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[P69] HOT SPOTS IN ARCTIC SOILS: ARE ANCIENT ARCTIC SETTLEMENTS POSSIBLE RESERVOIRS FOR KNOWN OR POTENTIAL PATHOGENIC AGENTS?

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The history of Greenland is marked by repeated waves of Paleo-Inuit immigration from North America. From the 10th to 15th century, Norse settlers immigrated from Europe and flourished in southwest Greenland with the introduction of domestic livestock. The different Inuit and Norse cultures created middens by dumping and accumulating domestic waste. Today, animal bones, excrements, mollusc shells and other artefacts associated with past human occupation are a valuable resource for archaeologists to study these past societies' diets, habits, life, and death. However, these archaeological features might also represent unique microbial reservoirs of organisms from mixed origins (soil, human or animal associated) within an organic rich matrix- A latent source of microbes, including potential pathogens, that is currently exposed to climate change. Drastic increase in temperature observed in Greenland leads to thawing of the protective permafrost layer and midden material may be carried away by enlarged melting water from snowdrifts. Rising sea levels and loss of sea ice also accelerates the erosion of middens that are most often situated along the coast and might be washed out into the sea. This raises the question whether these sites represent a disease emergence threat. Especially that the increase in plant production in West Greenland is opening for the development of sheep farming in the Nuuk area, exactly where sheep farms were situated during the Norse era and abandoned for the past 500 years. In the VEO project, we aim to evaluate if ancient Arctic settlements are possible hot spots for pathogenic agents, and if potential pathogens may spread to the surrounding environment. Using metagenomics, we compared the microbial communities of middens from different age and location in West and South Greenland (Paleo-Inuit, Norse, and Modern Inuit middens) to pristine surrounding soils. We found that even after hundreds of years, the middens harbor a distinctive microbial signature enriched in host-associated and/or pathogenic bacteria belonging to Clostridium and other firmicutes; commensal bacteria from human faecal microbiome *C. massilliamazoniense*, *Ramboutsia* hominins and *Eubacterium tenue*, food poisoning agent *C. perfringens*, opportunistic pathogens *Paeniclostridium sordellii* causing toxic shock in humans, or agents associated to rare infant or adult botulism such as *C. baratii* and *C. thermobutyricum*. The next step is to identify and characterize pathogenicity markers, relatedness to currently circulating pathogens as well as model potential dissemination.