

METAGENOMICS

MUNI
SCI

EVA CHOCHOLOVÁ

LABORATORY OF BIOLOGICAL AND MOLECULAR ANTHROPOLOGY

DEPARTMENT OF EXPERIMENTAL BIOLOGY

QUIZ

1. What is the difference between genomic and epigenomic research?

Genomics

Epigenomics

Change over long time

Environmentally responsive, plastic



2. What is taphonomic bias? What are some examples?

Taphonomic biases: biological and geological processes that occur between death, decay, and eventual fossilisation that result in over- or under-representation or even complete absence of specific skeletal elements, taxa, or demographic groups (e.g., different sexes or ages) in the fossil record.

3. What are the differences between mtDNA and nuclear DNA?

Nuclear DNA

3,000,000,000 base pairs

- Two copies
- Long
- Recombining
- Inherited from both parents
- Great amount of information

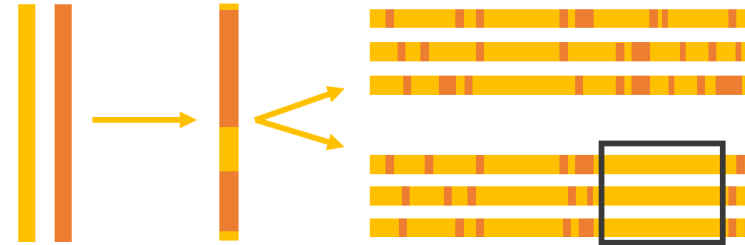
Mitochondrial DNA

16,500 base pairs

- More copies per cell
- Shorter, circular
- Generally without recombination
- Maternal
- Limited insight

4. What are introgression deserts?

- Introgression deserts – regions depleted of certain ancestry (Neanderthal in this case) compared to expected patterns without natural selection



5. What are some sources of ancient human genomes?

Human tissues



Artefacts



Settlements and environment



METAGENOMICS

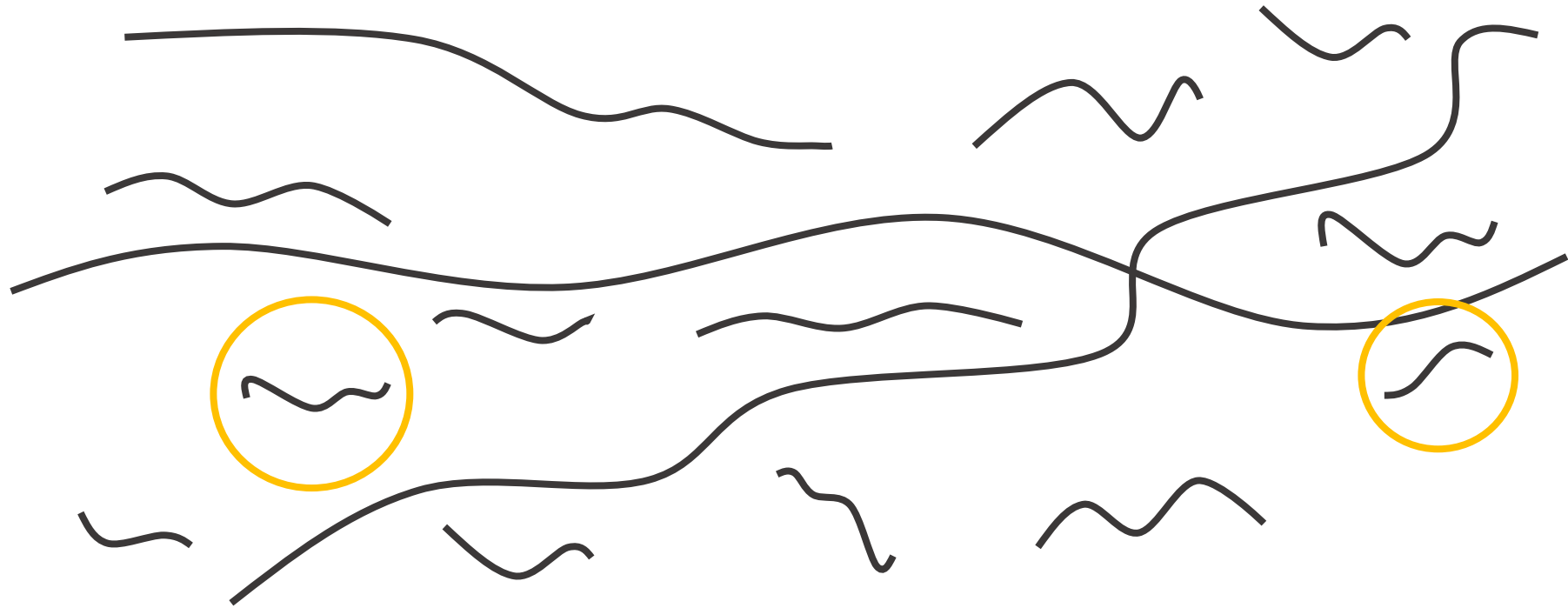
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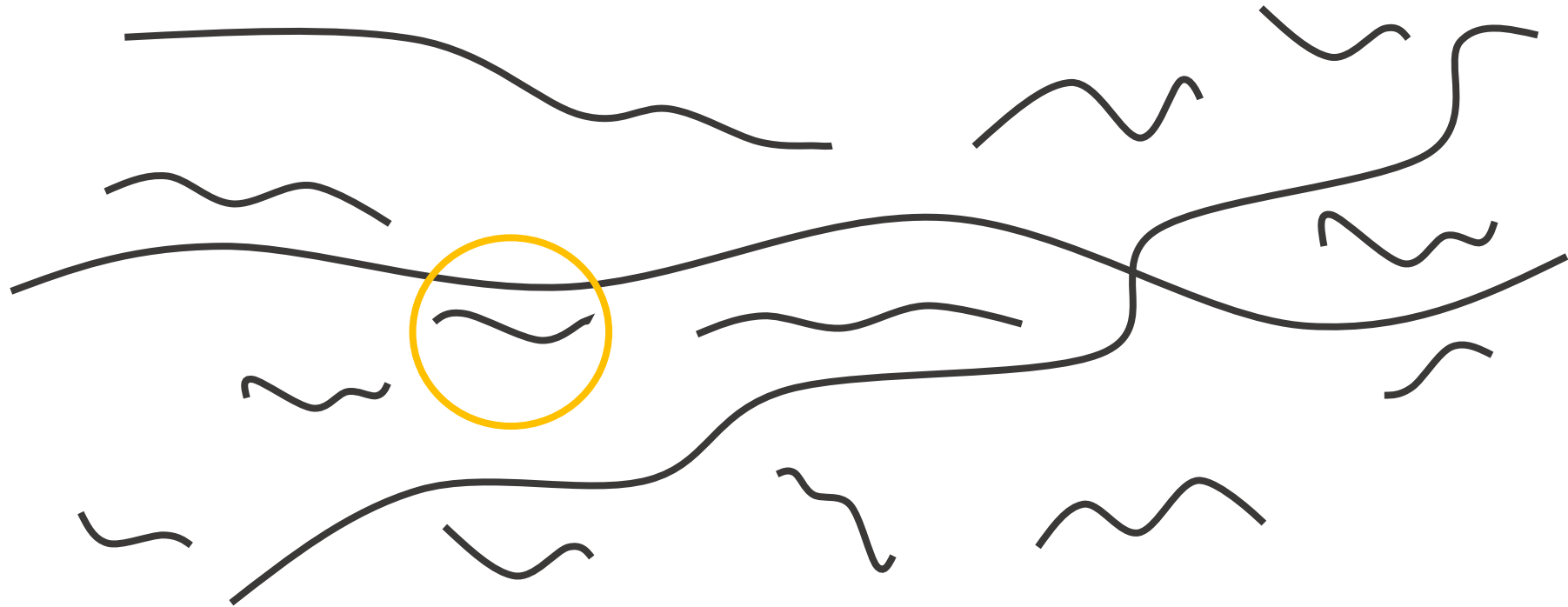
LABORATORY OF BIOLOGICAL AND MOLECULAR ANTHROPOLOGY

DEPARTMENT OF EXPERIMENTAL BIOLOGY

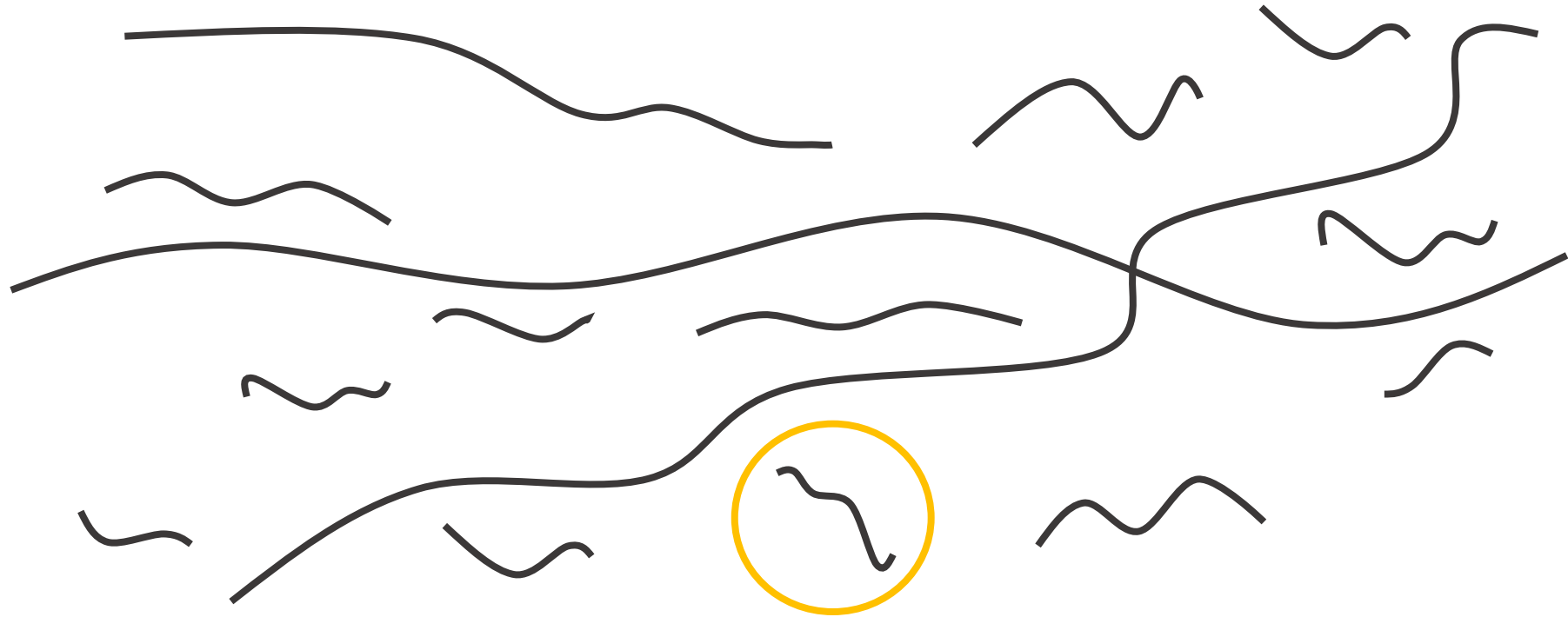
ONE ORGANISM (HUMAN GENOME)

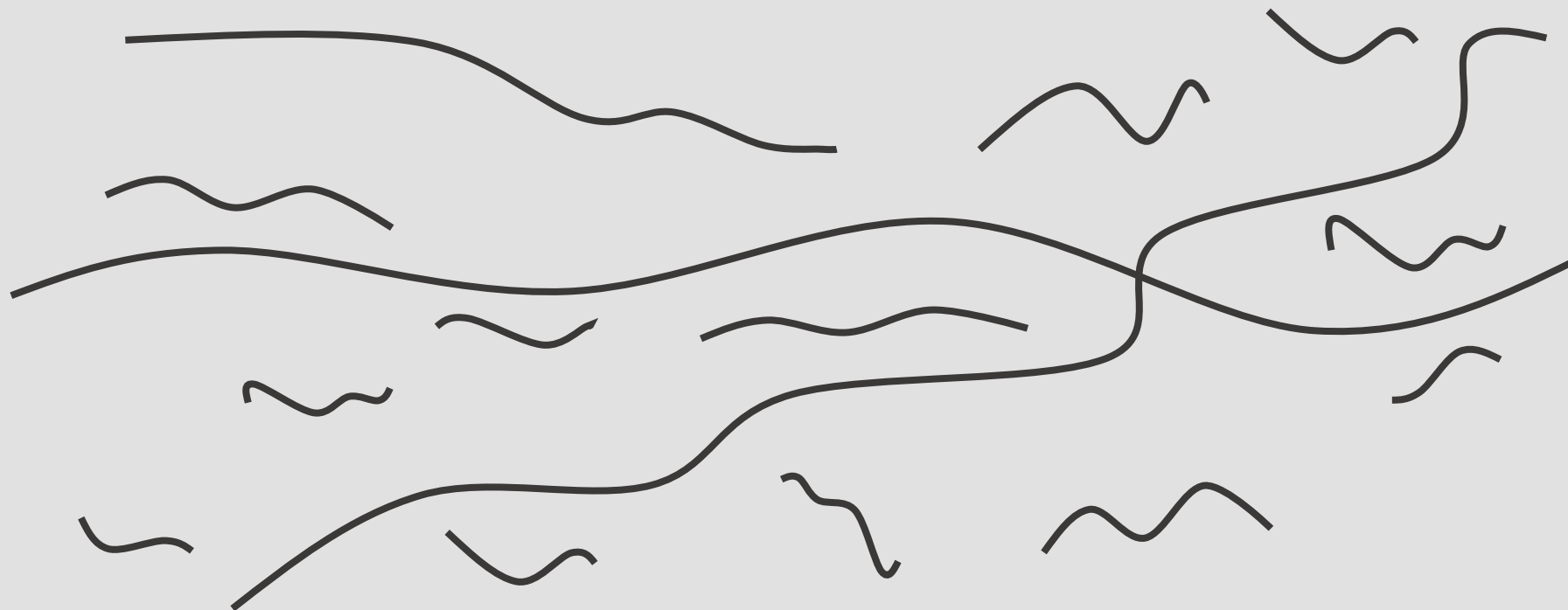


ONE ORGANISM (PATHOGEN GENOME)

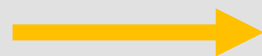


ONE ORGANISM (WHEAT GENOME)

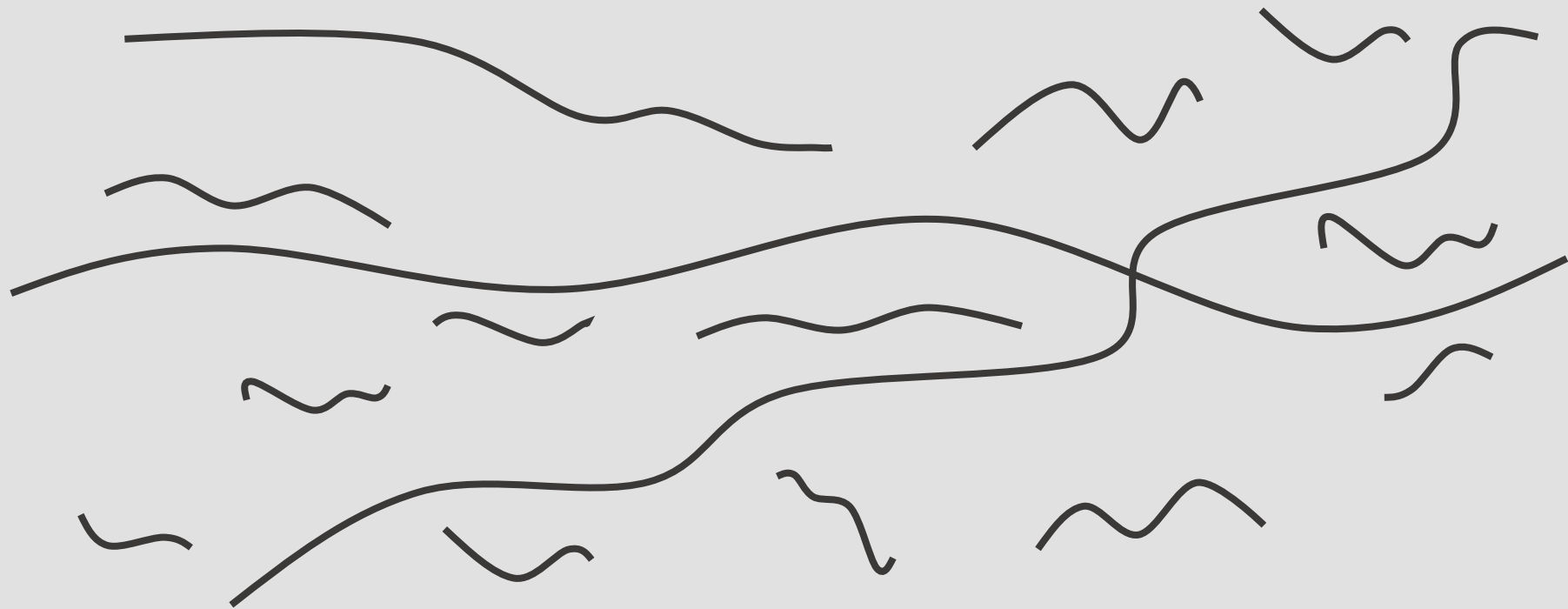




METAGENOME



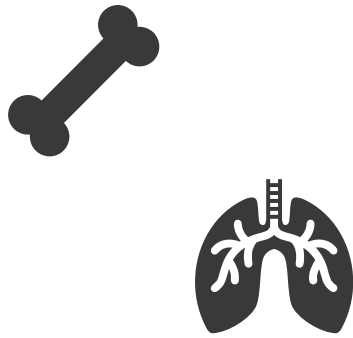
ALMOST ANYTHING



METAGENOME includes necrobiome!

SOURCES FOR ANCIENT METAGENOMICS

Human and non-human tissues



Artefacts



Settlements and environment



Coprolites

Dental calculus

Fermentation products

Museomics

...

SOURCES FOR ANCIENT METAGENOMICS

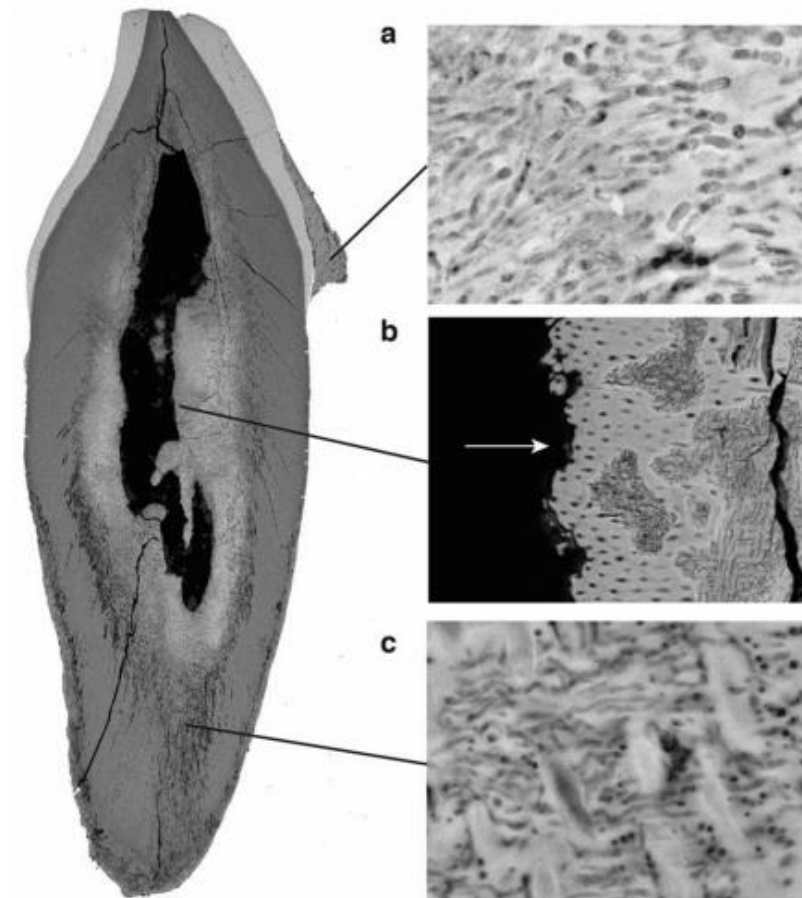


Figure 2. Key microbial locations within teeth. (a) Dental plaque calcifies to form dental calculus, a long-term reservoir of biomolecules from the oral microbiome. (b) Blood-borne pathogens leave behind their DNA on the inner surfaces of the dental pulp chamber; and (c) Microbes of the necrobiome and thanatomicrobiome can be found degrading and decomposing the tooth, especially in areas surrounding the root canal and pulp chamber, as well as cementum.

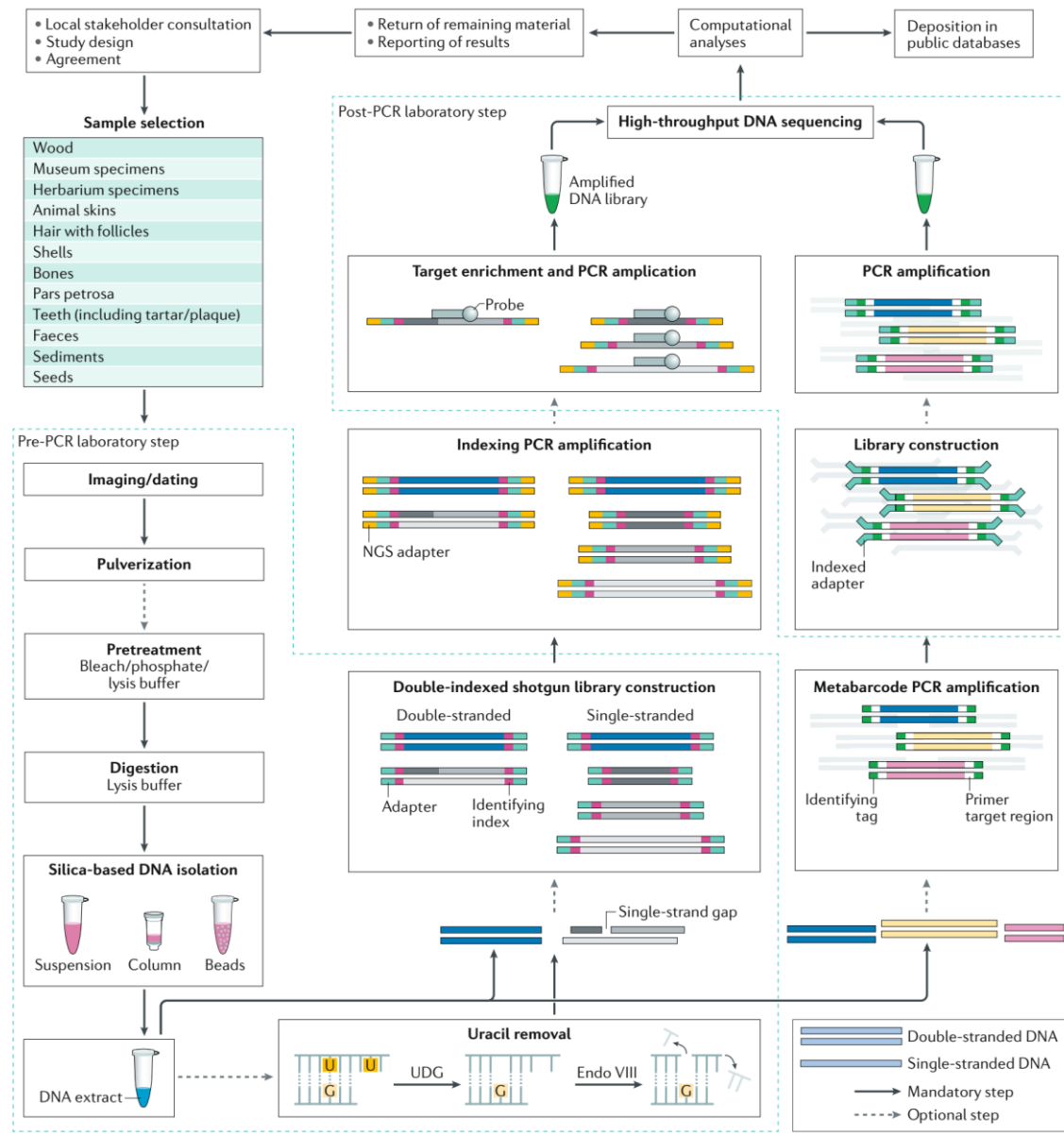


Fig. 2 | **Experimental workflow.** A wide range of remains are amenable to ancient DNA (aDNA) analysis. Prior to sample destruction, a research plan should be agreed amongst the different stakeholders. The different wet-laboratory procedures must be carried out in specific aDNA facilities, minimizing environmental contamination, and include all pre-amplification experimental steps, including sample preparation, DNA extraction, optional USER treatment and DNA library construction. Target enrichment and PCR amplification are carried out in regular molecular genetics facilities. Following next-generation sequencing (NGS), the sequence data are processed on computational servers and uploaded to public repositories. Results should be communicated to the stakeholders and any remaining sample should be returned as per the initial agreement. USER, uracil-DNA-glycosylase (UDG) and endonuclease VIII (Endo VIII) (New England Biolabs).

METAGENOMICS WORKFLOW EXAMPLE

Extraction → Library prep → (Enrichment) → Sequencing → Raw data processing → Mapping to reference /De novo assembly

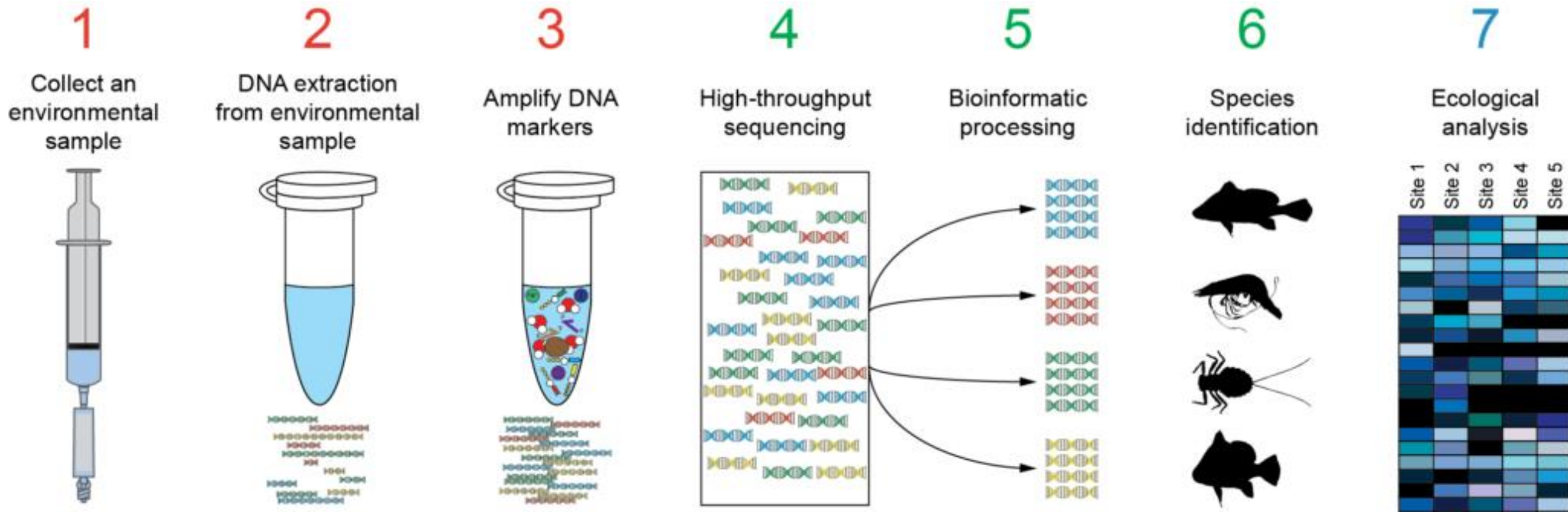
METATAXONOMICS

Technique	Advantages and challenges	Main applications
Metataxonomics using amplicon sequencing of the 16S or 18S rRNA gene or ITS	<ul style="list-style-type: none"> + Fast and cost-effective identification of a wide variety of bacteria and eukaryotes - Does not capture gene content other than the targeted genes - Amplification bias - Viruses cannot be captured 	<ul style="list-style-type: none"> * Profiling of what is present * Microbial ecology * rRNA-based phylogeny
Metagenomics using random shotgun sequencing of DNA or RNA	<ul style="list-style-type: none"> + No amplification bias + Detects bacteria, archaea, viruses and eukaryotes + Enables <i>de novo</i> assembly of genomes - Requires high read count - Many reads may be from host - Requires reference genomes for classification 	<ul style="list-style-type: none"> * Profiling of what is present across all domains * Functional genome analyses * Phylogeny * Detection of pathogens
Meta-transcriptomics using sequencing of mRNA	<ul style="list-style-type: none"> + Identifies active genes and pathways - mRNA is unstable - Multiple purification and amplification steps can lead to more noise 	<ul style="list-style-type: none"> * Transcriptional profiling of what is active

„Metataxonomics is a term we propose and define as the high-throughput process used to characterize the entire microbiota and create a metataxonomic tree, which shows the relationships between all sequences obtained.“

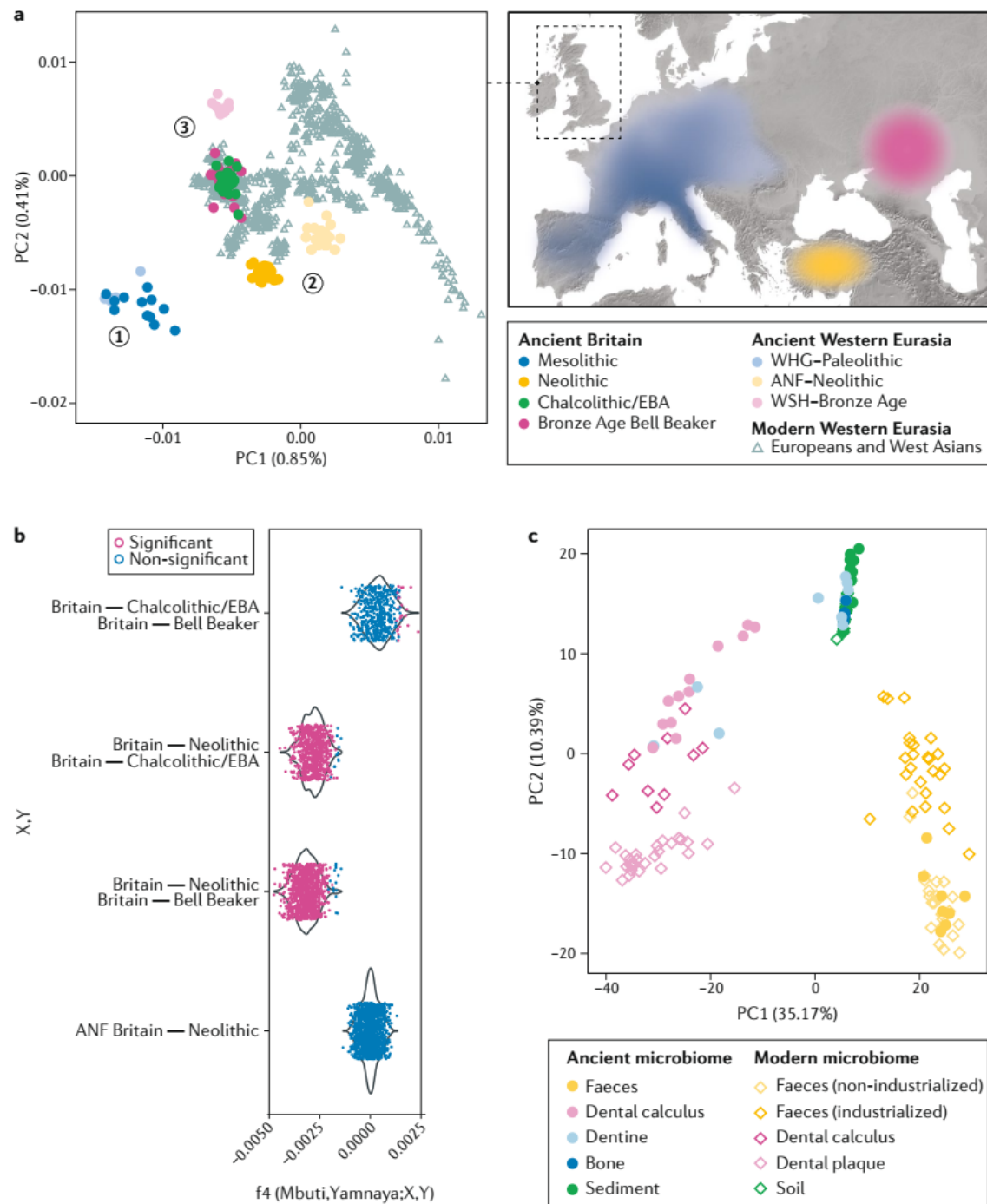
Marchesi et al., 2015; DOI: 10.1186/s40168-015-0094-5

METABARCODING



AMPLICON SEQUENCING, METATAXONOMICS, AMPLICON METATAXONOMICS...

Fig. 4 | Examples of standard aDNA statistical analyses applied to human and microbiome data. **a** | Principal component analysis (PCA) of prehistoric individuals from Britain (circles), projected on the diversity of present-day Europeans and West Asians (triangles, data from REFS^{158,206,352}). The gene pool of people who lived in present-day Britain has considerably changed through time, reflecting a complex migration and admixture history. During the Paleolithic and Mesolithic periods (group 1), individuals in Britain genetically resembled western hunter-gatherers (WHG; blue) found at that time throughout much of Western Europe. During the Neolithic (group 2), the arrival of farming populations dramatically shifted the genetic profile of individuals in Britain towards Anatolian Neolithic farmers (ANF; yellow). Then, beginning in the Chalcolithic period and continuing through the Bronze Age (Early Bronze Age (EBA)) (group 3), the genetic profile of individuals in Britain shifted again, this time towards western steppe herders (WSH; pink) from the Pontic steppes associated with the expansion of the Bell Beaker cultural phenomenon across Europe. **b** | Genetic hypotheses generated using PCA can be formally tested using f_4 statistics. Here, we show f_4 statistics of the form (Mbuti, Yamnaya; X, Y), where X and Y are pairs of ancient individuals from Britain associated with the Neolithic, Bell Beaker and Chalcolithic/EBA. Scores significantly different from 0 ($|Z \text{ score}| > 3$) are shown in pink, whereas non-significant scores are shown in blue. Individuals from Britain and associated with the Bell Beaker culture and the Chalcolithic/EBA show a significant excess of genetic sharedness with Bronze Age WSH associated with the Yamnaya culture of the Pontic steppes. **c** | Principal coordinate analysis of genus-level taxonomic frequency profiles of ancient (circles) and modern (diamonds) microbiota reconstructed from faeces, dental calculus, dental plaque, dentine, bone, soil and sediments (data from REF.³⁵³). Ancient dental calculus samples have metagenomic diversity profiles similar to modern dental calculus, whereas paleofaeces resemble modern faeces from non-industrialized populations. Microorganisms colonizing skeletal material generally originate from soil, but some dentine samples show evidence of being decomposed by the dental plaque bacteria. aDNA, ancient DNA.



THE CARP STORY

Garbage in, garbage out. But first you need to know what garbage looks like.



Figure 1. Carp in the soil. https://en.wikipedia.org/wiki/File:Cyprinus_carpio.jpeg

VALIDATION

Authentication based on damage

Competitive mapping

Good reference, database choice!!

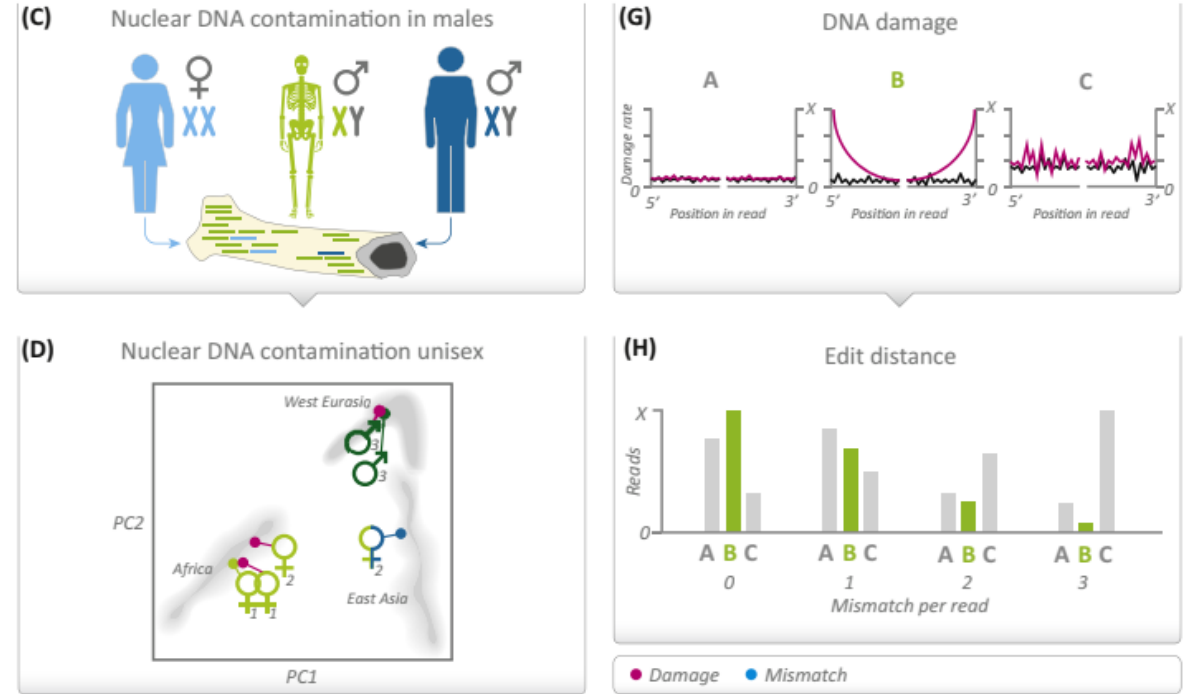
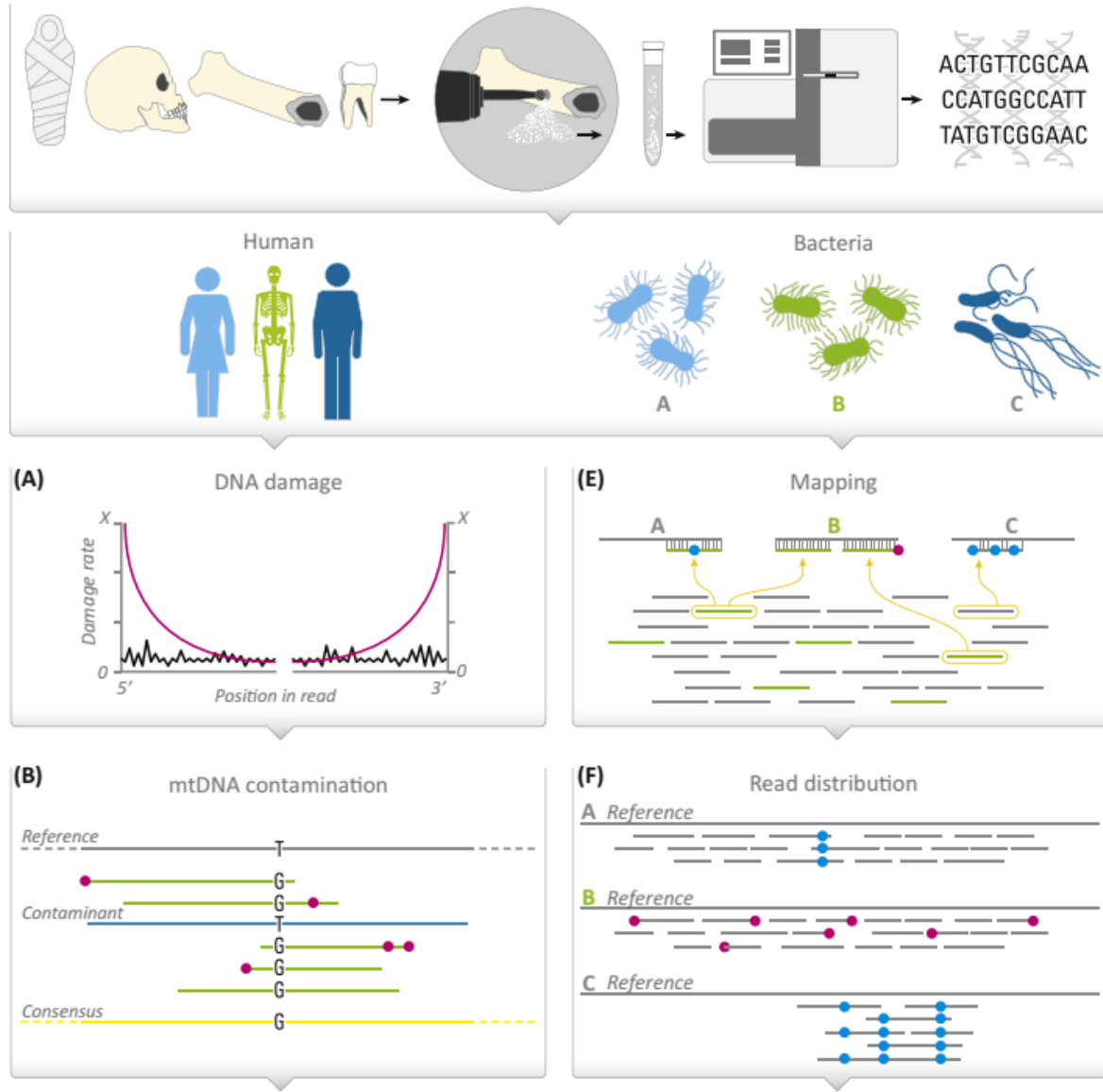
Unique markers

Does it make biological and historical sense?

Review

Mining Metagenomic Data
Sets for Ancient DNA:
Recommended Protocols for
Authentication

Felix M. Key,^{1,*} Cosimo Posth,¹ Johannes Krause,¹
Alexander Herbig,¹ and Kirsten I. Bos^{1,*}



Trends in Genetics

Figure 1. Schematic Illustration Detailing the Conceptual Process of Species Authentication in Ancient Metagenomic Data. After sample processing and sequencing, the analytical techniques for ancient human and bacterial DNA authentication differ. (A–D) For the human example, light blue indicates female contamination, dark blue indicates male contamination, and green indicates ancient sequences. Abbreviation: mtDNA, mitochondrial DNA. Pink dots indicate reads with damage expected of ancient DNA. In the principal component analysis (PCA), female individual ‘1’ and male individual ‘3’ potentially have low nuclear DNA contamination since all sequences and only those with damage occupy close positions in the PCA space. By contrast, female individual ‘2’ is contaminated, since all sequences occupy a position in the PCA space that differs from those only with damage. (E–H) For the bacterial example, organism ‘a’ is a modern bacterium with close homology to an ancient target, ‘b’ is the ancient target, and ‘c’ is a modern contaminant with lower homology to the ancient target. In 1E, green DNA sequences are ancient, and grey stem from environmental sources. Blue dots denote nucleotide differences from the reference sequence. Figure produced by Annette Günzel.

PLoS One. 2020; 15(5): e0232936.

Published online 2020 May 22. doi: [10.1371/journal.pone.0232936](https://doi.org/10.1371/journal.pone.0232936)

PMCID: PMC7244142

PMID: [32442164](https://pubmed.ncbi.nlm.nih.gov/32442164/)

Museomics for reconstructing historical floristic exchanges: Divergence of stone oaks across Wallacea

[Joeri S. Strijk](#), Conceptualization, Data curation, Formal analysis, Funding acquisition, Investigation, Methodology, Project administration, Resources, Supervision, Validation, Visualization, Writing – original draft, Writing – review & editing,^{1,2,3,*} [Hoàng Thi Binh](#), Writing – review & editing,⁴ [Nguyen Van Ngoc](#), Writing – review & editing,⁴ [Joan T. Pereira](#), Resources,⁵ [J. W. Ferry Slik](#), Resources, Writing – review & editing,⁶ [Rahayu S. Sukri](#), Resources, Writing – review & editing,⁶ [Yoshihisa Suyama](#), Methodology, Software, Writing – review & editing,⁷ [Shuichiro Tagane](#), Resources, Writing – review & editing,⁸ [Jan J. Wieringa](#), Resources, Writing – review & editing,⁹ [Tetsukazu Yahara](#), Resources, Writing – review & editing,¹⁰ and [Damien D. Hinsinger](#), Conceptualization, Data curation, Formal analysis, Funding acquisition, Investigation, Methodology, Resources, Software, Visualization, Writing – original draft, Writing – review & editing^{2,3,11}

Tony Robillard, Editor

JOURNAL ARTICLE

From museums to genomics: old herbarium specimens shed light on a C₃ to C₄ transition

[Guillaume Besnard](#) ✉, [Pascal-Antoine Christin](#), [Pierre-Jean G. Malé](#), [Emeline Lhuillier](#), [Christine Lauzeral](#), [Eric Coissac](#), [Maria S. Vorontsova](#)

Journal of Experimental Botany, Volume 65, Issue 22, December 2014, Pages 6711–6721,

<https://doi.org/10.1093/jxb/eru395>

Published: 25 September 2014

Trends in
Ecology & Evolution

Review

Mining museums for historical DNA: advances and challenges in museomics

Christopher J. Raxworthy^{1,*} and Brian Tilston Smith¹

 CellPress
OPEN ACCESS



Museum Genomics

Annual Review of Genetics

Vol. 55:633-659 (Volume publication date November 2021)
First published as a Review in Advance on September 23, 2021
<https://doi.org/10.1146/annurev-genet-071719-020506>

[Daren C. Card](#),^{1,2} [Beth Shapiro](#),^{3,4} [Gonzalo Giribet](#),^{1,2} [Craig Moritz](#),⁵ and [Scott V. Edwards](#)^{1,2}

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JOURNAL ARTICLE

Next-Generation Museomics Disentangles One of the Largest Primate Radiations

[Katerina Guschanski](#), [Johannes Krause](#), [Susanna Sawyer](#), [Luis M. Valente](#), [Sebastian Bailey](#), [Knut Finstermeier](#), [Richard Sabin](#), [Emmanuel Gilissen](#), [Gontran Sonet](#), [Zoltán T. Nagy](#) ... Show more

Author Notes

Systematic Biology, Volume 62, Issue 4, July 2013, Pages 539–554,

<https://doi.org/10.1093/sysbio/syt018>

Front Plant Sci. 2020; 11: 819.

Published online 2020 Jun 26. doi: [10.3389/fpls.2020.00819](https://doi.org/10.3389/fpls.2020.00819)

PMCID: PMC7333454

PMID: [32754167](https://pubmed.ncbi.nlm.nih.gov/32754167/)

Museomics Unveil the Phylogeny and Biogeography of the Neglected Juan Fernandez Archipelago *Megalachne* and *Podophorus* Endemic Grasses and Their Connection With Relict Pampean-Ventanian Fescues

[María Fernanda Moreno-Aguilar](#),¹ [Itziar Arnelas](#),² [Aminael Sánchez-Rodríguez](#),² [Juan Viruel](#),³ and [Pilar Catalán](#)^{1,4,5,*}

*

ÖTZI

> Science. 2016 Jan 8;351(6269):162-165. doi: 10.1126/science.aad2545.

The 5300-year-old *Helicobacter pylori* genome of the Iceman

Frank Maixner ^{# 1}, Ben Krause-Kyora ^{# 2}, Dmitrij Turaev ^{# 3}, Alexander Herbig ^{# 4 5}, Michael R Hoopmann ⁶, Janice L Hallows ⁶, Ulrike Kusebauch ⁶, Eduard Egarter Vigl ⁷, Peter Malfertheiner ⁸, Francis Megraud ⁹, Niall O'Sullivan ¹, Giovanna Cipollini ¹, Valentina Coia ¹, Marco Samadelli ¹, Lars Engstrand ¹⁰, Bodo Linz ¹¹, Robert L Moritz ⁶, Rudolf Grimm ¹², Johannes Krause ^{4 5}, Almut Nebel ², Yohan Moodley ^{13 14}, Thomas Rattei ³, Albert Zink ¹

Affiliations + expand

PMID: 26744403 PMCID: PMC4775254 DOI: 10.1126/science.aad2545

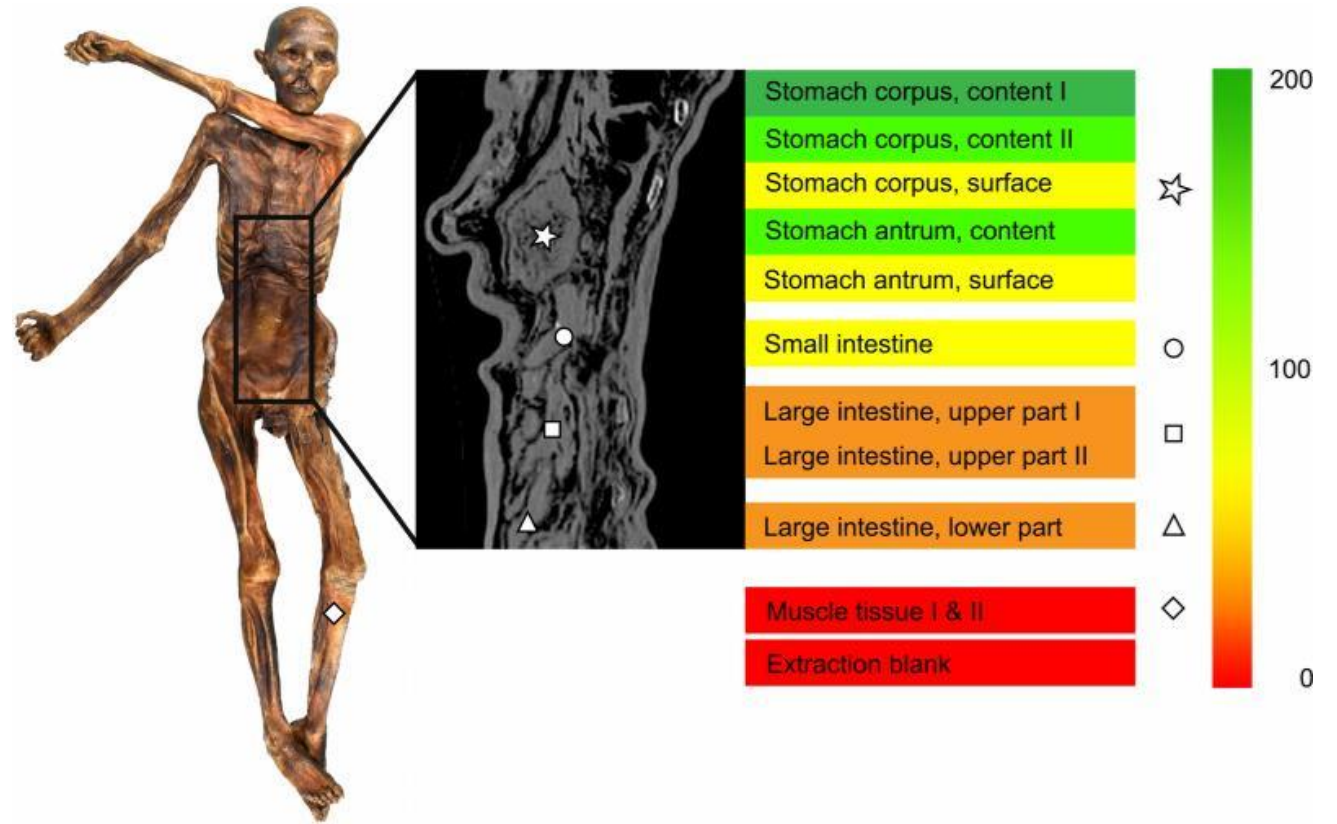


Fig. 1 *H. pylori* specific reads detected in the metagenomic datasets of the Iceman's intestine content samples. The color gradient displays the number of unambiguous *H. pylori* reads per million metagenomic reads. Control metagenomic datasets of the Iceman's muscle tissue and of the extraction blank were included in the analysis. The different intestinal content sampling sites are marked in the radiographic image by the following symbols: * stomach content, ○ small intestine, □ upper large intestine, △ lower large intestine. The sampling site of the muscle control sample is highlighted in the Iceman overview picture (◇).

CALCIFIED ABSCESS

Microbiology and Infectious Disease

A molecular portrait of maternal sepsis from Byzantine Troy

Alison M Devault, Tatum D Mortimer, Andrew Kitchen, Henrike Kiesewetter, Jacob M Enk, G Brian Golding, John Southon, Melanie Kuch, Ana T Duggan ... Caitlin S Pepperell [see all »](#)

McMaster University, Canada; MYcroarray, United States; School of Medicine and Public Health, University of Wisconsin-Madison, United States; University of Wisconsin-Madison, United States; University of Iowa, United States; Tübingen University, Germany; University of California, United States; Biotechnology Center, University of Wisconsin-Madison, United States; Lawrence Livermore National Laboratory, United States [see all »](#)

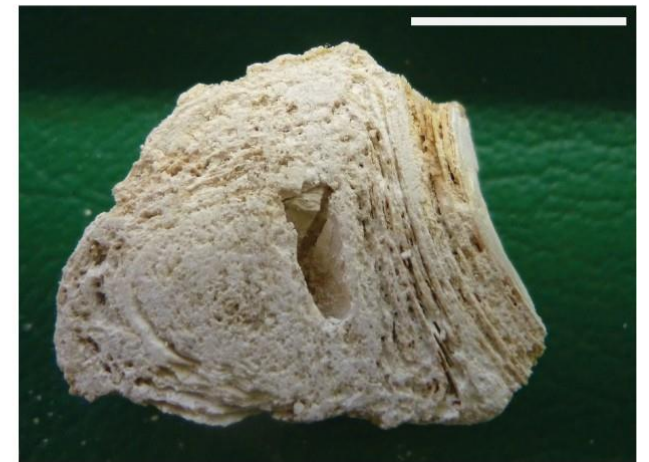
Jan 10, 2017 · <https://doi.org/10.7554/eLife.20983> 

Pregnancy complications are poorly represented in the archeological record, despite their importance in contemporary and ancient societies. While excavating a Byzantine cemetery in Troy, we discovered calcified abscesses among a woman's remains. Scanning electron microscopy of the tissue revealed 'ghost cells', resulting from dystrophic calcification, which preserved ancient maternal, fetal and bacterial DNA of a severe infection, likely chorioamnionitis. *Gardnerella vaginalis* and *Staphylococcus saprophyticus* dominated the abscesses. Phylogenomic analyses of ancient, historical, and contemporary data showed that *G. vaginalis* Troy fell within contemporary genetic diversity, whereas *S. saprophyticus* Troy belongs to a lineage that does not appear to be commonly associated with human disease today. We speculate that the ecology of *S. saprophyticus* infection may have differed in the ancient world as a result of close contacts between humans and domesticated animals. These results highlight the complex and dynamic interactions with our microbial milieu that underlie severe maternal infections.

A



B



C



Palaeogenetic analysis of (pre)historic artifacts and its significance for anthropology*

Joachim Burger¹, Susanne Hummel¹, Ina Pfeiffer² and Bernd Herrmann¹

¹ Historical Anthropology and Human Ecology, Institute of Zoology and Anthropology, University of Göttingen

² Institute of Veterinary Medicine, University of Göttingen

With 2 figures and 2 tables

Table 1. Taxonomic identification of organic traces from archaeological and museum/ collection samples.

Sample number	Sample	Period/Date Taxon	GenBank Taxon	Consensus
1	Aztek vessel 1; Museum für Völkerkunde Berlin	IV Ca 1905c ante 1500 AD	Hypoxis leptocarpa Hypoxis densiflora	Hypoxis
2	Aztek vessel 2; Museum für Völkerkunde Berlin	IV Ca 1855 ante 1500 AD	Martinella obovata Podranca ricasoliana	Bigoniaceae
3	parchment	FU 2 modern times	Oryctolagus cuniculus Sylvilagus nuttallii, Sylvilagus palustris, Sylvilagus audobonii	Oryctolagus cuniculus
4	“sausage-end”	1151-I Latène A (2400 BP)	Salvia hispanica Salvia uliginosa Salvia divinorum Plectranthus barbatus Nepeta faassenii	Salvia

Analysis of Parchment Fragments from the Judean Desert Using DNA Techniques

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GILA KAHILA, PATRICIA SMITH,
CHARLES GREENBLATT
Hebrew University, Jerusalem

JOE ZIAS
Rockefeller Museum, Jerusalem

MAGEN BROSHI
Shrine of the Book, Jerusalem

Analysis of Parchment Fragments from the Judean Desert Using DNA Techniques

In: [Current Research and Technological Developments on the Dead Sea Scrolls](#)

Authors: SCOTT R. WOODWARD, GILA KAHILA, PATRICIA SMITH, CHARLES GREENBLATT, JOE ZIAS, and MAGEN BROSHI

Type: Chapter

Pages: 215–238

DOI: https://doi.org/10.1163/9789004350229_012

ARTEFACTS

Decoding the biological information contained in two ancient Slavonic parchment codices: an added historical value

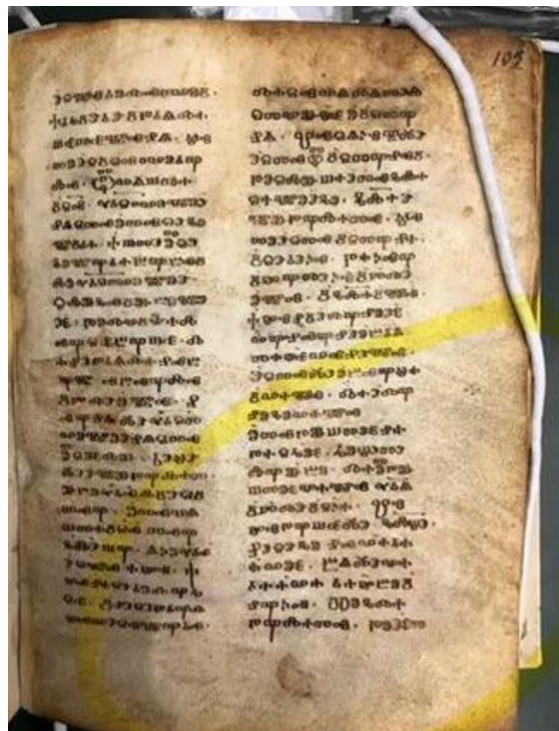
Guadalupe Piñar ✉, Hakim Tafer, Manfred Schreiner, Heinz Miklas, Katja Sterflinger

First published: 12 May 2020 | <https://doi.org/10.1111/1462-2920.15064> | Citations: 14

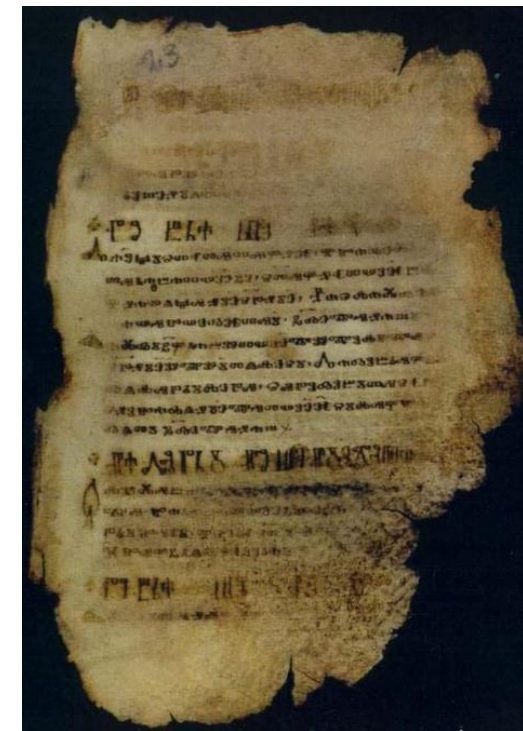
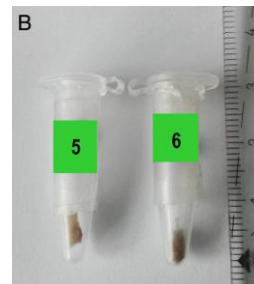
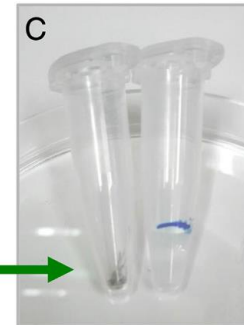
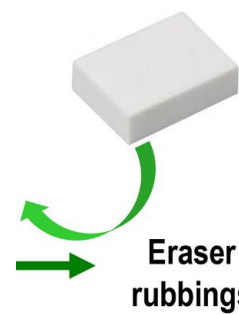
Biocodology is an emerging field that studies the biological information stored in ancient manuscripts and is currently revolutionizing the field of codicology (Fiddymont *et al.*, 2019) by incorporating high-throughput molecular techniques such as proteomics (Fiddymont *et al.*, 2015), genomics and metagenomics (Teasdale *et al.*, 2015, 2017). These technologies make it possible to extract the biological information stored for centuries in ancient manuscripts, especially in parchment objects.

Table 2. Animal species identified in the *Codex Liturgiarium Sinaiticum* and *Codex Assemanianus*, showing the total numbers of reads as well as the relative proportion of the total sequences (%) affiliating with each species.

Species	<i>Codex Liturgiarium Sinaiticum</i>		<i>Codex Assemanianus</i>	
	Reads sample 5	Reads sample 6	Reads sample P	Reads sample R
<i>Homo sapiens</i>	208 416 (0.5%)	64 370 (0.15%)	7 852 951 (17%)	143 268 (0.4%)
<i>Ovis aries</i>	49 223 (0.12%)	483 (0.001%)	55 146 (0.12%)	24 465 (0.06%)
<i>Bos taurus</i>	15 204 (0.035%)	4630 (0.01%)	13 544 (0.03%)	19 958 (0.05%)
<i>Capra hircus</i>	8803 (0.02%)	174 (0.0004%)	11 576 (0.025%)	3972 (0.01%)
<i>Sus scrofa</i>	4615 (0.01%)	945 (0.002%)	19 598 (0.04%)	3698 (0.01%)



Codex Assemanianus





Liturgiarium Sinaiticum (commonly *Missale Sinaiticum*)

ARTEFACTS

Review | [Open access](#) | [Published: 07 June 2019](#)

So you want to do biocodicology? A field guide to the biological analysis of parchment

[Sarah Fiddymment](#) , [Matthew D. Teasdale](#) , [Jiří Vnouček](#), [Élodie Lévêque](#), [Annelise Binois](#) & [Matthew J. Collins](#)

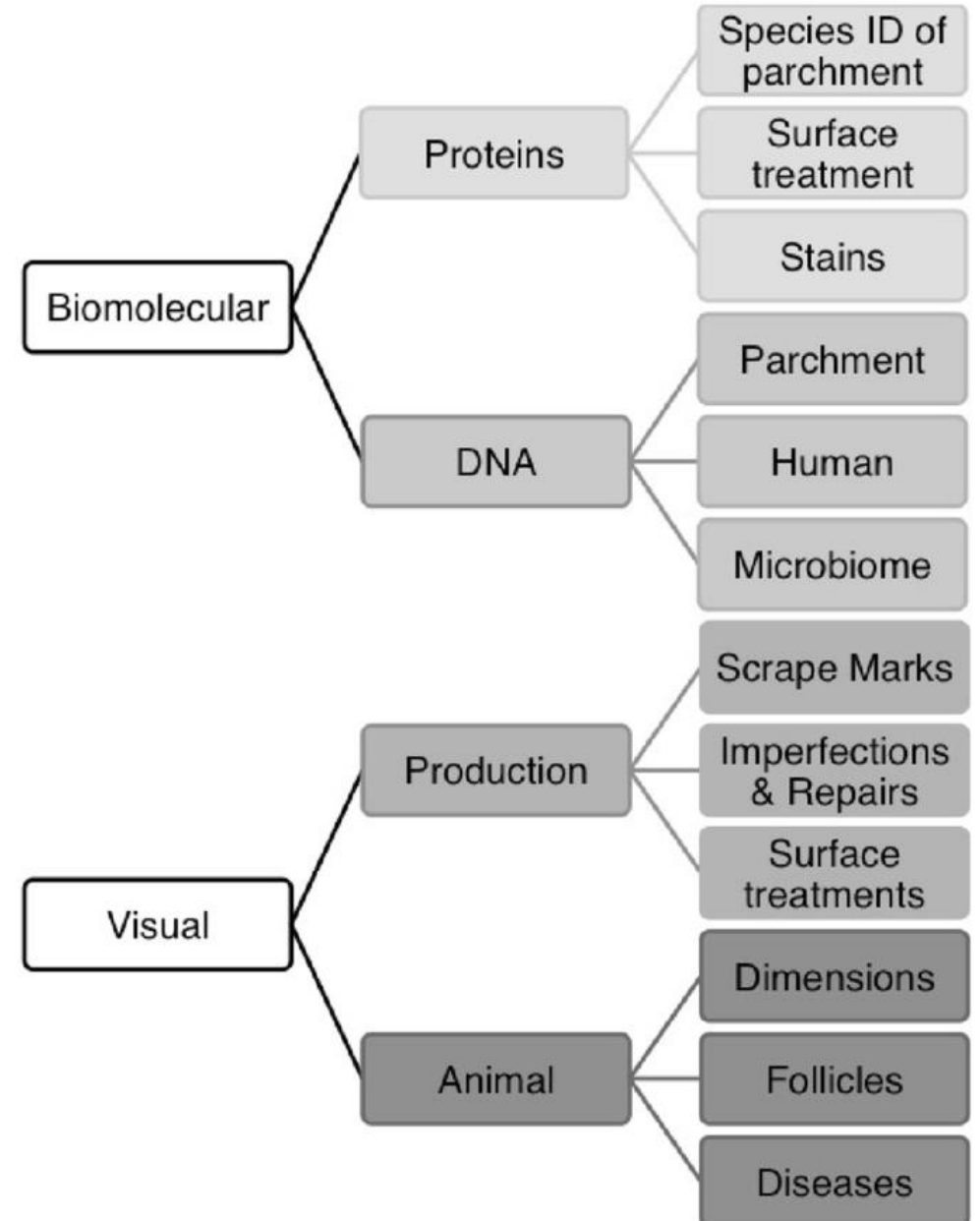
[Heritage Science](#) **7**, Article number: 35 (2019) | [Cite this article](#)

„What species of animal is this particular document made from?”

Are these two fragments related?

What is this stain?



I am concerned about the condition of a document, could there be potentially damaging bacteria or fungi present?”



ARTEFACTS

Review | [Open access](#) | [Published: 07 June 2019](#)

So you want to do biocodicology? A field guide to the biological analysis of parchment

[Sarah Fiddymment](#) , [Matthew D. Teasdale](#) , [Jiří Vnouček](#), [Élodie Lévêque](#), [Annelise Binois](#) & [Matthew J. Collins](#)

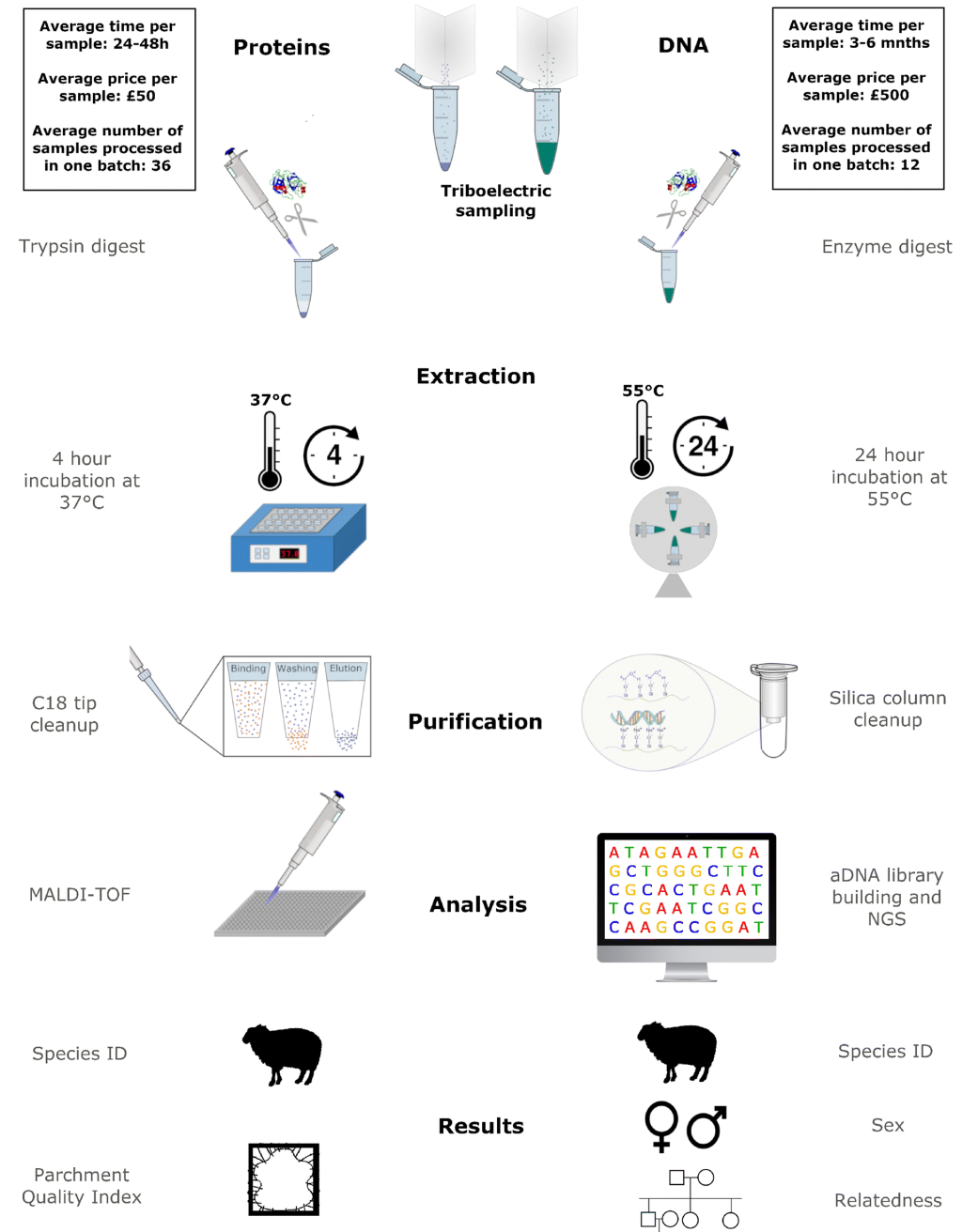
[Heritage Science](#) **7**, Article number: 35 (2019) | [Cite this article](#)

„What species of animal is this particular document made from?”

Are these two fragments related?

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I am concerned about the condition of a document, could there be potentially damaging bacteria or fungi present?”



ARTEFACTS – BIRCH PITCH

Article | [Open access](#) | [Published: 15 May 2019](#)

Ancient DNA from mastics solidifies connection between material culture and genetics of mesolithic hunter-gatherers in Scandinavia

[Natalija Kashuba](#) , [Emrah Kirdök](#), [Hege Damlien](#), [Mikael A. Manninen](#), [Bengt Nordqvist](#), [Per Persson](#) & [Anders Götherström](#)

[Communications Biology](#) **2**, Article number: 185 (2019) | [Cite this article](#)


Birch pitch – heating birch bark, mostly for adhesion

Betulin – antiseptic, medicinal use

The studied material and its origin. **a** One of the chewing gums from Huseby Klev, (Fynd 2037), with two plastelina casts for each side. The cast to the left captures several teeth imprints from the left side of the maxilla, the one to the right is of the corresponding teeth from the mandible. The presence of the second molar and analysis of tooth wear suggest that the individual, who left these imprints was in the early teens (12–14 years old)¹¹. Scale bar: 50 mm (photo by Verner Alexandersen). **b** The location of the sites, genomes from which were used in this study. 1—LaBrana; 2—Loschbour; 3—Bichon; 4—Hummervikholmen; 5—Huseby Klev; 6—Steigen; 7—Motala; 8—Stora Bjers; 9—Stora Förvar; 10—Yuzhny Oleni Ostrov; 11—Samara



On the performance of birch tar made with different techniques

[Patrick Schmidt](#) , [Matthias A. Blessing](#), [Tabea J. Koch](#) & [Klaus G. Nickel](#)

Heritage Science **9**, Article number: 140 (2021) | [Cite this article](#)

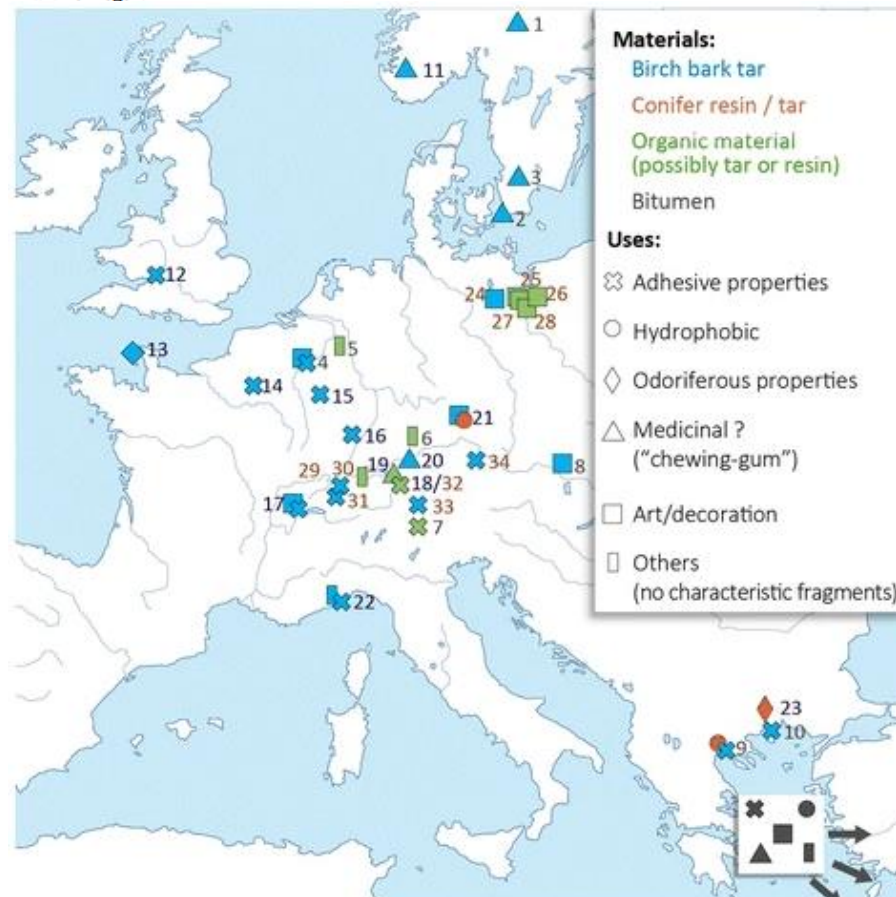
Fig. 1



Experimental set up for the aceramic birch tar making experiments. **a** Condensation method using several stones simultaneously and the resulting tar (**b**); **c** two raised structures during construction. Birch bark rolls are placed on grates bade from fine sticks. The lower chamber is covered by aluminium foil to minimize loss of the tar; **d** finished raised structure with the sediment covering the bark rolls; **e** tar produced in one of the raised structures, still adhering to the aluminium foil receptacle

Birch Bark Tar Production: Experimental and Biomolecular Approaches to the Study of a Common and Widely Used Prehistoric Adhesive

Maxime Rageot^{1,2,3} · Isabelle Théry-Parisot¹ · Sylvie Beyries¹ · Cédric Lepère^{1,4} · Alain Carré¹ · Arnaud Mazuy¹ · Jean-Jacques Filippi² · Xavier Fernandez² · Didier Binder¹ · Martine Regert¹



Plant tars and resins exploitation in Europe during recent Prehistory (6000–2500 BC). Information is based solely on published works which involved chemical investigation. 6th millennium BC: 1: Ringsjöholm; 2: Segebro; 3: Bokeberg; 4: Podri l'Cortri; 5: Erklelenz-Kückhoven; 6: Henuhof Nord II; 7: Gaban rockshelter; 8: Brunn am Gebirge; 9: Makriyalos; 10: Paliambela. Second part of 5th millennium and first part of 4th millennium BC: 11: Ovre Storvatnet; 12: Sweet Track; 13: La Hougue Bie; 14: Beaurieux; 15: Waldbillig Karelslé; 16: Rosheim; 17: Clairvaux VII and XIV; 18: Zürich Seefeld; 19: Burgäschi-Ost, Seeberg; 20: Hornstaad Hornle I; 21: Ergolding Fischergasse; 22: Nice-Giribaldi; 23: Dikili Tash. Transition 4th and 3rd millennium BC: 24: zulawka mala; 25: Bakowo Site 3; 26: Jeznicka Struga; 27: Opatowice Site 42; 28: Papros Site 6B; 29: Chalain 2, 3 and 4; 30: Portalban; 31: Montilier; 32: Zürich Seefeld; 33: Örtzi; 34: Mondsee.

BIRCH PITCH

Article | [Open access](#) | [Published: 17 December 2019](#)

A 5700 year-old human genome and oral microbiome from chewed birch pitch

[Theis Z. T. Jensen](#), [Jonas Niemann](#), [Katrine Højholt Iversen](#), [Anna K. Fotakis](#), [Shyam Gopalakrishnan](#), [Åshild J. Vågane](#), [Mikkel Winther Pedersen](#), [Mikkel-Holger S. Sinding](#), [Martin R. Ellegaard](#), [Morten E. Allentoft](#), [Liam T. Lanigan](#), [Alberto J. Taurozzi](#), [Sofie Holtsmark Nielsen](#), [Michael W. Dee](#), [Martin N. Mortensen](#), [Mads C. Christensen](#), [Søren A. Sørensen](#), [Matthew J. Collins](#), [M. Thomas P. Gilbert](#), [Martin Sikora](#), [Simon Rasmussen](#) & [Hannes Schroeder](#) 

[Nature Communications](#) **10**, Article number: 5520 (2019) | [Cite this article](#)

„The DNA is so exceptionally well preserved that we were able to recover a complete ancient human genome from the sample (sequenced to an average depth of coverage of 2.3×), which is particularly significant since, so far, no human remains have been recovered from the site. The results highlight the potential of chewed birch pitch as a source of ancient human and non-human DNA, which can be used to shed light on the population history, health status, and even subsistence strategies of ancient populations.“



BIRCH PITCH

„DNA preservation and genome reconstruction“

„Sex determination and phenotypic traits“

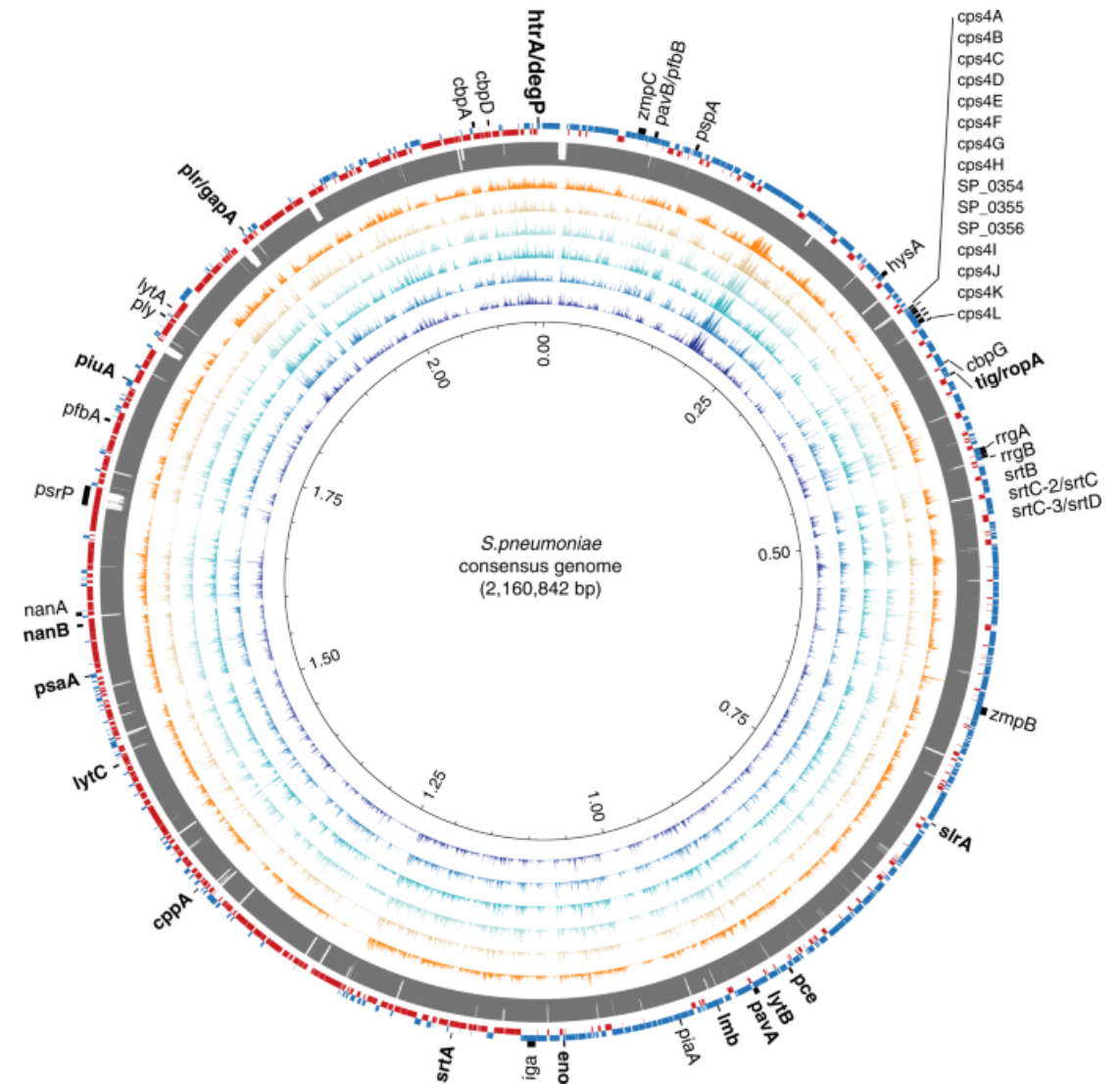
„Genetic affinities“

„Metataxonomic profiling of non-human reads“

„Oral microbiome characterisation“ (including EBV)


„Pneumococcal DNA“

„Plant and animal DNA“ (birch, hazelnut, mallard)“



Article | [Open access](#) | [Published: 18 January 2024](#)

Metagenomic analysis of Mesolithic chewed pitch reveals poor oral health among stone age individuals

[Emrah Kırdök](#) , [Natalija Kashuba](#), [Hege Damlien](#), [Mikael A. Manninen](#), [Bengt Nordqvist](#), [Anna Kjellström](#), [Mattias Jakobsson](#), [A. Michael Lindberg](#), [Jan Storå](#), [Per Persson](#), [Björn Andersson](#), [Andrés Aravena](#) & [Anders Götherström](#)

[Scientific Reports](#) **14**, Article number: 22125 (2024) | [Cite this article](#)

Abstract

Prehistoric chewed pitch has proven to be a useful source of ancient DNA, both from humans and their microbiomes. Here we present the metagenomic analysis of three pieces of chewed pitch from Huseby Klev, Sweden, that were dated to 9,890–9,540 before present. The metagenomic profile exposes a Mesolithic oral microbiome that includes opportunistic oral pathogens. We compared the data with healthy and dysbiotic microbiome datasets and we identified increased abundance of periodontitis-associated microbes. In addition, trained machine learning models predicted dysbiosis with 70–80% probability. Moreover, we identified DNA sequences from eukaryotic species such as red fox, hazelnut, red deer and apple. Our results indicate a case of poor oral health during the Scandinavian Mesolithic, and show that pitch pieces have the potential to provide information on material use, diet and oral health.

WAX SEALS

Research | [Open access](#) | [Published: 17 January 2023](#)

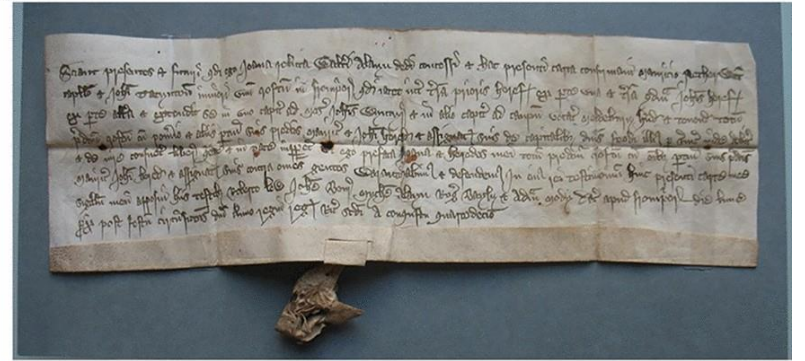
ArcHives—combined palynological, genomic and lipid analysis of medieval wax seals

[Tuuli M. Kasso](#) , [Renée Enevold](#), [Samuel Johns](#), [Guillermo Rangel-Piñeros](#), [Alberto J. Taurozzi](#), [Alister Sutherland](#), [Max Ramsøe](#), [Lora V. Angelova](#), [Mélanie Roffet-Salque](#), [Matthew J. Collins](#) & [Christian Cargø](#)

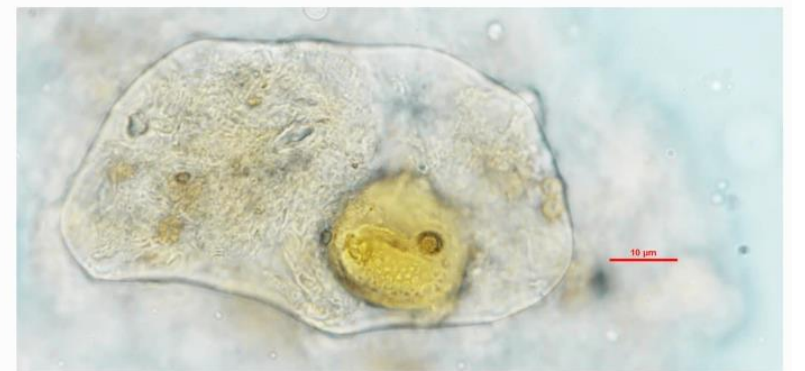
[Heritage Science](#) **11**, Article number: 11 (2023) | [Cite this article](#)

- Pollen
 - Lipids
 - Metagenomics
- „DNA analysis on medieval wax specimens seems to be very limited, not only due to the poor preservation of DNA, but also the composition of taxa and limited usefulness of this. We therefore suggest further work with this type of material, as there is still more potential for unlocking the unseen archives of medieval wax seals.“


a



b



Pollen from the family *Fabaceae* cf. *Trifolium* found in a wax-resin lump in sample DA122

- 
- Biocodicology
 - Fermentation
 - Yeast
 - Calcified abcess
 - Necrobiome
 - Competitive mapping

THINK - FEEL - CARE

Think: How does this person understand this system and their role within it?

Feel: What is this person's emotional response to the system and to their position within it?

Care: What are this person's values, priorities, or motivations with regard to the system? What is important to this person?

What can we learn about them, how and why? How would it motivate you to carry out such research?

