, AND CAROLINE TOKARSKI Authors Info & Affiliations

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SEDIMENTARY ANCIENT DNA, FLORA AND FAUNA

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DEPARTMENT OF EXPERIMENTAL BIOLOGY

SEDIMENTARY ANCIENT DNA

- Abbreviated to sedaDNA
- Proxies (indirect sources of information) – e.g., fossil assemblages, indicator species, geochemical proxies…
- Before HTS mostly limited to fossil record (molluscs, diatoms, foraminifera…)
- Often for study of palaeoenvironment, climate change, biodiversity
- Greater resolutions compared to pollen analysis
- Best preservation in anoxic and cold environment, high clay, borate and organic content
- Organisms underrepresented in databases, missing references, unknown organisms

SEDIMENTARY ANCIENT DNA

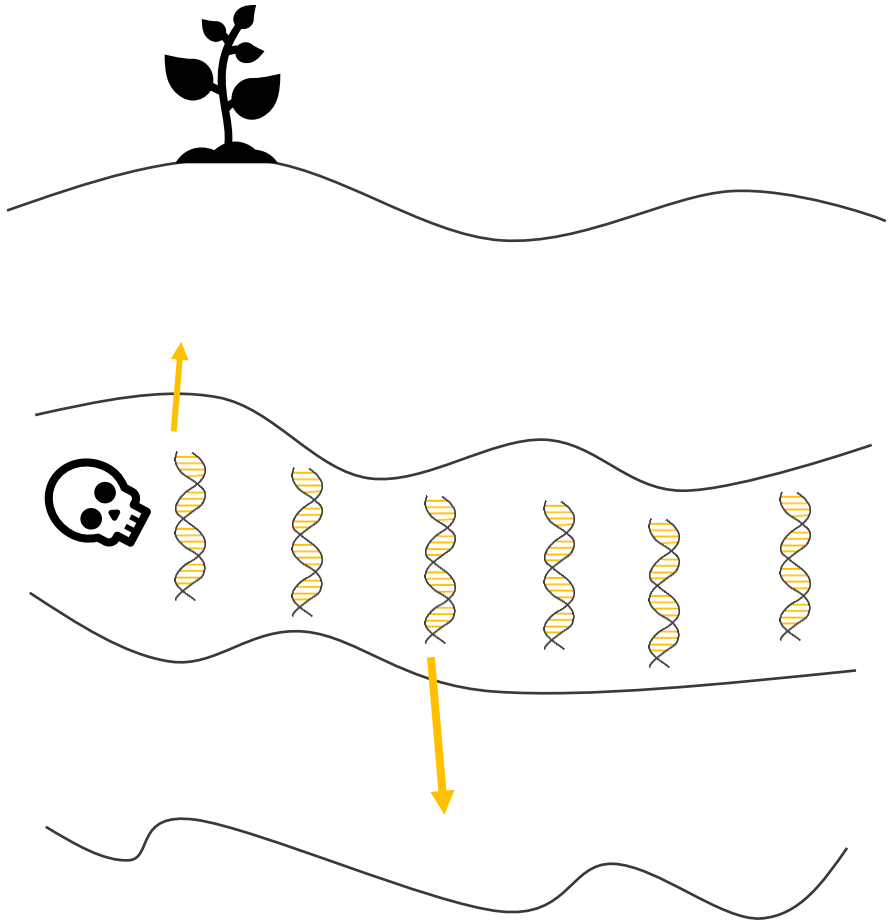
Table 1. Terms commonly used in marine *sed*aDNA research and their definition. aDNA terms are listed hierarchically, all other terms are listed alphabetically.

aDNA Terms	Definition	References
Ancient DNA (aDNA)	Biomolecular analysis of non-modern genetic material preserved in a broad range of biological samples.	Shapiro and Hofreiter, 2012
Palaeoenvironmental DNA (PalEnDNA)	Disseminated genetic material found in ancient environmental samples such as sediment, soil, paleosols, coprolites, water and ice.	Rawlence et al., 2014
Environmental DNA (eDNA)	DNA isolated from environmental samples (e.g., soil, water, air), usually a complex mixture of genomic DNA from various organisms.	Taberlet et al., 2012a; Stat et al., 2017
Sedimentary aDNA (*sed*aDNA)	Ancient DNA isolated from sediments.	Willerslev et al., 2003; Jørgensen et al., 2012
Marine *sed*aDNA	Ancient DNA retrieved from marine sediment cores.	This review

SEDIMENTARY ANCIENT DNA

Cryosphere	Area of Earth that experiences temperatures below 0 °C for at least part of each year.	Van Everdingen, 1998
Deep Biosphere	Sediment depths below 1 m below seafloor (mbsf).	Parkes et al., 1994; Fry et al., 2008
DNA leaching	Movement of DNA vertically across sediment layers.	Ceccherini et al., 2007; Haile et al., 2007; Pote et al., 2007

Observed in cave sediments and non-frozen soil



SOURCES

- Lakes and other freshwater sources
- Marine
- Cave
- Burials
- Settlements
- Permafrost
- (Ice, glacier)
- (Latrines)
- (Extraterrestrial sources)

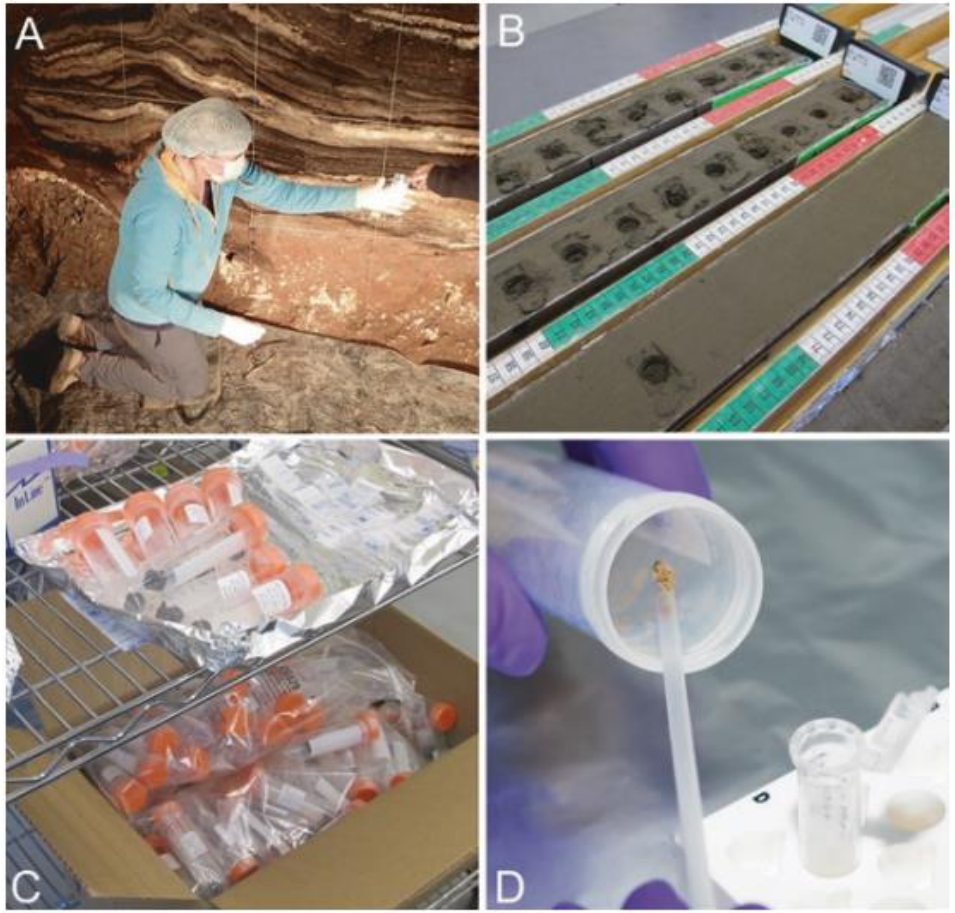


Fig. 3.1 Examples of (**a**) researchers sampling an accessible cave sediment profile in the field; (**b**) a freshly subsampled lake core, where the rectangular areas represent discarded sediment surface for access to underlying pristine sediment, and the circular holes correspond to the material that was sampled for DNA analysis. Alternative core sectioning and subsampling strategies can be used for higher resolution analyses; (**c**) subsamples that were taken in a non-cleanroom space; and (**d**) a subsample to be used as input for DNA extraction in a cleanroom space. Images are copyright of Dr. Richard G. Roberts (**a**), Dr. Peter D. Heintzman (**b**, **c**), and the Max Planck Institute for Evolutionary Anthropology (**d**)

Heintzman et al., 2023 DOI: 10.1007/978-3-031-43799-1_3

METHODOLOGICAL CONSIDERATIONS

Table 3.1 Taxon-specific methodological considerations for the *sed*aDNA workflow, with signposts to other chapters of this volume

Group	Fresh cores recommended	Contamination potential	Suitable for		Further reading
			Amplicon	Metagenomics[d]	
Prokaryotes	Yes	High	No[b]	Yes	Chapters 4, 5
Microbial eukaryotes	Yes	High	No[b]	Yes	Chapters 6, 7
Fungi	Yes	High	Yes[c]	Yes	Chapter 6
Wildlife[a]	No	Low	Yes[c]	Yes	Chapters 8–11
Domesticated/ farmed taxa[a]	No	Intermediate	Yes[c]	Yes	Chapters 10, 11
Human	Yes	High	No	Yes	Chapter 11

aWildlife and domesticated/farmed taxa include both animal and plant taxa
bAmplicon methods may be appropriate for taxa that are unable to have colonised the sediment after collection or be present in the modern sampling or laboratory environment
cData are prone to contamination and so need to be interpreted carefully. See also Chap. 11
dThe feasibility of metagenomics may be limited by the availability of reference genome data for certain taxonomic groups

Heintzman et al., 2023 DOI: 10.1007/978-3-031-43799-1_3

SEDIMENT CORING

- Cold storage, subsampling ideally on board in case of marine sediments

- Horizontal (accessible profiles – permafrost, soil, cave)
  - from bottom to top to prevent cross-contamination
- Vertical (inaccessible profiles – marine, lake, ice)

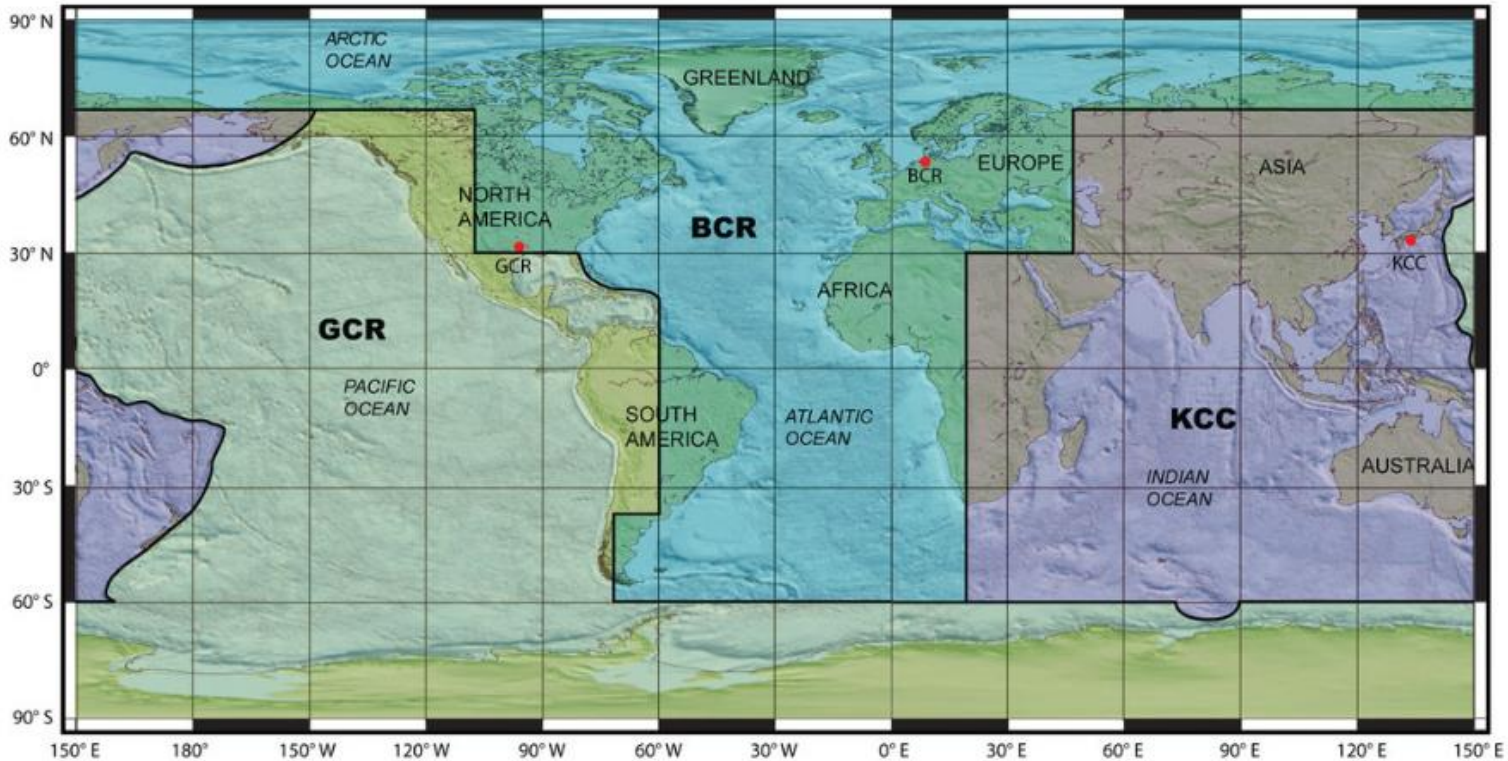
- Contamination monitoring by addition of exotic DNA or synthetic tracers

- Archiving in specialized facilities, e.g., LacCore facility in Minnesota, Permafrost ArChives Science (PACS) Laboratory at the University of Alberta, International Ocean Discovery Program

Geographic Assignment of Core Samples to Repositories

Repository	Institution	Amount of Core	Program(s) Generating Core	Geographic Location
GCR	Texas A&M University	152 km	DSDP, ODP, and IODP	Pacific (Pacific plate east of western boundary); Caribbean Sea and Gulf of Mexico; Southern Oceans (S of 60° except Kerguelan Plateau)
BCR	University of Bremen	185 km	DSDP, ODP, and IODP	Atlantic and Arctic Oceans (north of Bering Strait); Mediterranean, Black, and Baltic Seas
KCC	Kochi University / JAMSTEC	149 km	DSDP, ODP, and IODP	Pacific (west of western boundary of Pacific plate); Indian Ocean (N of 60°S), all of Kerguelan Plateau, and the Bering Sea
Rutgers/NJGS	Rutgers / NJGS	4.1 km	ODP Leg 150X & 174AX	Land-based New Jersey and Delaware cores

DSDP: Deep Sea Drilling Program ODP: Ocean Drilling Program IODP: Integrated Ocean Drilling Program / International Ocean Discovery Program



U. Röhl adapted from Firth, JV, Gupta, LP and Röhl, U (2009) New focus on the Tales of the Earth - Legacy Cores Redistribution Project Completed. Scientific Drilling, 7. 31-33. doi:10.2204/iodp.sd.7.03.2009. [Map Mar 15, 2016]. Retrieved from http://www.marum.de/en/Cores_at_BCR.html

https://www.iodp.org/resources/core-repositories

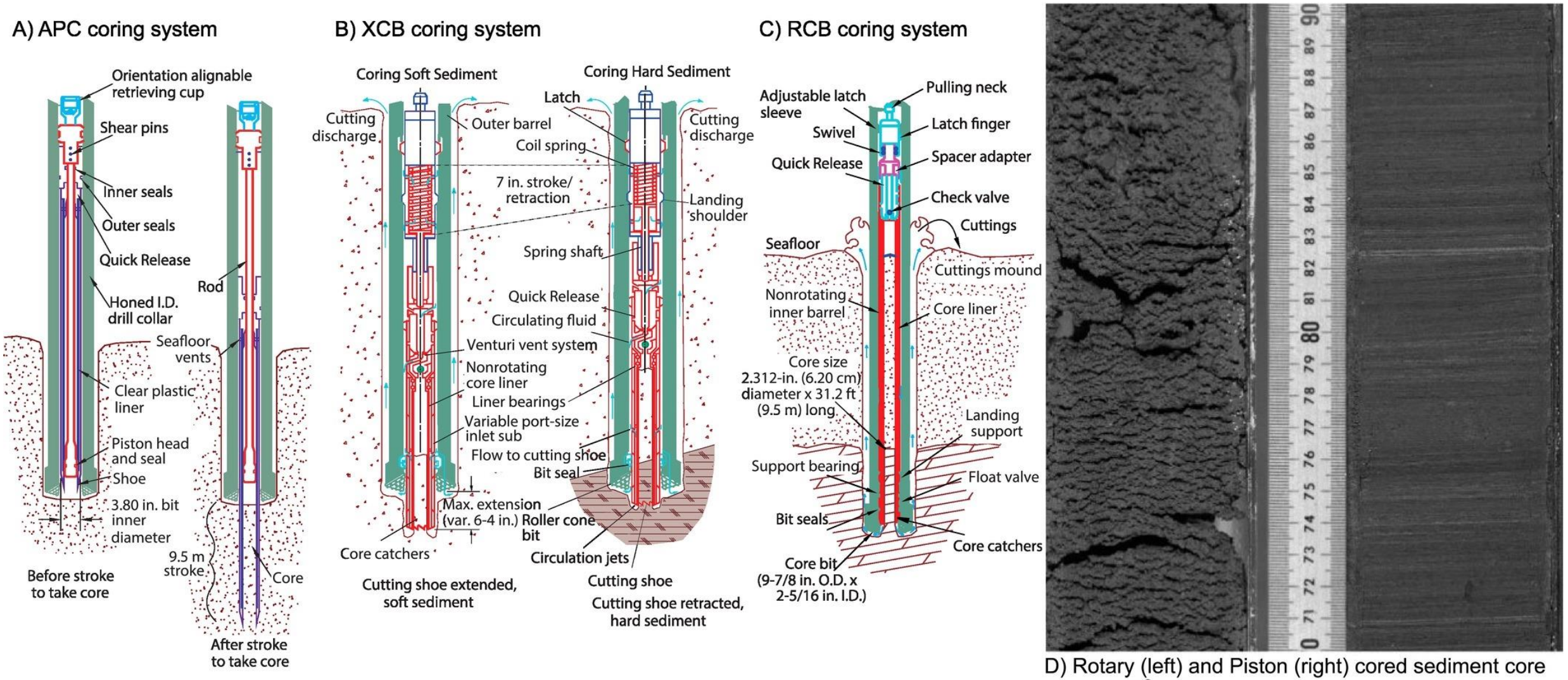


Fig. 2. Overview of IODP coring systems. A) Advanced piston coring system (APC), shown before and after stroking; only small volumes of drill fluid can enter the space between the core barrel and collar from above after stroking, greatly reducing the risk of contamination. B) Extended core barrel system (XCB) and C) Rotary core barrel system (RCB); both containing circulation jets at the bottom of the core barrel through which drill-fluid enters and removes coring debris by transporting it upwards within the drill hole to the surface. D) Comparison of rotary and piston cored sediments demonstrating the well-preserved lamination in Piston cored material. Figure adapted from Sun et al. (2018) and IODP (iodp.tamu.edu/tools/index.html)

Armbrecht et al., 2019 DOI: 10.1016/j.earscirev.2019.102887

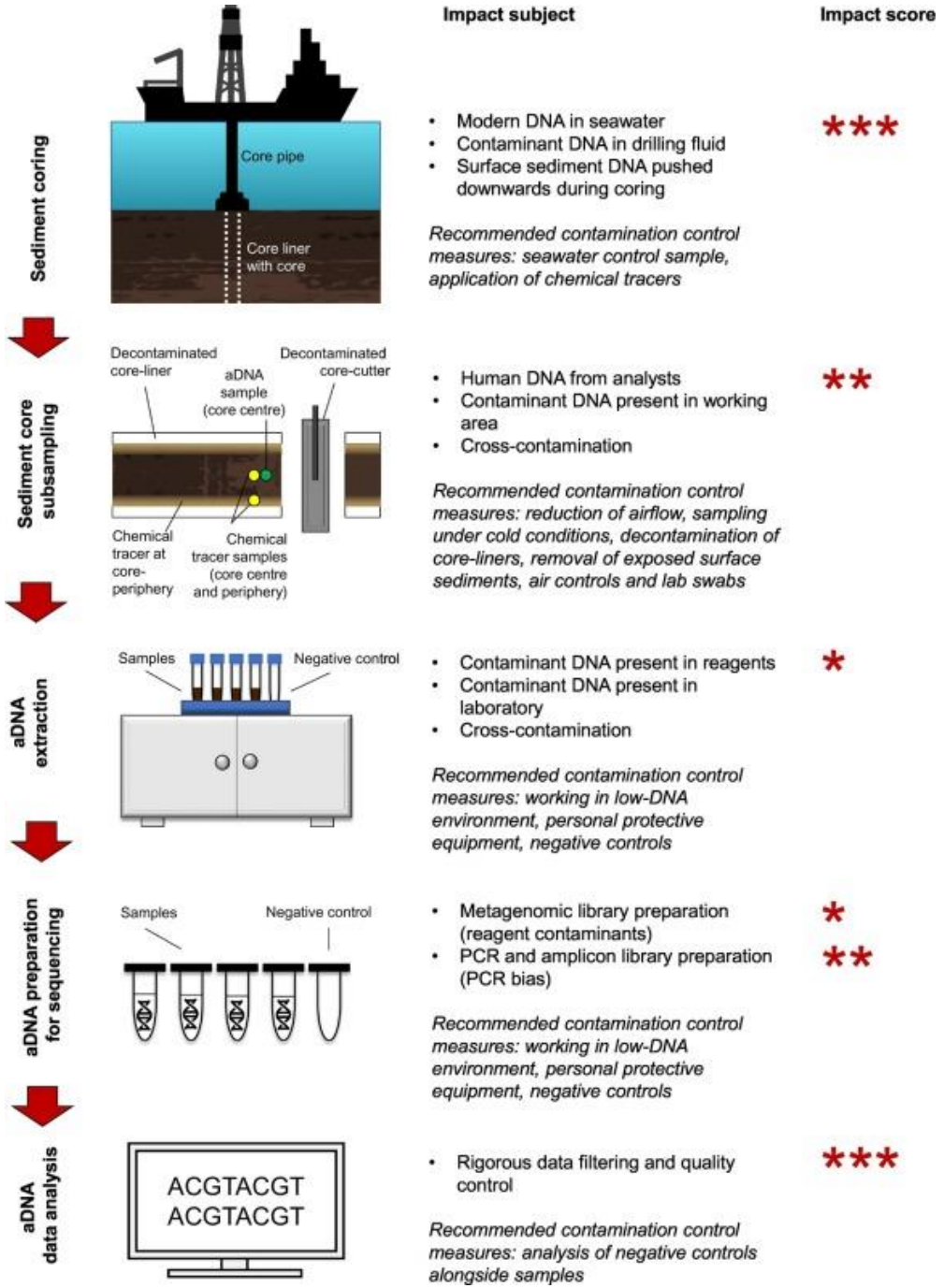
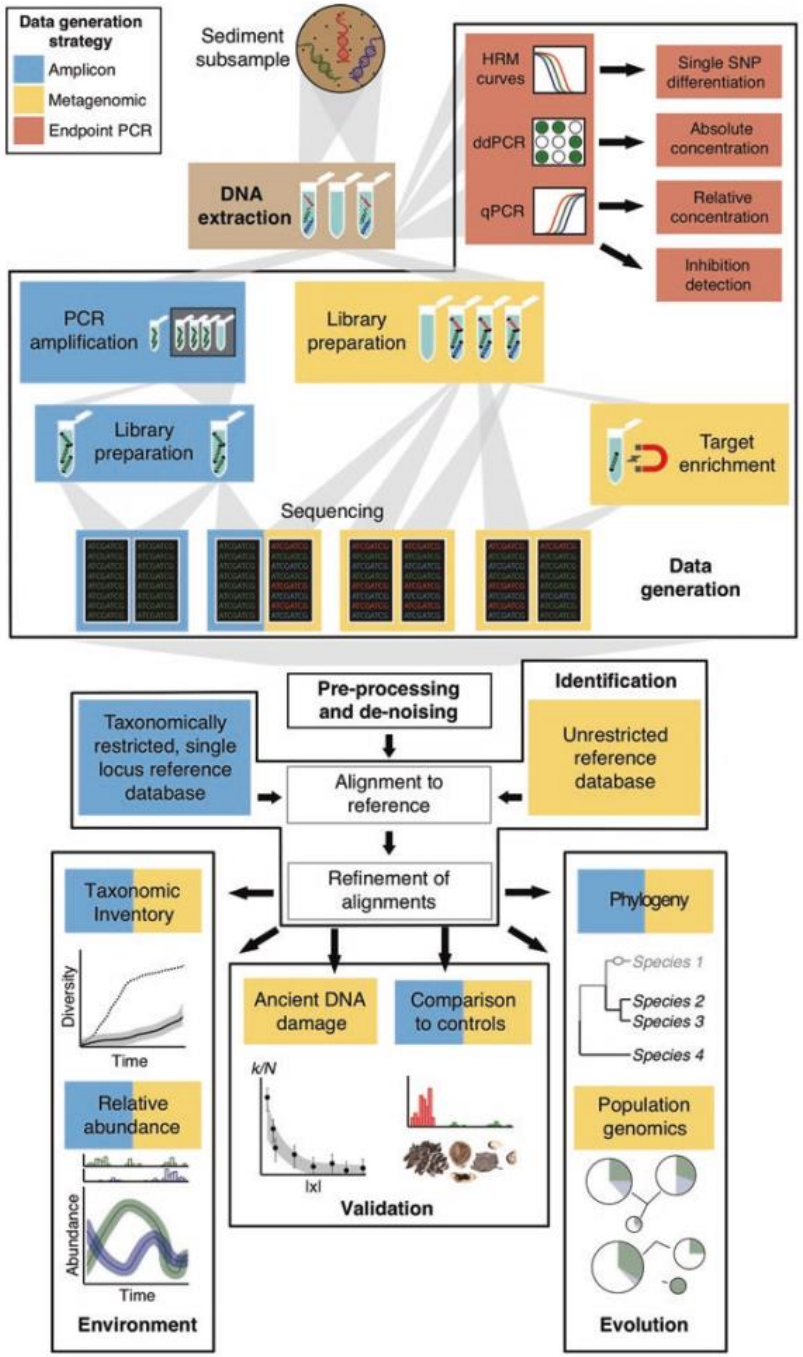


Fig. 1. Schematic showing the key steps involved in acquiring deep marine sediment cores, subsampling, DNA extraction, aDNA preparation for sequencing and data generation. Indicated are sources of potential contamination and reduction in data quality, as well as recommended precautions to be considered and/or controls to be taken. An impact score (1–3 stars) is given to indicate the severity of potential contamination or the impact that impaired data would have on the results at each step in the process. Schematic graphics are not to scale.

Armbrecht et al., 2019 DOI: 10.1016/j.earscirev.2019.102887



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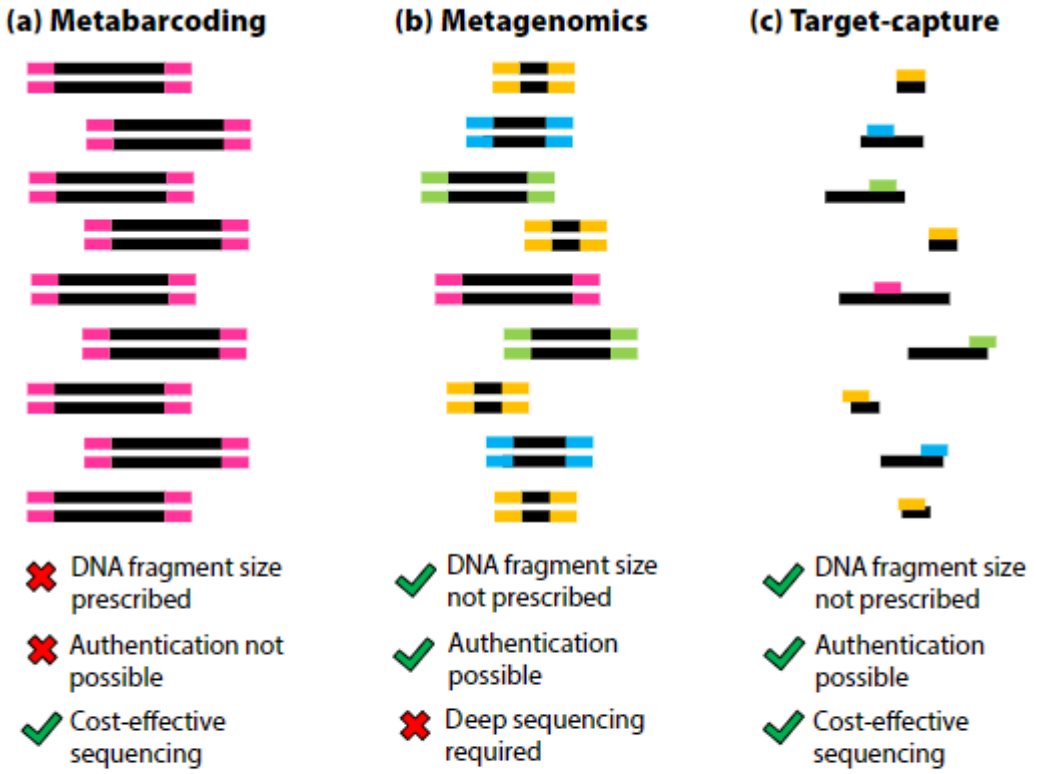


FIGURE 2. Schematic of different methodological approaches in modern and ancient marine genomics. (a) Metabarcoding is the amplification and analysis of equally sized DNA fragments from a total DNA extract. (b) Metagenomics is the extraction, amplification, and analysis of all DNA fragments independent of size. (c) Target-capture describes the enrichment and analysis of specific (chosen) DNA fragments independent of size from a total DNA extract.

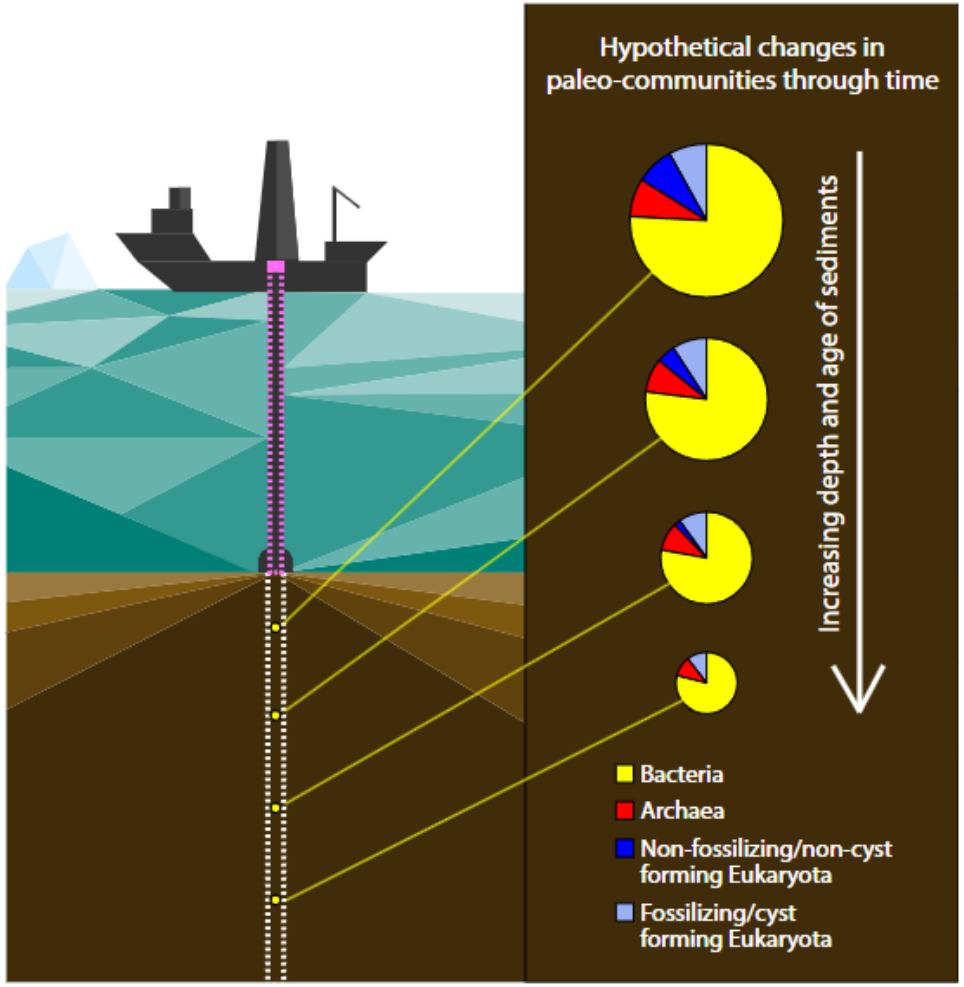
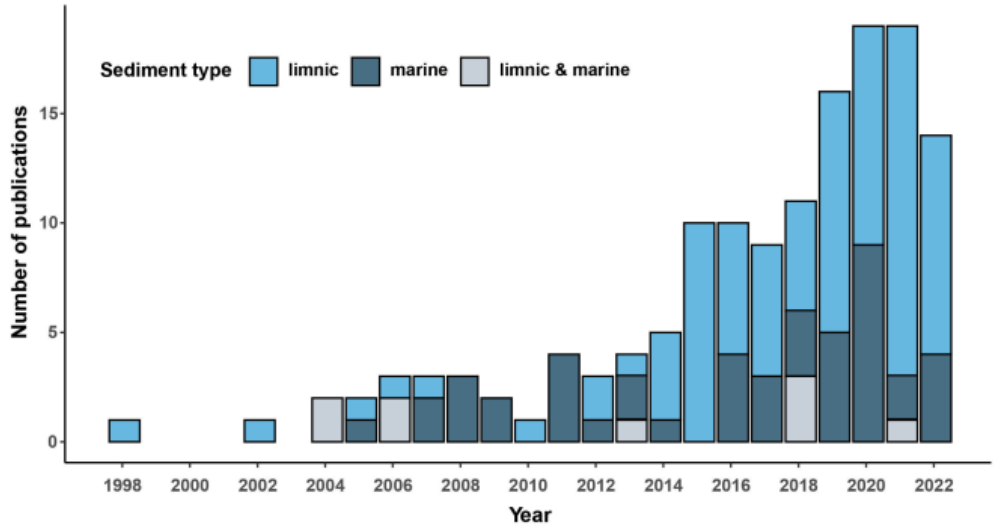


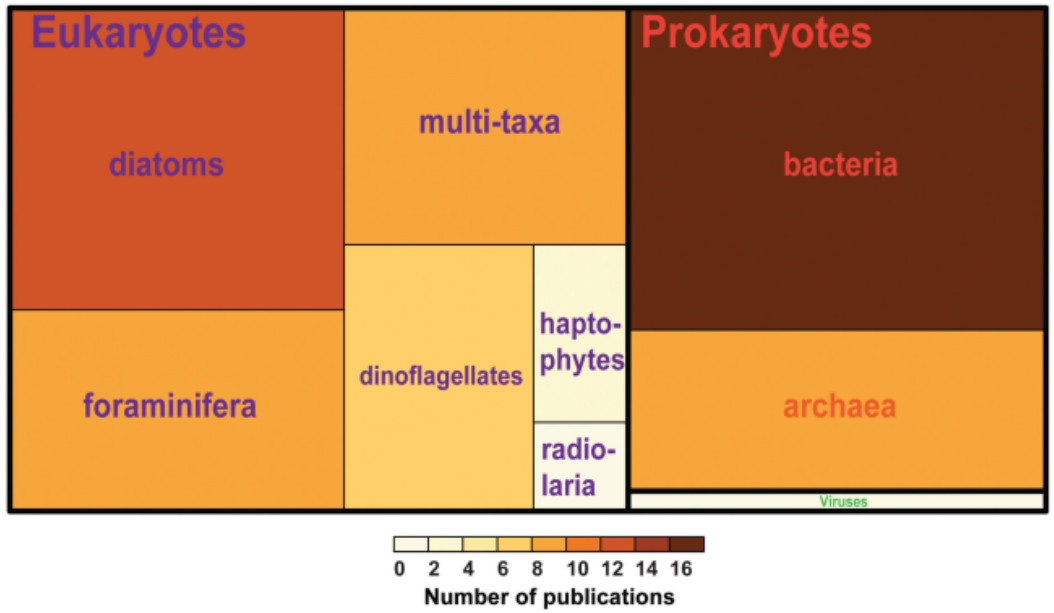
FIGURE 1. Schematic of a drilling vessel recovering a sediment core for *sed*aDNA analysis and hypothetical past marine community composition. The pink dashed line indicates the use of a chemical tracer for contamination tracking during coring. The white dashed line depicts the sediment core. Small yellow circles indicate theoretical *sed*aDNA sampling intervals, corresponding to pie charts on the right. Pie charts represent hypothetical paleo-communities detectable from *sed*aDNA shotgun analysis, where the majority (~75%, see text and Figure 3c) of the recovered *sed*aDNA sequences originate from bacteria, and where *sed*aDNA from fossilizing/cyst-forming taxa increases relative to non-fossilizing/non-cyst-forming taxa with subseafloor depth (assuming that *sed*aDNA of fossilizing/cyst-forming taxa preserves better than that of non-fossilizing/non-cyst-forming taxa). The decreasing size of the pie charts with subseafloor depth indicates an expected decrease in *sed*aDNA. Schematic not to scale.

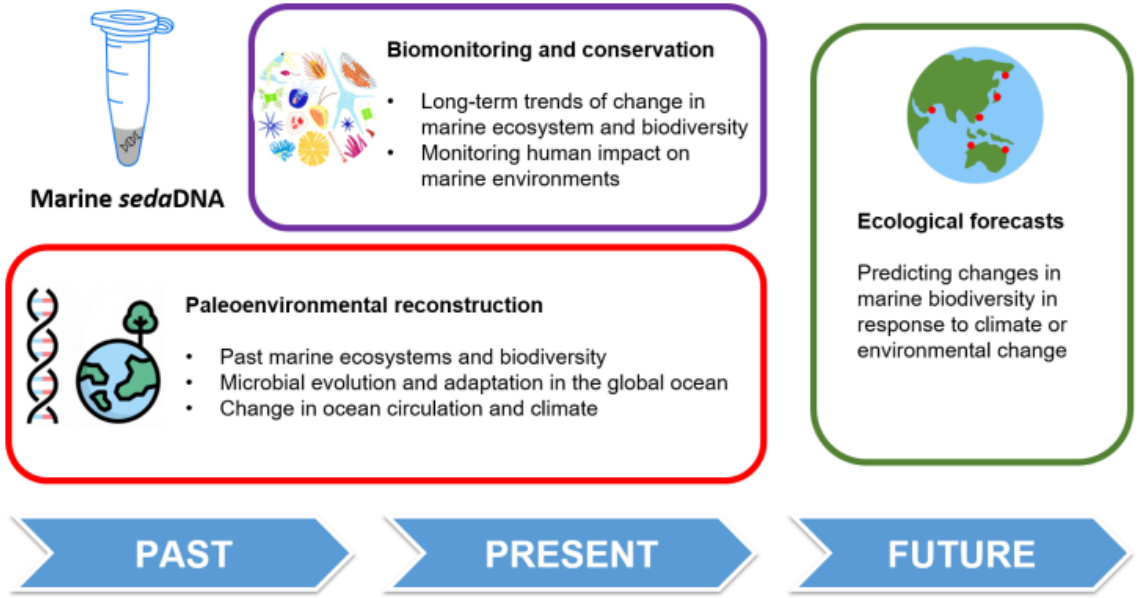
Armbrecht et al., 2020 DOI: 10.5670/oceanog.2020.211

MARINE sedaDNA

- Research always multidisciplinary – geology, organic and inorganic chemistry, geomorphology, palaeoceanography, micropaleontology…
- More dynamic environment than freshwater systems







Nguyen et al., 2023 DOI: 10.3389/fmars.2023.1185435

MARINE sedaDNA

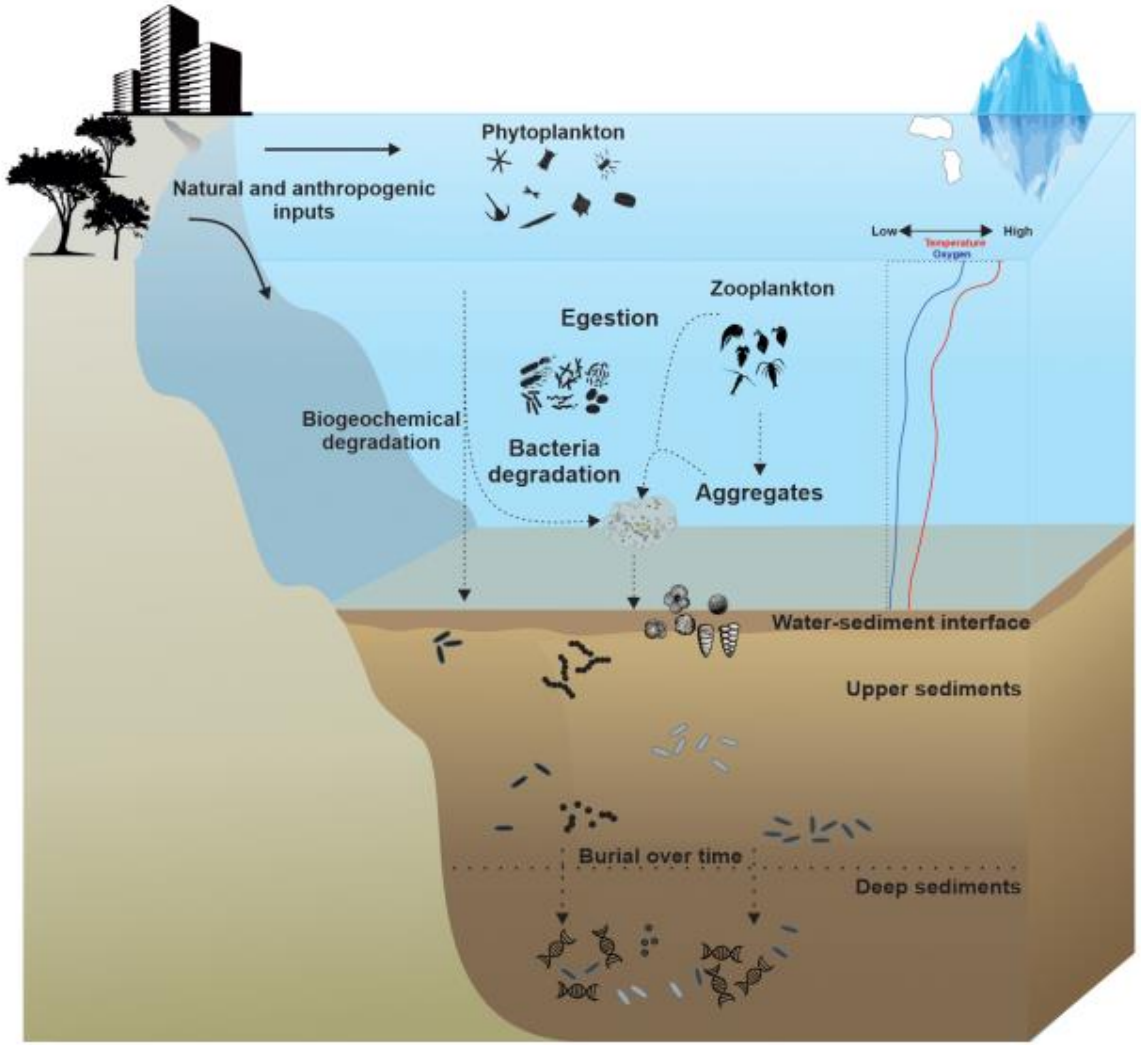
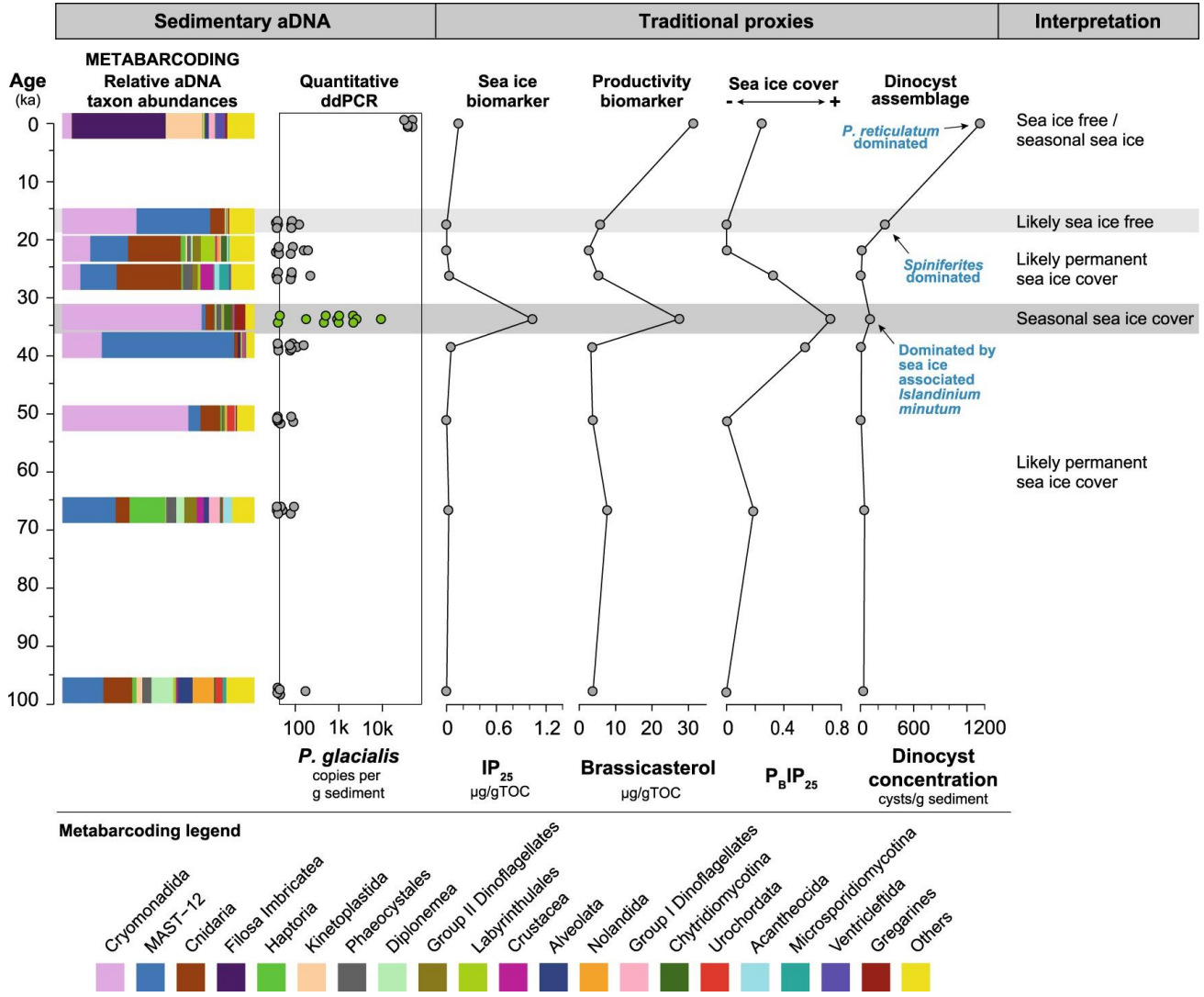


FIGURE 2
Schematic illustration of eDNA taphonomic processes in the marine environment. These processes involve eDNA distribution, degradation, and/or preferential preservation during the transition from the pelagic to the benthic zones, and from the water-sediment interface into subsurface sediment.

MARINE sedaDNA



Comparison of our novel sedimentary aDNA approach (metabarcoding and ddPCR) with traditional proxies (biomarkers and palynology) for sea ice reconstructions over the last ~100,000 years at Site GS15-198-38 in the Greenland Sea

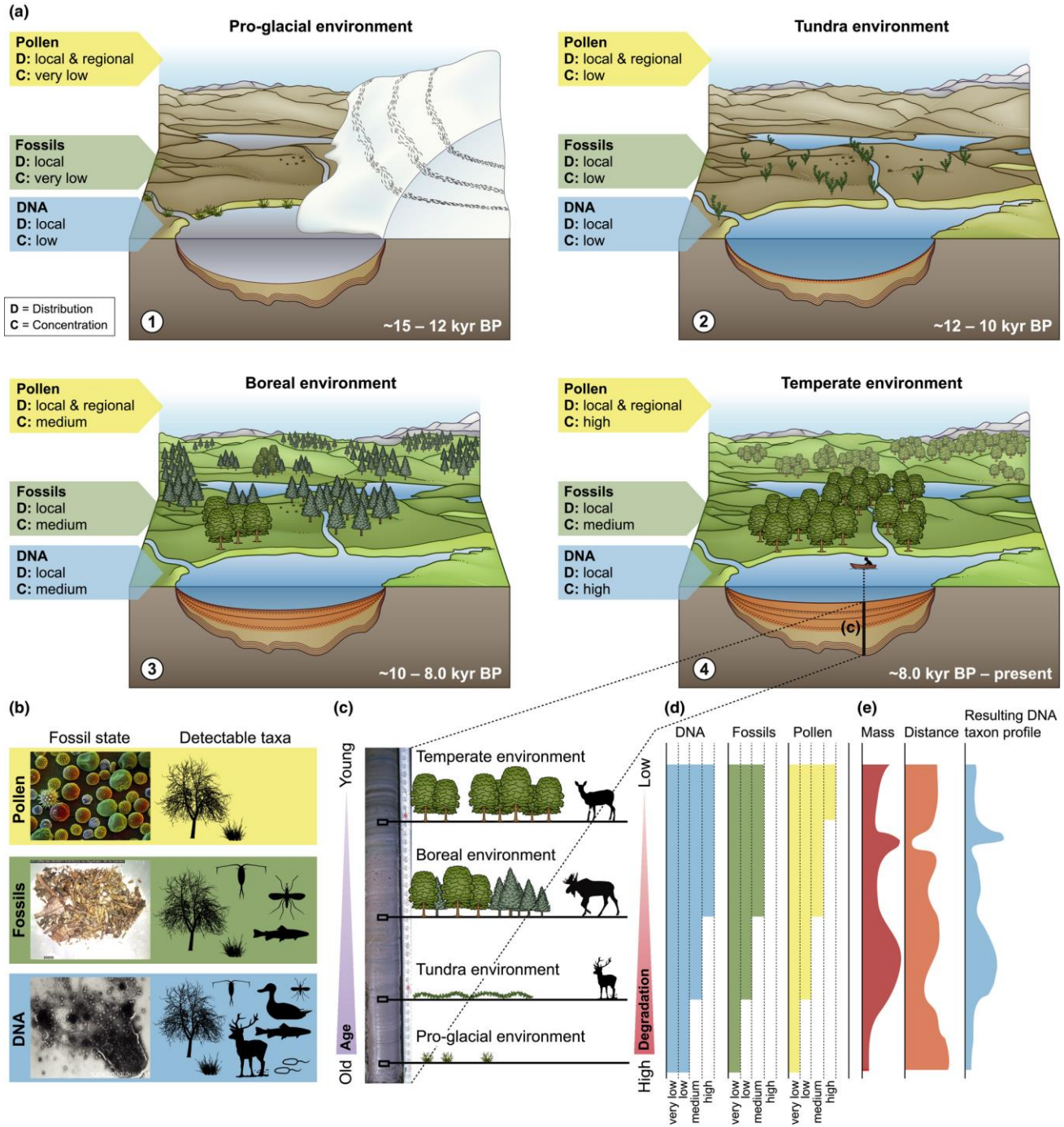
Schepper et al., 2019 DOI: 10.1038/s41396-019-0457-1

LAKE sedaDNA

- Accumulation of both aquatic and terrestrial environmental components
- Lower disturbance, temperature stability
- Preferencial winter sampling

A full bodysuit, shoe cover, hairnet, facemask, hood, gloves and sleeve guards are necessary during DNA extraction from a sediment core for ancient DNA (aDNA) analyses in an aDNA laboratory (a). During subsampling in a clean laboratory, surface contamination from the sediment core is removed with sterilized razors (b), and non-contaminated material from within the intact cores is extracted for DNA extraction (c).

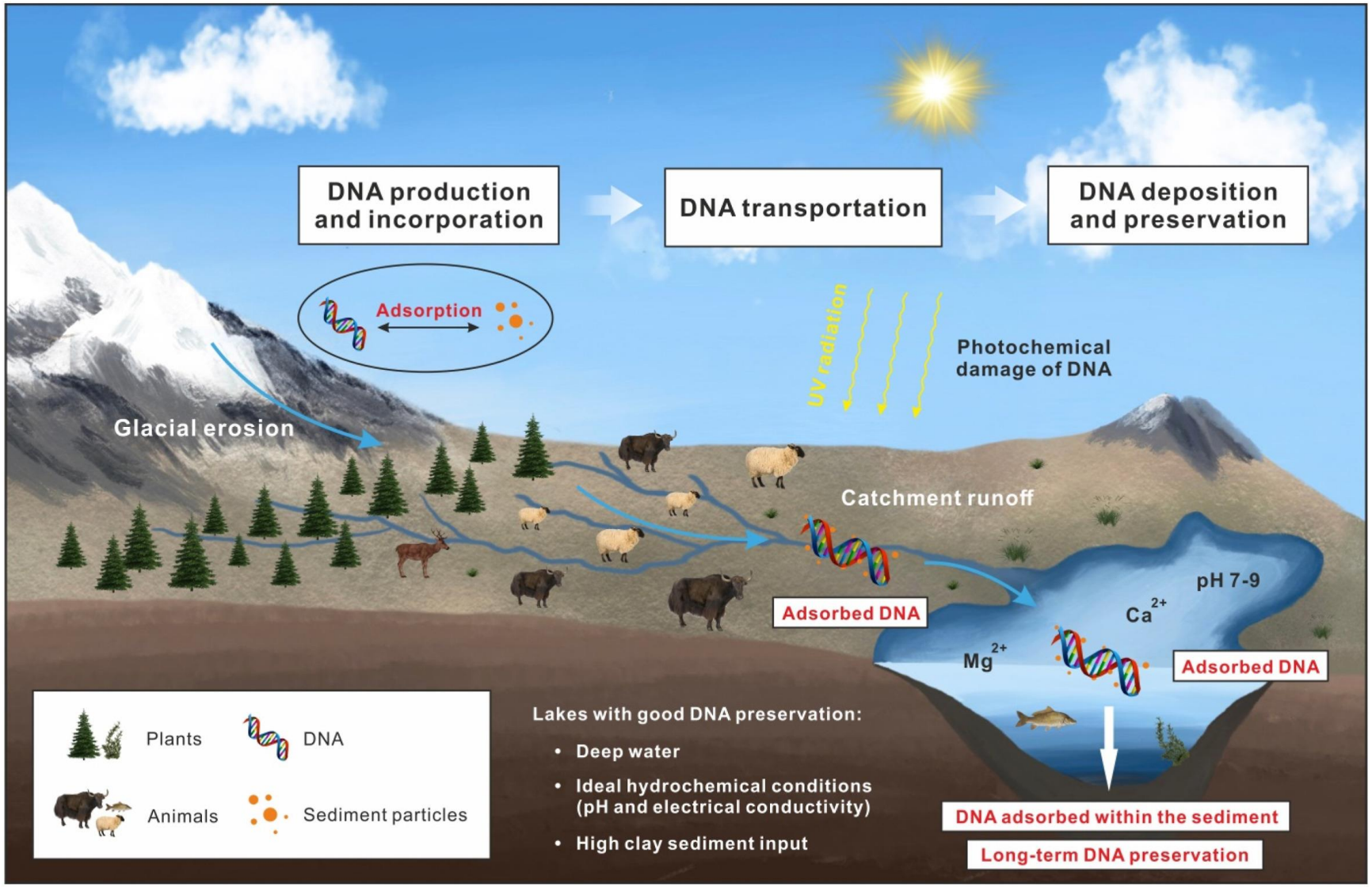
Parducci et al., 2017 DOI: 10.1111/nph.14470



Biotic palaeoenvironmental proxies in lake sediments. (a) Sequential environmental development for a temperate region, in which the lake sediments start to accumulate as the glacial ice retreats, incorporating glacially eroded debris and the sparse pioneering biota (1), which later is replaced by a tundra-steppe community (2); then the boreal forest establishes (3) before eventually being replaced by a temperate forest (4). By identifying organisms detectable by DNA, macro- and microfossils accumulated and preserved in the lake sediments (b), it is possible to reconstruct the environments through time (c). It is important to note that the rate of degradation is strongly correlated with the age of the sediments and that the input concentration (d) varies in different climatic environments from these three proxies. In addition, the resulting DNA profile (e), as well as macro- and microfossils, are influenced by taphonomic processes, such as differences in biomass production and the distance from source to deposit. This is why a combination of all three proxies makes a more robust palaeoenvironmental reconstruction. kyr BP, thousand years before present.

Parducci et al., 2017 DOI: 10.1111/nph.14470

Fig. 2. Conceptual model of the taphonomic processes of extracellular DNA from lake sediments. After having been released into the environment, extracellular DNA can be incorporated into soil or sediment particles by adsorbing to, for example, clay minerals and humic substances, which is the primary mechanism responsible for long-term DNA preservation. Adsorbed DNA can subsequently be transported into the lake through catchment runoff. Most large lakes on the Tibetan Plateau are expected to have high upstream DNA inputs because of diverse landscapes and well-developed hydrographical networks in their catchments. However, high-level ultraviolet (UV) radiation on the Tibetan Plateau might photochemically damage DNA over long transport distances. During the deposition stage, terrestrial adsorbed DNA is expected to be well preserved in deep lakes with neutral to slightly alkaline water pH (7–9), intermediate water conductivities (100–500 μS cm^{-1}; suitable cation concentrations), and high clay sediment input. On the other hand, DNA from aquatic organisms (e.g., fish and macrophytes) might still be preserved in many Tibetan lakes characterized by high water pH (≥9) and conductivity (>1000 μS cm^{-1}). After sediment particles are finally deposited and buried in the lake bottom, DNA is adsorbed within the sediment and stored in a cold and anoxic environment that limits bioturbation, sediment reworking, and microbial activity, which favors long-term DNA preservation. To conclude, we infer that some deep glacial lakes with freshwater and high clay sediment input, such as those from the southern and southeastern Tibetan Plateau, may have a high potential for sedimentary ancient DNA studies in the future.



Jia et al., 2022 DOI: 10.1016/j.quascirev.2022.107703

MORE ON sedaDNA

- Burials
  - Contamination control (comparison of samples and sedaDNA)
  - Non-destructive for remains
  - Have to be sampled early
  - Potentially human DNA, pathogens, parasites, diet, …

- Caves!

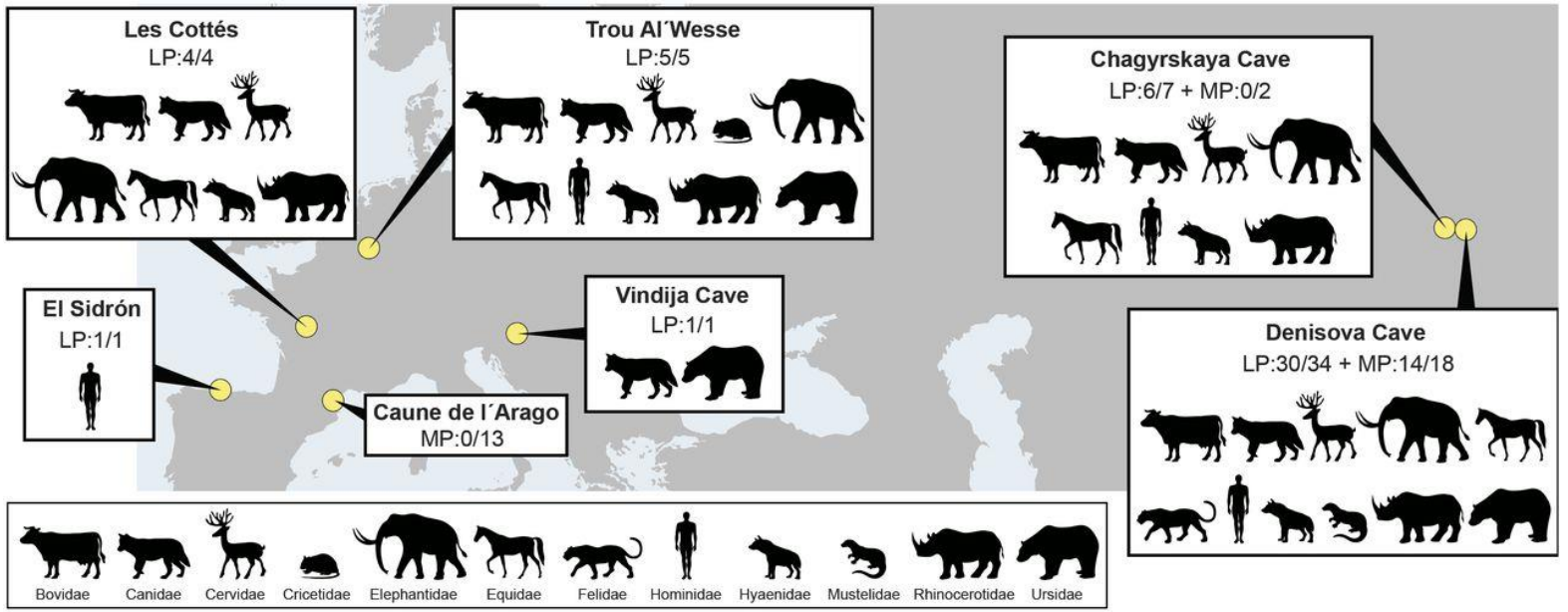
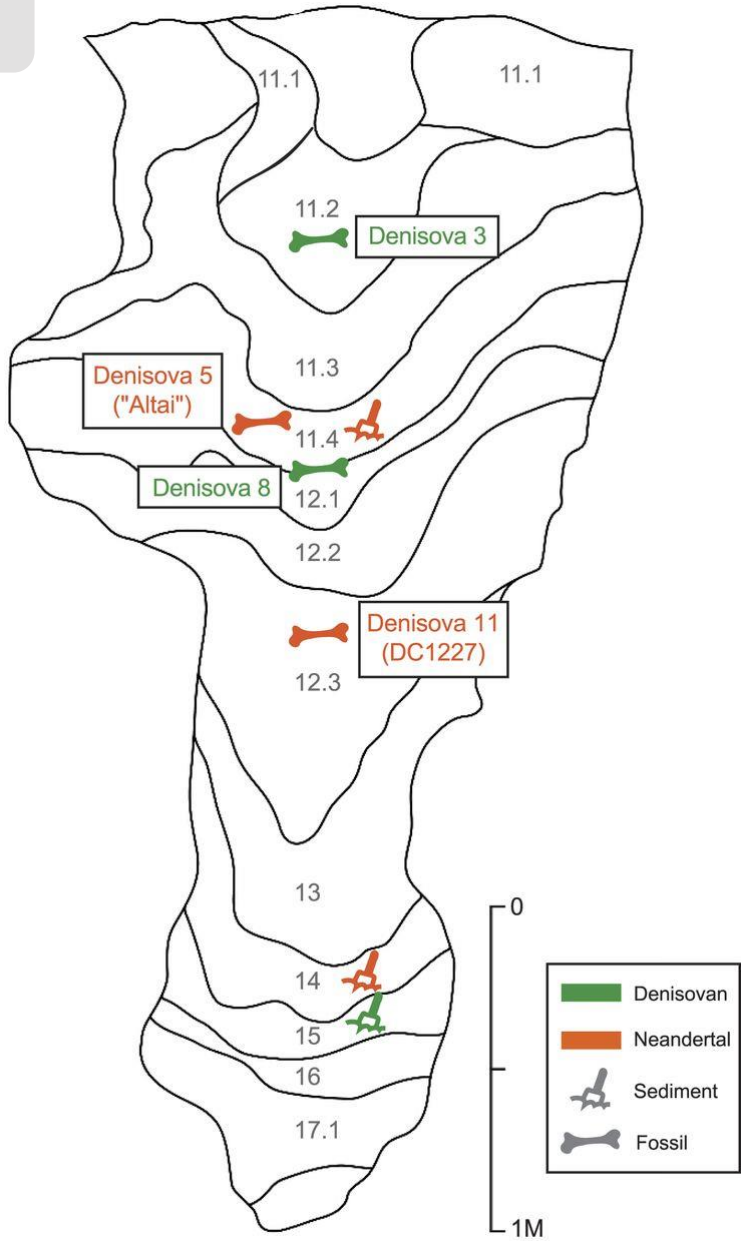


Fig. 1 Ancient taxa detected in Late Pleistocene (LP) and Middle Pleistocene (MP) sediment samples from seven sites.
For each time period, the fraction of samples containing DNA fragments that could be assigned to a mammalian family and authenticated to be of ancient origin is indicated. The shaded symbols representing each family are not to scale.
Slon et al., 2017; DOI: 10.1126/science.aam9695



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MORE ON sedaDNA

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  - Mostly megafauna and hominins

MORE ON sedaDNA

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  - Contamination control (comparison of samples and sedaDNA)
  - Non-destructive for remains
  - Have to be sampled early
  - Potentially human DNA, pathogens, parasites, diet, …

- Caves!
  - Mostly megafauna and hominins
  - Microstratigraphy

Microstratigraphic preservation of ancient faunal and hominin DNA in Pleistocene cave sediments

Diyendo Massilani[a,1], Mike W. Morley[b,1], Susan M. Mentzer[c,d], Vera Aldeias[e], Benjamin Vernot[a], Christopher Miller[c,d,f], Mareike Stahlschmidt[g], Maxim B. Kozlikin[h], Michael V. Shunkov[h], Anatoly P. Derevianko[h], Nicholas J. Conard[c,d], Sarah Wurz[f,i], Christopher S. Henshilwood[f,i], Javi Vasquez[j], Elena Essel[a], Sarah Nagel[a], Julia Richter[a], Birgit Nickel[a], Richard G. Roberts[k,l], Svante Pääbo[a,1], Viviane Slon[a,m,n,o], Paul Goldberg[d,k], and Matthias Meyer[a,1]

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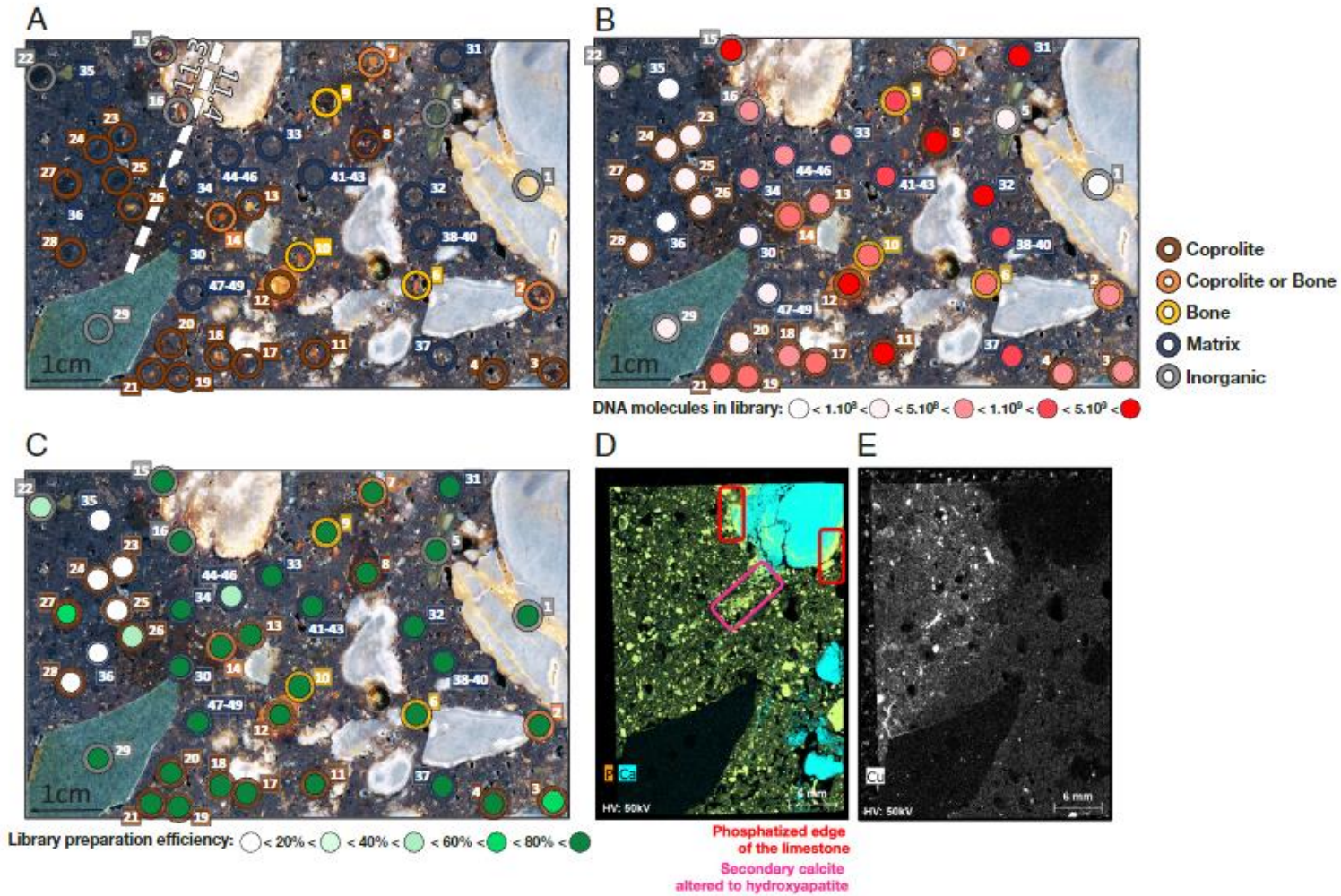

Fig. 3. Targeted sampling of microfeatures from block DCE5C. (*A*) Surface scan with sampling locations and layer designations. (*B*) Number of library DNA molecules recovered from each sample. (*C*) Library preparation efficiencies. (*D*) μXRF surface scan for P (orange) and Ca (aqua) produces a distribution map of calcium phosphate (yellow) that indicates fragments of hydroxyapatite from bone and coprolite as well as phosphatized limestone (red frames) and secondary calcite (magenta frame). (*E*) μXRF surface scan for Cu (white).

PLANTS

- Domestication!
- Greatest genome size, polyploidization allows subfunctionalization and neofunctionalization, transposable elements crucial
- aDNA offers insight into timing, number and locality of domestication events, processes behind domestication (human behaviour, genome changes)
- Research of wild and early-domesticated ancestors, adaptation to pathogens and environmental changes
- Palaeoecology
- Sources: seeds, herbarium specimens, wood, pollen, sediments, various plant fragments

Table 2 Ancient plant DNA

Species	Dating[a]	Site	Sample	Characterization[b]	Extraction[c]	Reference
Oak	500–9800 BP	Europe	Waterlogged wood	NGS	TrisHCL SDS $CaCl_2$ EDTA DTT PK/Phchlo/Column	[142]
Japanese cedar	3600 BP	Japan	Buried tree	PCR/sequencing	Column	[133]
Maize	1100–6000 BP	New World	Desiccated cob	PCR/sequencing	CTAB TrisHCL NaCl EDTA/ Chlo	[111] [112]
Maize	360–1320 BP	New World	Desiccated cob	PCR/sequencing	Column	[114]
Maize	670–5280 BP	New World	Desiccated cob	Capture, NGS	SDS DTT PK/Phchlo/Column	[115]
Maize	650–4300 BP	New World	–	PCR/sequencing	SDS DTT PK/Phchlo/EDTA PTB/Column	[113]
Maize	4700 BP	Chile, Peru	Charred and non-charred grain	PCR/sequencing	SDS DTT PK/Phchlo	[110]
Maize	5310 BP	Mexico	Desiccated grain	NGS	TrisHCL SDS $CaCl_2$ EDTA DTT PK/Phchlo/Column	[116]
Maize	5300 BP	Mexico	Desiccated cob	NGS	–	[117]
Sunflower	3100 BP	USA	Desiccated disk fragment, pericarp, kernel	NGS	TrisHCl NaCl SDS $CaCl_2$ EDTA DTT PK/Phchlo/Column	[119]
Radish	350–550 AD	Egypt	Desiccated seed	Chemical analysis/ PCR/sequencing	CTAB TrisHCL NaCl EDTA/Chlo	[124]
Sorghum	2800 BP	Egypt	Desiccated seed	PCR/sequencing	–	[125]
Rice	1200–2400 BC	China	Desiccated seed and chaff	PCR/sequencing	Magnetic beads	[127]
Grape	1600–2500 BP	Europe	Waterlogged and charred pip	PCR/sequencing	DTAB /Chlo/CTAB	[120]
Grape	7^{th}–15^{th} century AD	Italy	Waterlogged pip	PCR	SDS DTT PK/Phchlo/Column	[121]
Grape, maize, olive, dogwood, cotton	400–2400 BP	New World, Europe	Non-carbonized remain	PCR/sequencing	SDS DTT PK/Phchl	[122]
Barley	6200–5800 BP	Israel	Desiccated seed	NGS	CTAB TrisHCL PVP βME/Phchlo/ Column	[104]
Barley	3000 BP	Egypt	Desiccated grain	PCR/sequencing	SDS DTT PK EDTA PTB/Column	[103]
Barley, wheat	150–5250 BC	Spain	Charred, partially charred, waterlogged seed	PCR/sequencing	TrisHCL SDS EDTA PK/Phchlo or Column	[105]
Wheat	700 AD–8400 BP	Anatolia	Charred grain	PCR/sequencing	CTAB TrisHCL NaCl EDTA/Chlo	[109]
Wheat	340–3500 BP	Spain	Charred and desiccated seed	PCR/sequencing	Tris EDTA CTAB βME/Column	[108]
Cotton	750–3750 BP	Brazil, Peru, Egypt	Desiccated seed	NGS	CTAB/Column	[132]
Arabidopsis	300 BP	USA	Herbarium	NGS	CTAB or PTB DTT/Column	[131]

Summary of ancient plant nuclear DNA recovery listing species, dating, location site, sample type, characterization method, extraction protocol, and associated references. [a]Datings are referenced as in the publication concerned using BC, AD, or BP. [b]*PCR/sequencing* polymerase chain reaction and sequence capture, *NGS* next-generation sequencing. [c]*DDT* dithiothreitol proteinase K, *Phchlo* phenol-chloroform, *Ph* phenol, *Chlo* chloroform, *SDS* sodium dodecyl sulphate, *EDTA* ethylene-diamine-tetraacetic acid, *CTAB* cetyltrimethylammonium-bromide, *PTB* phenacylthiazolium bromide, *DTAB* dodecyltrimethylammonium bromide, *βME* β-mercaptoethanol, *Tris* tris(hydroxymethyl) aminomethane, *PK* proteinase K

Pont et al., 2019 DOI: 10.1186/s13059-019-1627-1

FAUNA

- Domestication!, introgression, loss of diversity, migrations and contact
- Domestication – commensal, directed, prey
- Wild animals, extinct species such as mammoth

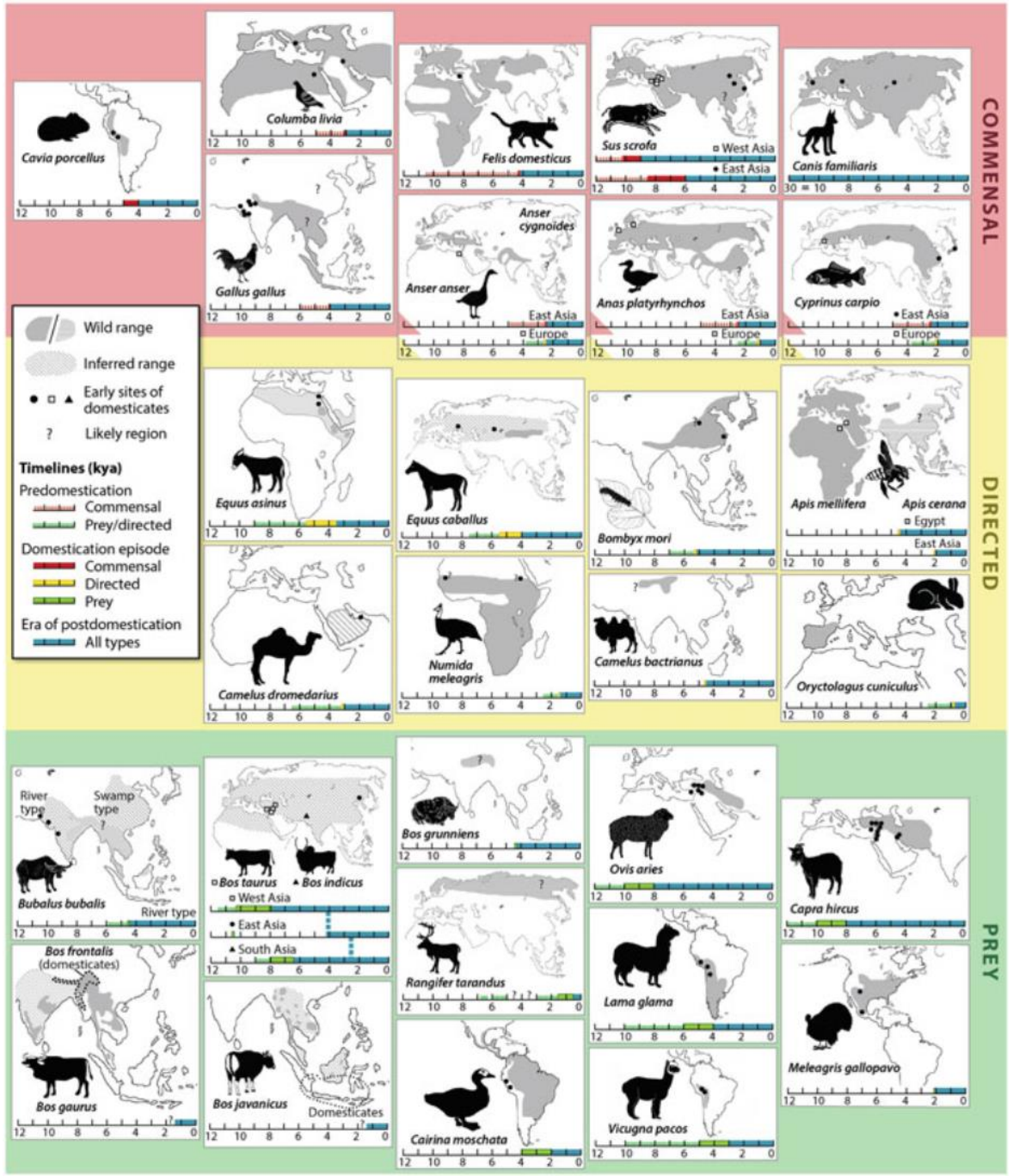

Fig. 1 Geographical/chronological time frame of domestication and potential pathways for major domestic animals. The timelines are in ky (1,000 years) increment. Adapted after Larson and Fuller (2014)

CONSERVATION AND aDNA

- Biodiversity levels:
  - Diversity of ecosystems
  - Species diversity
  - Genetic diversity

- Loss of biodiversity usually in presented in lost species, genetic diversity often unknown

REVIEWS AND SYNTHESES | Open Access

Estimated six per cent loss of genetic variation in wild populations since the industrial revolution

Deborah M. Leigh, Andrew P. Hendry, Ella Vázquez-Domínguez, Vicki L. Friesen

First published: 07 May 2019 | https://doi.org/10.1111/eva.12810 | Citations: 131

CONSERVATION AND aDNA

- Biodiversity levels:
  - Diversity of ecosystems
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  - Genetic diversity

- Loss of biodiversity usually in presented in lost species, genetic diversity often unknown

- Museum collections and sedaDNA

ORIGINAL RESEARCH article

Front. Ecol. Evol., 03 March 2020
Sec. Paleoecology
Volume 8 - 2020 | https://doi.org/10.3389/fevo.2020.00037

This article is part of the Research Topic
Applied Uses of Ancient DNA
View all 14 Articles >

Unveiling the Ecological Applications of Ancient DNA From Mollusk Shells

Clio Der Sarkissian[1*] Per Möller[2] Courtney A. Hofman[3,4] Peter Ilsøe[5] Torben C. Rick[6] Tom Schiøtte[7]
Martin Vinther Sørensen[7] Love Dalén[8,9] Ludovic Orlando[1,5]

limit for shell DNA recovery to ≥100,000 years

CONSERVATION AND aDNA

- Biodiversity levels:
  - Diversity of ecosystems
  - Species diversity
  - Genetic diversity

- Loss of biodiversity usually in presented in lost species, genetic diversity often unknown

- Museum collections and sedaDNA

- Ancient and historical DNA can help:
  - Set baselines for genetic diversity
  - Assess introgression, identify source populations
  - Assess evolutionary impacts of past events
  - Study effective population size, subpopulations and their distinctness
  - …

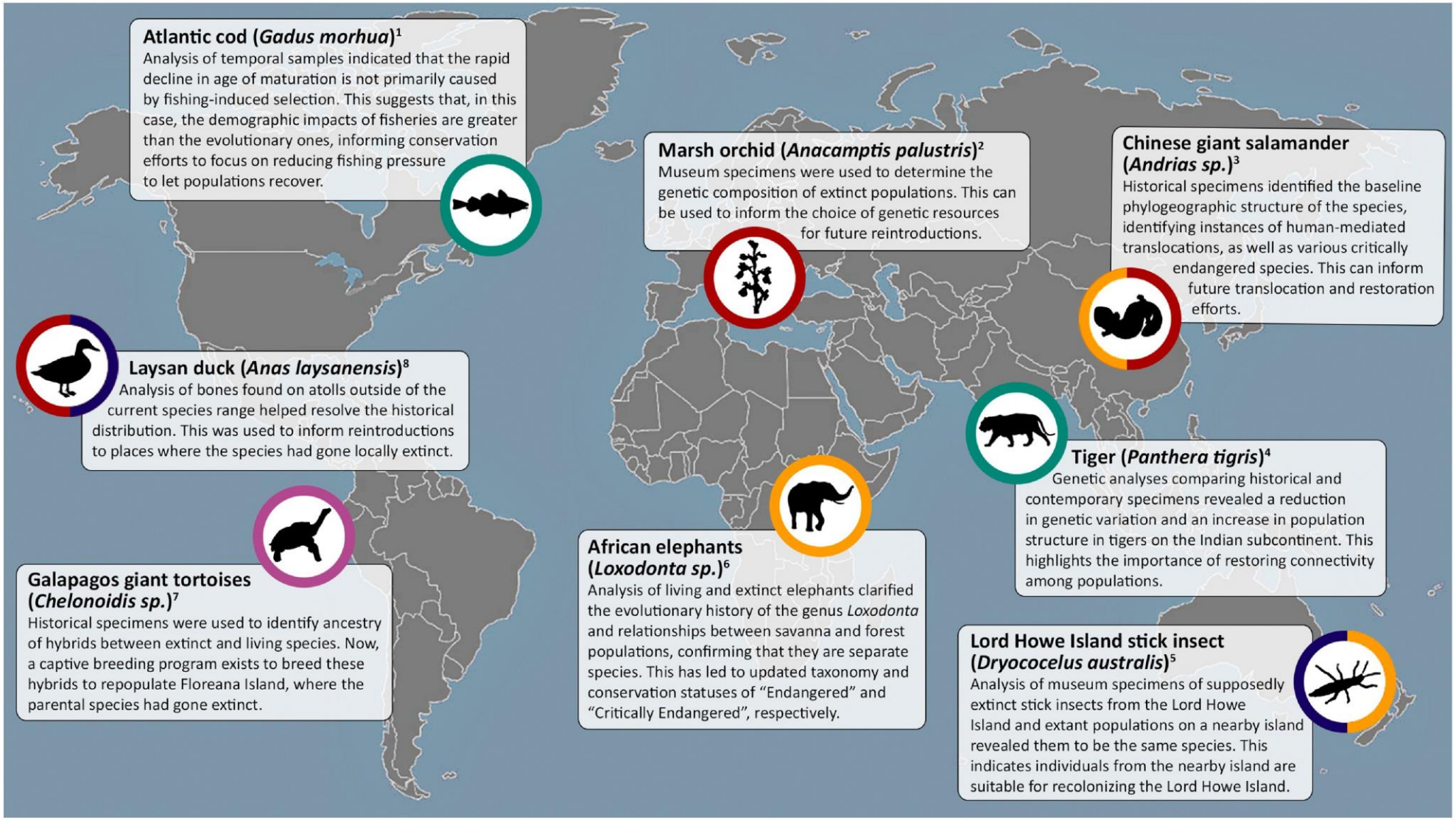


Figure 1. Examples of studies where ancient and/or historical DNA has provided important conservation insights.

Colours around the icons indicate the type of provided conservation insight or informed policy action: blue, determining the historical distribution of species; purple, guiding conservation breeding; red, informing translocations/reintroductions; teal, assessing anthropogenic impacts on genetic diversity; yellow, resolving taxonomic issues.

Jensen et al., 2022 DOI: 10.1016/j.tree.2021.12.010

DEEXTINCTION

- Bringing extinct species back to life

Jurassic Park (1993), Universal Pictures

DEEXTINCTION

- Bringing extinct species back to life
- Similar phenotype by cross-breading

Founder population, selected in Etosha in 1987 **Ricky**

Rain Current population, Nuwejaars Wetland 2022

DEEXTINCTION

- Bringing extinct species back to life

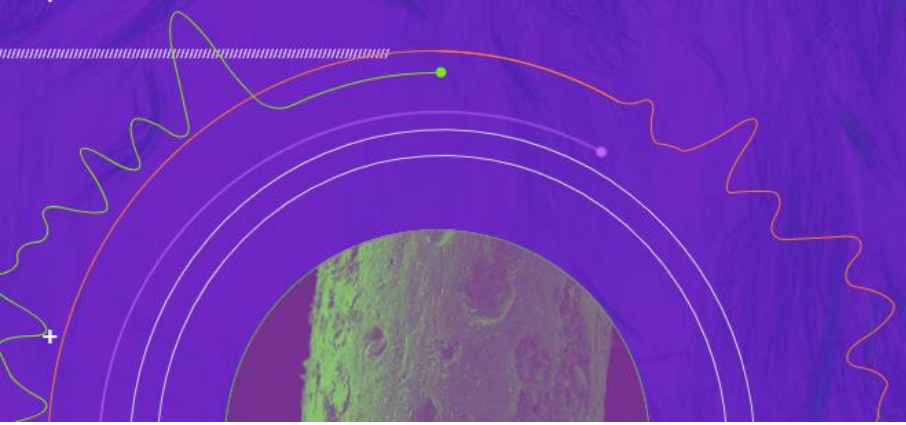
- Similar phenotype by cross-breading
- Genome editing of close related species

| EARTH'S OLD FRIEND |

THE MAMMOTH

MAY 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.



COLOSSAL PROJECT 001

- Goals more general, e.g.:
  - Elephant genome
  - Elephant tracking technologies
  - Artificial womb
  - Ecological restoration
  - Synthetic biology applications
  - Vaccine
  - Sustainable agriculture
  - …

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- Cloning

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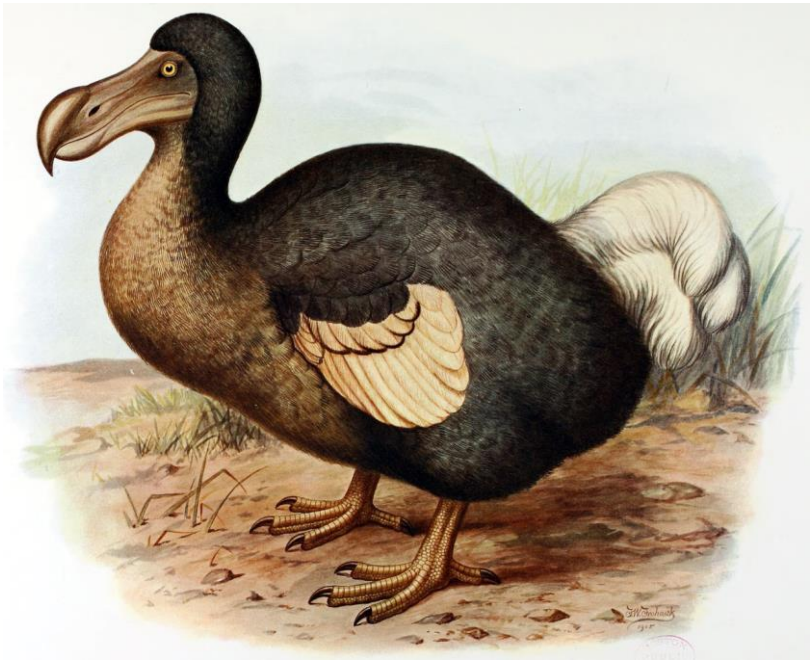
- Thylacine, Dodo, Quagga, Mammoth, Passenger pidgeon



Extinct birds (1907), Frederick William Frohawk

Birds of New York (1910), Louis Agassiz Fuertes

DEEXTINCTION

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- Efficiency of funding

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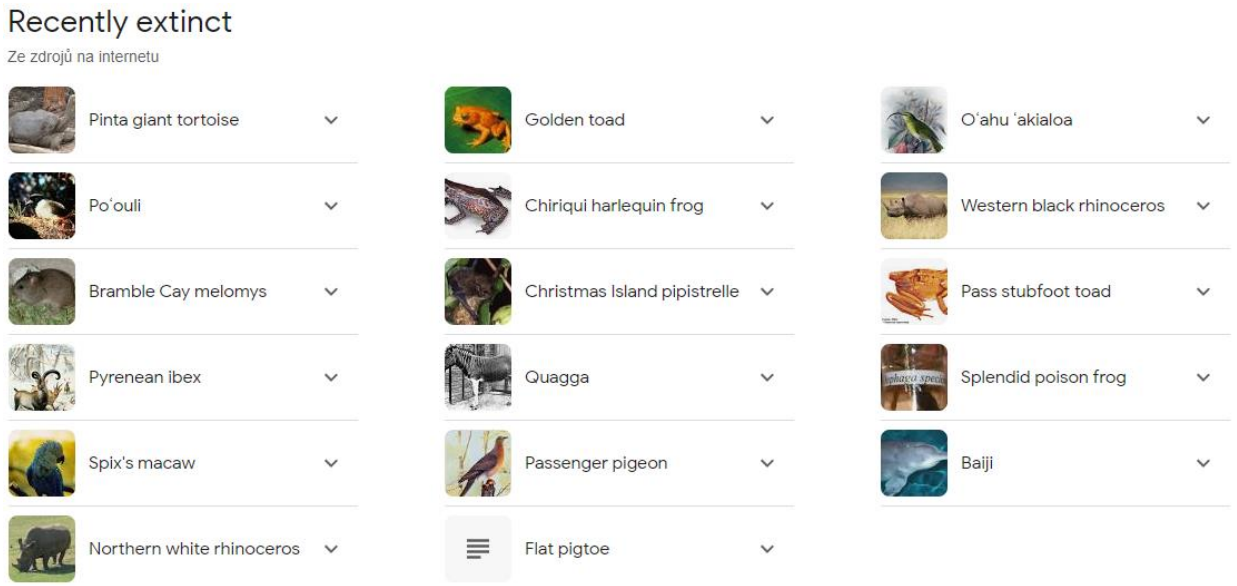

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- Ecosystem, habitat – do extinct species have a place?
- Efficiency of funding

- Recently extinct species!
- At least about 200-2000 species every year

- Rhino and recently extinct species for deextinction
- Deextiction types
- sedaDNA subsampling (on boats in marine sedaDNA)
- Plant domestication
- Extraterrestrial sediment
- Climate change and sedaDNA
- Sampling in winter (lake sedaDNA)
- Domestication types
- Reintroduction of genetic diversity from past populations to current ones