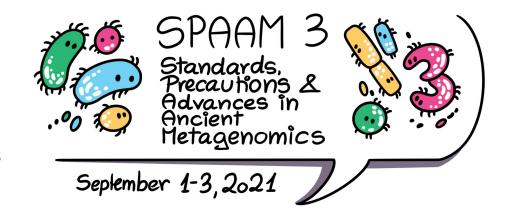


Standards,
Precautions &
Advances in
Ancient
Metagenomics

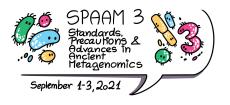


Session 2: Current challenges and biases in ancient patho(meta)genomics

Miriam Bravo | September 1st, 2021 | SPAAM3







Objectives for this Session

01

Hear the current challenges and biases in lab and bioinformatic techniques in ancient patho(meta)genomics.

02

Exchange views on the key steps during the detection and reconstruction of ancient pathogen genomes.

03

Discuss the importance of paleopathological evidence in ancient patho(meta)genomics.







Session 2 Agenda



4 Speakers

Richell Ramírez Molina
UNAM

Dr. Meriam Guellil

University of Tartu

lan Light

Max Planck Institute for Infection Biology

Dr. Kelly Blevins

Durham University



Discussion

A joint discussion with the presenters. All attendees can ask questions and participate in this discussion of key topics presented in this session.

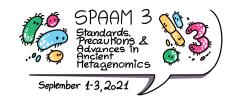


Break

Session 2 will begin at:
8:45 Pacific Time
17:45 Central European Summer Time







Suggested Topics of Discussion

Ancient pathogen DNA detection

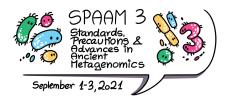
What metagenomic profiling software do you use? Does it require a custom database?
 How often do people design custom databases for their projects?

Ancient pathogen genome reconstruction

 What sort of bias is introduced when a reference based mapping is used? Is competitive mapping a strategy that you use to overcome this bias?

Ancient pathogens and closely related nonpathogenic microbes from the environment of burial contexts, coexist in the archeological remains we analyze. How do you exclude the elements of environmental contaminants from the pathogen genome reconstructed? How confident can we be that the genomic diversity we are observing is authentically deriving from the ancient pathogen?





Suggested Topics of Discussion

- Ancient pathogen genome reconstruction
 - Which criteria have you followed to select the samples suitable for capture-enrichment strategy? Do you normally buy a custom target capture kit or synthetize your own baits using an in-house protocol?

