Title: Investigating the role of diet on the intestinal microbiota of Greenland sled dogs (*Canis lupus familiaris borealis*) using genome resolved metagenomics: a *One Health* approach

Authors:

Elsa MK Brenner ^{1,2**}	elsa.brenner@sund.ku.dk
Ostaizka Aizpurua ²	ostaizka.aizpurua@sund.ku.dk
Emilie Ulrikka Andersen-Ranberg ³	emilie.ranberg@sund.ku.dk
Pernille Klein-Ipsen ⁴	pernille.klein-ipsen@sund.ku.dk
Rosalina Rotovnik ⁴	rosalina.rotovnik@sund.ku.dk
Nanna Gaun ²	nanna.gaun@sund.ku.dk
Jorge Langa ^{2,5}	jorge.langa@sund.ku.dk
Raphael Eisenhofer ²	raphael.eisenhofer@sund.ku.dk
Antton Alberdi ²	antton.alberdi@sund.ku.dk
Garazi Bideguren ²	garazi.bideguren@sund.ku.dk

1- University Centre of the Westfjords, 2- University of Copenhagen Globe Institute, 3- University of Copenhagen, Department of Veterinary Clinical Sciences, 4- University of Copenhagen, Department of Veterinary and Animal Sciences, 5- University of the Basque Country UPV/EHU, ** primary contact

Abstract: The Greenland sled dog (*Canis lupus familiaris borealis*, GSD) is a breed of working dog unique to the Greenlandic Arctic. GSDs have distinct connections to their surrounding environment; they are housed outside, where they are fed primarily raw marine mammals and fish -a reflection of the hunted foods that many settlements in Greenland rely on for a significant portion of their livelihood. Moreover, GSDs almost exclusively drink from surrounding natural water sources, e.g., ice and small water bodies. Due to GSD's connectivity to both humans and the natural environment, GSDs are an excellent species for monitoring the role of diet and environment on intestinal health. This study applies the One Health framework to investigate differences in the intestinal microbiota of two populations of working GSDs. We compare GSDs in Ittoqqortoormiit, who are fed game and managed as described above, to the population in Daneborg, who are fed dryfeed, given clean drinking water, and managed by the Danish military. We used genome-resolved metagenomics to characterize the diversity, composition, and functional traits of the intestinal microbiota from 58 fecal samples, resulting in 555 metagenomic assembled genomes (MAGs), of which 44% had no species level annotation. Results indicate significantly different microbial communities in Ittoqqortoormiit and Daneborg, with pathogenic bacteria - including the genera Clostridium, Enterococcus, and Escherichia – more abundant in Ittoqqortoormiit. Functional analysis of the microbiome reveals significantly different profiles between the two populations, related to differing diet and environmental exposure. Higher levels of antibiotic degradation in Ittoqqortoormiit, where dogs do not receive formal veterinary care, suggests antibiotic pollution in the coastal system or through contact with human waste. Elevated degradation activity for butanediol, catechol, and propylene glycol further reveal the extent of anthropogenic compounds in the Arctic environment. This research contributes to *QimmeqHealth*, a broader effort to conserve the GSD breed, improve GSD health, and advance knowledge of diseases that impact coastal Arctic communities. Further, it highlights the value of applying metagenomics to monitor Arctic coastal, animal, and human health.