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The importance of vertical resolution in sea ice algae production models

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ABSTRACT

In this study an ice-algal mathematical model is used to resolve the vertical fine structure of sea ice with ice algae, and results are compared to simulations with ice algae located only at the bottom ice layer and to those where ice algae are distributed homogeneously across part of the ice column. Ice algae are reported to contribute 4–26% of overall Arctic Ocean primary production and are an important food source for the ice-associated ecosystem. Thus, it is important to estimate the future impacts of global warming on the contribution of ice algae to Arctic primary production. Primary production models, describing the relationships between ice-algal physiology and population dynamics, with environmental forcing and trophic interactions involving bacteria and grazers, can be applied to quantify such impacts. One important aspect in these models is how to represent the vertical distribution of ice algae in sea ice. In most models, only the bottom ice layer is considered where most of the algal biomass tends to be concentrated. However, since ice algae are also present along the entire ice column, this may lead to underestimation of ice-algal production. Some empirical data and model results suggest that ice algae located in the surface and interior layers may be kept at lower concentrations, in spite of high growth rates, due to grazing by micro- and meiofauna. Results obtained in this study show the importance of resolving vertically the distribution of ice algae to avoid bias in primary production estimates, well in line with empirical studies.

1 . Introduction

Previous estimates of Arctic ice-algal primary production (PP) based on a limited number of measurements ranged from 9–73 Tg C year^{-1}, corresponding to 4–26% of total Arctic PP (Legendre et al., 1992). In a recent modeling study, Jin et al. (2012) estimated an average Arctic ice-algal PP of 21.7 Tg C year^{-1} for the period 1992–2007. This accounts for roughly 5% of pelagic PP, considering estimates of the same authors and those of Pabi et al. (2008) of >400 Tg C year^{-1} for the period 1998–2006. Whilst the contribution of ice-algal PP appears to be relatively low at a Pan-Arctic level when compared to pelagic PP, ice algae mediate important biogeochemical processes through the ice–water and ice–atmosphere interfaces (Nomura et al., 2013; Vancoppenolle et al., 2013) and provide an early, highly concentrated and nutritious food source for specialized ice-associated and pelagic grazers (Leu et al., 2011; Poltermann, 2001; Søreide et al., 2010). A tight sympagic (sea ice)–pelagic-benthic coupling in Arctic waters around Svalbard was also revealed by stable isotopes and fatty acid trophic markers (Tamelander et al., 2006; Søreide et al., 2013). Recent results seem to support the hypothesis that sea ice thinning (e.g., Kwok and Rothrock, 2009; Polyakov et al., 2012) and increasing melt pond cover (e.g., Rösel and Kaleschke, 2012) in the Arctic Ocean may enhance under-ice productivity and ice-algal export, with ecological consequences from the surface ocean to the deep sea (Boetius et al., 2012). Ice-algal production may be higher than phytoplankton production in some shelf areas of the Chukchi and Beaufort Seas, according to Gradinger (2009) from data obtained in May/June 2002. The declining ice extent may lead to a reduction in the contribution of ice algae to organic matter produced in the Arctic Ocean (Arrigo, 2014).

In spite of the potential importance of sea ice for global biogeochemistry, it is represented as biologically and chemically inert in Earth system models (Vancoppenolle et al., 2013). Most of the modeling efforts of sea ice biogeochemistry have focused on ice algae and associated biogeochemistry. Tedesco and Vichi (2014) presented a synthesis of ice biogeochemical models published over the last 10 years (cf. — Table 1 of the cited authors). These may be roughly classified in three groups, according to how different authors represented the vertical distribution of ice algae and associated biogeochemical processes: a) One-layer models of fixed thickness, b) one-layer models of variable thickness and c) multi-layer models. The first type simulates ice algae only at the ice bottom assuming some specific thickness for the bottom ice layer (Jin et al., 2006, 2008). The second type simulates ice algae only in one layer but of variable thickness – the Biological Active Layer (BAL) – (Tedesco et al., 2010, 2012; Tedesco and Vichi, 2014). The third type resolves vertically the concentration of ice algae and biogeochemical processes considering a number of layers within the ice (e.g., Arrigo et al., 1993; Vancoppenolle et al., 2010; Pogson et al., 2011; Saenz and Arrigo, 2012).

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The rationale to justify using only one ice layer in models applied to the Arctic Ocean is based on the fact that ice algae are, usually, found in highest concentrations near the bottom of sea ice (Tedesco and Vichi, 2014). This common assumption is reflected in the Los Alamos Sea Ice Model (CICE) which simulates biogeochemical processing and ice algae in a single layer attached to the sea ice bottom (Elliott et al., 2012; Hunke et al., 2013).

None of the modeling studies cited above evaluated the effects of neglecting/resolving vertically the ice-algal distribution. Tedesco et al. (2010) compared results obtained with a one-layer model of fixed ice-algal layer thickness with those of a one-layer model of variable thickness (the BAL model) concluding that the former underestimates ice-algal biomass. However, comparisons with multi-layer models were not carried out.

Several empirical studies (e.g., Gradinger, 1999; Mundy et al., 2011) have shown peaks in ice-algal concentrations throughout the entire ice column, although with uneven distribution. Cota et al. (1991a) mentioned that ice algae tend to be concentrated at the bottom of land-fast ice. This is not necessarily true in pack ice, where more surfaces bathed by seawater are available along the sides and in the relatively porous interior (Garrison et al., 1986; Gradinger, 1999). In the Barents Sea there are six possible assemblages of ice algae in drifting sea ice, divided among surface, interior and bottom assemblages, according to Syvertsen (1991). In addition, pressure ridges with rafted sea ice may contain additional communities. According to Gradinger (1999), high ice-algal biomass accumulations were found at the surface, in the interior and in the bottom layer of ice floes in Arctic pack ice. The same authors indicated that studies dealing only with the bottom few centimeters of the ice floes may underestimate algal biomass and production by factors of up to 25. Mock and Gradinger (1999), using a method of measuring ice-algal primary production that resolved its vertical variability, concluded that traditional methods restricted to the study of bottom communities may have severely underestimated Arctic as well as Antarctic primary production. Chlorophyll peaks were observed high in the ice during advanced stages of ice melt in July in Darnley Bay, a coastal Arctic bay along the southern shore of Amundsen Gulf (Mundy et al., 2011). At this time, the sub-ice-algal layer had disappeared due to melting, but good growth conditions still existed inside the congelation ice, which consists of columnar ice with well-oriented crystals. Moreover, it may be hypothesized that, even when most of ice algae are concentrated at the bottom layer, the small amount of algae higher in the ice may have an important contribution to ice primary production due to a higher exposure to irradiance. Also, empirical and model results presented by Tedesco et al. (2010) provide further evidence that ice-algal biomass and production higher in the ice may be important. In a recent winter survey (February 2014) north of Svalbard in connection with the Centre for Ice, Climate and Ecosystems (ICE) project "N-ICE2015" (www.npolar.no/n-ice2015) sampled ice cores exhibited a chlorophyll maximum of 1.5 $\mu g\ L^{-1}$ at the middle of the ice column (P. Assmy et al., unpubl. data). All these arguments point out to the potential relevance of ice algae located above the bottom layer of sea ice, in spite of the overwhelming evidence for their dominance in the latter.

The main goal of the present study is to evaluate the importance of resolving the vertical distribution of ice algae in primary production models for ice-covered waters, by comparing results obtained with the three types of model approaches (a–c) described above with regards to their primary production and biomass dynamics forecasts. A complementary objective is to discuss some structural aspects of ice-algal models where different paradigms are followed concerning the role of nutrient limitation and the way multiple factor limitation is handled. Obtained results may contribute to the definition of the requirements for an ice-algal model applicable at regional spatial scales, integrated in coupled physical–biogeochemical models.

2 . Methodology

The modeling approaches described herein are based on three model setups. In the first approach it is assumed that all biomass is concentrated in the bottom 3 cm of sea ice, i.e., at the bottom layer (Jin et al., 2006, 2008). Hereafter this will be referred to as the 0D model setup. In the second approach, it is also assumed that algae are concentrated in only one layer but the thickness of it may change, according to ice properties and following the Biologically Active Layer (BAL) concept (Tedesco et al., 2010, 2012; Tedesco and Vichi, 2014). Hereafter, this will be referred to as the BAL setup. The third approach resolves vertically ice-algal biomass across the whole ice column, sensu Arrigo et al. (1993). Hereafter, this will be referred as the 1D model setup. Results obtained with the three approaches are compared. All model setups were designed for possible coupling with regional 3D models simulating hydrodynamics, ice dynamics and biogeochemical processes in the Arctic Ocean.

In the 0D model, all ice biogeochemistry and ice-algal growth takes place at the bottom layer, similarly to the model of Jin et al. (2006). In the BAL and in the 1D model, ice is divided in one bottom layer and 19 congelation ice layers. The thickness of the former remains constant during the simulation, whereas the thickness of the latter ones is kept equal among them but reduced/increased proportionately as the total ice thickness decreases/increases. Therefore, at each model time step, the vertical geometry of the model grid is adjusted implying the recalculation of properties at each "adjusted" layer by a weighted average of the properties of adjacent layers. When ice grows, it is assumed that the bottom layer remains with the same thickness implying that the layer above will "receive" a part of the previous bottom layer. Similar transfers occur from the first congelation layer to the one above it and so forth until the surface. The net result is that all 19 congelation layers will have their thickness increased by the same amount. When ice melts, it is assumed that part of the lower congelation layer becomes part of the bottom layer to maintain its thickness. This loss will partly be compensated by incorporating a fraction of the layer above it and so forth until the surface. The net result is that all 19 congelation layers will have their thickness decreased by the same amount. Fig. 1 synthesizes the main differences between the three model setups.

In the case of the BAL model, the layers are used only to resolve vertically ice physical and chemical properties. These properties are then averaged vertically across the BAL layer and used to force ice-algal physiology. Ice-algal concentration is considered homogeneous in the BAL. At each model time step, the thickness of the BAL is adjusted according to brine channel volume — the upper limit of the BAL is set at the bottom of the layer where brine channel volume is $\leq 5\%$ (Tedesco et al., 2010).

In the case of the 1D model, the layers are used to resolve the biological properties, and ice-algal distribution is calculated with the same vertical resolution as ice physical and chemical properties. In this model there are two different ways of handling ice-algal "behavior": the passive and the active way. In the passive version, as ice grows, the existing ice algae remain at their original location in the ice. The active way implies that ice-algal cells are capable of some motility and tend to move towards the bottom layer, in accordance with Arrigo et al. (1993). It was implemented by shifting downward ice-algal biomass in block when ice grew and its vertical displacement was equivalent to the magnitude of ice growth. This is the configuration used in the present work since it allows a more realistic vertical distribution of chlorophyll. Without this feature turned on, ice algae become shifted further away from ice bottom during periods of ice grow; this is not supported by most empirical observations showing higher biomasses at bottom ice (e.g. Gradinger, 1999). In all three models, ice thinning related to ice melting leads to a loss of ice algae. In case of the BAL model, this loss is distributed through the BAL layer, whereas in the 0D and in the 1D model this loss occurs only at the bottom layer.