

ACQUARONE

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

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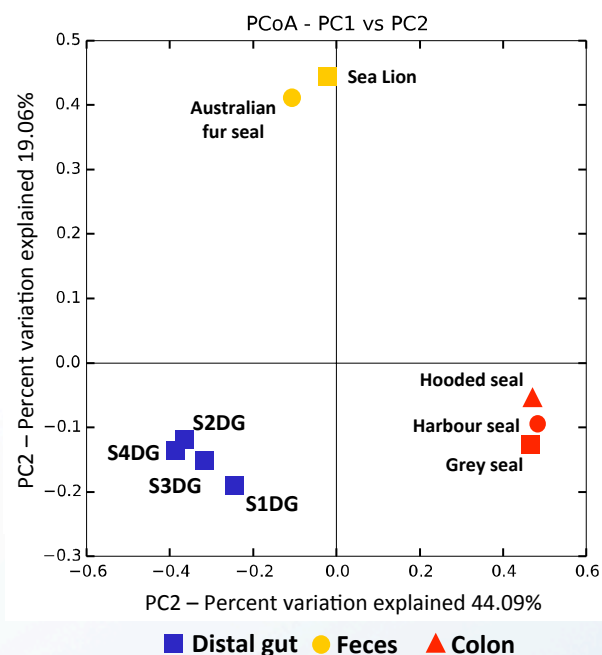
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## ABSTRACT

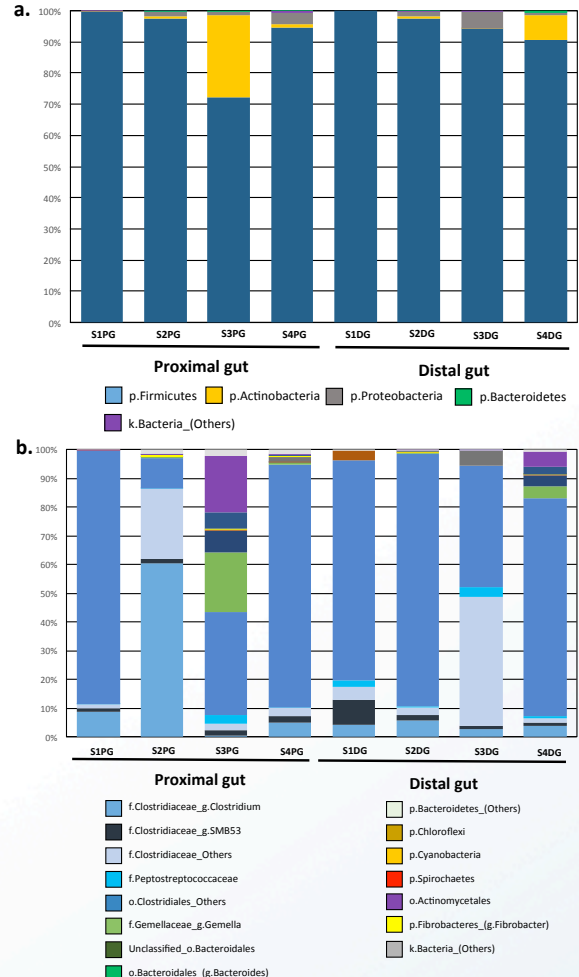
Symbiosis between mammals and their gut microbiome is important for the extraction of energy and nutrients from food and influences immune response and brain development. The sterile foetal gut is first colonized during passage through the birth canal and then by maternal, social and environmental contact. 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 93.4% of 389,359 sequences assigned to 'core' OTUs (i.e. phylotypes found in all the samples and accounting at least 1% of total shared sequences) gave no designations at genus level with RDP classifier. 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.

## COMPARISON WITH OTHER PINNIPEDS



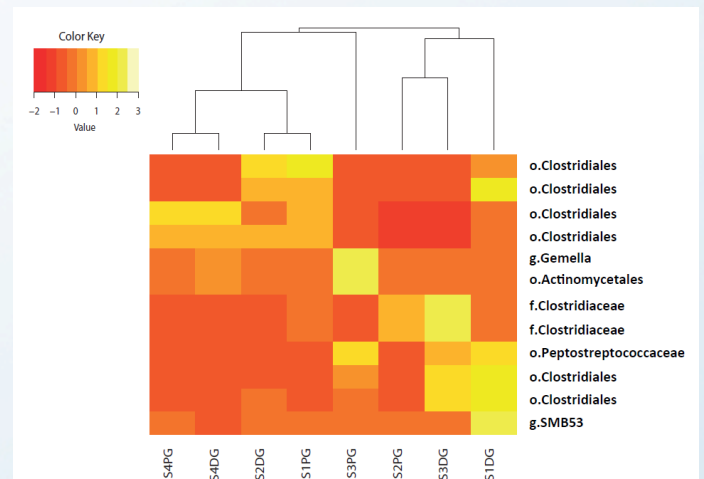
**Interspecies comparison of gut samples from different marine mammals and hooded seals.** PCoA plots were created from principal coordinates calculated based on unweighted UniFrac distance matrices. Samples presented variable shape and color depending on the animal source and sampling site: hooded seals, distal small intestine (this study; blue square); <sup>1</sup>Australian fur seal, feces (orange circle); <sup>2</sup>Sea lion, feces (orange square); Hooded seals feces (red triangle); <sup>3</sup>Harbour seal (red circle); <sup>4</sup>Grey seal feces (red square). <sup>1</sup>Smith et al. 2013: doi: 10.1111/1574-6941; <sup>2</sup>Bik et al. 2015: doi: 10.1038/ncomms10516. <sup>3</sup>Glad et al. 2010: doi: 10.1007/s00248-010-9690-x.

## MAJOR BACTERIAL PHYLA AND GENUS



**Bacterial taxonomical characterization from the proximal and distal gut sections of the small intestine in hooded seals.** Taxonomical classification is shown at a) phylum and b) genus level. Classification was performed with partial sequences of the bacterial 16S rRNA gene against the RDP-II database using RDP classifier tool.

## MAJOR BACTERIAL PHYLOTYPES



**OTU heatmap plot representing the main bacterial phylotypes shared by all the samples from proximal and distal small intestine in hooded seal.** The heatmap plot was created using z-score values of the most representative (accounting at least 0.01% total shared sequences) bacterial phylotypes found in all the samples.