Patterns in the Juan Fernandez fur seal faecal microbiome

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Abstract

As apex predators, pinnipeds are considered to be useful bioindicators of marine and coastal environments. Endemic to a small archipelago in the South Pacific, the Juan Fernandez fur seal (JFFS) is one of the less-studied members of the pinniped family Otariidae. This study aimed to characterize the fecal microbiome of the JFFS for the first time, in order to establish a baseline for future studies of host-microbial-environment interactions and monitoring programs. During two consecutive reproductive seasons, 57 fecal samples were collected from 7 different JFFS colonies within the Juan Fernandez Archipelago, Chile. Bacterial composition and abundance were characterized by sequencing the V4 region of the 16S rRNA gene. The overall microbiome composition was dominated by five phyla: Firmicutes (40 %), Fusobacteria (30 %), Bacteroidetes (22 %), Proteobacteria (6 %) and Actinobacteria (2 %). Alpha diversity was higher in Tierras Blancas. However, location was not found to be a dominant driver of microbial composition. Interestingly, the strongest signal in the data was a negative association between the genera *Peptoclostridium* and *Fusobacterium*, which explained 29.7 % of the total microbial composition variability between samples. The genus *Peptoclostridium* has not been reported in other pinniped studies and its role here is unclear, with interpretation challenging due to a lack of information regarding microbiome functionality in marine mammals. As a first insight into the JFFS fecal microbiome, these results contribute towards our understanding of the natural microbial diversity and composition in free-ranging pinnipeds.

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