

Extended abstract - Brilliant Marine Research Idea 2020

Title of the idea	Microbiome and diet turnover as indicator of rapid environmental change in the Arctic Ocean
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Extended abstract

Climate change is rapidly altering the Arctic marine ecosystem and threatening cold-adapted species. Changes in community composition and increased predation and competition are expected to disrupt trophic interactions among organisms in the Arctic marine ecosystem, including the microbial community. Despite the essential role of the microbial diversity in host health, trophic ecology and close interaction with the environment, studies on the gut microbial communities of Arctic fish remain scarce. Polar cod (*Boreogadus saida*), an abundant endemic circumpolar fish, functions as key species in the Arctic marine food web and might be used as indicator for the environmental status of the Arctic pelagic biosphere. In particular, diet composition could be used as a proxy to monitor seasonal trophic links and borealization of prey species. Furthermore, the use of certain bacterial groups to evaluate fish health and environmental status has been suggested. The aim of this project was to extract maximal information from individual polar cod sampled in the Barents Sea during summer and the understudied Beaufort and Chuckchi Sea in autumn. We used DNA metabarcoding of the COI and 16S rRNA gene to determine baseline dietary and microbiome levels, monitor seasonal dynamics and ecological effects such as borealization in the Arctic marine ecosystem.

First, we investigated the use of DNA metabarcoding for prey item composition compared to traditional visual analysis (Maes & Schaafsma, *in prep*). Second, we optimized the 16S rRNA metabarcoding protocol for polar cod specifically. Metabarcoding yielded high-resolution taxonomic assignments for both COI (mostly species-level) and 16S rRNA data (genus-level). We described the polar cod diet at high taxonomic detail, showing previously undescribed prey items. We found a high diversity of prey species in both the Barents Sea and Alaskan region. Polar cod in the Barents Sea mainly fed on amphipods, krill and fish, whereas polar cod in the Alaskan region mainly consumed copepods and ostracods. The presence of several Atlantic fish species and the temperate-boreal Northern krill indicate an increasing presence of boreal species in the Barents Sea. Interestingly, we found jellyfish in the diet of Alaskan polar cod. Increasing presence of these gelatinous predators may affect the distribution of polar cod, yet here we see that juvenile jellyfish might be a food source as well.

We unraveled a high diversity of bacteria in the gut microbiome that is significantly different between the Barents Sea summer polar cod and under-ice juvenile Alaskan polar cod. In the Barents Sea, Firmicutes was the dominating phylum, followed by Proteobacteria and Deinococci. In the Alaskan region, the microbial diversity was higher and Proteobacteria dominated the microbial communities, followed by Firmicutes and Planctomycetota. Among bacteria that can tolerate extreme cold (i.e. psychrophiles), we also found members of bacterial groups with metabolic activity supposedly unfit for

the Arctic region according to the literature. This only confirms that a lot of bacterial strains are yet to be detected in the polar regions. In addition, we found bacterial groups that might be of particular importance to the Arctic marine food web.