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Microzooplankton community structure and grazing impact on major phytoplankton in the Chukchi sea and the western Canada basin, Arctic ocean

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ABSTRACT

We investigated the microzooplankton community and its grazing impact on major phytoplankton groups in the Chukchi Sea and in the western Canada Basin during the period July–August 2010. The study area was divided into three regions based on topography, hydrographic properties and trophic conditions: (1) a productive region over the Chukchi Sea shelf (CSS) with high phytoplankton biomass dominated by diatoms, (2) an oligotrophic region over the Northwind Abyssal Plain (NwAP) with low phytoplankton biomass dominated by picophytoplankton, and (3) the Northwind Ridge (NwR), over which waters were dominated by picophytoplankton and diatoms. The spatial distribution of microzooplankton biomass and its composition were related to differences in phytoplankton biomass and assemblage composition in the three water masses. Heterotrophic dinoflagellates (HDF) and ciliates were significant components of microzooplankton populations. Athecate HDF was the most important component in the CSS, where diatoms were dominant. Naked ciliates were dominant microzooplankton in the NwR. Microzooplankton grazing rate varied by the assemblage composition of both phytoplankton and microzooplankton. Microzooplankton was capable of consuming an average of 71.7 ± 17.2% of daily phytoplankton production. Growth rates of smaller phytoplankton (i.e., picophytoplankton and autotrophic nanoflagellates) and grazing rates on them were higher than rates for diatoms. Microzooplankton grazed more on picophytoplankton (PP grazed = 89.3 ± 20.5%) and autotrophic nanoflagellates (PP grazed = 82.3 ± 22.5%) than on diatoms (PP grazed = 62.5 ± 20.5%). The dynamics of predator and prey populations were almost balanced in waters in which smaller phytoplanktons were dominant. Picophytoplankton production was consumed by microzooplankton allowing transfer to larger consumers. On average, microzooplankton grazed 62.5% of the diatom production in the waters we studied, indicating that the classical food chain (with carbon flux from diatoms to copepods) is likely operational and of significance in this region. Overall, microzooplankton grazing was an important process controlling phytoplankton biomass and composition in the Chukchi Sea and the western Canada Basin during early summer.

1. Introduction

Microzooplankton are key components of pelagic food webs. They are important grazers of phytoplankton and act as a food source for consumers at higher trophic levels. These micro-grazers are highly abundant, ubiquitous in the world's oceans, grow rapidly and have unique feeding mechanisms that allow ingestion of wide spectrum of food particle sizes. This combination of attributes makes micrograzers essential elements in the functioning of pelagic ecosystems (Hansen et al., 1994; Sherr and Sherr, 2002; Calbet and Landry, 2004; Calbet and Saiz, 2005; Saiz and Calbet, 2011). Microzooplankton community structure and grazing pressure are drivers of top-down control pressure on phytoplankton in pelagic ecosystems. These drivers may restructure phytoplankton assemblages when grazing is selective, and they influence the functioning of the microbial food web (Burkill et al., 1987; Reckermann and Veldhuis, 1997; Irigoien et al., 2005; Calbet, 2008; Yang et al., 2012). Consequently, the details of microzooplankton community structure and the net grazing impact on phytoplankton are crucial for an expanded understanding of carbon flow and the fate of primary production in marine ecosystems.

In the western Arctic Ocean, the broad and shallow Chukchi shelf links the Pacific and the Arctic Oceans. During transit through

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the Chukchi Sea, Pacific waters flowing from the Bering Strait are significantly modified by oceanic and atmospheric forcings. These mechanisms play a significant role in the stratification and circulation of the western Arctic Ocean (Aagaard et al., 1981). A combination of seasonally variable environmental factors and the inflow of warm Pacific water result in spatial and temporal variability of the water mass in the western Arctic Ocean (Carmack and Wassmann, 2006). Thus, productivity and plankton composition in this region are regulated by physical forcing and hydrographic characteristics of the water mass (Ashjian et al., 2003; Grebmeier and Harvey, 2005; Lane et al., 2008; Sukhanova et al., 2009). The Arctic Ocean is currently undergoing rapid environmental change resulting from natural and anthropogenic drivers, which include accelerated warming (Steele et al., 2008; Zhang et al., 2010), decreased extent of sea ice cover (e.g., Comiso et al., 2008) and other physical changes. These changes will have a major impact on ecosystem functioning and biogeochemical cycling in the Arctic Ocean (e.g., Sakshaug and Slagstad, 1992; Walsh et al., 2004). Because of ongoing changes in the Arctic, there is an urgent imperative for better characterization and understanding of food web structures that are key elements of the Arctic pelagic ecosystem.

Comprehensive studies of pelagic Arctic microzooplankton assemblages have generally been limited to the central Arctic Ocean, including the Chukchi Sea (Sherr et al., 1997; Sherr et al., 2003; Sherr et al., 2009), the Bering Sea (Olson and Strom, 2002; Strom and Fredrickson, 2008; Sherr et al., 2013), western Greenland (Nielsen and Hansen, 1995; Levinsen et al., 1999, 2000; Levinsen and Nielsen, 2002), and the Barents Sea (Verity et al., 2002). Previous studies have emphasized the importance of microzooplankton in microbial assemblages and their role as major consumers of phytoplankton. Campbell et al. (2009) reported that microzooplankton were generally preferred over phytoplankton as prey for copepods in the western Arctic Ocean. However, other studies have described low levels of microzooplankton grazing on phytoplankton during the spring and summer seasons in portions of the high Arctic Ocean (Sherr et al., 2009; Calbet et al., 2011). Most Arctic studies of microzooplankton have been conducted in eastern Arctic waters, coastal, bays and/or relatively low latitude sites. At the present time, the high-latitude marine ecosystem is particularly sensitive to climate change because small temperature differences can have large effects on the extent and thickness of sea ice (Holland et al., 2006). However, the role of microzooplankton in food webs of the high-latitude sectors of Arctic Ocean remains uncertain. The work reported here is a first step toward improved understanding of the role of microzooplankton in high-latitude waters of the western Arctic Ocean (73–78°N).

The results of this study emphasize the need for further research for a broader perspective on the phytoplankton–microzooplankton trophic link in pelagic ecosystems of high-latitude Arctic Ocean. We investigated spatial variation of microzooplankton assemblages and their grazing impacts on phytoplankton in different waters during early summer to determine the relative importance of microzooplankton composition in different geographic regions through its effect on the grazing pressure exerted on major phytoplankton groups.

2. Materials and methods

The Korea Arctic Research Program mounted a multidisciplinary expedition in the Pacific sector of the Arctic Ocean aboard the *IBRV* Araon icebreaker during the period 17 July–14 August 2010. The study area included (1) the Chukchi Sea shelf (CSS; stns 1, 38, 3, 4, 35), (2) the Northwind Abyssal Plain (NwAP; stns 33, 32, 31, 28, 29), and (3) the Northwind Ridge (NwR; stns 6, 8, 10, 13, 14) (Fig. 1).

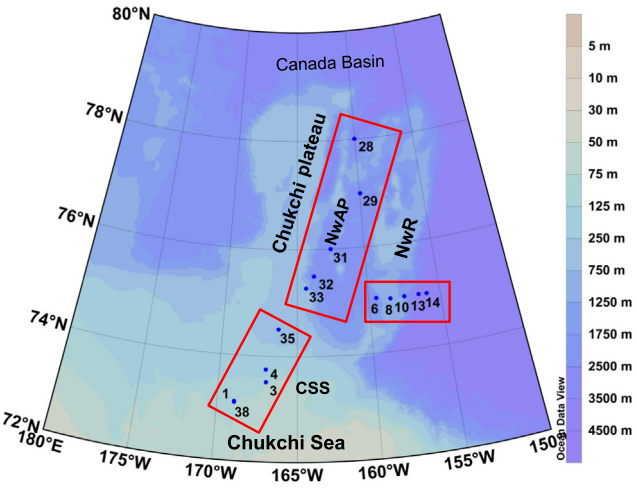

Fig. 1. Sampling stations in the western Arctic Ocean from 17 July to 14 August, 2010. NwAP, Northwind Abyssal Plain; NwR, Northwind Ridge; and CSS, Chukchi Sea shelf.

2.1. Collection and analysis of hydrographic data

At all the stations, we made hydrocasts to make measurements of conductivity/temperature/depth (CTD) (SeaBird Electronics, SBE 911plus) that were used to plot vertical profiles of temperature and salinity. Using traditional *T–S* (temperature–salinity) diagram analyses, we determined the mixing and transformation of water masses. To collect water samples for measurements of chlorophyll-*a* (Chl-*a*) concentration, we installed 12 Niskin bottles (20 l each) on the CTD frame to sample waters at depths of 3, 10, 20, 30, 75, 100 m and at the depth of the subsurface chlorophyll maximum (SCM). Water subsamples (1 l) were filtered through glass-fiber filter paper (25 mm; Gelman); Chl-*a* concentrations were measured with a Turner Designs fluorometer (TD-700) following extraction in 90% acetone (Parson et al., 1984). The fluorometer had been previously calibrated against pure Chl-*a* (Sigma-Aldrich).

2.2. Phytoplankton and microzooplankton

To determine abundances of microzooplankton by depth, we used a Niskin rosette sampler to collect water samples at 3, 10, 20, 30, SCM, 75, and 100 m depths. Water samples for phytoplankton biomass analysis were taken from 10 m and at the SCM depth, the two depths for which dilution experiments were conducted at each station. To determine the abundance of plankton other than ciliates and diatoms, we preserved 500 ml samples of water with glutaraldehyde (1% final concentration), then stored them at 4 °C before staining and filtration. Subsample of 100 ml was filtered onto nuclepore filters (0.8 μm pore size, black) for 3–20 μm sized plankton and 300 ml subsample was filtered onto nuclepore filters (8 μm pore size, black) for >20 μm sized plankton. For picophytoplankton (<3 μm sized), subsample of 20–40 ml was filtered onto nuclepore filters (0.2 μm pore size, black). Aliquots of the preserved samples were stained with proflavin (0.33%) for an hour before filtration. During filtration, the samples were drawn down until 5 ml remained in the filtration tower. Concentrated DAPI (50 μg ml^{-1} final concentration) was then added and allowed to sit briefly (5 s) before filtering the remaining sample until dry (Taylor et al., 2011). Filters were mounted onto glass slides with immersion oil and cover slips. For nano-and microplankton cells, at least 50 fields per sample were counted with an epifluorescence