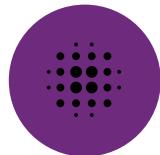


STANDARDS, PRECAUTIONS, AND ADVANCES IN ANCIENT METAGENOMICS



OCTOBER 12TH TO 14TH, 2022
Virtual Conference

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TIME ZONES



CALIFORNIA

7am to 11am



NEW YORK

10am to 2pm



LONDON

3pm to 7pm



GERMANY

4pm to 8pm



INDIA

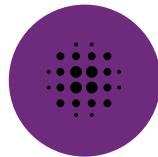
7:30pm to 11:30pm



ADELAIDE

11:30pm to 3:30am

SCHEDULE



DAY 1

Wednesday, 7am to 11am PST



WELCOME & INTRO TO SPAAM4

7 to 7:15am

KEYNOTE SPEAKER: MARIA SPYROU

7:15 to 8:15am



BREAK

8:15 to 8:40am

SESSION 1: ENVIRONMENTAL & SEDIMENT ADNA

8:40 to 9:40am

Vilma Perez: Using sedaDNA to reveal the microbial responses to Australian environmental change over the Holocene

Jordan Von Eggers: Deterministic processes drive sediment prokaryotic community assembly of disconnected mountain lakes

Carly B. Scott: Millennia-old coral holobiont DNA provides insight into future adaptive trajectories

BREAK

9:40 to 9:55am



SESSION 2: PATHOGENS

9:55 to 10:40am

Zoe Pochon: Infectious diseases in the Viking Age town of Sigtuna

Alina Hiss: Hepatitis B virus in early medieval Europe

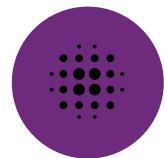
SPAMMILY GROUPS/BREAK

10:40 to 11am

AFTER-HOURS RECEPTION

11 to 12pm

SCHEDULE



DAY 2

Thursday, 7am to 11am PST



SESSION 3: BIOINFORMATIC TOOLS

7 to 8am

James Fellows-Yates: cuperdec: assessing endogenous community preservation in (ancient) microbiome samples through cumulative percent decay

Niolay Oskolkov: aMeta: an accurate and memory-efficient ancient Metagenomic profiling workflow

Reed Harder: Mapping and Visualizing Ancient Metagenomic Data in an Archaeological and Environmental Context

BREAK

8 to 8:15am

SESSION 4: WETLAB METHODS

8:15 to 9am

Josh Kapp: The Santa Cruz Reaction Method

Nasreen Broomand: Santa Cruz Reaction UDG Modifications

BREAK

9 to 9:30am

SESSION 5: LIGHTNING ROUND

9:30 to 10:15am

Tom Prys-Jones: Metagenomic analysis of coprolites from three Late Pleistocene megaherbivores from the Southwestern United States.

Davide Bozzi: Can metagenomics trace the geographical origin of ancient individuals?

Prashasti Singh: The reconstruction of diatom communities around Antarctica using marine sedimentary ancient DNA

Kadir Özdoğan: Exploring the lifestyle of people from Roman Limes through ancient environmental DNA

Sichao Huang: Arctic terrestrial ecosystem change over the last 54,000 years revealed by sedimentary ancient DNA on a lake sediment core from Far Eastern Russia

SESSION 6: MICROBIOMES

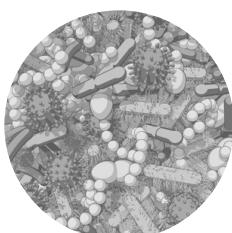
10:15 to 11am

Markella Moraïtou: Ecology, not host phylogeny, shapes the oral microbiome of closely related species

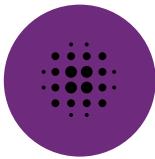
Maria Zicos: Diet and paleo-environment of Mylodon-darwini at Mylodon Cave (Ultima Esperanza, Chile)

SPAAMILY GROUPS DISCUSSION

11 to 11:15am



SCHEDULE



DAY 3

Friday, 7am to 11am PST

SPAAMILY GROUPS ACTIVITY

7 to 7:20am



KEYNOTE SPEAKER: MARIA AVILA-ARCOS

7:20 to 8:20am

BREAK

8:20 to 8:30am

SESSION 7: CAREER PANEL

8:30 to 9:30am

Kelly Harkins (CEO of Astrea)

Eadaoin Harney (23 & Me Researcher)

Andrew Farrer (Head of Programmes and Delivery at Cambridge Science Centre)

Jennifer Klunk (Lead Product Scientist, Daicel Arbor Biosciences)

Luíseach Nic Eoin (Senior Editor at Nature, Ecology & Evolution)



BREAK

9:30 to 10am



SESSION 8: FUTURE OF SPAAM

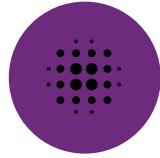
10 to 10:30am

Discussion of SPAAM goals and activities and selection of organizing committee of SPAAM5

CLOSING REMARKS & AWARDS

10:30 to 11am

CODE OF CONDUCT



TL;DR

- All attendees and members of SPAAM are expected to be respectful towards all members regardless of background, and actively participate in creating a welcoming and friendly community.
- Unacceptable or illegal behaviour will not be tolerated and the organizers reserve the right to remove anyone violating the Code of Conduct from both in-person or online channels.
- If at any point you feel unsafe or the code of conduct is violated, please contact any of the following SPAAM members who will deal with any issues respectfully and anonymously, as required.

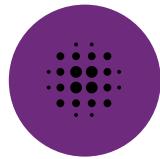
1. PURPOSE

- A primary goal of SPAAM4 is to be inclusive to the largest number of contributors, with the most varied and diverse backgrounds possible. As such, we are committed to providing a friendly, safe and welcoming environment for all, regardless of gender, sexual orientation, ability, ethnicity, socio-economic status, and religion (or lack thereof).
- This code of conduct outlines our expectations for all those who participate in our community, as well as the consequences for unacceptable behaviour.
- All attendees at our conference are required to agree to and comply with the following code of conduct. Organisers will enforce this code throughout the event. We expect cooperation from all participants to help ensure a safe and positive environment for everybody.

2. CITIZENSHIP

- A supplemental goal of this Code of Conduct is to increase 'citizenship' by encouraging participants to recognize and strengthen the relationships between our actions and their effects on our community.
- Communities mirror the societies in which they exist and positive action is essential to counteract the many forms of inequality and abuses of power that exist in society.
- If you see someone who is making an extra effort to ensure our community is welcoming, friendly, and encourages all participants to contribute to the fullest extent, we want to know (either in person, Slack, or email – see section 8).

CODE OF CONDUCT



3. EXPECTED BEHAVIOUR

The following behaviors are expected and requested of all community members:

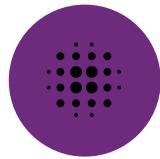
- Participate in an authentic and active way. In doing so, you contribute to the health and longevity of this community.
- Exercise consideration and respect in your speech and actions.
- Attempt to respectfully resolve issues before conflicts arise.
- Refrain from demeaning, discriminatory, or harassing behaviour and speech.
- Be mindful of your surroundings and of your fellow participants. Alert organisers if you notice a dangerous situation, someone in distress, or violations of this Code of Conduct, even if they seem inconsequential.
- Remember that events may be shared with members of the public; please be respectful to all patrons of these locations.

4. UNACCEPTABLE BEHAVIOUR

The following behaviors are considered harassment and are unacceptable within our community, both in person and online:

- Violence, threats of violence or violent language directed against another person.
- Sexist, racist, homophobic, transphobic, ableist or otherwise discriminatory jokes and language.
- Posting or displaying sexually explicit or violent material.
- Posting or threatening to post other people's personally identifying information ("doxxing").
- Personal insults, particularly those related to gender, sexual orientation, race, religion, or disability.
- Inappropriate photography or recording.
- Inappropriate physical contact. You should have someone's consent before touching them.
- Unwelcome sexual attention. This includes, sexualized comments or jokes; inappropriate touching, groping, and unwelcomed sexual advances.
- Deliberate intimidation, stalking or following (online or in person).
- Advocating for, or encouraging, any of the above behaviour.
- Sustained disruption of community events, including talks and presentations.
- Furthermore, we will follow all legal guidance from the European Commission on non-discrimination

CODE OF CONDUCT



5. CONSEQUENCES OF UNACCEPTABLE BEHAVIOR

Unacceptable behaviour from any attendee, including those with decision-making authority, will not be tolerated.

Anyone asked to stop unacceptable behaviour is expected to comply immediately.

If an attendee engages in unacceptable behaviour, the community organizers may take any action they deem appropriate, up to and including a temporary ban or permanent expulsion from the event without warning (and without refund in the case of any payments).

6. REPORTING GUIDELINES

If you are subject to or witness unacceptable behaviour, or have any other concerns, please notify any of the event organisers (see section 8) as soon as possible. Organisers will ensure that the report can be given in a safe space, and will be recorded as respectfully as possible.

Additionally, organizers are available to help attendees engage with local law enforcement or to otherwise help those experiencing unacceptable behaviour feel safe. In the context of in-person events, organizers will also provide escorts as desired by the person experiencing distress.

7. SCOPE

We expect all participants (contributors, paid or otherwise, and other guests) to abide by this Code of Conduct in all community venues—online and in-person—as well as in all one-on-one communications pertaining to community business.

This code of conduct and its related procedures also applies to unacceptable behaviour occurring outside the scope of community activities when such behaviour has the potential to adversely affect the safety and well-being of community members.

8. CONTACT INFO

- James Fellows Yates (EN, LMU, München, james_fellows_yates@eva.mpg.de)
- Aida Andrades Valtueña (CAT/ES/EN, MPI-EVA, Leipzig, aida_andrades@eva.mpg.de)
- Shreya Ramachandran (EN/ES, University of Chicago, shreya23@uchicago.edu)
- Elizabeth ‘Betsy’ Nelson (EN/ES, University of Connecticut, enelson@uconn.edu)

CODE OF CONDUCT

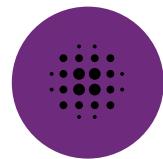


9. VIRTUAL CONFERENCE ADDENDUM

For SPAAM4, the following guidelines have been added to the code of conduct:

- Do not share the zoom link with anyone. If a lab mate or colleague requests it, please direct them to the conference organizers (pg. #)
- **Enter the zoom room with your own name.** Participants will be admitted based on conference registrations, so names such as 'iphone 6' will not be admitted.
- A zoom moderator will be online at all times and reserves the right to mute anyone whose audio is on inappropriately. The moderators also reserve the right to evict participants from the zoom room for code of conduct violations.
- If you would like to communicate or ask a question, please either raise your hand (zoom feature) or leave a comment in the chat, unless instructed otherwise by session moderators.
- Please pay attention to whether or not presenters want their work shared online. If the 'do not tweet' image is shown at the beginning of the presentation, please refrain from mentioning or citing the work online.

PRESENTATION ABSTRACTS



KEYNOTE PRESENTATIONS

Maria Spyrou



Maria Avila-Arcos

Most of the Global South territories were subjects of European colonialism from the 15th century onward. Along with peoples, pathogens arrived to the occupied lands, causing some of the most devastating epidemics worldwide and disproportionately affecting Native peoples. Understanding the molecular properties of these epidemic-causing ancient pathogens is of utmost interest for a number of disciplines, and ancient DNA research is particularly well positioned to answer many central questions in ancient pathogen research. Because the discipline is relatively new and not yet established in many global south countries, discoveries in this direction depend largely on Global North groups carrying out the research. In order to advance knowledge in this direction, the discipline needs to take careful consideration of the local context and do research in the most ethical way to avoid perpetuating colonialism.

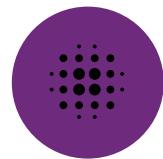
SESSION 1: ENVIRONMENTAL SEDIMENTS

Vilma Perez

Using sedaDNA to reveal the microbial responses to Australian environmental change over the Holocene

Over the last two centuries, Australia's diverse ecosystems have suffered substantial modifications mostly associated with anthropogenic impacts and climate change. However, the biological impacts of this historic shift remain unclear. Sedimentary ancient DNA analysis offers a novel and powerful tool for collecting long-term (millennia) monitoring data and investigating the distribution of species assemblages through time, to better predict how biological systems will respond in the future. Here we reconstructed past microbial communities – key indicators of environmental response – using shotgun data of sedaDNA preserved in Australian lacustrine sediments. These sedimentary genetic records were correlated with existing geochronological, geochemical, and charcoal records to examine past changes in microbial assemblages in response to Holocene environmental change. We detected vertical changes in microbial communities significantly correlated with depth, charcoal records and salinity, suggesting ecological shifts over time associated to a major shift in fire regime and aridity. Specifically, we observed an increase of halotolerant and halophilic families (e.g., Halobacteroidaceae and Halobacteriaceae) reflecting a period of high salinity after a drought episode. While these species presented authentic ancient DNA signals, the shifts in the community composition also indicated changes in the past community structure in response to the drastic changes in lake conditions associated with a reworking of physicochemical conditions at certain depths. Overall, these observations indicate that changes in sedimentary microbial communities change can provide insights to both past environmental conditions and geochemical changes of the sediment during burial.

PRESENTATION ABSTRACTS



Jordan Von Eggers

Deterministic processes drive sediment prokaryotic community assembly of disconnected mountain lakes

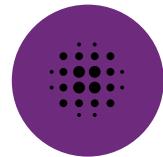
Complex microbial communities are assembled through dynamic deterministic and stochastic processes, yet how the relative importance of each process varies with local and regional factors remains unclear. Lake sediments are a model system to study ecological assembly because they possess varying dispersal potentials in disconnected mountain ranges, distinct physicochemical characteristics, and microbes in sediments experience a drastic shift in ecological setting during the burial process. Here, we produced 16S rRNA metabarcoding data to study the diversity and composition of archaeal and bacterial communities of 46 sediment cores from 35 lakes in four mountain ranges of Wyoming, USA. Community composition varied consistently with sediment depth, and between shallow, warm and deeper, cooler lakes. Dominant phyla and families at similar depths were highly similar across lakes, regardless of geographic distance. Community similarity distance- and environmental-decay relationships and quantitative ecological process estimates using a null model approach supported our findings. Overall, deterministic processes (homogenous and variable selection) accounted for 89.5% of pairwise comparisons, whereas stochastic processes (homogenizing dispersal, dispersal limitation, drift) were responsible for 10.5%. Homogenous selection dominated in intra-lake, intra-horizon comparisons, however, variable selection increased across horizon comparisons and across a lake environmental gradient, highlighting phylogenetically divergent microbes between sediment layers and different lakes. Despite dispersal barriers, distinct sedimentary environments select for taxa that can survive in extreme conditions. Understanding the spatial variation of microbial diversity and assembly of lake sediments is essential to using sedimentary microbes to understand past and current dynamics of lake ecosystems.

Carly B. Scott

Millenia-old coral holobiont DNA provides insight into future adaptive trajectories

Ancient DNA (aDNA) has been applied to evolutionary questions across a wide variety of taxa. Here, for the first time, we utilized aDNA from millennia-old fossil coral fragments to gain new insights into a rapidly declining western Atlantic reef ecosystem. We sampled twelve *Acropora* spp. fragments (dated 4215 BCE to 1776 CE) obtained from seven Caribbean and Western Atlantic reef cores. From these samples, we established that it is possible both to sequence aDNA from reef cores and place the data in the context of modern-day genetic variation. We recovered varying amounts of nuclear DNA exhibiting the characteristic signatures of aDNA from the Acroporid fragments. To describe the holobiont sensu lato, which plays a crucial role in reef health, we utilized metagenome-assembled genomes as a reference to identify a large additional proportion of ancient microbial DNA from the samples. The samples shared many common microbes with modern-day coral holobionts from the same region, suggesting remarkable holobiont stability over time. Despite efforts, we were unable to recover ancient Symbiodiniaceae reads from the samples. Comparing the ancient *Acropora* spp. data to whole-genome sequencing data from living acroporids, we found that while slightly distinct, ancient samples were most closely related to individuals of their own species. Together, these results provide a proof-of-principle showing that it is possible to carry out direct analysis of coral holobiont change over time, which lays a foundation for studying the impacts of environmental stress and evolutionary constraints.

PRESENTATION ABSTRACTS



SESSION 2: PATHOGENS

Zoé Pochon

Infectious diseases in a medieval urban environment: Sigtuna as a case study

Infectious diseases are not easy to detect in paleopathology. Long-lasting diseases such as tuberculosis, leprosy, syphilis and brucellosis can leave visible traces on the bones, but this is not the case for most infectious diseases. With the development of next-generation sequencing techniques, it is now possible to recover the genomes of ancient humans but also of the pathogens they were hosting at the time of death such as Yersinia pestis, the agent of plague.

Here we focus on the impact of urbanization on infectious disease with the Viking Age town of Sigtuna as a case study. Over 40 individuals were subjected to shotgun sequencing and screening for potential pathogens using a new ancient metagenomics workflow developed in collaboration with the National Bioinformatics Infrastructure Sweden (NBIS), called aMeta and available on GitHub. Preliminary results are promising, with the detection of the foodborne pathogen *Yersinia enterocolitica* and the sexually transmitted infections *Neisseria gonorrhoeae* and Hepatitis B virus. This is an ongoing project and we would appreciate feedback on preliminary results and suggestions for downstream analysis and verification steps.

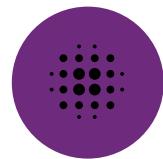
Authors : Zoé Pochon, Emrah Kirdök, Nikolay Oskolkov, Maja Krzewińska, Anders Götherström

Alina Hiss

Hepatitis B virus in early medieval Europe

When screening data from projects predominantly focusing on human genetic analyses, the success rate regarding pathogens can be rather low, especially when the majority of the samples are petrous bones. However, we have been finding a number of individuals infected with the hepatitis B virus in these datasets. This virus is the causative agent of chronic hepatitis, cirrhosis and hepatocellular carcinoma in humans, which can be transmitted vertically from mother to child and horizontally as a sexually transmitted disease. Here, I will focus on samples from the early medieval time from the Carpathian basin and surrounding areas where genetic data for entire sites is available. Combining the analyses of this pathogen with knowledge about relatedness and kinship within social groups, makes it possible to interpret infections in more detail. We can gain insights about the impact this disease might have had on individuals in the past and, in some cases, make assumptions regarding the transmission of the virus. Here, I will present first genetic results about the hepatitis B virus from the Carpathian Basin in early medieval Europe and discuss implications for the transmission and spread of the virus in this confined space and time.

PRESENTATION ABSTRACTS



SESSION 3: BIOINFORMATIC TOOLS

James Fellows Yates

cuperdec: assessing microbial preservation in ancient samples via cumulative percent decay curves

A first step in any palaeogenomic study is assessing the level of DNA preservation in a sample. Ancient microbiome researchers need to be able to remove samples that no longer retain sufficient signal of the original microbial community of an ancient individual. Without such a step, it makes it difficult for researchers to distinguish between true biological differences from noise or contamination. However, to date, there are few formalised tools or approaches to address this step in ancient microbiome studies.

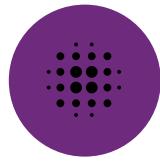
In this talk, I will introduce the R package 'cuperdec'. This package facilitates the creation and analysis of a new visualisation concept termed 'cumulative percent decay' curves. This visualisation allows researchers to distinguish between samples containing the 'expected' types of microbes of a given microbiome type, from those samples that mostly contain DNA from other sources. Additionally, the R package includes automated filtering methods that allow for reproducible decisions of 'keep' and 'discard' for each sample for downstream analysis. The package and a tutorial is available on the defacto 'standard' R package repository CRAN at <https://cran.r-project.org/package=cuperdec/>.

Nikolay Oskolkov

AncientMetagenome: an accurate ancient metagenomics analysis workflow with low false-positive detection rate

Analysis of microbial data from archaeological samples is a rapidly growing field with a great potential for understanding ancient environments, lifestyles and disease spread in the past. However, high error rates have been a long-standing challenge in ancient metagenomics analysis. This is also complicated by a limited choice of ancient microbiome specific computational frameworks that meet the growing computational demands of the field. Here, we propose aMeta, an accurate ancient Metagenomic profiling workflow designed primarily to minimize the amount of false discoveries and computer memory requirements. Using simulated ancient metagenomic samples, we benchmark aMeta against a current state-of-the-art workflow, and demonstrate its superior sensitivity and specificity in both microbial detection and authentication, as well as substantially lower usage of computer memory. aMeta is implemented into a Snakemake workflow to facilitate use and reproducibility.

PRESENTATION ABSTRACTS

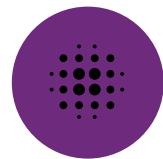


Reed Harder

Mapping and Visualizing Ancient Metagenomic Data in an Archaeological and Environmental Context

In recent years, there has been a significant increase in the publication of geotagged ancient DNA, including human, animal, and microbial data. This growth has paralleled the development of increasingly accessible repositories of geotagged archaeological, paleo-climatic and historical (textual) data. Historical, archaeological and archaeogenetic data shed light on past events and processes, including pandemics, climate/environmental shifts, demographic changes and population movements, all from different angles. Recent successes in integrating these domains have demonstrated the potential of interdisciplinary perspectives. However, existing publicly available datasets are presented in varied formats, and existing mapping tools often rely on propriety or closed-source software or are narrow in scope. This presentation will discuss ongoing efforts to develop an open-source library of software tools for interfacing with a range of archaeological and archaeogenetic datasets and for the interactive mapping of this data, drawing from similar integrative efforts in the geosciences. These software tools aim to offer an interface for interactively visualizing and analyzing archaeological data alongside microbial, environmental and animal genetic data as part of interactive maps and time-series. Planned future work includes the integration of further data sets and addition of extended tools for demographic analysis.

PRESENTATION ABSTRACTS



SESSION 4: WETLAB METHODS

Josh Kapp

The Santa Cruz Reaction Method

This talk will be an overview of the Santa Cruz Reaction library preparation method.

Nasreen Broomand

Santa Cruz Reaction UDG Modifications

This talk will be a brief overview of the updated UDG treatment protocol modified to appropriately accompany the Santa Cruz Reaction single-stranded library protocol

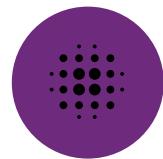
SESSION 5: LIGHTNING ROUND

Tom Prys-Jones

Metagenomic analysis of coprolites from three Late Pleistocene megaherbivores from the Southwestern United States.

Analyses of degraded endogenous bacterial DNA present in coprolites has the potential to shed light on life-history traits from extinct species such as diet or gut physiology, which would improve modeling studies of past ecosystems. However, an issue when evaluating the microbial composition of coprolites is the degree to which the microbiome is representative of the host's original gut community versus the changes that occur in the weeks following deposition due to desiccation. Shotgun sequencing was performed on ancient DNA (aDNA) extracted from coprolites of the Columbian mammoth (*Mammuthus Columbi*), Shasta ground sloth (*Nothrotheriops shastensis*) and paleontological bison (*Bison* sp.) collected from caves on the Colorado Plateau, Southwestern USA, which were compared to modern fecal specimens of the African savannah elephant (*Loxodonta africana*), the brown-throated sloth (*Bradypus variegatus*) and the modern bison (*Bison bison*). Both paleontological and modern bison fecal bacterial communities were also compared to those of progressively dried cattle feces to determine whether endogenous DNA from coprolites had a microbiome signal skewed towards aerobic microorganisms typical of desiccated fecal matter. There was a significant separation of samples in NMDS plots based on their classification as either paleontological or modern, and to a lesser extent, based on the host species. In addition, increasingly dried cattle feces formed a continuum between the modern and paleontological bison samples, highlighting that whenever coprolite metagenomes are compared to modern specimens, that the latter be desiccated and come from a closely related host fed a comparable diet to the paleontological species.

PRESENTATION ABSTRACTS



Davide Bozzi

Can metagenomics trace the geographical origin of ancient individuals?

Ancient DNA (aDNA) studies often rely on (human) remains from museum collections. In many cases, these collections were assembled centuries ago and their archives often lack key metadata making it difficult to trace the geographical origin of the individual samples. In recent years, genome sequencing of deceased individuals has helped to clarify their provenance; however, in some cases, their geographical origin remains mysterious. Here we investigate the possibility of tracing the origin of ancient humans using the sequenced metagenome constituted mostly by human-associated microorganisms or environmental DNA that has leaked into the sample after the death of the individual. To do so we developed a comparative framework in which the metagenome of an individual of interest is compared to different reference panels of ancient samples with known geographical location. Our framework consists of different analyses involving comparisons of (i) k-mers spectra, (ii) microbial taxa composition and (iii) phylogenomic analysis of selected species whose genome could be reconstructed at reasonably high coverage.

We apply our method to ancient individuals with Polynesian ancestry supposedly found in Brazil to evaluate their most-likely origin based on metagenomics data.

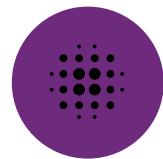
Our preliminary results of this case study suggest that the k-mers analysis might be capable of distinguishing clusters mirroring the geographical origin of the individuals, while the taxonomic analysis of the classified reads lack the power of differentiating the samples into separate clusters. We also observe that, for some human-associated microorganisms, phylogenomic analyses can shed light on the geographical distribution of specific clades, helping to discriminate between different hypotheses about the provenance of the humans that carried them.

Prashasti Singh

The reconstruction of diatom communities around Antarctica using marine sedimentary ancient DNA

Diatoms are important marine microorganisms often used in paleoenvironmental reconstructions because of their usefulness as indicators for changing climatic conditions. When diatoms die, they sink to the seafloor and gradually settle down in layers, making ocean sediments a storehouse of palaeoecological information. Analysis of ancient DNA from these sediments (sedaDNA) can be used to reconstruct the composition of past diatom communities and provide insights into Antarctic paleoenvironmental conditions. The Antarctic sea-floor provides an excellent setting for DNA preservation because of its constant low temperature, low oxygen concentrations and minimal disturbances. Overcoming the limitations of microfossil analyses, sedaDNA can detect diatom species that have little or no visible morphological features preserved, and, additionally, may provide insights into the evolutionary history of these organisms. Here, we introduce a project aiming to reconstruct diatom communities using sedaDNA from East and West Antarctica. In this pioneering work, we will extract sedaDNA from existing sediment cores, optimize these techniques to specifically target diatom sedaDNA, and analyse diatom composition changes in light of climatic changes over time. We aim to apply the optimized techniques to investigate changes in diatom community structures, in particular, sea-ice diatoms, over, at least, the Holocene. This project will generate significant new knowledge about one of Antarctica's most important marine primary producer groups' responses to past environmental change. Generating new information about how diatom communities adapt to climate change over large timescales will lead to improved prediction of how future climates will affect Antarctic primary production and aid conservation efforts for Antarctica.

PRESENTATION ABSTRACTS



Kadir Toykan Özdoğan

Exploring the lifestyle of people from Roman Limes through ancient environmental DNA

Since ancient environmental DNA (eDNA) methods are becoming one of the standard approaches for understanding the human past, the goal of my PhD project is to use this approach to explore the lifestyle and mobility of border people and other organisms with the focus on Roman Limes.

Therefore, we started collecting soil samples from Iron Age/Roman sites throughout the Netherlands and Belgium, we will be targeting even a broader region to cover entire Northwestern Roman borders. Our aim is using ancient eDNA to gather information about biological diversity in anthropogenic environments so that we can tell the impact of the Roman Empire within and outside the borders.

We are going to be using the shotgun metagenomics approach, however experimenting on target capture protocols to focus on mtDNA in order to recover insights about mobility of livestock and domestic plants is one of our near future goals.

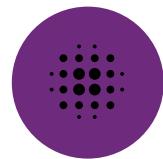
Although I will not have any presentable results by the date of the conference, in this presentation, I would like to talk about the current status and the goals of my PhD project, the methods I am planning to apply and the foreseeable possible struggles to hopefully start a conversation during the conference.

Sichao Huang

Arctic terrestrial ecosystem change over the last 54,000 years revealed by sedimentary ancient DNA on a lake sediment core from Far Eastern Russia

Arctic environments are threatened by recent warming and have experienced climate transitions in the past. Important environmental archives in poorly studied Siberian regions are lake sediment cores. We recovered a 10 m long sediment core from Lake Ilirney, located in a continuous permafrost zone in Eastern Chukotka (Russian Arctic), that covers the last 54,000 years including interglacial (at about 30–36 ka and from 16 ka-towards today) and glacial periods (at about 54–36 ka and 30–16 ka). We used sedimentary ancient DNA (sedaDNA) shotgun sequencing to discover past biodiversity changes of the terrestrial catchment community under different climate regimes. Our data reveal that the catchment vegetation around lake Ilirney changed from herb, with herbivorous mammals occurring during glacial times, to shrub dominated plants since 16 ka. Along with an increase in woody vegetation in warmer periods associated biota responsible for plant organic matter degradation, like saprotrophic fungi and lignin degrading bacteria, increased accordingly. Beside the reconstruction of past taxonomic composition, the sedaDNA data revealed changes in the functional biodiversity, which we investigated for carbon degrading enzymes that supported an increase in relative abundance of lignin and chitin degrading enzymes potentially degrading complex organic molecules during warmer periods. Thus, our results support that under future warming the expansion of shrubs, accelerated permafrost thaw and the increase of specified degraders in Arctic terrestrial environments might lead to enhanced degradation of plant organic material resulting in a potential positive climate feedback.

PRESENTATION ABSTRACTS



SESSION 6: MICROBIOMES

Markella Moraitou

Ecology, not host phylogeny, shapes the oral microbiome of closely related species

Placed at the contact zone between external and internal environments, the little-studied oral microbiome has important roles in host physiology and health. Here we investigate the contribution of host evolutionary relationships and ecology in shaping the oral microbiome in three closely related gorilla subspecies (mountain, Grauer's, and western lowland gorillas). We used shotgun metagenomics of 46 museum-preserved dental calculus samples deriving from two datasets, each processed in a different research facility, with somewhat different methods. The biological signal persists even after accounting for this potential confounding factor. We find that the oral microbiomes of mountain gorillas are functionally and taxonomically distinct from the other two subspecies, despite close evolutionary relationships and geographic proximity with Grauer's gorillas. Altitudinal differences in gorilla subspecies ranges appear to explain these patterns, proposing a close connection between dental calculus microbiome and the environment. Mountain gorillas show high abundance of nitrate-reducing oral taxa, which may contribute to high altitude adaptation by modulating blood pressure. Our results suggest that ecology, rather than evolutionary relationships and geographic proximity, primarily shape the oral microbiome in these closely related species.

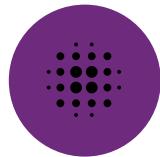
Maria Zicos

Diet and paleo-environment of Mylodon-darwinii at Mylodon Cave (Ultima Esperanza, Chile)

Sloths (Xenarthra, Folivora) were among the most diverse and widespread megafaunal mammals in the Americas from the Miocene to the Quaternary but underwent heavy levels of extinction in the latest Pleistocene and into the Holocene. No studies to date have investigated demographic dynamics of these species to understand whether their population crashed rapidly or underwent a slow decrease overtime. In this project I propose to tackle this question using ancient DNA (aDNA) and population genetics techniques to reconstruct the demographic history of extinct ground sloth Darwin's ground sloth (*Mylodon darwinii*) from Mylodon Cave (Ultima Esperanza, Chile), as well as their diet toward extinction.

The aim of the dietary investigation is to assess whether these sloths underwent major shifts in their diets as their environment shifted from steppes to Nothofagus forests as a result of climatic events existence. Studies have suggested that *Mylodon darwinii* from Mylodon cave were solely grazing, yet the diet of this species might have been able to be more flexible in other parts of this range. Shotgun metagenomics will be used to infer whether they were able to modify their diet, by inferring the plant and microbial diversity from ancient DNA in coprolites. Challenges of this study included recovery of informative DNA from the coprolites through laboratory protocols, as well as metagenomic analysis of the plant DNA, as there is no dedicated genomic database of Patagonian plants to correctly identify this material.

CONTACT INFORMATION



SPAAM4 CONFERENCE ORGANIZERS



Nasreen Broomand (nbrooman@ucsc.edu)

Nasreen is a PhD candidate in the Human Paleogenomics Lab at UC Santa Cruz. Her wide-ranging research interests include modern-day diseases and public health, evolutionary genomics of pathogens, the microbiome's role in the evolution of the human immune system, non-invasive DNA methods, research ethics, inclusive community-based participatory research, and the long-lasting impacts of colonialism on human health outcomes. In addition to her research, she is currently assisting the Monterey Bay Archaeological Archives in their NAGPRA compliance process and serves as co-president of UCSC Women in Science and Engineering in their fight for diversity and equity in the sciences.



Abby Gancz (asg5573@psu.edu)

Abby is a PhD candidate in Anthropology at the MicroARCH lab at Penn State University. Her research is on ancient systemic diseases and their associations with the human oral microbiome. In addition to her research, she works towards improving science education and outreach in the central Pennsylvania Area.



Gunnar Neumann (gunnar_neumann@eva.mpg.de)

Gunnar Neumann is a PhD candidate in archaeogenetics at the Max Planck Institute for Evolutionary Anthropology in Leipzig, Germany. His research focuses on ancient pathogens and pathogen evolution from the Chalcolithic to early modern times in Western Eurasia.



Pooja Swali (pooja.swali@crick.ac.uk)

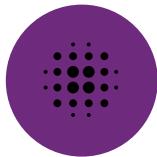
Pooja is Currently a PhD student at the Francis Crick Institute, looking at how ancient pathogens have evolved in time, with a predominant focus on prehistoric Britain. Alongside her PhD, she is using her background in science communication to develop activities and communicate why we study ancient DNA to the general public. She is also dedicated to widen participation and increase equality and diversity in STEM subjects.



Shreya Ramachandran (shreya23@uchicago.edu)

Shreya is a PhD candidate in the GenSCAPE lab at the University of Chicago, advised by Dr. Maanasa Raghavan. She is interested in microbial evolution across space and time, and studies ancient pathogenic bacteria and modern gut microbiomes in diverse populations. She is passionate about ethical community-based research, diversity and equity in science, academic writing pedagogy, and crossword puzzles.

SPAAMILY GROUPS



Neisseriaceae

Shreya Ramachandran, Yaxal Ponce Soto, Jasmin Frangenberg, Ian Light, Aida Andrades Valtueña, and Nikolay Oskolkov

Enterobacteriaceae

Yuti Gao, Eleanor Green, Maria Zicos, Andrea Quagliariello, and Tomos Prys-Jones

Bacteroidaceae

Abigail Gancz, Rupinder Kaur, James Fellows Yates, Mohamed Sarhan, and Irina Velsko

Fusobacteriaceae

Pere Gelabert, Maxime Borry, Sterling Wright, Allie Mann, and Ava Gabys

Lactobacillaceae

Cameron Pauly, Marica Baldoni, Sierra Blunt, Samantha Price, and Biancamaria Bonucci

Herpesviridae

Sreevatshan Kannurpatti Srinivasan, Merian van Os, Anna White, Bjørn Bartholdy, and Christine Ta

Clostridiaceae

Pan Long, Anan Ibrahim, Therese Balkenbush, Jamie Alumbaugh, Carly Scott, and Markella Moraitou

Chloroflexaceae

Jordan Von Eggers, Charlotte Greenall, Kadir Toykan Özdogan, Vilma Perez, and Valentina Vanghi

Streptomycetaceae

Mark Laurence Garcia, Lev Cosijns, Anne Marie Høier Eriksen, Sally Wasef, Dawn Lewis, and Harvey Palacios

Treponemataceae

Pooja Swali, Tre Blohm, Kelly Blevins, Hannah Moots, Miriam Bravo, and Zoé Pochon

Filoviridae

Alice Lee, Nasreen Broomandkhoshbacht, Kevin Daly, Elizabeth Nelson, Anne Kathrine Runge, and Olivia Smith

Poxviridae

Gunnar Neumann, Corrin Laposki, Laura Carrillo Olivas, Rémi Barbieri, and Davide Bozzi

Yersiniaceae

Reed Harder, Marcel Keller, Alina Hiss, Maria Lopopolo, and Iyunoluwa Ademola-Popoola

