Introduction

The *Roseobacter* clade is regarded to be a major bacterial lineage in marine environments. *Roseobacter*-affiliated bacteria represent a numerically significant part not only of pelagic, but also of benthic microbial communities.

To understand their biogeography, diversity and specific metabolic adaptations, we compared the *Roseobacter* clade within sediment and water samples from the eastern North Sea by cultivation-independent and cultivation-based methods.

Main questions

- Do we find specific distributions of pelagic and benthic *Roseobacter*-affiliated bacteria?
- Can we identify core taxa of benthic rosecobacters?
- Are rosecobacters specialized in utilizing different organic sulfur compounds?
- Do sediment-dwelling rosecobacters show specific adaptations that are different from their pelagic relatives?

Methods & Results

Strategy to unravel diversity and activity of benthic rosecobacters

Abundance and diversity of *Roseobacter* populations on the seafloor, sinking particles and free-living in the water column

- Clustering of DGGE profiles and amplicon-based analysis revealed specific localization of free-living and attached populations
- *Roseobacter* populations from sinking particles and sediments showed high similarities
- An increasing diversity of *Roseobacter* populations was observed from the sea surface to the seafloor

*Roseobacter*-affiliated isolates from the coastal North Sea

- Media amended with DMS, DMS+lactate or DMSP as substrates were suitable to isolate 20 *Roseobacter*-affiliated bacteria
- The isolates comprise 0.55% of all *Rhodobacteraeaceae* in a corresponding amplicon-based pyrosequence dataset
- Four strains (SK15, 21, 45 & 11) potentially might be new species

Phenotypical characteristics of *Shimia halotis* (strain SK13)

- Strain SK13 is closely related to *Shimia halotis* (99% sim.)
- Bundle forming pili are induced after incubation in artificial sea water medium amended with DMS & glutamate
- Similar bundles of pili were observed earlier in pathogens or biofilm-forming bacteria
- In order to get deeper insights into the genetic repertoire and physiology of strain SK13, whole genome sequencing is currently in progress

Conclusions

- The distribution of the *Roseobacter* clade in the North Sea samples followed regional patterns. A broad overlap was observed for sinking particles and the sediment surface.
- All media were sufficient to enrich and isolate *Roseobacter*-affiliated bacteria from MPN dilution series of North Sea samples with interesting phenotypic characteristics
- Strain SK13 might become a model organism to study adaptation mechanisms of rosecobacters in sediments