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Struck by pestilence: Investigating the ancient human pathogen landscape using metagenomics

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Tid: 15.00 – 17.00
Plats. Observera - Rum 111

Material:

Nedan återfinns en disposition för kappan och abstract för två av de publicerade artiklarna samt för två manuskript som snart skickas in till peer-review granskning. Som bilaga återfinns även pdf:er på två publicerade artiklar.

Please find below the kappa structure of the thesis and the abstracts of two published papers and two manuscripts close to submission. Attached to the mail are copies of two of the published papers.

Utskrifter/Printouts:

I receptionen vid institutionen finns två utskrifter av materialet som är bilagd här tillsammans med utskrifter även för de två manuskripten.

Two printouts of the material provided here and additionally those of two manuscripts will be available in the reception of the department.

Info for seminar: Struck by pestilence: Investigating the ancient human pathogen landscape using metagenomics

Zoé Pochon, PhD student, Archaeological Science

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Chapter 1: aMeta

aMeta: an accurate and memory-efficient ancient metagenomic profiling workflow

Analysis of microbial data from archaeological samples is a growing field with great potential for understanding ancient environments, lifestyles, and diseases. However, high error rates have been a challenge in ancient metagenomics, and the availability of computational frameworks that meet the demands of the field is limited. Here, we propose aMeta, an accurate metagenomic profiling workflow for ancient DNA designed to minimize the amount of false discoveries and computer memory requirements. Using simulated data, we benchmark aMeta against a current state-of-the-art workflow and demonstrate its superiority in microbial detection and authentication, as well as substantially lower usage of computer memory.

Keywords: Ancient metagenomics, Pathogen detection, Microbiome profiling, Ancient DNA

Chapter 2: Gobas

Five centuries of consanguinity, isolation, health, and conflict in Las Gobas: A Northern Medieval Iberian necropolis

Between the 8th and 11th centuries CE, the Iberian Peninsula underwent profound upheaval due to the Umayyad invasion against the Visigoths, resulting in population shifts and lasting demographic impacts. Our understanding of this period is hindered by limited written sources and few archaeogenetic studies. We analyzed 33 individuals from Las Gobas, a necropolis in northern Spain, spanning the 7th to 11th centuries. By combining archaeological and osteological data with kinship, metagenomics, and ancestry analyses, we investigate conflicts, health, and demography of these individuals. We reveal intricate family relationships and genetic continuity within a consanguineous population while also identifying several zoonoses indicative of close interactions with animals. Notably, one individual was infected with a variola virus phylogenetically clustering with the northern European variola complex between ~885 and 1000 CE. Last, we did not detect a significant increase of North African or Middle East ancestries over time since the Islamic conquest of Iberia, possibly because this community remained relatively isolated.

Keywords and pathogens found: Pathogen overview, Smallpox, *Erysipelothrix rhusiopatiae*, *Yersinia enterocolitica*, *Streptococcus pneumoniae*, *Leptospira interrogans*, *Borrelia recurrentis*

Chapter 3: Ibiza

Genetic Diversity in Medieval Ibiza: Unveiling North African, European, and Sub-Saharan Ancestries

This study examines the genetic and metagenomic landscape of medieval Ibiza, focusing on 13 individuals buried in the Islamic cemetery at 33 Bartomeu Vicent Ramon (AD 950–1150). By integrating genomic data with historical and archaeological contexts, we investigate migration patterns and cultural interactions within medieval Islamic populations. Using genome-wide imputation techniques, we identify and quantify the genetic contributions from European, North African, and sub-Saharan African populations, revealing a high level of genetic diversity within the sample. Individuals exhibit varying degrees of admixture, reflecting the complex social structure of medieval Iberia. Despite this diversity, we also identify two individuals with high levels of consanguinity, indicating endogamic practices within the community. Notably, two sub-Saharan African individuals display distinct ancestry profiles, underscoring the extensive networks of the

Islamic world. Additionally, metagenomic analyses provide evidence of leprosy in one individual, offering insights into the health challenges faced by these communities. This research enhances our understanding of medieval Iberia's demographic transformations, highlighting population changes during Islamic rule.

Keywords and pathogens found: Pathogen overview, Leprosy, Hepatitis B virus, Human Parvovirus B19

Chapter 4: B19

Parvovirus B19 in sailors from sunken warships from the 16th and 17th centuries

Naval warships of the 16th and 17th centuries housed hundreds of individuals in confined quarters, creating ideal conditions for pathogen transmission. We screened human remains from two such shipwrecks, *Mary Rose* (1545) and *Kronan* (1676), and recovered parvovirus B19 (B19V) DNA from multiple individuals. Two complete and four partial genomes were reconstructed, all belonging to genotype 2—a lineage historically widespread in Europe but now largely replaced by genotype 1. Post-mortem damage patterns confirm the authenticity of the sequences, while genomic divergence between individuals suggests independent infections acquired prior to embarkation. These genomes fill a temporal gap between the most recent medieval sequences (~950 CE) and early 20th-century data, documenting the continued circulation and genomic stability of genotype 2 in early modern Europe. Our findings show that viral DNA can persist in submerged human remains for centuries and highlight the potential of shipwreck contexts to illuminate the evolutionary history of human pathogens.

Keywords and pathogens found: Human parvovirus B19, Genotype 2, Historical gap