Microbial polysaccharide utilization in sandy surface sediments of Isfjorden (Svalbard)

SEBASTIAN MIKSCH[1], DAVID PROBANDT[1], MONIKE OGGERIN DE ORUBE[1], MARIA JENSEN[2], RUDOLF AMANN[1], KATRIN KNITTEL[1]

[1]Max Planck Institut for Marine Microbiology,Celsiusstr.1
D-28359 Bremen, smiksch@mpi-bremen.de
[2]University Centre in Svalbard , P.O. Box 156
N-9171 Longyearbyen, maria.jensen@unis.no

In the ocean, utilization of polysaccharides by heterotrophic microorganisms is a key process for the marine carbon cycle. Spring algae blooms cause a succession of the bacterioplankton in reaction to the algae-derived organic matter. At the shallow shelf, a significant portion of organic matter from the water column is sinking to the sediments. In sediments that are still shallow enough to be reached by sunlight there is also input of polysaccharides by benthic algae. Rate measurements showed that in oxygenated sandy sediments up to 40% of the total organic input is remineralized, but so far it is not completely resolved what components, how and by whom. Seasonal changes might be caused – among other factors- by the availability of different polysaccharides as substrates for heterotrophic bacteria.

For this study we sampled sandy surface sediments from Isfjorden (Svalbard) at 78°N, an environment with extreme seasonality with respect to sunlight and primary production, with the aim to investigate benthic microbial remineralization. Sediments were sampled at three time points during polar night (December 2017), twilight (February 2018) and polar day (May 2018) and were used for microbial diversity analysis, metagenomics, metatranscriptomics, substrate incubations and fluorescence in situ hybridization (FISH). We found evidence for seasonal differences on taxonomic and functional level. Relative abundance of *Bacteroidetes* 16S rRNA increased (~20% in December vs. ~26% in May) together with abundance of chloroplasts in the presence of light. Profiles of carbohydrate-active enzymes (CAZymes) showed obvious changes in read abundances of different glycoside hydrolase (GH) families in metagenomes and metatranscriptomes. Changes were most pronounced in GH families mediating glycoproteins degradation (e.g. GH18, GH33 or GH109) and in families responsible for degradation of internal carbon storage compounds such as glycogen or starch (e.g. GH4, GH110 or GH133). Degradation of these storage compounds was highest in sediments from February indicating the investigated microbial communities were starving.