Pelagic bacterial communities across the Arctic-Atlantic boundary zone

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Introduction

In recent decades, the Eurasian Basin of the Arctic Ocean has undergone remarkable variations as part of the large-scale environmental changes facing the planet. The Fram Strait connects the Arctic Ocean to the North Atlantic, and provides the main gateway for water exchange between the Arctic and the global oceans. Two major current systems are present in Fram Strait: the West Spitsbergen Current (WSC) carries Atlantic water northwards, and the East Greenland Current (EGC) brings cold Arctic waters and ice southwards (Fig 1 and 2). The proximity of these two distinct current systems creates a valuable opportunity for studying differences in microbial community composition across strong gradients of temperature and ice cover. Here we present a first preliminary investigation of both free-living and particle-associated pelagic bacterial communities in the upper water column across a longitudinal transect of the entire Fram Strait, conducted during RV Polarstern expedition PS85 (ARK-XXVIII/2) in June 2014.

Hydrographical conditions

- During the sampling campaign in June 2014 the western part of the Strait was still covered by sea ice
- There was a strong gradient in surface temperature between eastern and western parts of the Strait
- Low chlorophyll a concentrations in the ice-covered region are potential evidence for low phytoplankton biomass in the western part of the Strait

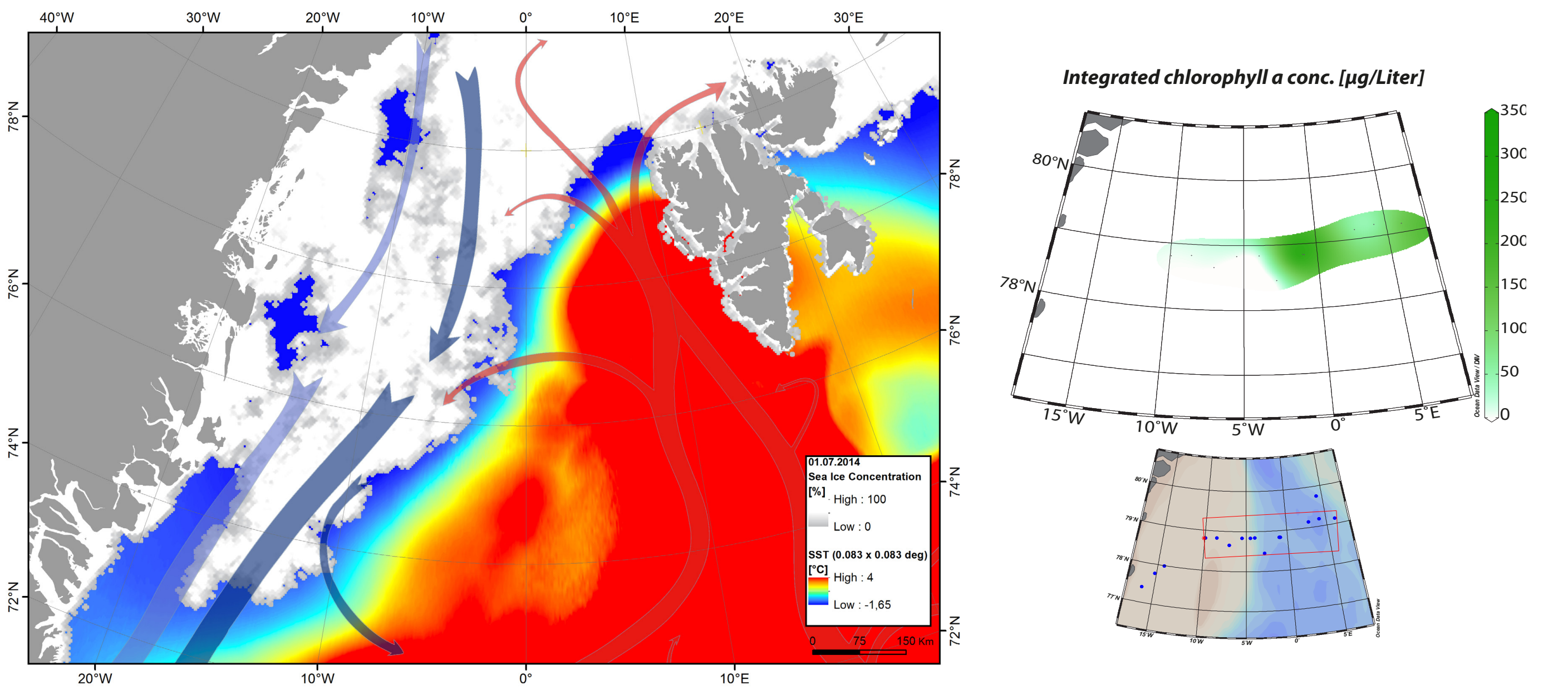


Figure 2: The hydrographic conditions in Fram Strait during June 2014. The satellite remote sensing sea ice concentration data were obtained from http://www.meereisportal.de (Spreen *et al.* 2008). The ice concentration is represented by inverted gray scale (gray-low, white-high). Sea surface temperature was obtained from NOAA NCEP real-time analysis (http://polar.ncep.noaa.gov/sst/rtg_high_res/). The arrows represent general directions of the WSC (in red) and the EGC (in blue). Map: AWI/ Laura Hehemann. The chlorophyll *a* conc. were measured as part of the long term sampling of the 'Plankton Ecology and Biogeochemistry in a Changing Arctic Ocean' group (PEBCAO) and kindly provided by Eva-Maria Nöthig (AWI, unpub. data).

Bacterial community composition

- Bacterial community richness is higher in the EGC compared to the WSC
- In contrast, absolute cell numbers are higher in WSC waters

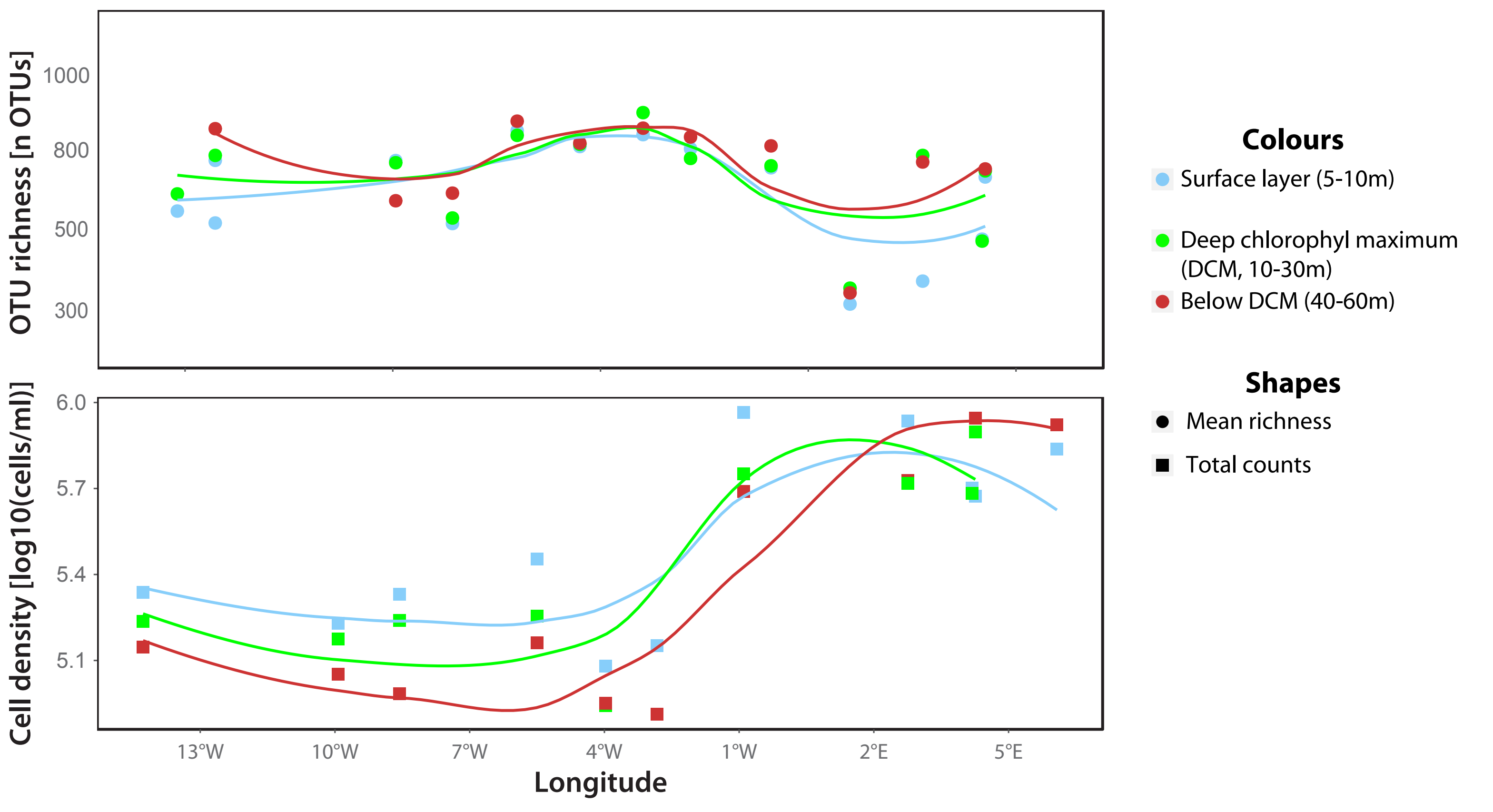


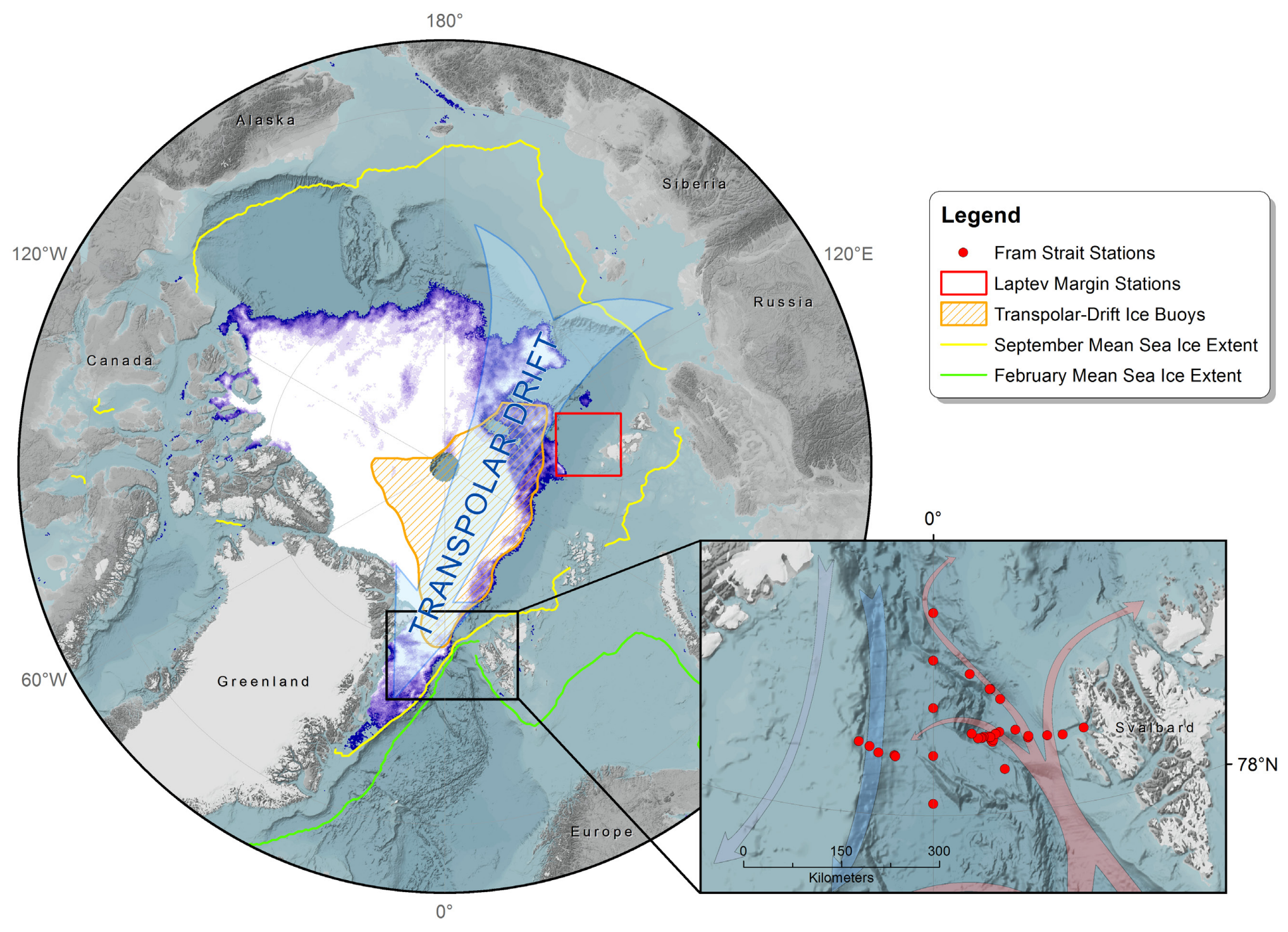
Figure 3: Bacterial richness and abundance along the longitudinal transect. Mean OTU richness was calculated based on separate estimates for free-living and particle-associated fractions, based on 16S tag-sequencing analysis. Total bacterial cell densities were measured as part of the long term sampling of the PEBCAO group. The color code represents the different water layers that were sampled at each station.

Material and methods

- The collected water samples were sequentially filtered through 3 and 0.22 µm filters to separate particle-attached and free-living communities. DNA extracts were sequenced on an Illumina machine using 16S primers targeting the V3V4 region.
- The OTU table was generated using swarm (Mahé et al. 2015, PeerJ. 2015; Vol. 3) and taxonomically assigned using SINA (Pruesse et al. 2012, Bioinformatics. 2012; Vol. 28); statistical analyses were done in R using the package phyloseq (McMurdie and Holmes 2013; Plos One; 2013; Vol. 8)
- Total cell counts were acquired from water samples using flow cytometry

Ocean Observing System FRAM

The mission of Frontiers in Arctic Marine Monitoring (FRAM) is to establish an infrastructure capable of providing synchronous year-round observations in the Arctic. One important component of this infrastructure is to establish a microbial observatory that addresses the response of ecosystem structure to on-going environmental change. The autonomous sampling and sensing technologies of the FRAM infrastructure are complemented with annual summer expeditions to the long-term observatory HAUSGARTEN. To date, microbial research in the water column has focused mainly on eukaryotes. Therefore our results will provide a knowledge baseline for long-term monitoring of pelagic bacterial communities in the highly dynamic Arctic-Atlantic boundary zone.



FRAM

Figure 1: The Fram Strait as part of FRAM research areas (Map: AWI/ Laura Hehemann, Ingo Schewe)

Taxonomic composition

- **Alphaproteobacteria** have higher relative abundances in the EGC water
- **Flavobacteria** are significantly enriched in the WSC, both in the free-living and particle-associated fractions
- **Gammaproteobacteria** are significantly enriched in the free-living fraction of WSC, while in the EGC they have higher relative abundances in the particle-associated fraction

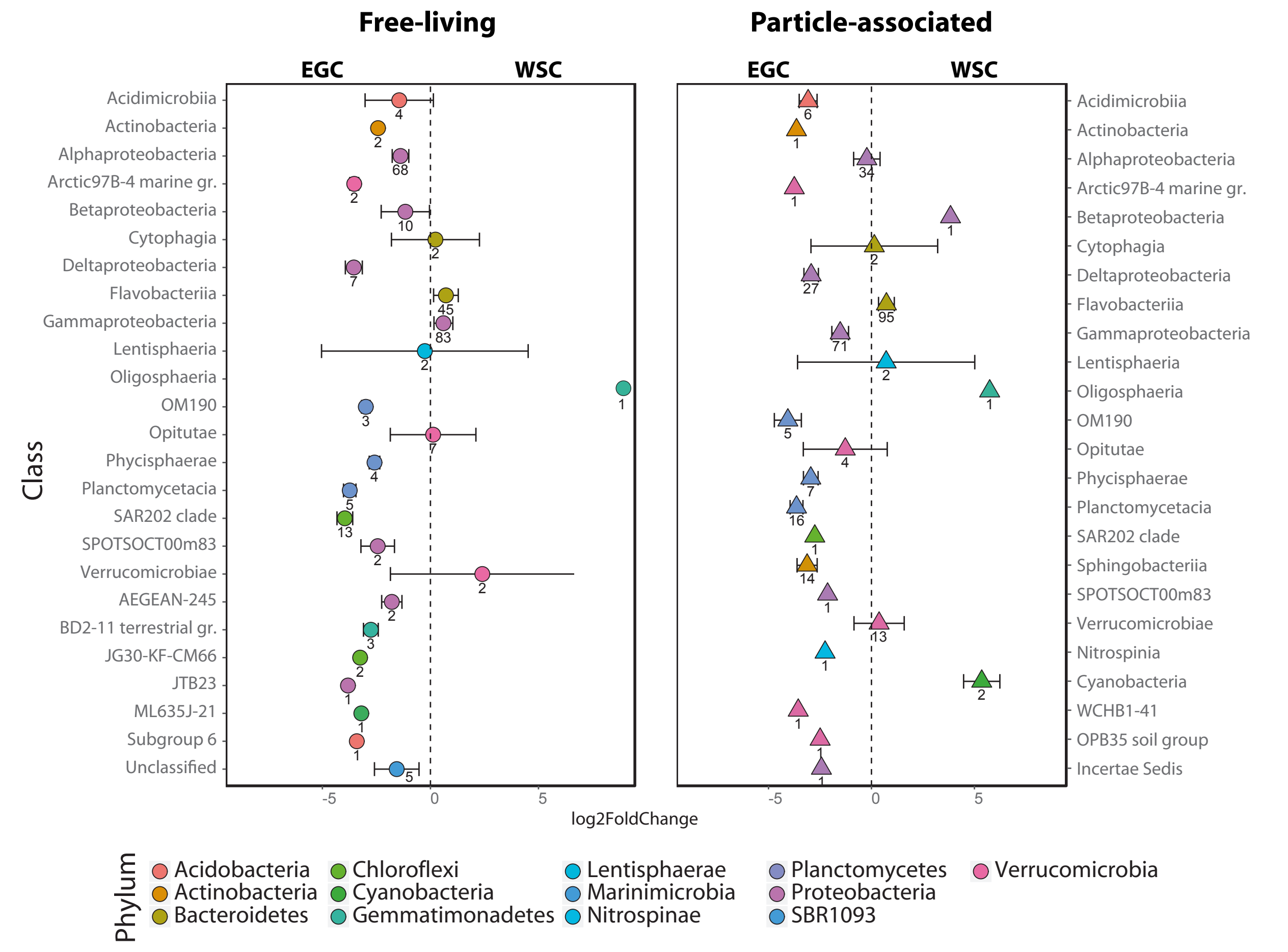


Figure 4: Bacterial taxonomic groups enrichment in the waters of the different current systems. The enrichment test was conducted separately on free-living and particles-associated fractions, based on 16S tag -sequencing analysis. Only taxonomic groups with statisticly significant enrichment were included in the figure (p<0.001). The numbers represent the amount of OTUs included in each taxonomic group.

Summary & Outlook

- Bacterial community abundance, diversity and composition revealed strong trends associated with longitudinal gradients of temperature, ice coverage and phytoplankton biomass
- Higher cell densities in the WSC are supported by higher chlorophyll a concentrations suggesting that the bacterial community is driven by eukaryotic phytoplankton blooms
- Further analyses will help to identify potential dynamics between bacterial and microbial eukaryotic communities across Fram Strait (coll. K. Metfies, AWI)

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