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

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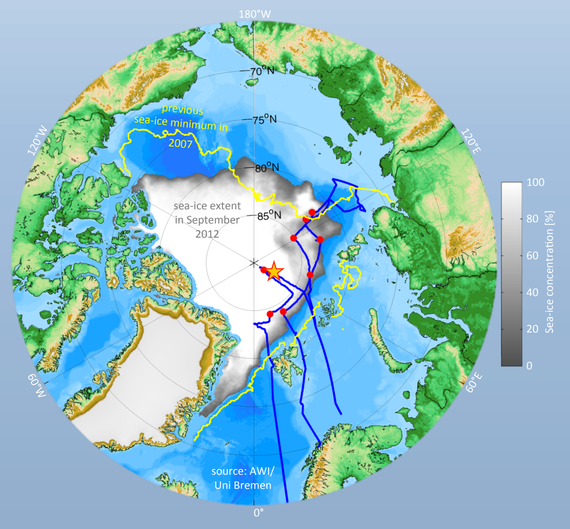


**Figure 1**: Cruise track of IceArc2012 (ARK-XXVII/3) from August to October, 2012. Red dots indicate the nine sampling sites, the star indicates station 7, for which Illumina sequences were obtained.

## 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

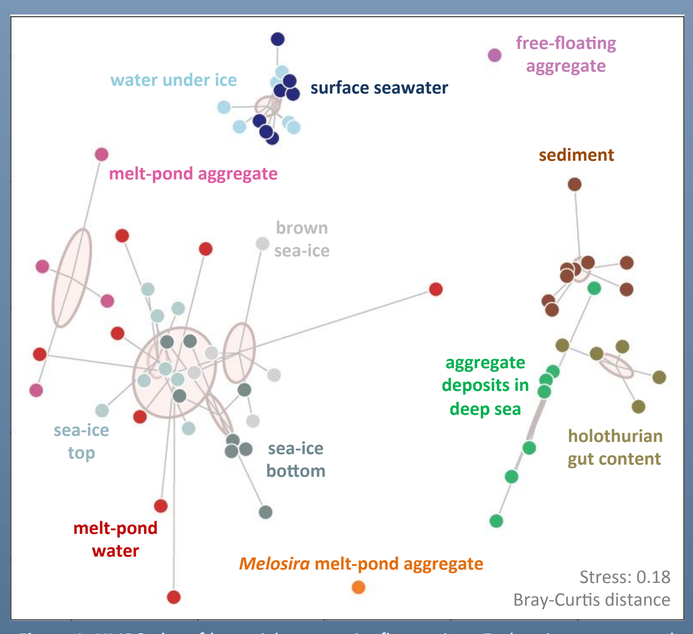


**Figure 1**: NMDS plot of bacterial community fingerprints. Each point represents the bacterial community of one sample. The distance between points reflects the relative differences in community structure between samples. Points within each group are connected to their group centroid with a spider diagram. The light pink ellipses show 95% dispersion of each group.

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

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

## 2. Bacterial community overlap

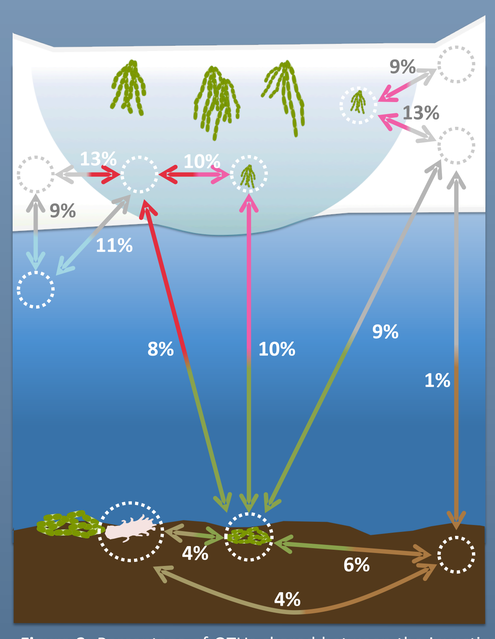


**Figure 2**: Percentage of OTUs shared between the investigated environments as detected by Illumina sequencing. Percentages are based on a Jaccard-distance-matrix of normalized data.

**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

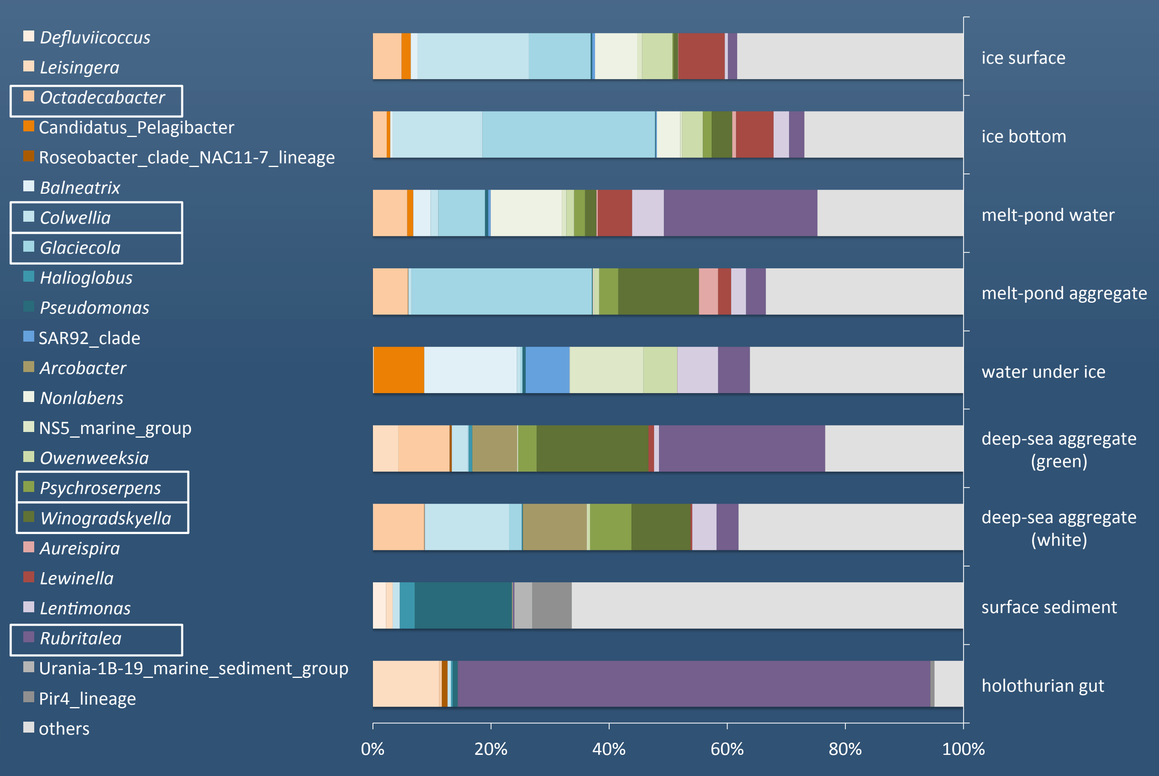


**Figure 3**: Bacterial community composition based on relative sequence abundances of the five most abundant classes detected over all environments.

Of **175 classified genera**, only **3** were **common** to all environments (***Rubritalea***, ***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. ***Octadecabacter***, ***Glaciecola***), indicating a **transport of cells** to the **deep sea**

## Materials & Methods

**Broad-scale comparison of bacterial community structures**

69 samples from nine Central Arctic stations → Molecular fingerprinting, i.e. Automated Ribosomal Intergenic Spacer Analysis (ARISA) → subset of 9 samples

**In-depth insights into community composition and identification**

Illumina next generation sequencing of the V4-V6 region of the 16S rRNA gene

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**References**

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