Defining unknown members of the *Roseobacter* group in marine sediments

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Introduction

- The *Roseobacter* group is known to be highly abundant in the marine environment. Especially in the water column, roseobacters are present in high numbers. In surface waters of the Southern Ocean, they make up more than 20% of the bacterial community.
- Although ~25% of all cultured representatives of the *Roseobacter* group were isolated from marine sediments, the role of the *Roseobacter* group in sediments is poorly understood.

Main questions

- What is the abundance of roseobacters in sediments worldwide?
- Can we define core taxa of the *Roseobacter* group in marine sediments?
- Are different regions of the ocean colonized by characteristic benthic members of the *Roseobacter* group?
- Do we find specific *Roseobacter* populations in different sediment horizons?

Methods & Results

Comprehensive data set from worldwide distributed sampling sites

![Worldwide distribution of sampling sites](image1.png)

- Sediments from deep and shallow oceanic regions
- Surface sediments and sediments from several meters below seafloor
- Different geochemical settings, e.g. TOC content and sulfate concentration
- Total number of RNA sequences from all sampling sites: 885,894

88% of all *Rhodobacteraceae* sequences can not be affiliated to known genera

![Rhodobacteraceae community composition in different sediment horizons](image2.png)

- Number of sequences classified as *Rhodobacteraceae*: 5,952 (6.7% of all), 743 *Rhodobacteraceae* could be affiliated to described genera
- For the *Roseobacter* group, only 7% of the sequences could be affiliated to the described genera

Definition of new benthic clusters within the *Roseobacter* group

- An ARB database was created, consisting of all sequences classified as *Rhodobacteraceae* with one type strain of every genus as backbone
- Phylogenetic trees were calculated using the neighbour joining and the maximum likelihood algorithm
- Clusters were defined when more than 10 sequences branched together in both trees

64% of all *Rhodobacteraceae* sequences were assigned to new clusters

![Clusters containing](image3.png)

- 115 clusters were identified as monophyletic branches within the *Rhodobacteraceae*
- 3,822 of the *Rhodobacteraceae*-affiliated sequences were affiliated to the new clusters
- 45% of these sequences formed 19 clusters, comprising more than 50 sequences, each

Outlook

- Designing specific primers and probes for the new clusters to detect and quantify them within the environment
- Answer main questions on worldwide distribution of benthic roseobacters
- Identifying the co-existence of known genera and unknown clusters
- Correlating specific geochemical conditions to the presence of members within the new clusters