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Abundance and biomass of bacteria in two Arctic glacial fjords

Katarzyna JANKOWSKA[1], Maria WŁODARSKA-KOWALCZUK[2] and Piotr WIECZOREK[2]

[1] *Wydział Inżynierii Lądowej i Środowiska, Politechnika Gdańska, ul. Narutowicza 11/12, 80-952 Gdańsk, Poland < kjank@pg.gda.pl>*

[2] *Instytut Oceanologii, Polska Akademia Nauk, ul. Powstańców Warszawy 55, 81-712 Sopot, Poland < maria@iopan.gda.pl>*

Abstract: The total numbers and biomass of bacterioplankton in two Arctic glacial fjords off west Spitsbergen were studied. Samples were collected from different water depth layers – from the surface to 80–90 m depth. Total bacterial number (TBN), biomass and morphological structure (shape of bacteria) were determined using the acridine orange direct count method. The highest values of TBN and biomass in the water column were found in Kongsfjorden in the stations adjacent to Kongsbreen Glacier, and the lowest values in the outer part of the Krossfjorden. The local maxima of bacterioplankton were observed in water layers around pycnocline. The morphological structure was similar in all samples – the bacteria were dominated by rods (over 65%), followed by cocci (16–20%) and vibrios (11–15%).

Key words: Arctic, Spitsbergen fjord, bacteria, epifluorescence methods.

Introduction

The fjords of the west coast of Spitsbergen belong to the rapidly changing Arctic coastal areas. Climate warming is causing glacier retreat, increase in melt-water inflow and inorganic suspensions sedimentation, salinity and temperature fluctuations. Therefore this area has been treated as a model site for studies on the impact of climate change in the Arctic (*e.g.* Włodarska-Kowalczuk and Węsławski 2001). Kongsfjorden and Krossfjorden, two fjords situated off the west coast of Spitsbergen, have attained much attention during the last few years. The fjords are regarded as key European sites for Arctic biodiversity monitoring (Hop *et al.* 2002). The intensive international investigations of these fjords (Ny Ålesund LSF, BIODAFF, BIOMARE programs) have focused both on the physical characteristics of the environment and the biotic components of the ecosystem. Overviews of the existing knowledge concerning the physical environment and marine ecosystem of the

fjords were recently published by Svendsen *et al.* (2002) and Hop *et al.* (2002). However, in contrast to the existing extensive data sets on the phyto- and zooplankton, nekton and benthic flora and fauna, bacteria have been not studied in the fjords. Bacteria cannot be disregarded in any model of an ecosystem structure and functioning in as much as they transform particulate organic matter to soluble forms and detritus (Zdanowski 1988) and transfer dissolved organic matter (DOM) to higher trophic levels (Azam *et al.* 1983). The present preliminary study of bacteria in the Kongsfjorden/Krossfjorden fjordic system is aimed at the evaluation of the densities and biomass of bacteria present in fjordic waters in the summer season as well as studying the distribution of bacteria along the fjord axis and among the water layers.

Investigated area

Kongsfjorden and Krossfjorden (79° N, 12° E) are two fjords of about 25 km length each, connected by a common mouth demarcated by two capes: Kapp Mitra and Kvadehuken (Fig. 1). Eight active tidal glaciers terminate in the waters of the inner parts of the fjords. Kongsbreen, situated in the innermost part of Kongsfjorden, is recognised to be the most active glacier in the Svalbard Archipelago, with the highest rate of calving (0.23 km^3/year) and with a front retreating at an average speed of 200 m/year (Lefauconnier *et al.* 1994). Each year the glacier erodes about 0.3 mm over 800 km^2 of its drainage area, which results in an input of 2.6×10^5 m^3 of mineral material into fjord waters per season (Elverhøi *et al.* 1980). The mineral material, carried by glacier meltwaters, sediments mostly in the inner parts of the fjord close to the glacier front (Svendsen *et al.* 2002). The strong inflow of glacier meltwater results in the formation of a surface water layer of relatively high temperature and very low salinity. This surface water overflows the Atlantic waters of high salinity and temperature originating on the Spitsbergen shelf, and the local fjordic waters of intermediate salinity and low temperature. The waters flowing into the fjord are transported along the southern coast, while the outflowing waters are transported along the northern coast (Svendsen *et al.* 2002). High amounts of inorganic suspension limit the abundance of phytoplankton and primary production in the inner basins in summer (Keck *et al.* 1999). The low salinity of surface water results in the mass mortalities of zooplankton observed in glacial bays (Węsławski and Legeżyńska 1998).

Materials and methods

Bacteriological investigations were carried out in Kongsfjorden and Krossfjorden in July 1999. Water samples were taken from five depths in five sampling stations (Figs 1, 3). At all stations, except for station IV, the salinity and temperature were measured with the use of OceanSeven 316 Idonaut. Water was sampled

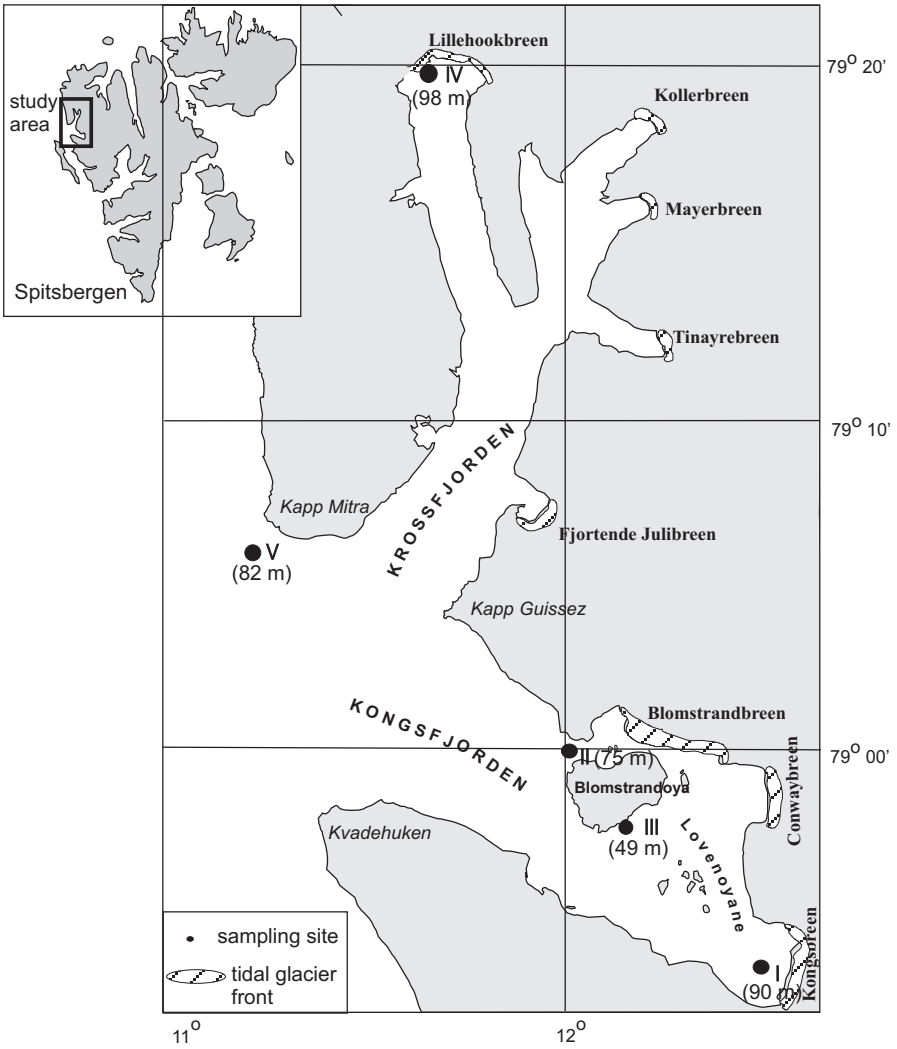

Fig. 1. Investigation area. Depth of sampling stations in brackets.

using Niskin bottles. Samples were stored in sterile glass bottles (250 ml) and fixed with particle-free formaldehyde (2% total concentration). The total bacterial number, biomass and morphology were determined using the acridine orange direct count method (Hobbie *et al.* 1977). Three 2 ml subsamples of each seawater sample were filtered on 25 mm irgalan-black-stained polycarbonate filters (0.2 µm diameter). The bacteria were stained with a 0.01% solution of acridine orange for 2 minutes. Cells were counted using an Axioskop FL epifluorescence microscope under 1200-fold magnification. An HBO-50 W high pressure mercury burner, 410–485 nm excitation filter, 515 nm barrier filter and 505 nm dichroic mirror were used (Świątecki 1997). The image analysis system of Świątecki (1997) was

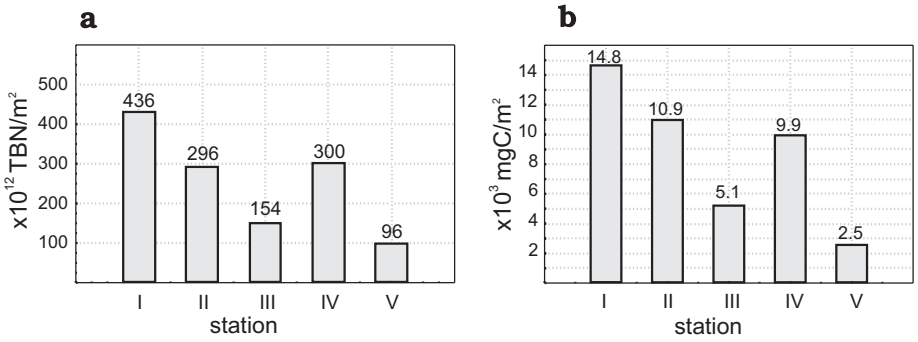

Fig. 2. a – total bacterial number (TNB), b – biomass (BB) at stations.

used. It included an attachment for the epifluorescence microscope, monochromatic camera and PC and MultiSkan Bace V.8.08 computer program for picture analysis. Bacterial cells were counted in 20 fields. The orange-red and greenish fluorescing particles were classified into five size classes and three morphological types (cocci, rod, and vibrio) were counted. The mean value of the three subsamples was calculated for each sample. The biomass of bacteria was estimated from the mean volume of cells with use of the Norland's formula (1993).

Results

The highest number of bacteria in the entire water column was recorded at station I adjacent to the Kongsbreen Glacier (436×10^{12} TBN/m^2) as well as in the surface waters of station II; the lowest values were observed at station V situated at the fjord mouth close to Kapp Mitra (96×10^{12} TBN/m^2) (Fig. 2a). The biomass distribution pattern in the investigated area and in the layers within the water column was similar to that observed for density (Fig. 2b). The biomass in the water column varied from 2.5×10^3 mgC/m^2 (at station V) to 14.8×10^3 mgC/m^2 (at station I) .

As regard the distribution in water layers the highest number of bacteria was noted in the surface water only at station V (Fig. 3). The maximum of TBN corresponded to the salinity gradient observed in 0–10 m water layer. At stations II and III, situated in the central part of Kongsfjorden, the highest values were recorded in the layers 5–10 m (80×10^5 TBN/cm^3) and 10 m (67×10^5 TBN/cm^3), respectively. At these stations strong salinity gradients were observed in the 0–20 m and 0–15m water layers, respectively. At stations I and IV, situated close to tidal glacier fronts, no single distinct peak of density was noted. At all stations, except for station I, the lowest bacterial numbers were observed in the bottom layers.

The proportions of bacteria of different shapes was very similar at all stations. Rods were the dominant bacterial forms – they made up from 66% (station II) to

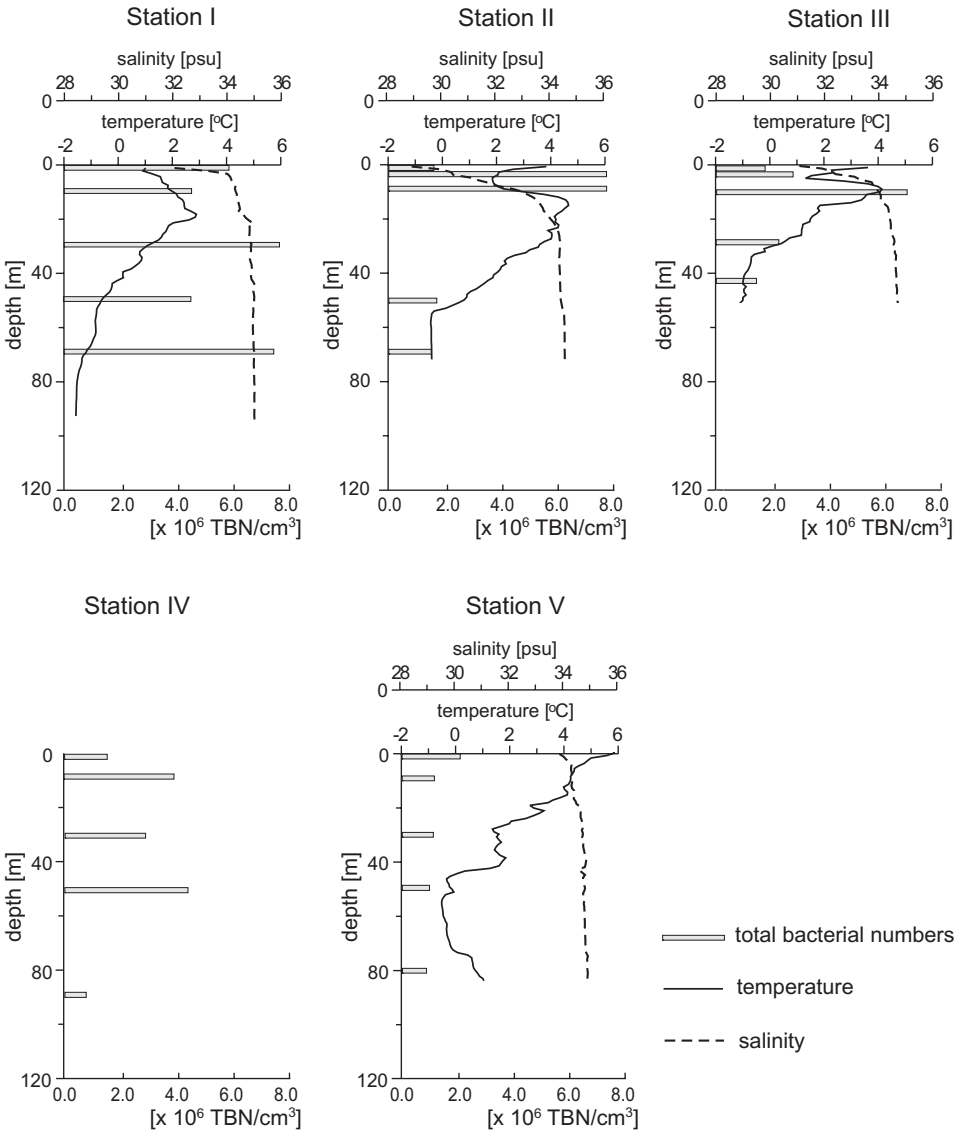

Fig. 3. Total bacterial number (TNB), depth, temperature and salinity at stations.

73% (station V) of all bacteria. The percentages of cocci and vibrios were much lower. Cocci made up between 16% (station IV) to 20% (station I), while vibrios accounted for 12% (station V) to 15% (station II).

The bacterioplankton was dominated by small forms (volume <0.1 μm³) – they made up 51–71% of TBN at stations I, II and II and 58–90% at stations IV and V. Bacteria of sizes ranging from 0.1 to 0.5 μm³ made up 8–18% of TBN, and bacteria larger than 0.5 μm³ made up from 2 to 8% of TBN.

Table 1

Total bacterial number (TBN) recorded in different polar habitats.

Habitat, area	$\times 10^5$ (TBN/cm^3)	Method	References
Fjordic water, Kongsfjorden Krossfjorden, Spitsbergen	7.8–80.0	AODC	present study
Fjordic water, Horsund, Spitsbergen	0.8–1.3	Light microscopic stained erytrosine	Zajączkowska and Zajączkowski 1989
Fjordic water, Admirality Bay, Antarctica	0.03–18.7	AODC	Zdanowski 1995
Open water, Antarctica	0.003–3.56	AODC	Zdanowski 1995
Open water, Beaufort Sea	1.8–8.7	AODC	Atlas and Morita 1986
Sea ice, Antarctica	0.03–440	AODC	Zdanowski 1995
Sea water under ice, Anatrctica	0.06	AODC	Zdanowski and Donachie 1993
Sea ice, Barents Sea and Laptev Sea	0.4–36.7	AODC	Gradinger and Zhang 1997

Discussion

The number and the biomass of bacteria decreased from the inner towards the outer parts of the fjords. The highest values of TBN and biomass were noted at the station adjacent to Kongsbreen, the glacier recognised to be the most active in the Svalbard archipelago. The abundance of bacteria was lower in the vicinity of less active glaciers – Blomstrandbreen and Lillehookbreen. The decrease in salinity in glacier-proximal areas results in mass mortalities of zooplankton (Węsławski and Legeżyńska 1998) and thus in high amounts of particulate organic carbon. These are potential food resources and available substrates for bacteria. In addition the high concentration of inorganic particles might be advantageous for bacteria. Bacterial colonization is important in processes such as flocculation of mineral particles (*e.g.* Syvitsky *et al.* 1989). Bacteria tend to attach to particles and aggregates of particles. The aggregates form a protective microhabitat for microorganisms and increase the availability of nutrients which are absorbed by particle surfaces (Logan and Hunt 1987, Droppo *et al.* 1998). Maximal bacterial densities were also observed by Zdanowski (1995) in the inner basin influenced by the glacier outflow in waters of an Antarctic fjord, Admiralty Bay (King George Island). A similar pattern was reported for sediments in the Baffin Island fjords by Syvitsky *et al.* (1989). They observed twice as high bacterial biomass in sediments close to the glacier than in sediments in the outer parts of the fjord.

The depth distribution of bacteria can be attributed to the hydrological stratification and/or phytoplankton distribution. Bacterioplankton and phytoplankton generally tend to accumulate in the layers around the pycnocline. Phytoplankton densities are very low in the area adjacent to Kongsbreen. In the central part of Kongsfjorden

phytoplankton concentrates at around 10–15 m, in the outer part of the fjord it concentrates in surface waters (Keck *et al.* 1999). This distribution pattern is followed by the bacteria in the central and outer parts of the fjord – maximal densities were found at 10 m at stations II and III and in the surface water at station V.

The only previous total bacterial counts done for water samples from Spitsbergen were published by Zajączkowska and Zajączkowski (1989) for Hornsund Fjord. The values found in Kongsfjorden are much higher. This stems from the difference in methodology – light microscopy by Zajączkowska and Zajączkowski (1989) and epifluorescence microscopy in our study. The values of bacterioplankton densities recorded in Kongsfjorden/Krossfjorden as well as in the Antarctic fjord – Admiralty Bay – were higher than the values recorded in the Arctic and Antarctic open waters (Table 1). This is a result of the higher concentrations of organic matter in inshore areas.

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