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Comparison of phytoplankton macromolecular compositions and zooplankton proximate compositions in the northern Chukchi Sea

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ABSTRACT

The macromolecular (proteins, lipids, and carbohydrates) composition of phytoplankton and the proximate (water, proteins, lipids, and ash) and elemental (carbon and nitrogen) compositions of mesozooplankton were determined in the northern Chukchi Sea to establish the relationship between zooplankton and their phytoplankton food source. Among the phytoplankton macromolecules examined in this study, lipids had the highest contents (58.4 ± 8.2%) and proteins had the lowest (16.1 ± 7.3%), which may be a consequence of a nitrogen deficiency in phytoplankton growth during the study period. In contrast, proteins (59.7 ± 10.6% DW) were the major proximate components in the mesozooplankton community, which was dominated by copepods up to 71% of total abundance. The low lipid contents (13.8 ± 12.4% DW) in the mesozooplankton community in this study might be due to the dominance of small species such as *Calanus glacialis*, which generally have relatively lower lipid contents than large copepods. Moreover, the spawning period of *C. glacialis* from April to June might be an additional reason for the low lipid contents, because copepods have normally very low lipid contents after spawning. The low lipid contents resulted in a low energy content in this mesozooplankton community in the northern Chukchi Sea. The different biochemical compositions of phytoplankton and zooplankton should be considered in order to understand the impacts of climate change on the quality of prey provided by lower trophic levels and subsequently on Arctic marine ecosystems.

1. Introduction

Arctic environments are currently experiencing rapid change. Higher temperatures and the ice export to Baffin Bay and Greenland Sea through the Fram Strait have decreased the extent and thickness of the perennial sea ice in the Arctic Ocean over several decades, producing more open water (Rothrock et al., 2003; Nghiem et al., 2007). Recently, areas in the Western Arctic Ocean such as the northern Chukchi Sea have experienced the most rapid changes in sea ice cover (Perovich and Richter-Menge, 2009). Other sub-Arctic and Arctic waters are subject to the effects of global warming because even a small change in the heat content in the water column causes significant impacts on the spatial distribution and dynamics of sea ice (e.g., Meier et al., 2005; Overpeck et al., 2005; Sarmiento et al., 2004). These changes in climate and ice conditions alter the quantity, quality, and timing of phytoplankton production and subsequently the seasonal distributions, geographic ranges, and nutritional structure of their primary consumers. Those lower trophic level changes are projected to alter the functioning of higher trophic levels (Tynan and DeMaster, 1997). Because seasonal cycles are strongly coupled to the timing of ice-break up and phytoplankton blooms (Smith and Schnack-Schiel, 1990), recent and projected changes in the sea ice cover can affect the protist and metazoan zooplankton communities (Hopcroft et al., 2008). Changes in zooplankton communities lead to changes at higher trophic levels, such as those of fish, seabirds, and marine mammals, because the seasonal success of the zooplankton communities determines the resources available to many higher trophic levels (Hunt and Stabeno, 2002; Hopcroft et al., 2008). Therefore, the current physiological status of phytoplankton to indicate food quality and their primary production to indicate food quantity are needed in order to better understand the impacts of ongoing changes in climate and sea-ice conditions on the Arctic marine ecosystem.

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The biochemical composition and biosynthetic patterns of phytoplankton can provide important clues to their physiological status (Morris, 1981; Smith et al., 1997a; Lee et al., 2009) and about the cycling and trophic transfer of photosynthetically fixed carbon in the marine food web (Laws, 1991; Parrish et al., 1995). Consequently, these photosynthetically synthesized biochemicals (proteins, lipids, polysaccharides, and low-molecular-weight metabolites (LMWM)) could influence the nutritional status of higher trophic levels (Scott, 1980; Lindqvist and Lignell, 1997).

The 3rd Korean Arctic expedition was conducted in the northern Chukchi Sea around the Chukchi Borderland and Mendeleyev Ridge from August 1 to September 10, 2012, onboard the Korean research icebreaker *ARAON*. The primary objective of this study was to find spatial distribution of the macromolecular compositions of phytoplankton in the northern Chukchi Sea. The second objective was to evaluate the nutritional status of the zooplankton community based on their proximate compositions related to macromolecular compositions of phytoplankton.

2. Materials and methods

2.1. Sampling

The vertical profiles of water temperature, salinity, and density were obtained from downcast measurements using a Seabird SBE-911+CTD profiler mounted on a rosette. Oceanographic water samples were collected from a total of 50 stations with a rosette sampler equipped with 20-L Niskin bottles. Samples for the macromolecular composition of phytoplankton were obtained at 25 selected stations (Fig. 1 and Table 1). Mesozooplankton samples were collected within the upper 200 m with a Bongo net (mesh apertures 330 and 500 μm) at 22 stations (Fig. 1 and Table 1) and then distributed for identification and compositional analysis.

2.2. Nutrient and chlorophyll a concentration measurements

The discrete water samples for dissolved inorganic nutrient concentrations (nitrite+nitrate, ammonium, phosphate, and silicate) were analyzed onboard immediately after collection, using an automated nutrient analyzer (SEAL, QuAAtro, UK) according to the manufacturer's instruction. The water samples used for the measurement of total chlorophyll *a* concentration were filtered through Whatman GF/F filters (25 mm). The size-fractionated chlorophyll *a* concentration was determined for samples that were passed sequentially through 20- and 5-μm Nuclepore filters (47 mm) and 0.7-μm Whatman GF/F filters (47 mm). Chlorophyll *a* concentrations were measured using a Trilogy fluorometer (Turner Designs, USA) following the method outlined by Parsons et al. (1984).

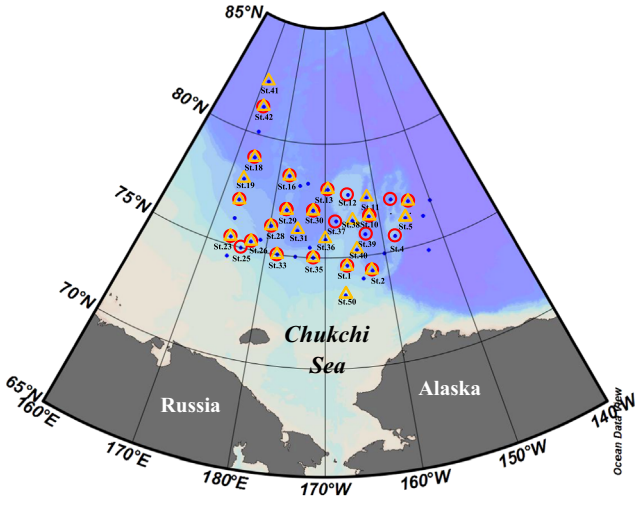

Fig. 1. Locations of sampling stations during the 2012 *ARAON* cruise in the northern Chukchi Sea. Red circles indicate mesozooplankton sampling stations. Yellow triangles indicate phytoplankton macromolecular stations.

Table 1
Location, the water depth (m), and the euphotic depth (Z_{eu}) for phytoplankton and mesozooplankton sampling stations in the northern Chukchi Sea, 2012.

Station	Location		Depth (m)	Z_{eu} (m)
	Latitude (°N)	Longitude (°W)		
1	74.6180	166.3970	374	76
2	74.3000	162.5000	1220	62
4	75.6560	157.7800	915	–
5	76.3249	155.3760	1010	68
6	76.9990	154.0000	1720	62
7	77.2520	157.1520	713	–
10	76.7120	161.8640	1061	76
11	77.5347	161.7760	2690	65
12	77.7500	165.3740	435	–
13	77.9970	169.4480	1232	65
16	78.5000	177.7500	1227	62
18	79.0000	186.0000	2452	41
19	77.9675	186.9585	1090	43
21	77.0350	186.6980	658	46
23	75.3450	186.2340	191	51
25	74.9930	184.1410	155	–
26	75.3710	182.7090	359	51
28	76.2180	179.8360	1193	57
29	77.0060	177.3630	1400	62
30	77.0760	172.3270	2013	65
31	76.1450	174.9480	2169	68
33	75.0000	177.9980	323	57
35	75.0000	171.9990	382	57
36	75.7970	169.9920	754	68
37	76.6000	168.0020	1783	–
38	76.5955	165.0040	567	62
39	75.9450	162.9400	2075	–
40	75.2819	164.6680	618	76
41	82.3237	188.3825	2758	41
42	81.2120	187.5970	2757	41
50	73.3137	165.0571	65	56

2.3. Macromolecular compositional analysis of phytoplankton

Water samples for macromolecular composition of phytoplankton were obtained from 3 light depths (100%, 30%, and 1%). One liter of each seawater sample was passed through a pre-combusted 47 mm GF/F filter (Whatman, 0.7 μm pore) and was then immediately stored at −80 °C until analysis. Quantitative protein analysis followed the method of Lowry et al. (1951), with absorbance measured at 750 nm using a spectrophotometer (Labomed, Germany). The concentration of proteins was calculated using calibration curves constructed using a protein standard solution (2 mg mL^{-1}, SIGMA). Carbohydrate analyses were performed following extraction using the phenol–sulfuric method of Dubois et al. (1956). The concentration of carbohydrates was determined by measuring the absorbance of samples at 490 nm with a glucose standard solution (1 mg mL^{-1}, SIGMA). Lipids were extracted with chloroform and methanol (1:2, v/v) according to Bligh and Dyer (1959) and Marsh and Weinstein (1966). Absorbance for lipids was measured at 360 nm. Tripalmitin solutions were used as the standards for lipid concentration. The calorific