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Characterization of the gut microbiome of hooded seals (*Cystophora cristata*)

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Symbiosis between mammals and their gut microbiome is important for the extraction of energy and nutrients from food and influences immune response and brain development. The sterile foetal gut is first colonized during passage through the birth canal and then by maternal, social and environmental contact. The composition of the adult microbial community depends on the initial colonization; food ingested, food deprivation periods and genetic factors in the host. Hooded seals (*Cystophora cristata*) are born isolated on sea ice; suckle high fat milk for three days and fast for four weeks before ingestion of solid food items. They represent an extreme example among mammals. We sampled and characterized the microflora from the proximal and distal gut contents of four seals of two years of age, two of each sex. The seals were born in the wild and taken in human care at the end of suckling where they were fed a herring diet (Permit 2012/030044 Norwegian Food Safety Authority). Molecular-based analysis using Illumina Hiseq resulted in 569 910 16S rRNA sequences from the four seals, and both sampling sites. Taxonomical classification applying a naive Bayesian algorithm in a total of 412 Operational Taxonomic Units (OTUs) showed *Firmicutes* as the major phylum across samples (93.3% of total sequences, on average), followed by *Actinobacteria* (4.6%) and *Proteobacteria* (1.8%). Strikingly, an average 75.2% of 433 158 sequences assigned to 'core' OTUs (i.e. phylotypes accounting at least 1% of total sequences) gave no designations at species level (<97% similarity percentage) with any phylotype from GenBank. Further analysis with hindgut and fecal samples from geographically diverse marine mammals highlighted similarities in the microbiome of those sharing comparable aquatic environments. Altogether, these analyses gave us the opportunity to obtain a reliable first glimpse of the small intestine microbiota in wild hooded seals.

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