

# Modeling the global cycle of marine dissolved organic matter and its influence on marine productivity



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## ARTICLE INFO

### Article history:

Received 23 October 2013

Received in revised form 16 May 2014

Accepted 17 May 2014

Available online 14 June 2014

### Keywords:

Global biogeochemical cycles

Marine dissolved organic matter

Microbial loop

Marine productivity, 3D numerical modeling

## ABSTRACT

A three-dimensional numerical model is developed for studies on the marine biogeochemical cycles by dealing with coupling of planktonic and microbial processes. The coupling is achieved by explicitly representing generation and consumption of dissolved organic matter (DOM). The model is applied to investigate mechanisms by which the global cycle of marine DOM influences marine productivity. Two categories, biodegradable ( $\text{DOM}_b$ ) and refractory ( $\text{DOM}_r$ ), are considered for DOM.  $\text{DOM}_b$  is generated through phytoplankton exudation, zooplankton excretion, detritus decomposition, and photodissociation of  $\text{DOM}_r$ . Bacteria consume  $\text{DOM}_b$  and generate  $\text{DOM}_r$ . After the long-term adjustment, the observed amount of DOM was reproduced from homogenous conditions of nutrients and plankton. Spatial distribution of bacterial abundance is reasonably validated against recently observed large-scale data. Sensitivity experiments indicated that: (i) over a multi-decadal timescale, contribution of  $\text{DOM}_r$  to global biogeochemical cycles is negligible, (ii) the existence of DOM significantly reduces the global marine primary productivity, and (iii)  $\text{DOM}_b$  originated from phytoplankton exudation is transported to subtropical regions, leading to enhanced primary productivity there as a consequence of nutrient supply associated with remineralization of transported  $\text{DOM}_b$ .

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## 1. Introduction

The ocean stores about 38,000 Pg of carbon, making it the largest carbon reservoir in the Earth system (Sarmiento and Gruber, 2006). Carbon in the ocean exists in various forms, from dissolved inorganic carbon (DIC) to biomass, and DIC accounts for more than 98% of the total marine carbon inventory. Although the abundance of dissolved organic carbon (DOC), which is estimated to be 662 Pg (Hansell et al., 2009) (hereafter referred to as H09), is far smaller than DIC, it represents the largest marine reservoir of reduced carbon and is an essential link between DIC and marine biomass (H09). DOC refers to the carbon part of dissolved organic matter (DOM) which exists as compounds of carbon with nitrogen, phosphorus, oxygen, and other various elements. There still remain many unknown aspects in marine DOM in terms of its chemical composition, spatial distribution, and production and decomposition processes (Hedges, 2002; Carlson, 2002; Ogawa and Tanoue, 2003). We need to reveal such unknown aspects of DOM in order to better understand the marine biogeochemical cycles. The amount of observational data of DOC has been increasing and analytical skill

has been refined (e.g., Hedges, 2002; Sharp, 2002; H09). However, our knowledge on oceanic DOM is still far from sufficient in order to provide rigorous quantitative description of its global distribution, assess its influence on marine productivity, and identify its controlling processes. We need the help of numerical modeling to obtain a global synthesis of marine DOM and associated biogeochemical cycles.

DOM is classified roughly into labile and refractory fractions, and longer-lived labile DOM is categorized separately as semi-labile DOM (Carlson, 2002). Both labile and semi-labile fractions are available to biota, and we hereafter call them collectively as biodegradable DOM ( $\text{DOM}_b$ ) according to Bendtsen et al. (2002) (hereafter referred to as B02).  $\text{DOM}_b$  is produced through various biogeochemical processes, such as phytoplankton exudation, “sloppy feeding” and egestion of grazers, viral-induced cell lysis and decomposition of detritus, and is consumed mostly by bacteria (Nagata, 2000; Carlson, 2002). Refractory DOM ( $\text{DOM}_r$ ) is unavailable to biota and accounts for a large fraction of bulk DOM pools in the ocean (Carlson, 2002). Production and decomposition processes of  $\text{DOM}_r$  are not well known, but it is considered that bacteria are one of its principal sources (Nagata and Kirchman, 2000; Ogawa et al., 2001; Jiao et al., 2010) and that photodissociation due to ultraviolet radiation near the sea surface is one of the principal sinks (Mopper and Kieber, 2002).

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Although production and consumption processes of DOM have been examined using various types of models (e.g., Archer et al., 1997; Anderson and Williams, 1999; Popova and Anderson, 2002; Pahlow and Vézina, 2003), there have been only a few three-dimensional global modeling studies on DOM and its role on marine productivity. Yamanaka and Tajika (1997) (hereafter referred to as YT97) extended a phosphorus cycle model, where particulate organic matter (POM) is produced in the euphotic layer depending on the phosphate concentration and photosynthetically active radiation (PAR) intensity. In their model, POM is remineralized in the aphotic layer by fitting its vertical profile to the observed POM flux (Martin et al., 1987) and DOM is included without explicit microbial processes. DOM is categorized into semi-labile and refractory fractions therein. Semi-labile DOM is produced at a rate proportional to POM production and remineralized with a fixed time constant of the order of 1 yr. Refractory DOM production is also proportional to POM production but at a smaller rate and decomposed in the euphotic layer at a fixed time constant of the order of 100 yrs. According to their results, the global export of DOM at the base of the euphotic layer accounts for a significant fraction of the total organic matter (DOM plus POM) export, but the downward DOM flux rapidly decreases with depth and becomes negligible below several hundred meters depth. Roussenov et al. (2006) used a similar model and showed that near surface horizontal transport of DOM significantly enhances the POM export (via conversion of DOM to POM) in the North Atlantic subtropical region. B02 constructed a simple model for the microbial processes where  $DOM_b$  consumption and  $DOM_r$  production are explicitly represented as consequences of bacterial activities. They succeeded in reproducing the observed high DOM concentration in the deep part of the northern North Atlantic as a result of temperature dependence of  $DOM_b$  consumption by bacteria. Their microbial loop model was driven by a given distribution of POM export from the euphotic layer which was calculated by a separate model, so the microbial processes did not influence the POM producing processes (planktonic processes) and marine productivity.

YT97 pointed out that the lifetime of semi-labile DOM is an important factor controlling its horizontal distribution and suggested that 0.5 yr is an optimal choice to reproduce an observed distribution in the surface water. While the lifetime is an external parameter in their model, it actually is determined by the microbial processes. The microbial model constructed by B02 explicitly deals with the processes which control the lifetime of  $DOM_b$ , but the horizontal distribution of  $DOM_b$  in the surface water was not discussed in their study. It is left to be investigated how the microbial processes control the lifetime of  $DOM_b$  and eventually its distribution and global cycle.

This study presents a global three-dimensional numerical model of the ocean general circulation and biogeochemistry using a combination of three existing models that deal with planktonic (Palmer and Totterdell, 2001), microbial (B02) and physical (Urakawa and Hasumi, 2009) processes. We demonstrate that combined use of these models, which were not used before as such, is instrumental to investigate basic system behavior after long term adjustment of  $DOM_r$ . We are aware that simplified assumptions with a use of coarse grid physical model poses limitations on our modeling results. Recently, studies have stressed the importance of stoichiometric variability and non-Monod type growth kinetics in planktonic processes (e.g., Flynn, 2010). Sophisticated models have been developed to consider stoichiometry in various functional components of ecosystems (Vichi et al., 2007; Vichi and Masina, 2009). However, the data are severely limited concerning stoichiometric balances of DOM-bacteria interactions and microbial growth controls in oceanic water columns especially in deep oceans (BD02; Arístegui et al., 2009; Nagata et al., 2010; Yokokawa et al., 2013). Thus, we use simple assumptions to focus on an

important, yet previously understudied, aspect of global biogeochemical cycles, i.e., role of DOM-bacteria-plankton couplings in regulation of global ocean productivity. Our model is based on nitrogen, similar to the model of Fasham et al. (1990), and carbon cycles are considered using prescribed carbon to nitrogen ratios (see Section 5 on the limitation of this assumption). Unlike the Fasham et al. (1990) model, ammonium is not included in our model. Although ammonium can be an important nitrogen substrate for microbes, it is typically much more diluted (<10 nM) than nitrate and dissolved organic nitrogen in oceanic water columns, contributing only marginally to the oceanic nitrogen inventory (Gruber, 2008). Our microbial model explicitly represents DOM-microbe interactions according to B02 and the model result is validated using recently published data on abundance distribution of free-living microbes (a principal consumer of  $DOM_b$ ) in the central Pacific, Atlantic and Southern Oceans (de Corte et al., 2012; Yokokawa et al., 2013). In our model, dissolution from detritus is one major source of  $DOM_b$ . Although microbial enzymatic hydrolysis plays a major role in detritus dissolution, this process is not explicitly resolved in our model because the validation data on abundance distribution of detritus-associated microbes are scarce (Nagata, 2008). We address the following issues: (1) how the existence of DOM affects marine productivity, (2) how the transport of DOM affects the global marine biogeochemical cycles, and (3) how the temperature dependence of bacterial DOM uptake and mortality affects the lifetime and spatial distribution of  $DOM_b$ .

## 2. Model description

The modeled biogeochemical components are dissolved nutrients, phytoplankton, zooplankton, detritus,  $DOM_b$ ,  $DOM_r$ , and bacteria. Only nitrate and iron are taken into account as dissolved nutrients. Each model component other than iron is represented by its nitrogen content. The flow of nitrogen and iron among the modeled components is summarized in Fig. 1. Note that iron also has external input and scavenging processes. Spatial distribution of these components is affected by oceanic flows and temperatures, which are given as monthly data by an ocean general circulation model. In the following sections, the model is described by dividing it into planktonic, microbial, and physical processes.

### 2.1. Planktonic processes

The formulation of planktonic processes is based on that of Palmer and Totterdell (2001), which is an NPZD-type lower trophic level model. Each component of the model variables (nutrient, phytoplankton, zooplankton, and detritus) is represented by its nitrogen content. The original model takes account also of the

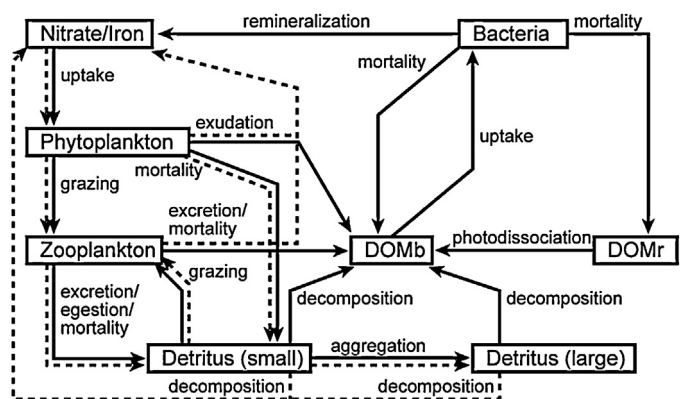


Fig. 1. Schematic diagram of the biogeochemical interaction of nitrogen (solid arrows) and iron (dotted arrows) among modeled components (boxes).

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