Sea ice-pelagic-benthic links of bacterial diversity during the Arctic summer sea ice record minimum in 2012

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Introduction

Microbial communities play an essential role in carbon and nutrient cycling not only at the seafloor but also in the sea ice and in the water column, contributing significantly to Arctic ecosystem functioning. Arctic sea-ice extent declined to a record minimum in summer 2012 and the observed rapid melting resulted in the sinking and widespread deposition of fresh ice algal aggregates of the centric diatom *Melosira arctica* to the deep-sea floor at 4400 m water depth (Boetius et al., 2013). Sediments with algal deposits showed elevated rates of oxygen consumption, indicating remineralization by bacteria, and evidencing a response of the entire ecosystem down to the deep sea to elevated carbon flux rates. Warming and its associated physical changes in the Arctic will also affect bacterial communities, but to understand the ecosystem consequences we lack baseline information on bacterial community composition and functions in different Arctic environments.

Conclusions

- Central Arctic sea ice, melt ponds, seawater, sediment and algal aggregates host distinct bacterial communities
- Strongest differences in bacterial community structure and composition between surface and deep-sea environments
- For melt ponds, community description differed from previous reports, potentially indicating community shifts
- High contribution of surface-derived bacterial cells to community composition in aggregate deposits in the deep sea, indicating a transport of cells from the surface to the deep sea by the rapidly deposited aggregates
- Increase in the export of sub-ice algae is expected, therefore the role of algal aggregates as transporters of bacteria to the deep sea may be underestimated

1. Bacterial community structure

Bacterial community structure clearly differs between sea ice, water column and deep sea environments.

Similar patterns of environment-specific community structures observed across different study sites

2. Bacterial community overlap

85% of OTUs unique to individual environments, only 0.2% of OTUs ubiquitously shared

Aggregate deposits in the deep sea shared relatively high percentages of OTUs with communities from melt ponds, sea ice, as well as with deep-sea sediment

3. Bacterial community composition

Of 175 classified genera, only 3 were common to all environments (*Rubritales*, *Colwellia*, *Pseudomonas*); 46 genera were unique to one environment

Predominance of *Verrucomicrobia* in melt pond water is in contrast to previous reports. This could be a first indication for ongoing shifts in community structure due to environmental changes

Communities in aggregate deposits in the deep sea contained several surface-derived genera also observed in the ice environment (e.g. *Octodendrobacter*, *Glaciecola*), indicating a transport of cells to the deep sea

Materials & Methods

<table>
<thead>
<tr>
<th>69 samples from nine Central Arctic stations</th>
<th>Broad-scale comparison of bacterial community structures</th>
<th>Molecular fingerprinting, i.e. Automated Ribosomal Intergenic-Spaced Analysis (ARIAS)</th>
<th>In-depth insights into community composition and identification</th>
</tr>
</thead>
<tbody>
<tr>
<td>Aggregate deposits in the deep sea</td>
<td>10%</td>
<td>8%</td>
<td>3%</td>
</tr>
<tr>
<td>4%</td>
<td>8%</td>
<td>1%</td>
<td>85%</td>
</tr>
</tbody>
</table>

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References


