Bacterial abundance, biomass and production during spring blooms in the northern Barents Sea

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ABSTRACT

To evaluate importance of bacterioplankton in the Barents Sea, we investigated the spatial and temporal distribution of bacterial abundance, biomass and production in relation to spring-bloom stages. During three cruises in 2003–2005, 12 stations were investigated. Average bacterial abundance ($\pm$S.D.) in the photic zone was $3.6 \pm 3.0 \times 10^5$ cells ml^{-1}, corresponding to 7.1 ± 6.1 mg C m^{-3}. Bacterial production in the photic zone was measured using dual labelling technique with ^{3}H-thymidine and ^{14}C-leucine, resulting in average production rates ($\pm$S.D.) of 1.5 ± 1.0 and 6.9 ± 4.8 mg C m^{-3} d^{-1}, respectively. In spite of low water temperature, the bacterial community was well developed and active. Similarity analysis of stations resulted in four distinct spring-bloom stages, covering pre- early-, late- and post-bloom stages. In the photic zone, bacterial biomass on average corresponded to $6 \pm 2\%$ of phytoplankton biomass. Highest integrated bacterial biomass was observed at mid- to late-bloom stages. Average bacterial production equalled $32 \pm 6\%$ ($\pm$S.E., $n = 24$) of particulate primary production. The bacterial production to primary production ratio tended to increase at late-bloom stages. The observed bacterial activity illustrates the importance of the bacterial pathway for channelling carbon from DOC through the microbial food web back into the classical food web, which previously has not been adequately considered in plankton ecosystem models of the Barents Sea.

1. Introduction

Arctic pelagic ecosystems are often used as an example of a short and linear classical food chain (e.g., Lentz, 1992), but during recent decades the importance of the microbial processes has been documented also for Arctic marine ecosystems (Nielsen and Hansen, 1995, 1999; Hansen et al., 1996; Lovejoy et al., 2002). Where investigated, the role of bacteria and the microbial food web in carbon transformation is now regarded as important as for lower-latitude ecosystems (e.g., Rivkin et al., 1996; Middelboe et al., 2002; Levinsen and Nielsen, 2002).

The Barents Sea is the largest shelf sea surrounding the Atlantic Ocean, and among the most productive of the world's oceans (Wassmann, 2002). The complex hydrography (Loeng, 1991; Sakshaug, 1997) is characterized by significant in- and out-flow of Atlantic, Arctic and modified water masses (Loeng et al., 1997) and heavy ice cover during winter and early spring. The latter gives rise to extended areas of melting ice and Marginal Ice Zones (MIZ), which are considered among the most dynamic areas in the world's oceans (Falk-Petersen et al., 2000). This complex

hydrodynamic plays an important role for production and distribution of small pelagic organisms such as phytoplankton, bacteria and their consumers in general (Backhaus et al., 1999) and in the Barents Sea in particular (Wassmann et al., 1999).

So far most investigations on the pelagic carbon cycle in the Barents Sea have focussed on the classical food chain, i.e., the key organisms, copepods of the genus *Calanus*, and its importance for fishery resources in the area (e.g., Conover et al., 1995; Sakshaug, 1997). During the last decade, however, parts of the microbial food web in the Barents Sea region have been investigated (Thingstad and Martinussen, 1991; Hansen et al., 1996; Hansen and Jensen, 2000; Jensen and Hansen, 2000; Allen et al., 2002; Howard-Jones et al., 2002; Rat'kova and Wassmann, 2002; Verity et al., 2002). Yet only the study by Hansen et al. (1996), covering four stations in the central Barents Sea, considers all components in the microbial food web, i.e. bacteria, heterotrophic nanoflagellates, ciliates and heterotrophic dinoflagellates. They proposed that bacterioplankton and microbial grazers play a major role for pelagic carbon turnover during spring bloom and throughout summer in the central Barents Sea.

The MIZ spring bloom is important for the production of the Barents Sea, but knowledge about the role of the bacterial community, in cycling of dissolved organic matter lost during

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the bloom is limited. Such knowledge from the Arctic is essential to understand the function of these ecosystems and the global carbon budget in general (Azam et al., 1983; Legendre and Le Fevre, 1995). Regional coupled ecosystem models are powerful tools to elucidate carbon flow and dynamics, but there is a substantial lack of high-resolution validation data for the ongoing effort of implementing the microbial food web in carbon flux models for the Barents Sea, especially in the seasonal transition from the spring bloom to regenerated summer production (Wassmann and Slagstad, 1993; Slagstad and Wassmann, 1996; Slagstad et al., 1999; Wassmann et al., 2006).

To evaluate the importance of the bacterial community for the carbon flow through the microbial food web and the bacterial potential of transporting carbon into the classical food web, we investigate the role of bacterioplankton on a spatial and temporal scale in the northern Barents Sea during spring-bloom development.

2. Material and methods

2.1. Study area

The present study was conducted in the northern Barents Sea aboard R/V "*Jan Mayen*" (University of Tromsø, Norway) during two summer cruises: 8–22 July 2003 (Stns. I, II, III and IV) and 20 July–4 August 2004 (Stns. VII, X, XI and XIII) and one spring cruise: 18 May–5 June 2005 (Stns. XIV, XVI, XVII and XVIII). Sampling sites were chosen to represent different stages of the spring-bloom succession (Fig. 1). Sampling Stns. I–XVIII roughly approach S–SE to N–NW transect, crossing the Polar Front. Stations were visited in numerical order due to movement and melting patterns of the ice cover. Generally, the MIZ moved northeast during the cruises.

2.2. Temperature, salinity and nutrients

At each station water-column characterization was based on temperature, salinity and nutrient concentration. Profiles of salinity, temperature and fluorescence were recorded from the surface layer and down to 200 m using a CTD Sealogger (SBE Sea-bird Electronic) equipped with a fluorometer (Seapoint Chlorophyll Flourometer; Seapoint Sensors, Inc.). Chlorophyll-*a* (chl-*a*) maximum depths were identified from the fluorescence profiles. Water samples were collected from 12 fixed depths, (1, 5, 10, 20, 30, 40, 50, 60, 90, 120, 150, 200 m) and one additional depth for the chl-*a* maximum if not covered by one of the fixed depths. From the upper eight depths and the chl-*a* maximum depth, water was sampled with a 20 and 30-L Go Flo bottle (model 1080, General Oceanics). Water from the lower four depths (90 m and below) was collected with 5-L Niskin bottles (model 1010C) mounted on a rosette together with the CTD Sealogger. Nitrate, phosphate, silicate and chl-*a* concentrations were measured for each sampling depth from 0 to 200 m. Nutrients were analysed on an automatic nutrient analyser (Dansk Havteknik) according to Grasshoff (1976) with a precision of 0.06, 0.09 and 0.12 µM for nitrate, phosphorus and silicate, respectively.
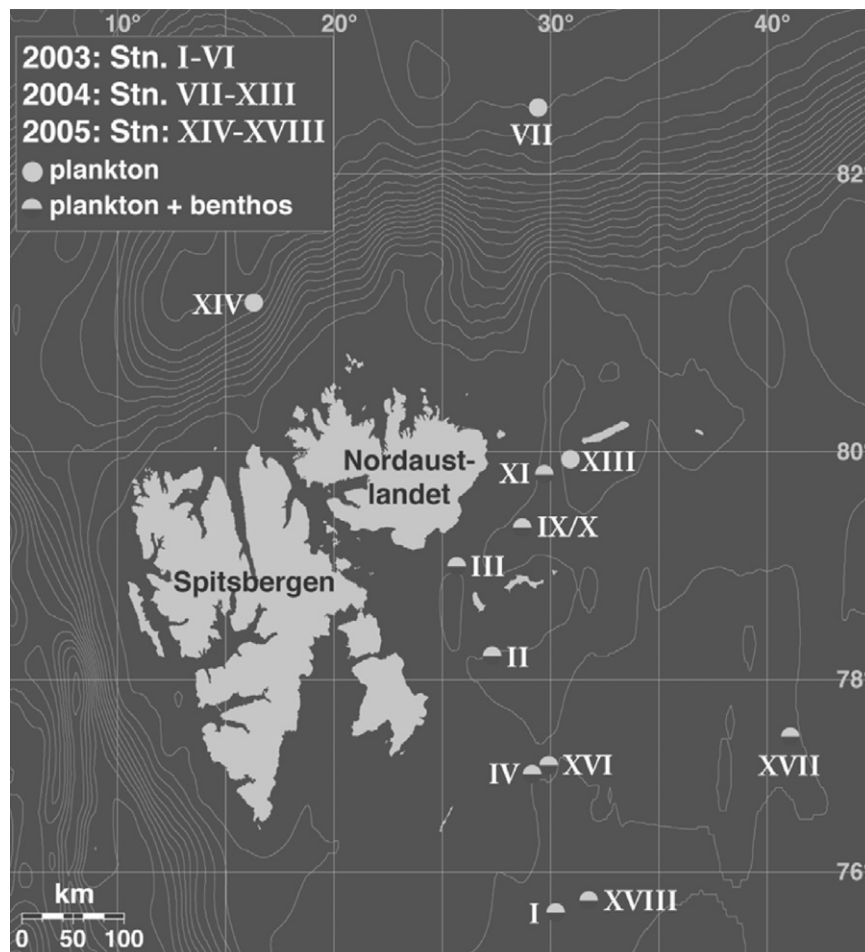

Fig. 1. The study area of the northern Barents Sea. Roman numbers indicate sampling stations.