



A dynamic Biologically Active Layer for numerical studies of the sea ice ecosystem

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ARTICLE INFO

Article history:

Received 29 June 2009

Received in revised form 23 May 2010

Accepted 26 June 2010

Available online 7 July 2010

Keywords:

Sea ice

Ecosystem modelling

Primary production

BFM

Ice bottom communities

Arctic

Baltic

ABSTRACT

This work introduces a novel approach for the modelling and coupling of sea ice biology to sea ice physics. The central concept of the coupling is the definition of the Biologically Active Layer, which is the time-varying fraction of sea ice that is connected to the ocean via brine pockets and channels, and acts as a rich habitat for many microorganisms. A simple but comprehensive physical model of the sea ice thermohalodynamics is coupled to a novel sea ice microalgal model of growth in the framework of the Biogeochemical Flux Model. The physical model provides the key physical properties of the Biologically Active Layer and the biological model simulates the physiological and ecological response of the algal community to the physical environment. Numerical simulations of chl-*a* were compared with observations at two different ice stations, in the Baltic and off the coast of Greenland, showing that this new coupling structure is sufficiently generic to represent well the temporal and spatial distribution of sea ice algae during the whole ice season at both sites. This model implementation and coupling structure is viable as a new component of General Circulation Models, allowing for estimates of the role and importance of sea ice biology in the local and global carbon cycle.

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1. Introduction

Sea ice is a stable environment where vertical motion is prevented and organisms may not face the problem of maintaining their position in the euphotic zone or near available food. Consequently, many species have developed several strategies to anchor to the ice matrix, where conditions are more favourable than in the underlying waters (Thomas and Papadimitriou, 2003). Except for those areas where snow cover is extremely thick, light is usually sufficient for net photosynthesis during the polar spring and summer (Grossi et al., 1987). Once the snow cover has melted, light is not a limiting factor anymore, and algae blooms usually occur in and underneath sea ice (Lavoie et al., 2005). Typically, the amount of light regulates the onset of ice algal blooms whereas the availability of nutrients constrains the magnitude of the bloom in polar areas (Kirst and Wiencke, 1995). However, the winter chlorophyll concentration can be occasionally high. For instance, during the mild winter of 2000 in the Gulf of Finland, high chl-*a* concentrations were found already in mid-January, showing no light-limitation at any stage of the ice season due to the thin ice sheet without snow cover (Granskog et al., 2003).

The vertical structure of sea ice displays distinct separate layers whose physical properties, like brine content and light extinction coefficient, have large differences. These properties evolve in time and govern light conditions inside the ice and the exchange of nutrients at the oceanic boundary layer. Biological observations show that microorganisms also are not homogeneously distributed along the depth of the sea ice. Sea ice biology assemblages may be found: (a) in regions of the pack that become flooded with seawater, as a result of either rafting or snow loading (Arrigo, 2003); (b) in the internal layers, the so-called “gap-layers” (Ackey et al., 2008), where organisms are often subject to large environmental fluctuations (Lizotte and Sullivan, 1991); (c) at the ice bottom, extending upward depending upon nutrient availability and salinity (Arrigo and Sullivan, 1992); (d) in a strand layer just beneath the sea ice, where algae are loosely attached to the underside of the sea ice and extend well into the water column (Melnikov and Boudarchuk, 1987; Johnsen and Hegseth, 1991); (e) in the platelet ice of Antarctic regions, where ice crystals nucleate in the water and at the ice-water interface, thus forming a porous and isothermal stable environment with salinity similar to seawater, and where the highest chl-*a* (greater than 1000 mg m⁻³) have been reported (Bunt and Lee, 1970; Arrigo et al., 1993; Thomas and Dieckmann, 2002).

Bottom ice communities exhibit the highest algal biomass accumulation of any sea ice habitat, higher than 500 mg chl-*a* m⁻²

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(Riaux Gobet et al., 2000), with the exception of the platelet ice, which has the highest biomass ever registered. Besides, landfast ice accumulates more algal biomass than pack ice in both Arctic and Antarctic regions: the reported peak biomass accumulation in pack ice has been less than $100 \text{ mg chl-}a \text{ m}^{-2}$ in both polar regions, while in landfast ice biomass has been greater than $200 \text{ mg chl-}a \text{ m}^{-2}$ in the Antarctic and in the Arctic as well (Arrigo, 2003).

Most of our knowledge on sea ice biology still relies on sparse localized observations, mostly concerning sea ice diatoms, whose frustules are better preserved than other microorganisms. Modelling thus represents an auxiliary tool to help qualifying and quantifying the role of sea ice biogeochemistry in the ocean dynamics.

To date, very few studies have dealt with the modelling of sea ice biogeochemistry. Nishi and Tabeta (2005) developed an ice-ocean-ecosystem model and applied it to Lake Saroma, in the bottom 0.02 m of sea ice. They used a 10-layer Maykut–Untersteiner thermodynamic sea ice model, 1-D vertical equations for heat, salinity and momentum, and an intermediate complexity ecosystem model consisting of two submodels: a pelagic one with 13 compartments and an ice one with 12 compartments. Jin et al. (2006) developed

a 1-D ice-ocean-ecosystem model to determine the factors controlling the bottom ice algal community of the landfast ice off Barrow, Alaska. The biology was assumed to develop in a bottom layer of constant thickness of 0.02 m. Snow and ice data were provided from observations. Arrigo et al. (1993) are the only ones that have developed a comprehensive fast-ice ecosystem model, which was tested in the Antarctic sea ice. They coupled a simple first-year sea ice thermodynamic model with an intermediate–complexity model of microalgal growth. The growth of the biological component was based on a temperature-dependent function, which was further controlled by light, nutrient availability and suboptimal salinity. Arrigo et al. (1997, 1998) simplified the physics of the 1-D model of Arrigo et al. (1993) to produce a quasi 3-D model to investigate the temporal and large-scale horizontal variation in standing stock and rates of primary production of ice algae in the Southern Ocean. However, productivity was allowed only in a prescribed interfacial layer of 0.02 m at the ice-snow interface and in a prescribed freeboard layer of 0.1 m, while sea ice bottom communities were not considered. Lavoie et al. (2005) developed a simplified version of the ice algae model of Arrigo et al. (1993) but considered more physical

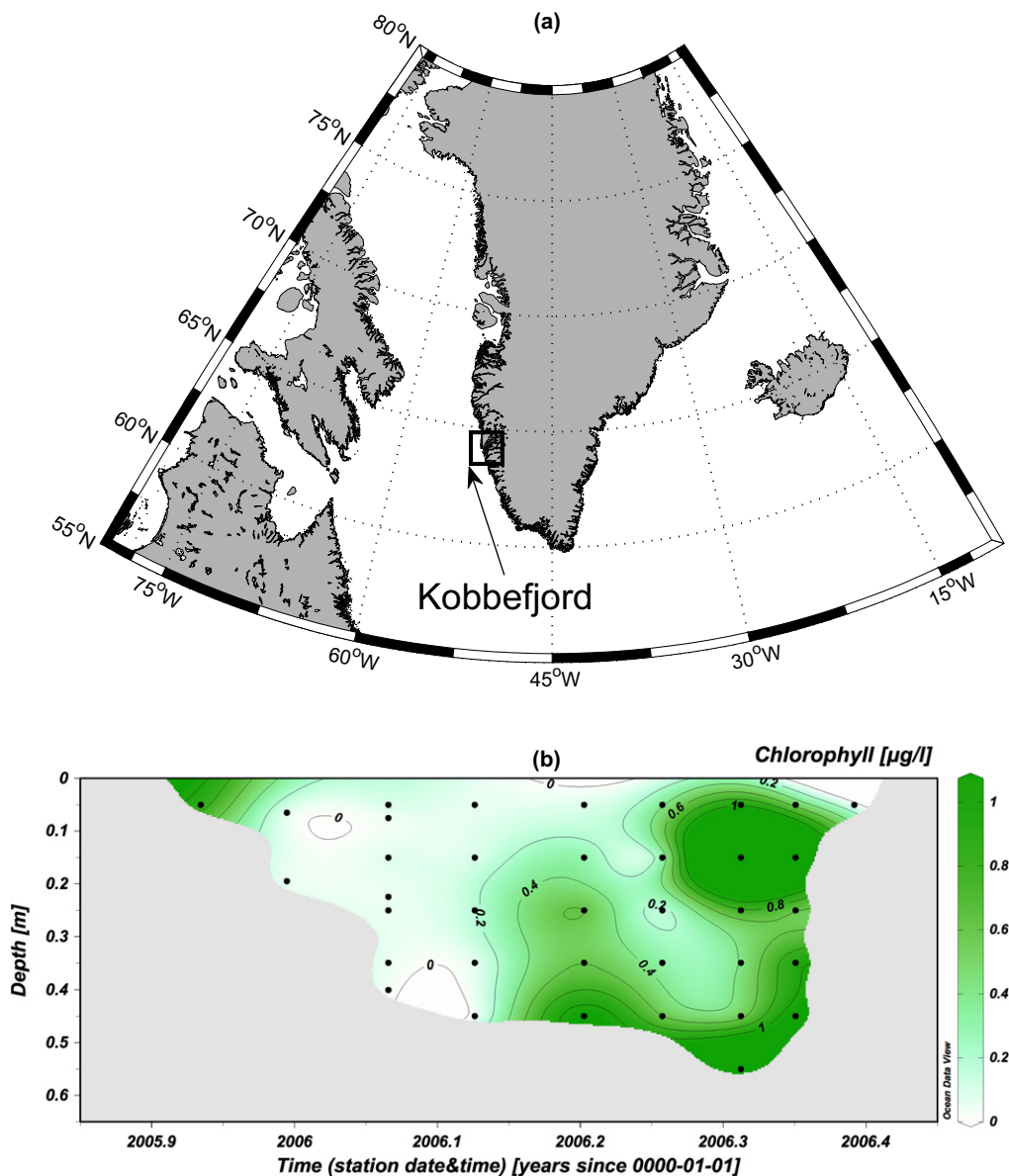


Fig. 1. Location and chlorophyll observations in 2005–2006 at Kobbefjord, the subarctic test-case site (data from Mikkelsen et al., 2008).

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