

Title

Metagenomic analysis of past populations with a focus on infectious diseases: A new workflow and the cases of Sigtuna and Kronan

Abstract

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.

For the first chapter of my thesis, we focused on developing a new ancient metagenomics workflow in collaboration with the National Bioinformatics Infrastructure Sweden (NBIS), called aMeta and available on GitHub. As the field of ancient metagenomics is quite new, it was necessary to develop a tool that could both detect the microbes present in a sample and verify whether they are ancient or just modern contamination.

Unfortunately, we will not be talking about chapter II, as the zoom presentation is open to all, and I would rather save these results for after the manuscript's acceptance.

The third chapter looks at the impact of urbanization on infectious diseases, with the Late Viking Age town of Sigtuna as a case study. Over 60 individuals were subjected to shotgun sequencing and screening for potential pathogens. Preliminary results are promising, with the detection of *Mycobacterium leprae*, *Yersinia enterocolitica*, Hepatitis B virus and other pathogens responsible for past epidemics. Today, *Yersinia enterocolitica* is mainly a foodborne zoonosis, but transmission through close contact with cattle cannot be ruled out in the context of an early urban town.

For the fourth chapter, I helped supervise a master student in our lab, Alicia Muriel, who successfully applied a single-stranded protocol to some interesting samples from the Kronan warship. These samples had shown traces of Human parvovirus B19 in a previous double-stranded analysis, and Alicia was able to obtain more data on them with this new method as they are predominantly single-stranded viruses. Human parvovirus B19 is responsible for fifth disease or slapped cheek syndrome, but is also known to remain in the body after the infectious phase.