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Variable C : N : P stoichiometry of dissolved organic matter cycling in the Community Earth System Model

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Abstract

Dissolved organic matter (DOM) plays an important role in the ocean's biological carbon pump by providing an advective/mixing pathway for ~20 % of export production. DOM is known to have a stoichiometry depleted in nitrogen (N) and phosphorus (P) compared to the particulate organic matter pool, a fact that is often omitted from biogeochemical-ocean general circulation models. However the variable C : N : P stoichiometry of DOM becomes important when quantifying carbon export from the upper ocean and linking the nutrient cycles of N and P with that of carbon. Here we utilize recent advances in DOM observational data coverage and offline tracer-modeling techniques to objectively constrain the variable production and remineralization rates of the DOM C / N / P pools in a simple biogeochemical-ocean model of DOM cycling. The optimized DOM cycling parameters are then incorporated within the Biogeochemical Elemental Cycling (BEC) component of the Community Earth System Model and validated against the compilation of marine DOM observations. The optimized BEC simulation including variable DOM C : N : P cycling was found to better reproduce the observed DOM spatial gradients than simulations that used the canonical Redfield ratio. Global annual average export of dissolved organic C, N, and P below 100 m was found to be 2.28 Pg C yr^{-1} (143 Tmol C yr^{-1}), 16.4 Tmol N yr^{-1}, and 1 Tmol P yr^{-1}, respectively with an average export C : N : P stoichiometry of 225 : 19 : 1 for the semilabile (degradable) DOM pool. DOC export contributed ~25 % of the combined organic C export to depths greater than 100 m.

1 Introduction

Dissolved organic matter (DOM) is an important pool linking nutrient cycles of nitrogen (N) and phosphorus (P) to the ocean's carbon cycle. Following its net production in the surface ocean, DOM provides an advective pathway for removal of biologically fixed carbon (C) to the deep ocean, accounting for ~20 % of the C exported within the ocean's biological pump (Hansell, 2013). Remineralization of DOM in the ocean's interior is carried out by microbial heterotrophs, respiring C while releasing inorganic N and P nutrients back to the water column. The concept of the Redfield ratio (Redfield, 1958; Redfield et al., 1963) has been a unifying paradigm in ocean biogeochemistry linking the stoichiometry of biological production and phytoplankton cellular material to that of the remineralization of detrital organic matter (OM) and inorganic nutrient ratios in the water column. At the global scale, production/decomposition of particulate OM (POM) in the ocean is thought to largely follow the canonical Redfield ratio of 106 : 16 : 1 for C : N : P, however some recent studies have suggested more variable C : N : P ratios (i.e., Martiny et al., 2013a, b). Large deviations from the Redfield ratio have been documented for DOM (Aminot and Kérouel, 2004; Hopkinson and Vallino, 2005). Hopkinson and Vallino (2005) found DOM production and decomposition to follow a stoichiometry of 199 : 20 : 1, indicating the more efficient export of C within DOM per mol of N and P relative to sinking POM. This finding is significant in light of evidence that future perturbations to the ocean from global climate change may favor enhanced partitioning of production to DOM (Wohlers et al., 2009; Kim et al., 2011). Thus accounting for variable stoichiometry within the DOM pool that deviates from the Redfield ratio requires a re-evaluation of the controls on C export and their response to future perturbations due to climate change.

Here we aim to incorporate variable production and decomposition stoichiometry within the DOM tracers of the Biogeochemical Elemental Cycling (BEC) model to improve representation of this important carbon export flux and associated nutrient cycles. The BEC tracks the cycling of key biogeochemical tracers (e.g. C, N, P, Fe, etc.) and runs within the ocean general circulation component of the Community Earth System Model (CESM) (Moore et al., 2004). The current release of CESM v1.2.1 contains five DOM related tracers: semilabile DOC, DON, and DOP pools as well as refractory DON and DOP pools (Moore et al., 2014). Here we have added a sixth DOM tracer, refractory DOC. We employ a novel approach to optimize the BEC DOM parameters using available observations, by applying a fast offline solver based on a direct-matrix inversion (DMI) of a linear model of DOM cycling. The 3-D ocean circulation is obtained from the offline tracer-transport model for the ocean component of the CESM (Bardin et al., 2014). The DMI solver uses a parallel multifrontal sparse matrix inversion approach as implemented in the MUMPS solver (Amestoy et al., 2001, 2006) to quickly obtain the equilibrium solutions needed to objectively calibrate the biogeochemical parameters of the DOM cycling model by minimizing the misfit between the model and observations. The DOM cycling parameters from the equilibrium solution of the offline model are then incorporated within the BEC and optimized with only minor additional tuning.

The remainder of this article is organized as follows. Section 2 describes: (1) the current representation of DOM cycling in the BEC v1.2.1, (2) the global ocean dataset of DOM observations utilized for the optimization, (3) structure of the offline DOM cycling model and the DMI solver, and (4) the modified BEC model with improved DOM cycling parameters with the metrics employed for optimization. Section 3 details the results of (1) the offline DOM cycling model solution, (2) the reference CESM-BEC v1.2.1 simulation, as well as (3) the BEC simulation with optimized DOM cycling, including a comparison of DOM cycling metrics. Sections 3.4 and 3.5 describe a comparison of multiple DOM cycling schema and an evaluation of direct uptake of DOP by phytoplankton in the BEC model, respectively. We conclude with a discussion and summary of our results (Sect. 4).

2 Methods

2.1 DOM cycling in the Standard BEC v1.2.1

Model simulations with the optimized DOM parameters are compared against a reference simulation using the standard version of the CESM-BEC v1.2.1, which we refer to as “REF”. The BEC model runs within the ocean physics component of CESM1 (Gent et al., 2011), which is the Parallel Ocean Program, v2 (Smith et al., 2010). Detailed description and evaluation of the ocean general circulation model is given by Danabasoglu et al. (2011). Additional documentation, model output, and model source code are available online (www2.cesm.ucar.edu). The REF simulation has a nominal horizontal resolution of 1° with 60 vertical levels ranging in thickness from 10 m (in the upper 150 m) with increasing layer thickness increasing with depth below 150 m. Results are presented for the final twenty-year annual average from a 310 year simulation.

A flow chart of organic matter cycling in the BEC is shown in Fig. 1 and a list of DOM parameter values from REF are given in Table 1. Primary production is carried out amongst 3 phytoplankton groups, which take up available inorganic nutrients and have losses to zooplankton grazing, sinking particulate organic matter (POM), and semilabile DOM. Organic matter is produced with a C : N : P stoichiometry set to the slightly modified Redfield ratio of Anderson and Sarmiento (2004), 117 : 16 : 1. Additional sources to semilabile DOM include grazing losses when phytoplankton are grazed by zooplankton as well as direct zooplankton losses. A variable fraction of DOM production is sent to the refractory DOM (DOMr) pool, with different fractions going to the dissolved organic N and P pools. Approximately fifteen percent of modeled primary production (PP) is sent to the DOM pool via these sources, with the remainder of PP cycling as POM. It is important to note that the BEC does not specifically track the total production/decomposition of DOM, which is estimated to be 30–50 % of net primary production (NPP) (Carlson, 2002; and references therein). Rather, BEC semilabile and refractory DOM tracers track the *accumulating* DOM pools that cycle on timescales of years to centuries and represent a smaller portion of NPP, ~ 5–10 % (Hansell, 2013). The labile DOM pool, which cycles on timescales of minutes to days (Hansell, 2013) is not explicitly modeled and is instead rapidly converted to inorganic carbon and nutrients at each time step.

Microbial remineralization is the dominant sink for both POM and DOM pools and is parameterized by assigned remineralization rates. POM is remineralized following a prescribed remineralization vs. depth curve, with a length scale that increases with depth (Moore et al., 2014). Semilabile DOM pools are assigned lifetimes (1/remineralization rate) that depend on the light field with model grid cells where photosynthetically active radiation (PAR) is > 1 % of surface irradiance being assigned a euphotic zone lifetime. Semilabile DOM in model grid cells with PAR < 1 % is assigned a mesopelagic zone lifetime. Remineralization is more rapid for semilabile DOM in the euphotic zone, with lifetimes on the order of 5 months for DON + DOP and ~ 8 months for DOC. Longer lifetimes for semilabile DOM are assigned in the mesopelagic zone with the order of remineralization lifetimes following C > P > N. Remineralization of refractory DOM follows a similar light dependence with a faster remineralization rate given to DOMr in euphotic zone grid cells to parameterize a sink via UV oxidation (Carlson, 2002). DOMr below the euphotic zone is remineralized over centennial timescales.

2.2 Database of DOM ocean observations

We compiled publicly available and literature observations of DOM concentrations into a single database for use in both the DMI-enabled linear DOM model as well as to evaluate our BEC DOM optimization model runs. Briefly, the database contains over 34 000 observations of DOC, > 18 000 observations of DON, and > 2000 observations of DOP. Geographic coverage for the 5 ocean basins is moderately balanced for observations of DOC and DON, however the Atlantic Ocean dominates available DOP observations with DOP data completely lacking for the Indian, Southern, and Arctic Oceans. Semilabile DOM is defined as the total observed DOM concentration less the refractory concentration as determined from the asymptotic concentration of DOM depth profiles. Refractory DOC concentrations vary by ocean basin in the range 37.7 µM (South Pacific) to 45.0 µM (Arctic). Globally constant concentrations are used for refractory DON (1.8 µM) and refractory DOP (0.03 µM). Full details of this DOM database are given elsewhere (Letscher et al., 2014).

2.3 Application of the DMI-enabled solver with a linear DOM cycling model

2.3.1 1st iteration – DOM source from BEC PP

The linear DOM cycling model cycles DOM with one source/sink and uses an idealized annual ocean circulation in offline mode from the CESM-POP2 ocean circulation model (Bardin et al., 2014); nominal 1° horizontal resolution with 60 vertical levels, i.e. the same grid as the standard BEC v1.2.1. In this simple model of DOM cycling, two tracers of DOM are simulated for each element, C, N, and P: semilabile (SLDOM) and refractory (RDOM). The source for each DOM tracer is parameterized as some variable fraction, f, of primary production and is formed within the top model grid level with a thickness of 10 m. The sink for each DOM fraction is microbial remineralization parameterized with an assigned remineralization rate, κ, that differs for the euphotic zone and deep ocean layers in the case of SLDOM. The conservation equations for each DOM tracer are:

$$\frac{\partial}{\partial t}\mathrm{SLDOM} + \mathbf{T}\mathrm{SLDOM} = \begin{cases} f_1\mathrm{PP} - \kappa_1\mathrm{SLDOM} & \text{if } z < 100\,\mathrm{m} \\ f_2\mathrm{PP} - \kappa_2\mathrm{SLDOM} & \text{if } z > 100\,\mathrm{m} \end{cases} \tag{1}$$

$$\frac{\partial}{\partial t}\mathrm{RDOM} + \mathbf{T}\mathrm{RDOM} = f_3\mathrm{PP} - \kappa_3\mathrm{RDOM} \tag{2}$$

where $\mathbf{T}$ = advection-diffusion transport operator (a sparse matrix constructed using output from the dynamical CESM-POP2 model as described in Bardin et al., 2014) and PP = the annual average 3-D primary production field from the coupled ocean-atmosphere run of the CESM for the 1990s (Moore et al., 2013).

We tested the sensitivity of the linear DOM model results to multiple production functions (CESM PP, DOM production flux from the BEC, satellite estimated PP), however results suggest the differing source functions do not appreciably alter modeled DOM distributions or parameter values.

The direct-solver technique makes it possible to objectively calibrate the parameters $f_i, \kappa_i | i = 1\ldots3$ by using a numerical optimization algorithm to minimizing an objective function that measures the misfit between the model-predicted and observed DOM concentration (e.g. Kwon and Primeau, 2006). A separate linear DOM model (Eqs. 1 and 2) is solved for the DOC, DON, and DOP cases. The DMI solver allows us to determine very efficiently the optimal lifetimes for the various DOM pools. It is not practical to determine these using multiple forward simulations of the full CESM-BEC, which would require years to decades of computer time.

2.3.2 Optimized DOM parameter incorporation into the BEC model

The optimized parameter values obtained from the DMI-enabled linear DOM model were incorporated within the BEC to improve its representation of DOM cycling. The BEC model has two tracers for each DOM pool, semilabile and refractory, with differing lifetimes for the euphotic vs. mesopelagic zones. Thus the SLDOM lifetimes, κ_1 and κ_2, from the DMI-enabled DOM model were applied to the BEC model semilabile tracers for the euphotic zone and mesopelagic, respectively. The RDOM lifetime from the DMI-enabled DOM model was applied throughout the full water column of the BEC model. Further fine tuning of DOM lifetimes was carried out to provide the best DOM optimized case, using the mean bias of the modeled concentrations vs. the observations and the log-transformed regression correlation coefficient between simulated and observed DOM in the upper ocean, 0–500 m, as comparison metrics. The BEC simulation containing the set of improved DOM cycling parameters following the first iteration of the DMI-enabled linear DOM model is termed "DOM DEV".

2.3.3 2nd iteration of DMI-enabled linear DOM model – DOM source from BEC DOM production flux

Initial improvements to DOM cycling metrics within the BEC model were large upon incorporation of the DMI-enabled linear DOM model parameter values, however because of differences between the offline model and the full BEC model further improvements to the DOM tracer lifetimes was possible. To achieve this the DMI-enabled linear DOM model was modified such that the production fraction, f, for each tracer was held constant allowing only the remineralization rate, κ, to be optimized. The values of f were diagnosed from the relative proportions of each tracer residing in the euphotic or deep layers at the end of the DOM DEV simulation of the BEC (see Fig. 2). Rather than using PP to get the production flux of each DOM tracer, the semilabile and refractory DOM production fluxes (SLDOMprod, RDOMprod) were extracted from the DOM DEV simulation and used in the modified DMI-enabled DOM model. At this step it was also desired to solve for the remineralization rate associated for a secondary sink for DOMr due to photo-oxidation in the surface layer. Thus Eqs. 1 and 2 were modified to become Eqs. 3 and 4 as follows:

$$\frac{\partial}{\partial t}\mathrm{SLDOM} + \mathbf{T}\mathrm{SLDOM} = \begin{cases} f_1\mathrm{SLDOMprod} - \kappa_1\mathrm{SLDOM} & \text{if } z < 100\,\mathrm{m} \\ f_2\mathrm{SLDOMprod} - \kappa_2\mathrm{SLDOM} & \text{if } z > 100\,\mathrm{m} \end{cases} \tag{3}$$

$$\frac{\partial}{\partial t}\mathrm{RDOM} + \mathbf{T}\mathrm{RDOM} = \begin{cases} f_4\mathrm{RDOMprod} - \kappa_4\mathrm{RDOM} & \text{if } z < 10\,\mathrm{m} \\ f_3\mathrm{RDOMprod} - \kappa_3\mathrm{RDOM} & \text{if } z > 10\,\mathrm{m} \end{cases} \tag{4}$$

The results obtained from the modified DMI-enabled linear DOM model were incorporated into the final DOM OPT simulation of the BEC following minor tuning of the κ parameter values.

3 Results

3.1 DOM parameter output from the DMI-enabled linear DOM model

3.1.1 1st iteration – DOM source from BEC PP

The objectively optimized DOM parameter values from the solutions to the DMI-enabled linear DOM model (DMI-DOM solver) are shown in Table 1. The fraction of the PP flux that accumulates as DOC, DON, and DOP is ∼ 10 %, with the percent-

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age cycling as refractory DOM: DOCr = 0.6 %, DONr = 0.4 %, and DOPr = 0.15 %. Optimized semilabile DOC exhibited the longest lifetimes with a lifetime of 34 years in the euphotic zone (EZ) and 2.9 years in the mesopelagic zone (MZ). Semilabile DON had an intermediate lifetime with respect to DOC and DOP, with an EZ lifetime of 8.7 years and MZ lifetime of 1.7 years. Semilabile DOP had the shortest lifetimes, with EZ lifetime = .8 years and MZ lifetime = 0.8 years. Optimization of the parameters for the refractory pools yielded lifetimes of 20 000 years, 9000 years, and 5000 years for DOCr, DONr, and DOPr, respectively.

3.1.2 2nd iteration of DMI-enabled linear DOM model – DOM source from BEC DOM production flux

Results from the modified DMI-enabled linear DOM model (MOD DMI-DOM solver), which used the BEC DOM production flux from the DOM DEV simulation are shown in Fig. 2 and Table 1. Approximately 7 % of primary production (PP) is routed to production of DOM, which is divided amongst semilabile (SLDOM) and refractory pools (RDOM). Remineralization lifetimes (κ_i^{-1}) differ for SLDOM depending on location in the water column with longer lifetimes for the euphotic zone (depths where PAR > 1 %) than for the mesopelagic zone. A similar faster rate of RDOM remineralization is assigned in the surface layer (< 10 m) to parameterize a sink due to photo-oxidation. The parameter f_i represents the percentage of the DOM production flux that is remineralized within each depth horizon on an annual basis with the sum of $f_1 + f_2 + f_3 + f_4 = 100\,\%$ and is diagnosed from the DOM DEV simulation. The relative magnitude of SLDOM remineralization that occurs within the EZ vs. the MZ was found to be ~ 1.8 : 1 (Fig. 2). Only a small percentage of RDOM remineralization occurs in the surface layer, i.e. 0.01–0.03 % (Fig. 2). The optimal tracer lifetimes from the modified DMI-DOM model were: 15 years for SLDOC in the EZ, 5 years for SLDOC in MZ, 15 000 years for RDOC, and 15 years for RDOC whilst in the surface layer (< 10 m). DON tracer lifetimes were: 15 years for EZ SLDON, 5 years for MZ SLDON, 8000 years for RDON, and 15 years for RDON at the surface. DOP tracer lifetimes were: 62 years for SLDOP in the EZ, 4.5 years for MZ SLDOP, 6000 years for RDOP, and 15 years for photo-oxidation removal.

3.2 Modeled DOM in the standard CESM-BEC v1.2.1 (REF simulation)

A set of metrics were used to assess the performance and improvements to DOM cycling for the CESM-BEC simulations including the global integrals of DOM production, export, and C : N : P stoichiometry (Table 2) as well as the mean bias and correlation coefficient (r) of the simulated DOM concentrations against the observational dataset in the upper 500 m (Table 3). Results and comparison of DOM cycling metrics from the REF simulation are presented in Tables 2 and 3.

DOC – total DOC production in the euphotic zone (upper 100 m) for the REF simulation is 10.5 Pg C yr^{-1} (Table 2). About 85 % of this DOC production is remineralized within the euphotic zone, yielding DOC export from the euphotic zone of $\sim$ 1.7 Pg C yr^{-1}. Modeled semilabile DOC concentrations from the REF simulation are shown for the surface (Fig. 3a) with observations overlain by the colored dots. The spatial extent of regions with elevated (> 30 µM) semilabile DOC concentrations (i.e. the subtropical gyres) is too large in the REF simulation compared to observations. Large overestimates of simulated DOC are found in the Southern Ocean. Modeled semilabile DOC concentrations for the REF simulation at 200 m are shown in Fig. 3b. Model underestimates (up to $\sim$ 75 %) are observed in the oxygen deficient zones in the eastern basins of the equatorial regions. Note that CESM v1.2.1 lacks a DOCr tracer so that simulated DOC is for the semilabile pool only (here we have subtracted the observed deep ocean DOC concentration for each basin from the DOC observations).

DON – total euphotic zone DON production is 120 Tmol N yr^{-1} with > 100 m export of 25.0 Tmol N yr^{-1} (Table 2). Modeled total DON concentrations (semilabile + refractory) at the surface are similarly overestimated in the REF simulation (Table 3) by up to 100 % within the subtropical gyres of the Pacific and the eastern South Atlantic Oceans (Fig. 4a). Model-observation misfit is better at 200 m (Fig. 4b), however biases of 15–

25 % remain (Table 3) in a number of regions (e.g. central equatorial Pacific, South Indian Oceans).

DOP – total euphotic zone DOP production is 7.43 Tmol P yr^{-1} with export out of the euphotic zone valued at 1.30 Tmol P yr^{-1} (Table 2). Modeled DOP distributions are shown in Fig. 5a (surface) and b (200 m), with observations mostly limited to the Atlantic Ocean. The region of elevated simulated DOP (> 0.25 µM) in the eastern South Atlantic surface waters is located further to the east than is observed (Fig. 5a), possibly owing to the snapshot nature of the observations (collected in January–February) compared to the annually averaged simulation. Modeled DOP in the subsurface agrees reasonably well with the Atlantic observations, except for a ~ 70 % model overestimate in the South Atlantic subtropical gyre (Fig. 5b).

3.3 Modeled DOM in the DOM OPT simulation

Results and comparison of DOM cycling metrics from the DOM OPT simulation against the observational dataset and REF simulation are presented in Tables 2 and 3. For a comparison of the set of DOM cycling parameter values between the REF and DOM OPT simulations, see Table 1.

DOC – total DOC production in the euphotic zone (upper 100 m) for the DOM OPT simulation is 4.16 Pg C yr^{-1} (Table 2). About 45 % of this DOC is remineralized within the euphotic zone, yielding DOC export from the EZ of 2.28 Pg C yr^{-1}, which is ~ 20 % larger than the result from a separate DOC data assimilative modeling study (Table 2; Hansell et al., 2009). Combined with the particulate organic carbon export from 100 m in the DOM OPT simulation of 7.01 Pg C yr^{-1}, DOC contributes ~ 25 % to the total 9.29 Pg C yr^{-1} of export production in the CESM-BEC. Modeled total DOC concentrations (semilabile + refractory) from the DOM OPT simulation are shown for the surface (Fig. 3c) and at 200 m (Fig. 3d). There is generally good agreement between the simulated fields and observations (colored dots) with the mean bias being < 20 % for the upper ocean (0–500 m; Table 3). Slightly larger model overestimations (up to ~ 30 %)

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exist at the surface for certain low-latitude ocean basins (e.g. tropical Atlantic, Indian Ocean).

DON – total euphotic zone DON production is 30.7 Tmol N yr^{-1} with > 100 m export of 16.4 Tmol N yr^{-1} (Table 2). Modeled total DON concentrations are improved over the REF simulation at 200 m (Fig. 4d), however overestimations of DON at the surface remain in DOM OPT (Fig. 4c). Simulated surface DON overestimation is largest in the low to mid latitudes, reaching ~30 %. Opposite the pattern obtained for the low latitudes, high latitude simulated DON is underestimated at the surface in the Southern Ocean (Fig. 4c) by up to ~35 %. However, overall DON mean biases are small in the DOM OPT simulation, i.e. < 10 % (Table 3).

DOP – total euphotic zone DOP production is 2.94 Tmol P yr^{-1} with export out of the euphotic zone of ~1 Tmol P yr^{-1} (Table 2). Modeled DOP distributions are shown in Fig. 5c (surface) and d (200 m). The DOM OPT simulation captures the low observed DOP concentrations in the North Atlantic, largely due to enhanced phytoplankton direct uptake of DOP (see Sect. 3.5). The region of elevated simulated DOP (> 0.25 µM) in the eastern South Atlantic surface waters continues to be located further to the east than is observed (Fig. 5c) in the DOM OPT simulation as was also the case in the REF simulation. Modeled DOP in the subsurface agrees reasonably well with the Atlantic observations, reducing the large overestimates in the REF simulation (Fig. 5b and d). Overall mean DOP biases are similarly < 10 % for both the total and semilabile pools (Table 3).

3.4 Comparison of multiple DOM cycling schemes in the CESM-BEC

We also wished to test other hypotheses for DOM cycling formulations such as non-variable C : N : P cycling stoichiometry (i.e. DOM cycling occurs at the Redfield ratio) as well as more rapid turnover of DOM in the EZ compared to the MZ (the DOM OPT and REF simulations contain more rapid turnover of DOM in the MZ, following the work of Carlson et al., 2004; Letscher et al., 2013a). To test these hypotheses, we performed two additional BEC simulations termed REDFIELD and EZRAPID using a coarser resolution version of the BEC model with a nominal 3° horizontal resolution. The optimized cycling parameter values obtained for DOC from the DOM OPT simulation were assigned to the DON and DOP pools for the REDFIELD simulation to allow all DOM (C/N/P) to cycle at the same rate and in the same proportions. The ability for phytoplankton to directly utilize DOP is also turned off in the REDFIELD simulation. The optimized EZ and MZ lifetimes for each DOM tracer from the DOM OPT simulation were reversed for the EZRAPID simulation such that the shorter lifetime (more rapid remineralization rate) was assigned to SLDOM in the EZ.

Results from 310 year simulations of these are compared against ~ 3° simulations of REF and DOM OPT in Table 4. Results are similar for DOC when comparing the DOM OPT and REDFIELD simulations, which is to be expected as the REDFIELD simulation used the same DOC cycling parameters as the DOM OPT simulation. Faster turnover of DOC in the EZ (EZRAPID simulations) had a detrimental effect on DOC mean biases, resulting in large overestimations in the upper 500 m (Table 4) when compared with faster turnover in the MZ (DOM OPT). Large positive mean biases were also found for DON within the REDFIELD and EZRAPID simulations when compared to the DOM OPT (Table 4). Similar positive biases were found for DOP within the REDFIELD and especially for the EZRAPID simulations, i.e. up to ~ 50–65 % (Table 4).

3.5 Direct DOP uptake by phytoplankton

The longer lifetimes for semilabile DOP in the DOP OPT simulation (on the order of years) allow for significant horizontal advection of DOP from the more productive gyre margins (e.g. the NW African upwelling region) towards the Sargasso Sea, providing an additional phosphorus source to the western North Atlantic. Each phytoplankton group within the BEC model can directly utilize DOP to satisfy their phosphorus requirements when phosphate concentrations are low (Moore et al., 2014). Literature reports of this phenomenon are numerous (e.g. Bjorkman and Karl, 2003; Casey et al., 2009; Lomas et al., 2010; Orchard et al., 2010) whereby phytoplankton make use of extracellular alkaline phosphatases to cleave phosphate groups from DOP moieties such as phosphate mono- and di-esters (Dyhrman and Ruttenberg, 2006; Sato et al., 2013) for subsequent uptake of the liberated phosphorus. Sohm and Capone (2006) provide half-saturation constants for DOP uptake by *Trichodesmium* spp. (a diazotroph) and bulk phytoplankton (dominated by nano- and pico- phytoplankton) from the subtropical North Atlantic, and suggested *Trichodesmium* species obtained much of their required phosphorus from DOP in this region. Based partly on this study, the diazotrophs have been given a lower half-saturation constant for DOP uptake than the other phytoplankton (Moore et al., 2014). Diatoms also exhibit alkaline phosphatase activity albeit at lower rates than other plankton groups (Dyhrman and Ruttenberg, 2006; Nicholson et al., 2006), and were thus assigned a greater half-saturation for DOP uptake than the other phytoplankton groups in the BEC (consistent with their reduced efficiency in taking up dissolved inorganic phosphorus in the model).

The fraction of total phosphorus uptake that is sustained by DOP uptake for each phytoplankton group in the DOM OPT simulation is shown in Fig. 6. DOP uptake is largest by diazotrophs (Fig. 6b), with generally ~ 20 % of P uptake from DOP in the subtropical gyres, increasing to ~ 30–50 % in the subtropical North Atlantic, western side of the subtropical South Atlantic, and the eastern Mediterranean Sea. DOP uptake represents a small fraction (< 5 %) of P uptake by the small phytoplankton and diatoms (Fig. 6a and c) over much of the ocean, increasing to ~ 10 % in the subtropical ocean gyres.

4 Discussion and summary

This study utilized a novel rapid solver of a simple linear biogeochemical cycling ocean model, constrained by our compilation of marine DOM observations, to efficiently optimize DOM biogeochemistry in the larger complexity CESM-BEC model. This approach allows for a quicker and more quantitatively robust method for optimizing biogeochemical ocean model parameters over the traditional "hand"-tuning approach. Model parameters determined with the modified DMI-enabled linear DOM model carried over well when implemented in the full CESM-BEC (see Fig. 2). The DOM OPT simulation contains reduced mean biases, improved correlation coefficients, and is more consistent with the DOM observational constraints when compared to the REF simulation (Figs. 3–5; Tables 2 and 3).

Our results demonstrate that allowing for non-Redfield stoichiometry in the DOM pools significantly improves the match to observed DOM distributions. The order of lability follows $P > N > C$, diagnosed from the calculated effective tracer lifetimes in DOM OPT which include the net result of the sum of tracer sinks (∼ 3.2 vs. 6.3 vs. 6.8 years for semilabile P, N, C; ∼ 4300 vs. 6360 vs. 13 900 years for refractory P, N, and C). Our DOM OPT simulation estimated export C : N : P ratio of 225 : 19 : 1 for the semilabile DOM is in excellent agreement with the estimate of 199 : 20 : 1 by Hopkinson and Vallino (2005) and strongly supports the idea that DOC is exported efficiently relative to DOP compared with the canonical Redfield ratio. The calculated export efficiencies, that is the fraction of euphotic zone DOM production that is exported below 100 m, are 55 %, 53 %, and 17.5 % for DOC, DON, and DOP, respectively. In addition, the DOM lifetimes from the DOM OPT simulation are in general agreement with available estimates from the literature. Semilabile DOC lifetime has been estimated at ∼ 1–13 years in the mesopelagic of the Sargasso Sea (Hansell and Carlson, 2001), ∼ 7–22 years in the mesopelagic of the North Pacific subtropical gyre (Abell et al., 2000), and ∼ 1.5–30 years for the global ocean (Hansell et al., 2012). Semilabile DON lifetimes have been estimated at ∼ 3–12 years (Letscher et al., 2013a) or ∼ 11–20 years (Abell et al., 2000) for marine DON and ∼ 4–14 years for terrigenous derived DON in the Arctic Ocean (Letscher et al., 2013b).

We found that best agreement with observed DOM distributions required a more rapid degradation of semilabile DOM in the mesopelagic than in the euphotic zone. This result is consistent with some incubation studies of DOM degradation (Carlson et al., 2004; Letscher et al., 2013a). Possible hypotheses for this depth dependence on DOM lifetimes in the real ocean are numerous, including differences in DOM composition/quality (Skoog and Benner, 1997; Aluwihare et al., 2005; Goldberg et al., 2011),

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microbial community structure (Giovannoni et al., 1996; Delong et al., 2006; Treusch et al., 2009; Carlson et al., 2004; 2009; Morris et al., 2012), availability of inorganic nutrients for heterotrophic utilization (Cotner et al., 1997; Rivkin and Anderson, 1997; Caron et al., 2000), abundance of bacterial grazers (Caron et al., 2000), and the presence or specific affinity of microbial cell membrane nutrient transporters (Azam and Malfatti, 2007; Morris et al., 2010). However the relative importance of each of these mechanisms are not well constrained, nor are any considered in the BEC model formulation, and thus require further investigation.

Direct uptake of DOP by phytoplankton seemed necessary in our simulations to capture the observed very low surface DOP concentrations in the Sargasso Sea. Yet there are large uncertainties in the preference and uptake efficiencies for dissolved inorganic phosphorus vs. dissolved organic phosphorus by different phytoplankton groups. Future field and lab studies are needed to reduce these uncertainties and to better quantify the role of DOP in determining spatial patterns of nitrogen fixation. There is also a great need for additional DOP measurements in every basin except the North Atlantic, along with improved quality control and the development of a DOP standard reference material.

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Table 1. Optimized DOM parameters from the DMI-enabled linear DOM model (DMI-DOM solver) and the modified DMI model (MOD DMI-DOM solver) as well as the REF and DOM OPT simulations of the CESM-BEC. Euphotic zone = 0–100 m for the DMI-DOM models and depths where PAR > 1 % for REF and DOM OPT. The "flux to DOM" represents the fraction of primary production (PP) that accumulates as DOM while the "fraction of DOM flux" represents the portion of the DOM production flux that accumulates as semilabile (SL) or refractory (R) DOM. Parameters $fi, \kappa_i | i = 1 \ldots 4$ are defined in Eqs. 1–4. Surf = surface layer (< 10 m), reminR = remineralization rate, sp = small phytoplankton, diat = diatoms, diaz = diazotrophs, k = half saturation constant for DOP uptake, yr = year, and NA = not applicable.

Parameter	DMI-DOM solver	MOD DMI-DOM solver	Parameter	REF	DOM OPT
Flux to DOM		*Fraction of DOM flux*	*Flux to DOM*		
SLDOC:$f_1 + f_2$	0.09 + 0.009	0.99	f_PP_doc	0.15	0.06
SLDON:$f_1 + f_2$	0.077 + 0.023	0.9885	f_PP_don	0.15	0.04
SLDOP:$f_1 + f_2$	0.085 + 0.01	0.997	f_PP_dop	0.15	0.06
			parm_labile_ratio	0.85	0.94
DOCr: f_3	0.006	0.0098	DOCrefract	NA	0.01
DONr: f_3	0.004	0.01125	DONrefract	0.08	0.0115
DOPr: f_3	0.0015	0.0029	DOPrefract	0.03	0.003
DOCrsurf: f_4	NA	0.0002	f_to_don	NA	0.66
DONrsurf: f_4	NA	0.00025			
DOPrsurf: f_4	NA	0.0001	*DOP uptake*		
			sp_kDOP	0.26	0.25
DOP uptake	NA	NA	diat_kDOP	0.9	1.0
			diaz_kDOP	0.09	0.08
DOM lifetimes			*DOM lifetimes*		
– Euphotic Zone			*– Euphotic Zone*		
SLDOC: $1/\kappa_1$	34 yr	15 yr	DOC_reminR	250 d	15 yr
SLDON: $1/\kappa_1$	8.7 yr	15 yr	DON_reminR	160 d	15 yr
SLDOP: $1/\kappa_1$	5.8 yr	62 yr	DOP_reminR	160 d	60 yr
– Layer 1 (< 10 m)			*– Layer 1* (< 10 m)		
RDOC: $1/\kappa_4$	NA	15 yr	DOCr_reminR	NA	20 yr
RDON: $1/\kappa_4$	NA	15 yr	DONr_reminR	2.5 yr	20 yr
RDOP: $1/\kappa_4$	NA	15 yr	DOPr_reminR	2.5 yr	20 yr
– Mesopelagic Zone			*– Mesopelagic Zone*		
SLDOC: $1/\kappa_2$	2.9 yr	5 yr	DOC_reminR	10 yr	5.5 yr
SLDON: $1/\kappa_2$	1.7 yr	5 yr	DON_reminR	4.4 yr	5 yr
SLDOP: $1/\kappa_2$	0.8 yr	4.5 yr	DOP_reminR	8.8 yr	4 yr
– Layer 2 : 60 (> 10 m)			*– Layer 2 : 60* (> 10 m)		
RDOC: $1/\kappa_3$	20 000 yr	15 000 yr	DOCr_reminR	NA	16 000 yr
RDON: $1/\kappa_3$	9000 yr	8000 yr	DONr_reminR	670 yr	9000 yr
RDOP: $1/\kappa_3$	5000 yr	6000 yr	DOPr_reminR	460 yr	5000 yr

Table 2. DOM production, export, and stoichiometry metrics for the REF and DOM OPT simulations against observational constraints. Tmol = teramoles, 1 × 10^{12} mol; Pg = petagrams, 1 × 10^{15} g.

Metric	REF Tmol (Pg) yr^{-1}	DOM OPT Tmol (Pg) yr^{-1}	H09[a] Pg yr^{-1}	Metric *DOM stoichiometry*_100 m	REF	DOM OPT	OBS[b]
*DOM export*_100 m							
DOC prod	874 (10.5)	346 (4.16)	3.7	– *Total pools*			
DOC remin	731 (8.78)	157 (1.88)	1.8	C : N	–	15.9	14.0
DOC export	143 (1.72)	189 (2.28)	1.9	N : P	19.4	29.4	40.6
				C : P	–	468.7	580.8
DON prod	120	30.7	–				
DON remin	95.0	14.3	–	– *Semilabile pools*			
DON export	25.0	16.4	–	C : N	7.3	11.9	7.5
				N : P	16.4	18.8	32.2
DOP prod	7.43	2.94	–	C : P	119	223.5	272.7
DOP remin	6.13	1.96	–				
DOP export	1.30	0.98	–				

[a] Hansell et al. (2009) result from a DOC data assimilative biogeochemical/circulation model.

[b] Letscher et al. (2014) result from analysis of marine DOM database.

Table 3. DOM mean bias and correlation coefficient in relation to the DOM observations within the upper ocean (0–500 m depth) for the REF and DOM OPT 1° simulations. Observations of semilabile DOM are calculated as the total observed DOM concentration less the asymptotic concentration below 1000 m in each ocean basin.

Metric	REF		DOM OPT	
	Mean Bias	log r	*Mean Bias*	log r
Total DOM_0–500 m				
DOC	NA	NA	+4 %	0.834
DON	+16 %	0.626	+2 %	0.663
DOP	+32 %	0.362	+7 %	0.439
Semilabile DOM_0–500 m				
DOC	+24 %	0.734	+46 %	0.810
DON	−20 %	0.632	+7 %	0.658
DOP	+4 %	0.388	+4 %	0.431

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Table 4. DOM mean bias and correlation coefficient in relation to the DOM observations within the upper ocean (0–500 m depth) for the REF, DOM OPT, REDFIELD, and EZRAPID ~ 3° simulations. Observations of semilabile DOM are calculated as the total observed DOM concentration less the asymptotic concentration below 1000 m in each ocean basin.

Metric	REF		DOM OPT		REDFIELD		EZRAPID	
	Mean Bias	log *r*	*Mean Bias*	log *r*	*Mean Bias*	log *r*	*Mean Bias*	log *r*
*Total DOM_*0–500 m								
DOC	NA	NA	+3 %	0.772	−1 %	0.752	+15 %	0.764
DON	+6 %	0.556	0 %	0.622	+24 %	0.609	+16 %	0.601
DOP	+13 %	0.394	−16 %	0.383	+121 %	0.440	+7 %	0.300
*Semilabile DOM_*0–500 m								
DOC	+3 %	0.770	+30 %	0.800	+18 %	0.784	+71 %	0.799
DON	−33 %	0.648	−4 %	0.617	+36 %	0.605	+25 %	0.609
DOP	−10 %	0.418	−25 %	0.380	+136 %	0.441	+5 %	0.298

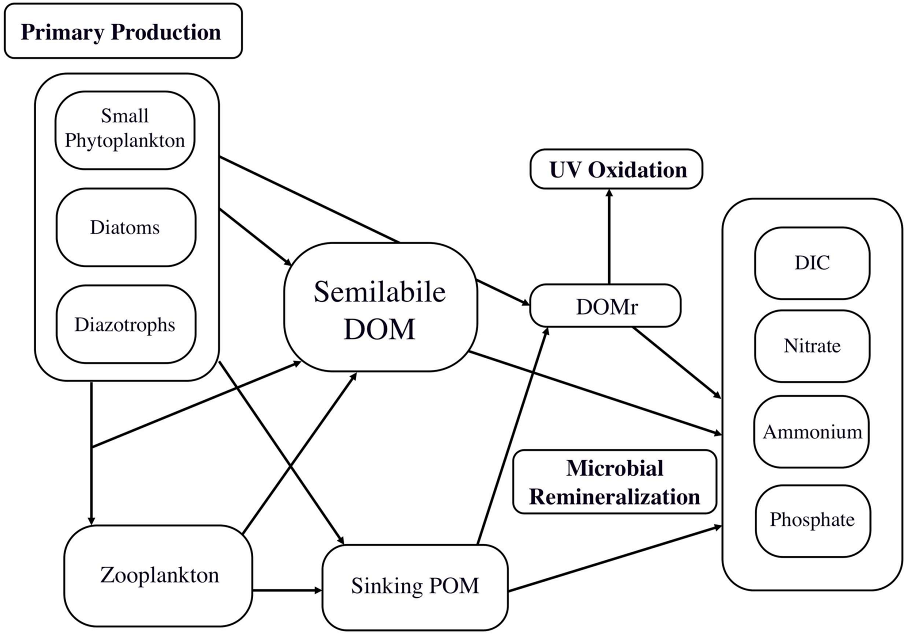

Figure 1. Schematic of organic matter cycling in the CESM-BEC. Primary production is carried out by three phytoplankton functional types: small phytoplankton (which also contains a subgroup of calcifying phytoplankton), diatoms, and diazotrophs. Sources to DOM include direct losses from phytoplankton/zooplankton and from zooplankton grazing of phytoplankton. The major sink for DOM is microbial remineralization, parameterized with an assigned lifetime which differs between the euphotic zone and the mesopelagic ocean. A small fraction of phytoplankton production is converted to refractory DOM in the upper ocean with an additional source to DOMr from degradation of sinking POM in the mesopelagic. DOMr is also lost via UV photooxidation in the surface layer ($< 10\,\mathrm{m}$). The products of organic matter remineralization are dissolved inorganic carbon, nitrate, ammonium, and phosphate.

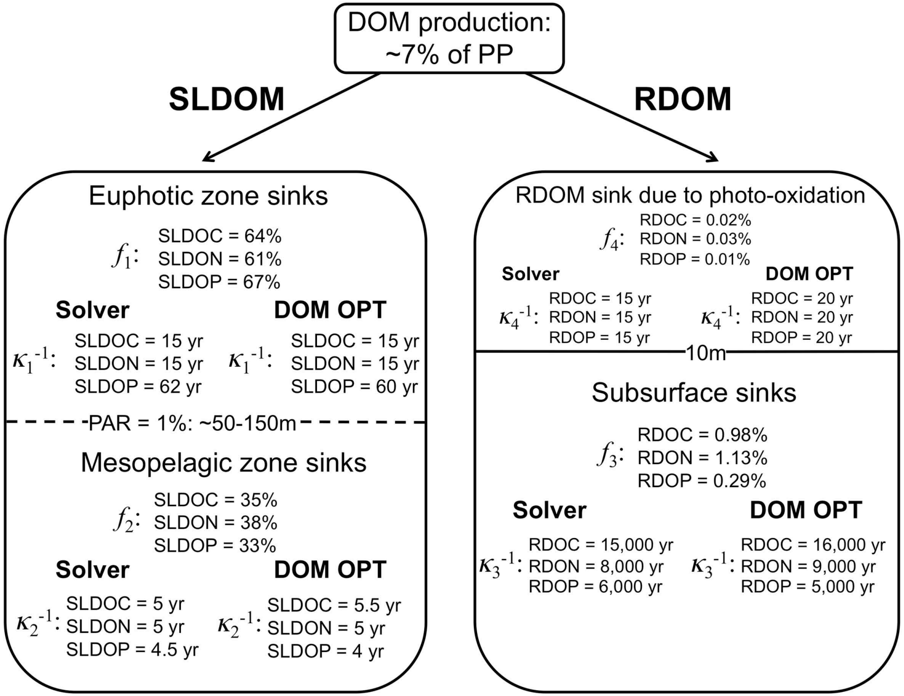

Figure 2. Configuration of the DOM remineralization scheme and parameter values from the modified DMI-enabled DOM model (Solver) and the DOM OPT simulation of the CESM-BEC. Note the only minor changes to tracer lifetimes, κ_i^{-1}, between the modified DMI-DOM model and the DOM OPT simulation. The parameter f_i represents the percentage of the DOM production flux that is remineralized within each depth horizon on an annual basis and is common to both models.

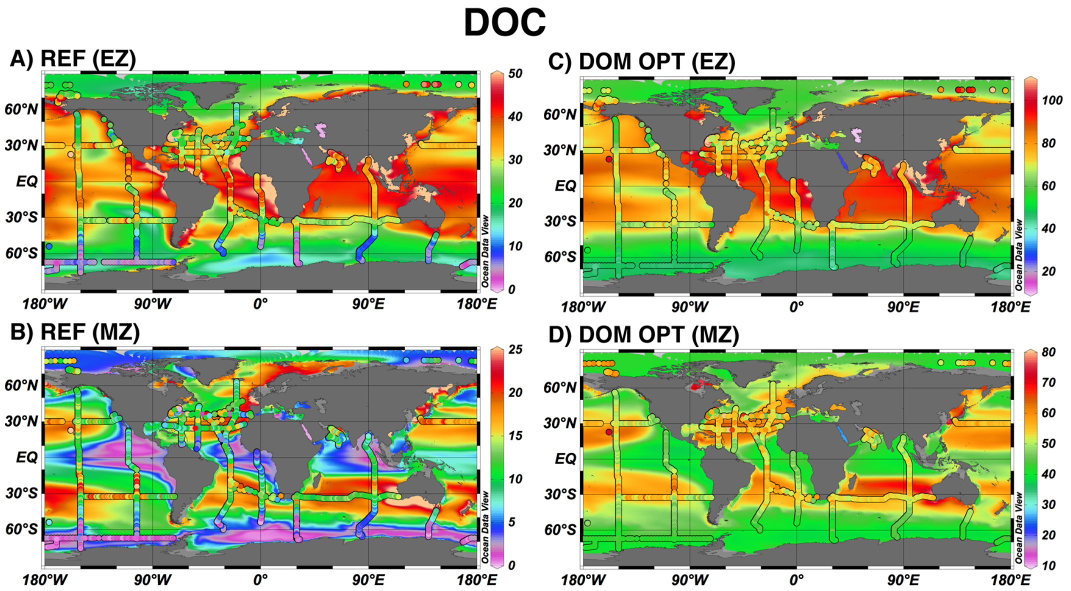

Figure 3. Plots of simulated semilabile [DOC] µM (colored contours) with observations (colored dots) for the REF simulation at **(A)** the surface (EZ) and **(B)** 200 m (MZ). Total [DOC] µM (semilabile + refractory) for the DOM OPT simulation is shown for **(C)** the surface (EZ) and **(D)** 200 m (MZ). Note the difference in color scales between plots **(A)** and **(C)**; **(B)** and **(D)** as the REF simulation lacks a DOCr tracer.

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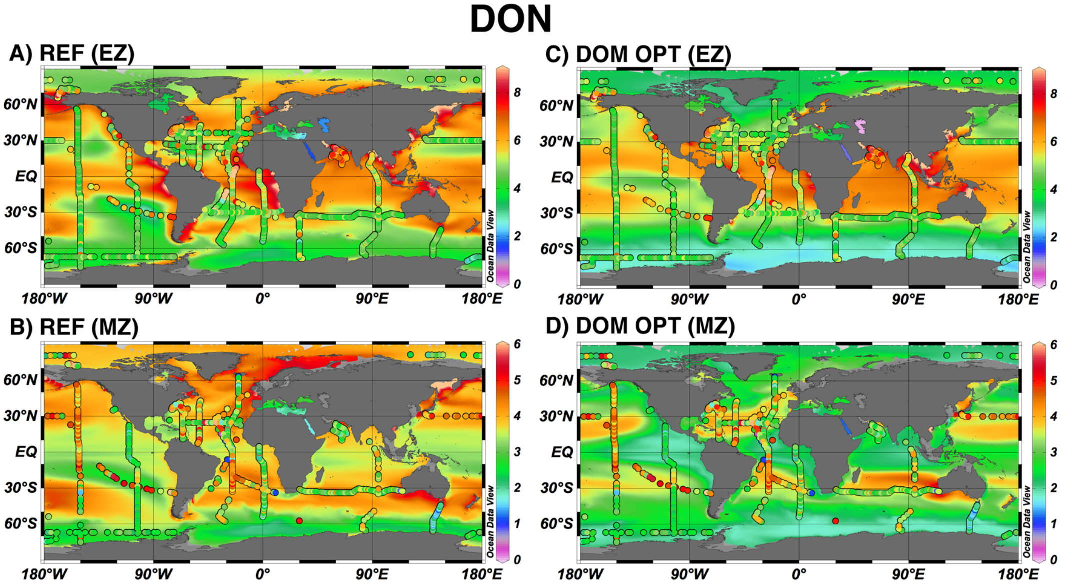


Figure 4. Plots of simulated total [DON] µM (colored contours) with observations (colored dots) for the REF simulation at **(A)** the surface (EZ), **(B)** 200 m (MZ), and for the DOM OPT simulation at **(C)** the surface (EZ), **(D)** 200 m (MZ).

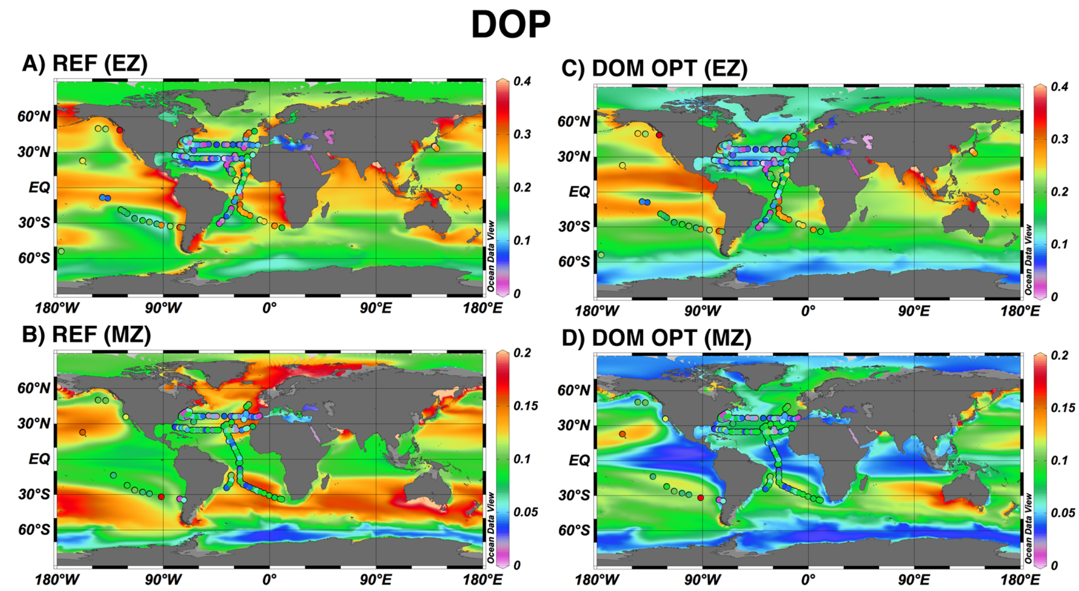
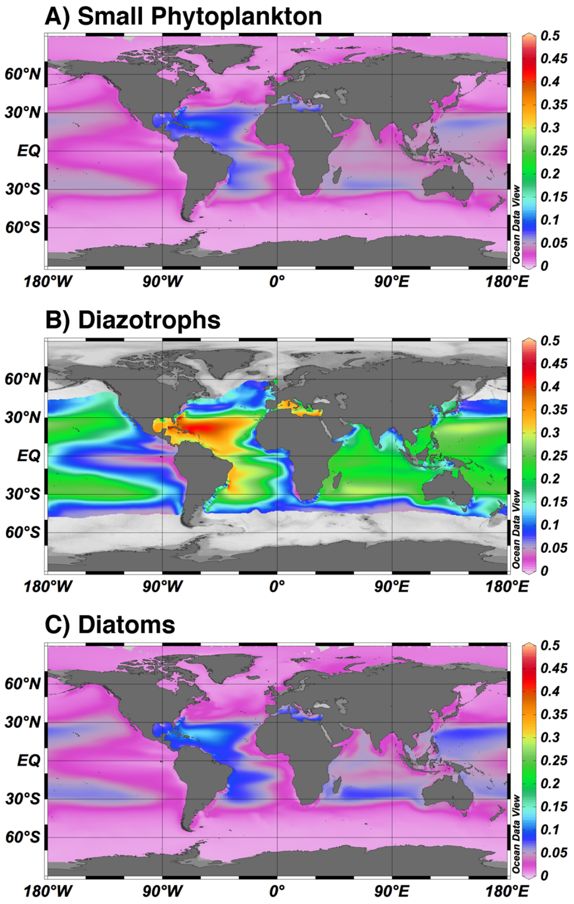


Figure 5. Plots of simulated total [DOP] µM (colored contours) with observations (colored dots) for the REF simulation at **(A)** the surface (EZ), **(B)** 200 m (MZ), and for the DOM OPT simulation at **(C)** the surface (EZ), **(D)** 200 m (MZ).


A) Small Phytoplankton

B) Diazotrophs

C) Diatoms

Figure 6. Fraction of total P uptake from DOP integrated over the euphotic zone (upper 100 m) for **(A)** small phytoplankton, **(B)** diazotrophs, and **(C)** diatoms in the DOP OPT simulation.

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