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Influence of glacial melt and Atlantic water on bacterioplankton community of Kongsfjorden, an Arctic fjord

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ABSTRACT

The Kongsfjorden, an Arctic fjord is experiencing warming due to increased input of Atlantic water masses. High-throughput sequencing was performed to examine bacterial diversity from the outer and inner zone of the fjord in summer and fall of 2012. A total of 11,999 operational taxonomic units (OTUs) were assigned into 19 known phyla and 5 genera *incertae sedis*. Significant variation (p = 0.001, n = 4) was observed between the bacterial community structure of outer and inner fjord while variation between summer and fall was minimum. *Proteobacteria* was the most abundant phylum (55.9-61.0%) in summer and fall. The most dominant alphaproteobacterial member of this phylum (OTU 263 *Pelagibacteriaceae*) contributed maximum to the observed dissimilarity between the outer and inner fjord community. Characterised by relatively fresher and warmer water, glacial meltwater input could be a major source of predominance of OTU 6968 *Flavobacteriaceae*, OTU 5552 *Psychrobacter*, OTU 7148 *Sphingomonadales* and OTU 5011 *Loktanella* in the inner fjord in summer. Thus, the significant variation in the bacterioplankton community composition of outer and inner fjord indicates strong and localized influence of glacial melt water in shaping the community structure.

1. Introduction

Kongsfjorden, located on the west coast of Spitsbergen (Svalbard) archipelago at 79° N is a glacial and open fjord in the Arctic. The water column in Kongsfjorden is influenced both by Atlantic and Arctic water masses (Hop et al., 2002). At the same time, tidal glaciers at the head of the fjord discharge freshwater and suspended loads that cause steep environmental gradients in salinity, temperature and sedimentation rates (Weslawski et al., 2000). Due to its location as a connecting channel between the Atlantic and Arctic Oceans, Kongsfjorden has received much research attention in the recent past. The current interest on the fjord is primarily based on the fact that Kongsfjorden is considered as an ecological indicator to study the impacts of climate change, with both Atlantic water influx and melting of tidal glaciers being linked to climate variability (Hop et al., 2002). The Kongsfjorden ecosystem is in a transition to a warmer state and the increased input of warm Atlantic water masses results in warm winters and Atlantification of the fjord (Polyakov et al., 2007; Huenerlage and Buchholz 2015). Hop et al. (2006) suggested that the Arctic–Atlantic boundary location of the Kongsfjorden (Spitsbergen) places this system in a good position as an indicator for climate-related changes.

In spite of its significance in studying the impacts of climate change, very little information is available on the phylogenetic composition of bacterioplankton in Kongsfjorden water, especially on a spatial as well as temporal perspective. Information on bacterial community structure of the fjord could provide insights on the taxonomy of members playing significant role in the biogeochemical cycles in this dynamic system. Recent developments in high throughput sequencing technologies enabled metagenomic analyses in a manner that exceeds the capacity of traditional Sanger sequencing-based approaches by several orders of magnitude with the possibility of detecting even very rare phylotypes (Tedersoo et al., 2010). Earlier, pyrosequencing was used to enumerate and contrast marine microbial diversity in the Arctic waters (Zeng et al., 2013; Bowman et al., 2012; Comeau et al., 2011; Kirchman et al., 2010). These studies have shown that the abundant phylogenetic groups represented in the pyrosequence data are generally similar to those reported by previous studies in the Arctic (Alonso-Sàez et al., 2008; Bano and Hollibaugh 2002; Garneau et al., 2006; Malmstrom et al., 2007; Zeng et al., 2009). Earlier studies from Svalbard fjord reported bacterial sequences that mostly fell under four major phylogenetic groups, which are the alpha and gamma subclasses of *Proteobacteria*, *Bacteroidetes* and *Verrucomicrobia* (Groudieva et al., 2004;

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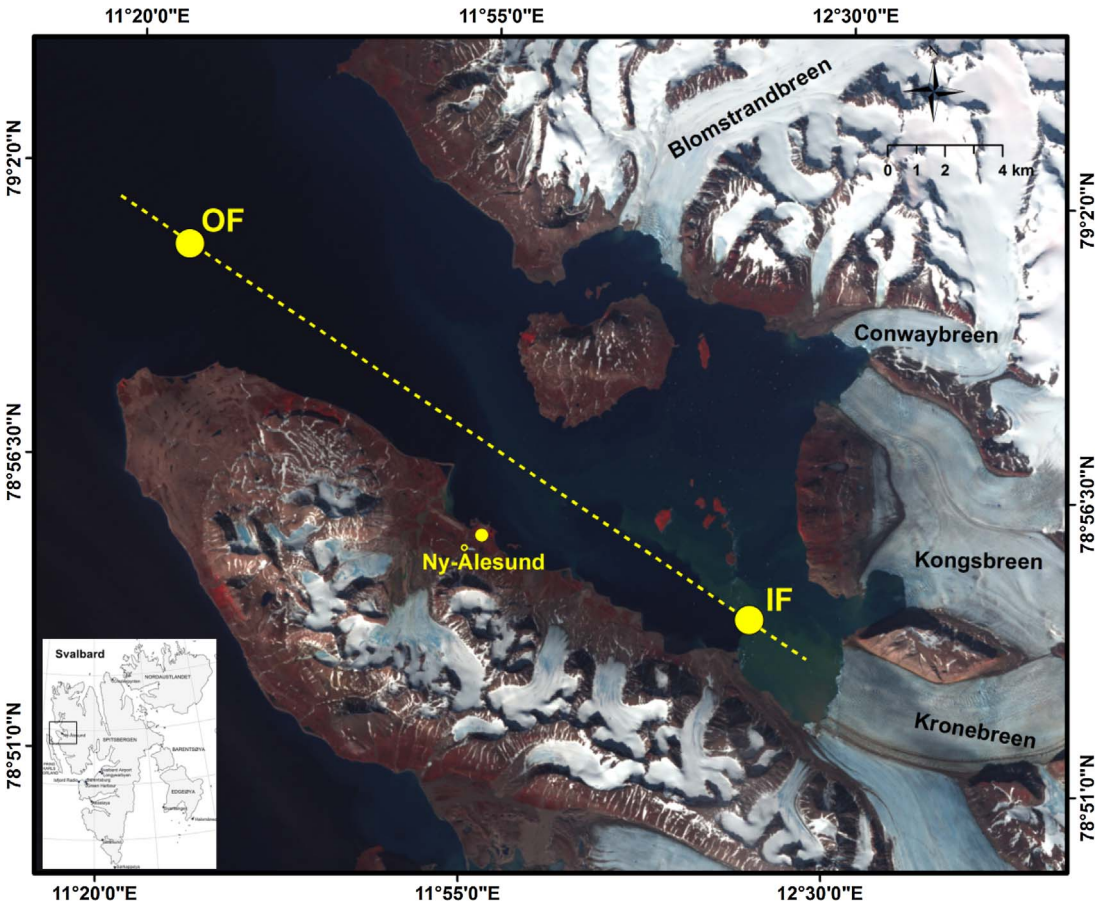

Fig. 1. Map of Kongsfjorden, Svalbard with sampling locations. Samples were collected from two stations located at outer fjord (OF) and inner fjord (IF) region in June and October 2012. Major transect where the CTD observations were made (broken line) is shown in the figure (map was created using Landsat 7 ETM (path/row:217/003) satellite data in ArcGIS 10.2).

Cardman et al., 2014).

Although there have been studies on spatial distribution of bacterioplankton communities in Kongsfjorden using 16S rRNA gene cloning and pyrosequencing (Zeng et al., 2009; Zeng et al., 2013; Cardman et al., 2014), examination of spatio-temporal variability is lacking. Such observations can provide insights in to variation in bacterial community structure in response to change in hydrographic properties over spatial and temporal scale. The present study attempts to understand the bacterioplankton diversity of Kongsfjorden in outer and inner fjord over temporal scale (summer and fall) using Illumina MiSeq platform. We hypothesize that the localized effect of glacial meltwater discharge may contribute to significant variation in the bacterioplankton community structure between outer and inner part of the fjord.

2. Materials and methods

2.1. Study site and sampling strategy

Kongsfjorden (Fig. 1) is a polar fjord situated between 78°04′N–79°05′N and 11°03′E–13°03′E on the west coast of Spitsbergen, Svalbard Archipelago. The fjord is characterised by a weak tidal range (~2 m) strongly influenced by topography and the adjacent ocean (Hop et al., 2002). One of the most remarkable characteristics of Kongsfjorden is that in spite of being located at high latitude it remains unfrozen in the winter in most years. At its inner end, the Kongsfjorden has mainly three glaciers viz. Kongsbreen, Conwaybreen and Blomstrandbreen draining into it and contributing to the major source of fresh water. Kongsbreen, situated in the innermost part of Kongsfjorden is recognized to be the most active glacier in the Svalbard Archipelago (Lefauconnier et al., 1994).

A Conductivity-Temperature-Depth (CTD) profiler (SBE 19 plus V2, Sea Bird Electronics, USA) equipped with a fluorescence sensor (Wet labs, Philomath, USA) was used to obtain information pertaining to the hydrographic features and fluorescence profiles along the major transect (nine stations) of Kongsfjorden in June and October 2012 using the research boat Teisten. Water samples were collected from a depth of 30 m showing primary chlorophyll maxima from the station OF (outer fjord) and IF (inner fjord) in June and October 2012 (Fig. 1). The water masses were delineated based on the redefined classification by Cottier et al. (2005) i.e., Surface ($S < 34.00$ and $T > 1$ °C), Intermediate (S-34.00–34.65 and $T > 1$ °C), Transformed Atlantic ($S > 34.65$ and T-1–3 °C) and Atlantic ($S > 34.65$ and $T > 3$ °C). Water samples were collected using Niskin bottles (10 l) attached onto the winch wire and triggered manually using messengers. Immediately upon collection, water samples were transferred to the pre-cleaned carboys. Further, they were analysed immediately after bringing it to the on-shore laboratory. Total microbial cells in the water samples were enumerated after staining with 4′, 6-diamidino-2-phenylindole (Hicks et al., 1992; Krishnan et al., 2009). Nitrite, nitrate, phosphate, silicate and dissolved oxygen were measured as described by Strickland and Parsons (1968). Chl *a* was quantified using HPLC (Agilent 1200, CA, USA) as per the protocol detailed by Van Heukelem (2002).

2.2. DNA extraction and V3 metagenomic library preparation

Two liters of water was filtered through 0.22 μm polycarbonate membrane filter (Merck Millipore, Germany) and stored at −80 °C until DNA extraction. DNA extraction from the microbial community collected over filter paper was performed using UltraClean soil DNA isolation kit (MOBIO, CA, USA). The filter paper was cut into thin pieces