

Diversity of hydrolytic enzymes among Arctic deep-sea sediment bacteria

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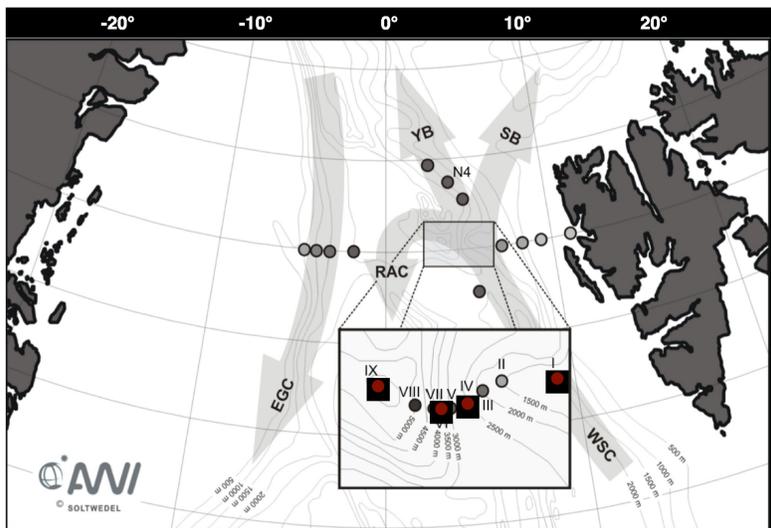


Figure 1 - Samples were taken in 2014 at the Arctic Long-Term Ecological Research (LTER) site HAUSGARTEN in Fram Strait. Red dots indicate the four sites that were included in this study, located along a water depth gradient from 1200 m down to 5500 m depth. WSC: West Spitsbergen Current; RAC: Return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

Introduction

- benthic communities are dominated by bacteria of mostly unknown identity and metabolism
- most deep-sea ecosystems are sustained by exported organic material from the productive, sunlit surface ocean
- organic matter availability generally decreases with increasing water depth
- previous studies showed a correlation between changes in bacterial community structure and organic matter availability

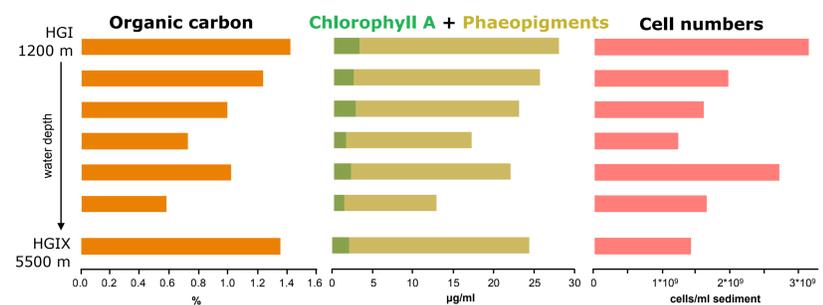


Figure 2 - Biogenic sediment compounds and bacterial cell numbers in surface sediments in 2014. Chlorophyll A represents the contribution of fresh material, phaeopigments represent more degraded material.

Main Questions

- Do we find differences between dominant and dominant active bacterial groups in Arctic deep-sea surface sediment at different water depth?
- Do communities residing at different water depths exhibit different capabilities to break down organic matter?
- Can we link specific hydrolytic enzymes to individual taxonomic groups?

- similar community composition along slope at low taxonomic resolution
- typically predominant sediment taxa, i.e. the JTB255 marine group, the Sh765B.TzT29 group or the OM1 clade, were underrepresented in the active part of the community
- other usually low-abundant taxa, i.e. *Flavobacteriia* and the
- high turnover across the depth gradient at species level
- the active community showed a higher turnover

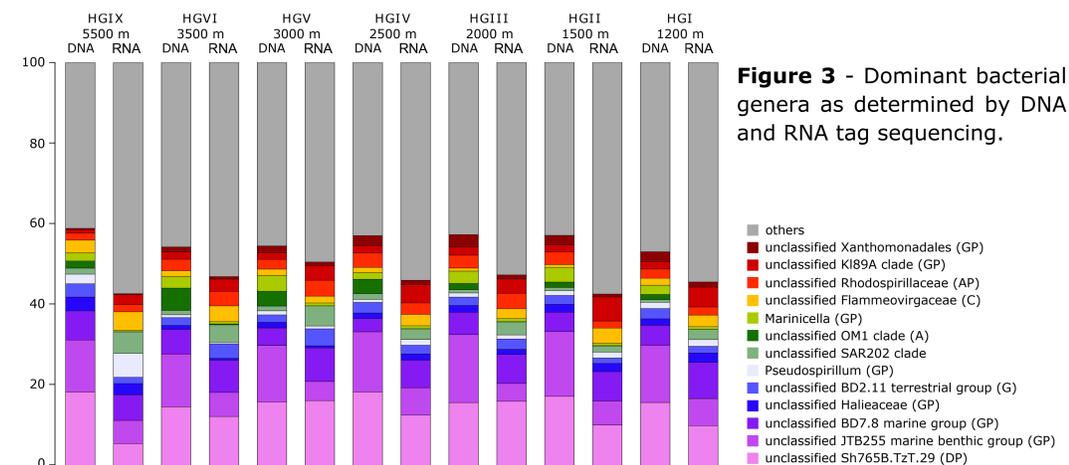


Figure 3 - Dominant bacterial genera as determined by DNA and RNA tag sequencing.

DNA	HGIX	HGVI	HGV	HGIV	HGIII	HGII	HGI
HGI	0.51	0.22	0.16	0.11	0.09	0.07	0.00
HGII	0.50	0.19	0.14	0.09	0.06	0.00	
HGIII	0.49	0.17	0.11	0.07	0.00		
HGIV	0.46	0.15	0.10	0.00			
HGV	0.44	0.13	0.00				
HGVI	0.42	0.00					
HGIX	0.00						

RNA	HGIX	HGVI	HGV	HGIV	HGIII	HGII	HGI
HGI	0.59	0.23	0.26	0.18	0.17	0.23	0.00
HGII	0.61	0.33	0.33	0.28	0.26	0.00	
HGIII	0.56	0.19	0.21	0.15	0.00		
HGIV	0.55	0.15	0.19	0.00			
HGV	0.51	0.14	0.00				
HGVI	0.53	0.00					
HGIX	0.00						

Figure 4 - Community turnover along the slope at OTU level. Displayed are Jaccard dissimilarities and OTUs > 99 reads.

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

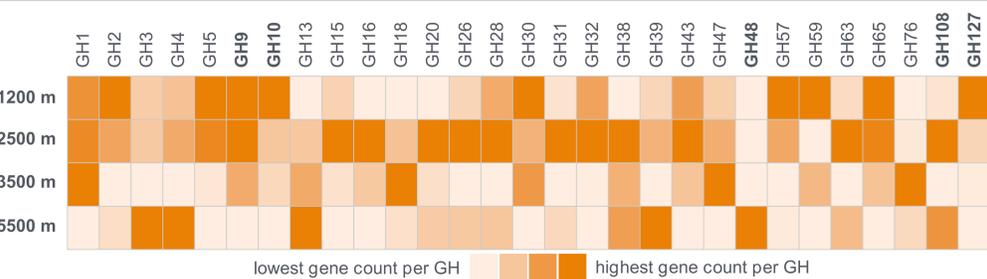


Figure 5 - Heat map of protein family gene counts associated with specific glycoside hydrolases (GH). Only GHs that could be detected both in metagenomes and -transcriptomes are displayed.

- 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

Results from the different molecular approaches were in good agreement and suggested similar community structures with the same dominant members.

Figure 6 - Community composition on class level as resolved by the different molecular approaches.

