Polysaccharide degradation potential of bacterial communities in Arctic deep-sea sediments (1200-5500 m water depth)

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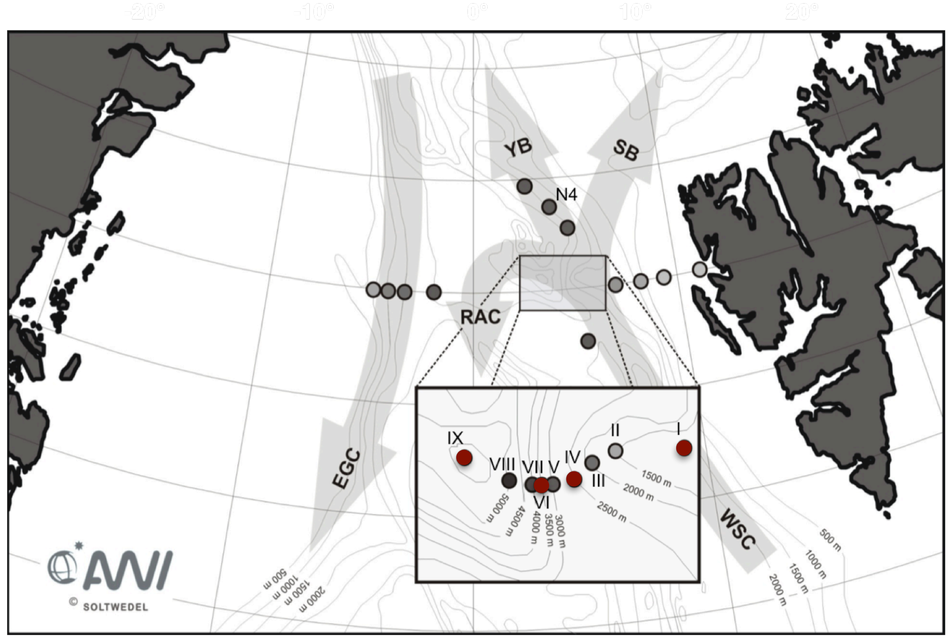


Figure 1 - Samples were taken in 2014 at the Arctic Long-Term Ecological Research (*LTER*) site *HAUSGARTEN* in Fram Strait. Red dots indicate the four sites that were included in this study, located along a water depth gradient from 1200 m down to 5500 m depth. WSC: West Spitsbergen Current; RAC: Return Atlantic Current; YB: Yermak Branch; Svalbard Branch; EGC: East Greenland Current (Ref. 3).

Introduction

- the majority of Earth's surface is covered by fine-grained deep-sea sediment dominated by bacteria of mostly unknown identity and metabolism
- benthic bacterial communities in deep-sea surface sediments depend on organic matter input from the upper ocean
- organic matter availability generally decreases with increasing water depth
- changes in bacterial community structure are correlated with water depth and with varying chlorophyll pigment concentrations, as a proxy for organic matter input (Ref. 1 & 2)

Conclusion

Benthic bacterial communities vary with water depth and exhibit a distinct enzyme machinery for the breakdown of polysaccharides depending on the type of exported material

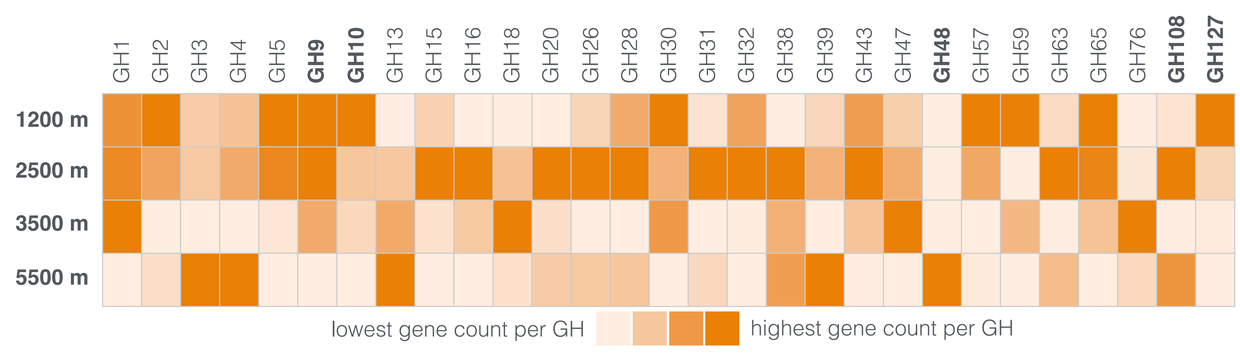


Figure 2 - Heat map of protein family gene counts associated with specific glycoside hydrolases (GH). Only GHs that could be detected both in metagenomes and -transcriptomes are displayed. At shallower depths we found more genes coding for hydrolases involved in polysaccharide degradation of algae material (e.g. GH9 for laminarin; GH10 for xylan, GH127 for plant cell walls), at deep stations more involved in the breakdown of bacterial cell walls (e.g. GH108 for components of peptidoglycan) and recalcitrant materials (e.g. GH48 for cellulose & chitin).

Figure 2

Results

- communities at **shallower depths** show a **greater proportion of protein domains** involved in **degradation of fresh algae material**
- communities at **deeper stations** show a **greater proportion of protein domains** involved in **breakdown** of **recalcitrant material** and **bacterial cell walls**

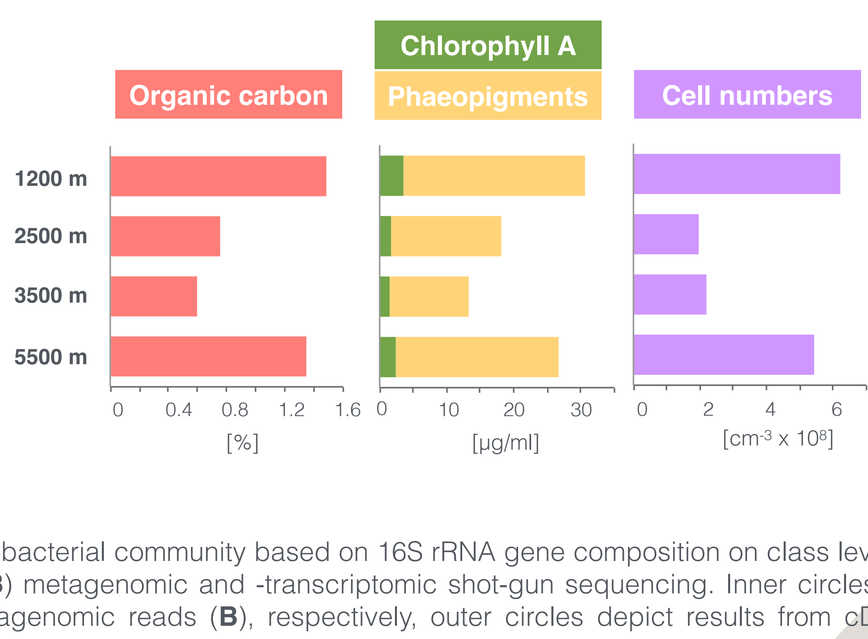
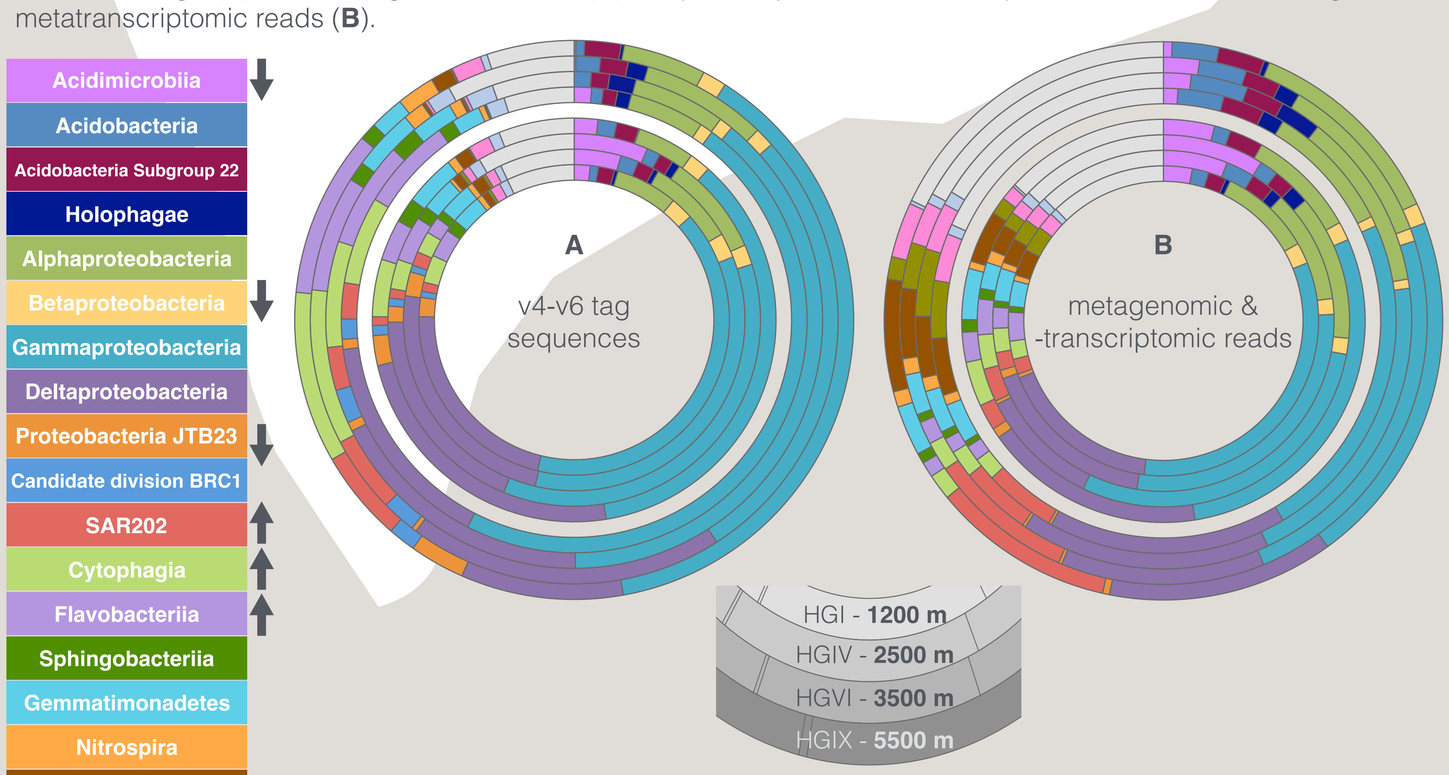


Figure 3 - Biogenic sediment compounds and bacterial cell numbers in surface sediment in 2014. Chlorophyll A represents the contribution of fresh material, while phaeopigments represent more degraded material.

- **lower organic matter** availability at **greater depth**
- **more fresh organic matter** at **shallower depth**
- deepest site accumulated more material due to topography (Ref. 3)

Figure 3

Figure 5 - Total versus active bacterial community based on 16S rRNA gene composition on class level obtained by (**A**) v4-v6 tag sequencing and (**B**) metagenomic and -transcriptomic shot-gun sequencing. Inner circles represent results from DNA tags (**A**) and metagenomic reads (**B**), respectively, outer circles depict results from cDNA tags (**A**) and metatranscriptomic reads (**B**).



- **over (↑)- or under (↓)-representation** of certain groups in the **active fraction** when compared to total community reads
- similar representation of community composition using tag sequences and -omic approaches

- **large differences** of total and active **bacterial communities on species level** along slope

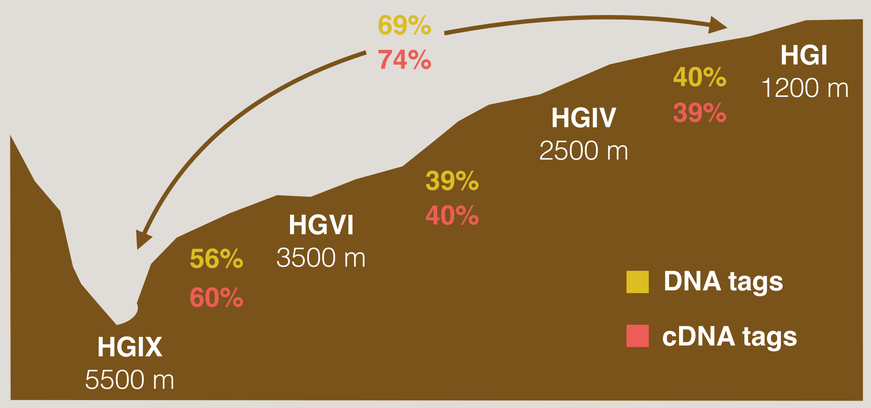


Figure 4 - Dissimilarity of communities along water depth gradient on species level based on presence-absence data with rare groups removed (<10 sequences).

Figure 4

Figure 5

Material & Methods

- DNA and RNA extraction from surface sediment (0-1 cm)
  - Tag diversity analysis using v4-v6 region of the 16S rRNA gene (Illumina MiSeq 300 bp paired-end libraries)
  - Metagenomes (4-5 Mio. reads, Illumina MiSeq 300 bp paired-end libraries, ~420 bp insert size)
  - Metatranscriptomes (4-5 Mio. reads, Illumina MiSeq 150 bp single-read libraries)

References
(1) Bienhold, C., Boetius, A. & Ramette, A. ISME Journal 6, 724–32 (2012).
(2) Jacob, M., Soltwedel, T., Boetius, A. & Ramette, A. PLoS One 8, e72779 (2013).
(3) Soltwedel, T. et al. Ecological Indicators 65, 89–102 (2016).

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