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RECEIVED 26 March 2026

REVISED 20 May 2026

ACCEPTED 30 May 2026

PUBLISHED 24 July 2026

CITATION

Bernish M, Gao M, Kim J, Pasquier B and
Inomura K (2026) Using a cell flux
model to investigate phytoplankton
growth and macromolecular allocation
under iron limitation.
Front. Earth Sci. 14:1839921.
doi: 10.3389/feart.2026.1839921

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Using a cell flux model to investigate phytoplankton growth and macromolecular allocation under iron limitation

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Global biogeochemical models are powerful tools used to interpret observations and empirical data, create hypotheses, and make predictions. Many of these models, however, represent marine microbes as static stoichiometric reactions that convert nutrients into biomass. To better constrain the biological processes that control nutrient cycling in the global ocean, we extend the Cell Flux Model of Phytoplankton to explore the impact of dissolved iron concentration on the allocation of macromolecules and elemental ratios within phytoplankton cells. This model is supported by data obtained from a range of incubation experiments conducted with phytoplankton of varying species and size categories. Model output is applied globally to highlights the effects of iron and light availability and physiological adaptation on the distribution of open ocean and neritic phytoplankton taxa. This research aims to elucidate the role of phytoplankton physiology within biogeochemical cycles, allowing for better characterization of marine microbial distribution and elemental makeup for interpretive and predictive models.

KEYWORDS

biogeochemical, iron limitation, marine ecology, microbial ecology, phytoplankton

Highlights

- A mechanistic model of phytoplankton is used to investigate the effect of iron limitation on cellular macromolecular allocation.
- The interacting effects of temperature and light on iron-limited phytoplankton physiology are incorporated into the model using existing formulations.
- Growth and allocation patterns of an oceanic phytoplankton taxon are evaluated on a global scale using modeling output and satellite data.

1 Introduction

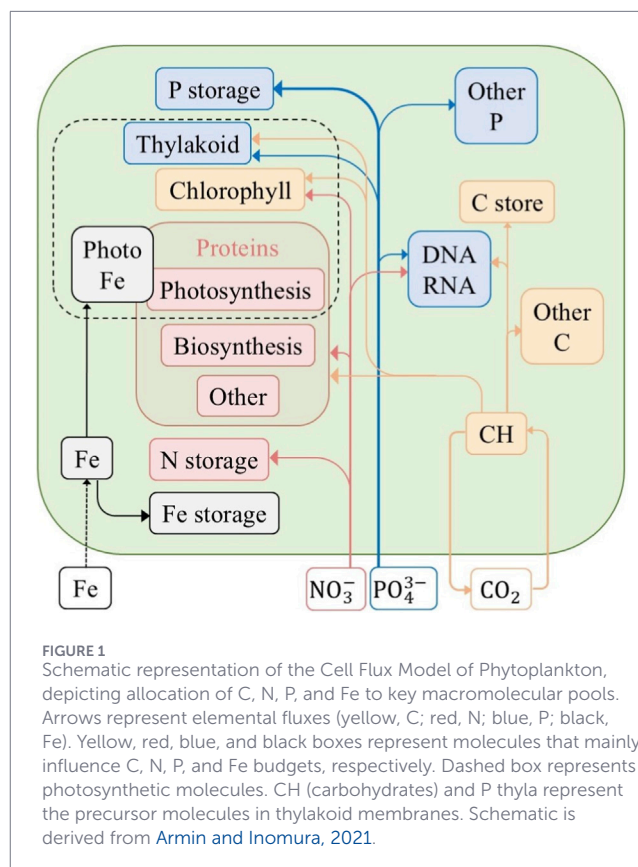
Phytoplankton play important parts in the biogeochemical cycling of carbon and other nutrients, contributing to almost 50% of the global net primary production

despite contributing to only 1% of the total photosynthetic biomass (Field et al., 1998). Variations in elemental proportions within phytoplankton are known to drive large-scale patterns of the stoichiometric makeup of organic matter (Finkel et al., 2016; Liefer et al., 2019). Shifts in nutrient input fluxes, surface ocean chemistry, and ocean circulation as a result of anthropogenic climate change will influence the availability of macro- and micro-nutrients in the future, driving changes in global marine microbial ecology and the export of organic matter (Eppley and Peterson, 1979; Steinacher et al., 2010).

Due to its flexible redox chemistry, iron is used within electron transfer reactions in both photosystems (Schoffman et al., 2016). In the ocean, dissolved iron sticks to sinking particles and is rapidly scavenged from the water column, rendering upwelled waters relatively low in iron compared to macronutrients (Tagliabue et al., 2014). Thus, despite only being required in trace amounts, iron limits primary production in approximately a third of the global surface ocean (Boyd et al., 2007; Breitbarth et al., 2010). In addition, other environmental factors, namely, light and temperature, have been demonstrated to influence the physiological responses of phytoplankton to iron limitation (Jabre and Bertrand, 2020; Sunda and Huntsman, 2011). For example, decreased light levels and photoperiods drive an increased cellular demand for iron, a result of the cell up-regulating the capacity of its photosynthetic machinery (Sunda and Huntsman, 1997; Feng et al., 2010). However, current earth system models do not explicitly represent the interacting effects of light, temperature, and iron concentration on cell physiology.

In this study, we extend a coarse-grained cellular physiology model to resolve the relationship between dissolved iron concentrations and macromolecular allocation. This model accounts for important physiological responses to different growth conditions, using two parameters optimized for various phytoplankton taxa. We implement the model on a global scale using gridded dissolved iron concentrations and observe how environmental factors (e.g., light intensity and temperature) affect the macromolecular allocation and elemental composition of neritic and oceanic phytoplankton taxa. Through focusing on the physiological context provided by model output, we interpret the relationship between micronutrient concentration and phytoplankton growth; namely, how macromolecular allocation is affected by external iron concentrations in conjunction with other environmental factors.

There has been a considerable effort by researchers to extend the breadth of ecological and biogeochemical models in order to describe how ocean systems have and will continue to change under various climate scenarios. However, linking limited incubation experiments to larger-scale models and understanding the effects of multiple stressors on phytoplankton physiology is a major challenge (Follows et al., 2007). This research will advance the predictive power of earth system models through providing a mechanistic understanding of the microbial processes that underlie the biological cycling of iron and other nutrients.



2 Materials and methods

2.1 The Cell Flux Model of Phytoplankton

The Cell Flux Model of Phytoplankton (hereby referred to as CFM-Phyto; Figure 1) is a mechanistic model used to estimate and quantify the growth rate, stoichiometry, and macromolecular allocation of phytoplankton under different environmental conditions (Inomura et al., 2020). Essential elements, such as carbon, nitrogen, and phosphorus, are assigned to major macromolecular groups, including proteins, RNA, DNA, and photosynthetic machinery, each with their own distinct stoichiometric ratios. CFM-Phyto has been demonstrated to reflect the observed growth rates and elemental stoichiometry of various species of phytoplankton (Inomura et al., 2020). It has also been used to estimate the temperature and light dependencies of stoichiometric ratios, as well as to predict the stoichiometric ratios of phytoplankton based on remote sensing data (Armin and Inomura, 2021; Kim et al., 2022; Tanioka and Matsumoto, 2020).

2.2 Calculation of μ

Before determining the cell's resource allocation and elemental makeup, the specific growth rate must be calculated. We first assume a steady state condition in which the change of cellular iron

concentration over time is equal to 0. As a result, the rate of iron uptake (V_{Fe} , in mol Fe (mol C d)⁻¹) is balanced by the growth rate (μ , in d⁻¹) multiplied by the cellular iron Q_{Fe} , in mol Fe (mol C)⁻¹.

$$\frac{dQ_{Fe}}{dt} = V_{Fe} - \mu Q_{Fe} = 0 \quad (1)$$

Cellular iron uptake is linearly proportional to the extracellular iron concentration with an affinity parameter a_{Fe} (in $\frac{\text{mol Fe}}{\mu\text{M Fe mol C d}}$):

$$V_{Fe} = a_{Fe}[Fe] \quad (2)$$

Major iron allocations are to photosystems, enzymes involved in nitrogen fixation (nitrogenase), and other pools, including storage (Saito et al., 2011). As this version of CFM-Phyto focuses on non-N₂ fixing phytoplankton, we assume that the allocation to nitrogen fixation enzymes is negligible. We also assume that iron storage is small. These assumptions lead to a further assumption that the cellular iron is approximate to the iron allocated to photosystems, described by Equation 3:

$$Q_{Fe} \sim Q_{Fe}^{Pho} \quad (3)$$

Relating the allocation of iron to photosystems to the investment in chlorophyll yields the following equation (Inomura et al., 2022):

$$Q_{Fe}^{Pho} = A_{Pho}^{Fe} Q_C^{Chl} \quad (4)$$

where A_{Pho}^{Fe} is a factor that represents the moles of iron required for each mole of chlorophyll (in units mol Fe (mol C in chlorophyll)⁻¹).

While the pigment to photosystem ratio has been observed to vary, this simplification allows for an explicit, mechanistically motivated representation of iron limitation (Strzeppek et al., 2019). Q_C^{Chl} represents the empirically-observed linear relationship between cellular chlorophyll to carbon ratio and growth rate under a given light intensity:

$$Q_C^{Chl} = \frac{1+E}{v_I} \mu + \frac{m}{v_I} \quad (5)$$

where E (dimensionless) represents growth-rate-dependent respiration, m (in d⁻¹) represents maintenance respiration (Inomura et al., 2020), and v_I represents the rate of carbon fixation in mol C (mol C in chlorophyll)⁻¹ d⁻¹ at light intensity I :

$$v_I = v_I^{max} (1 - e^{-A_I I}) \quad (6)$$

where v_I^{max} represents the maximum carbon fixation rate per chlorophyll in mol C (mol C in chlorophyll)⁻¹ d⁻¹ and A_I represents a coefficient characterizing the turnover time of the photosynthetic unit (Cullen, 1990). Inserting Equations 2, 4 and 5 into Equation 1 yields the following quadratic relationship between Q_{Fe} and μ :

$$-\frac{A_{Pho}^{Fe}(1+E)\mu^2}{v_I} - \frac{A_{Pho}^{Fe}m\mu}{v_I} + a_{Fe}[Fe] = 0 \quad (7)$$

The solution for μ is obtained by solving the standard quadratic equation,

$$\mu = \frac{-b + \sqrt{b^2 - 4ac}}{2a} \quad (8)$$

where $a = -\frac{A_{Pho}^{Fe}(1+E)}{v_I}$, $b = -\frac{A_{Pho}^{Fe}m}{v_I}$, and $c = a_{Fe}[Fe]$.

2.3 Data and parameter optimization

We compiled data from 9 published papers on phytoplankton growth under iron-limited conditions (Table 1). For each of these datasets, two parameters used in the calculation of cell growth under iron limitation, a_{Fe} and A_{Pho}^{Fe} (Equation 7), were optimized using the Metropolis-Hastings algorithm, a Markov Chain Monte Carlo (MCMC) method that introduces perturbations to initial estimates and converges to values that best fit the data (Metropolis et al., 1953; Hastings, 1970). The method consists of two parts: generation of parameters and testing. In the testing part, we compute the likelihood ratio based on the model data fit and generate a random value between 0 and 1. If the updated likelihood ratio is greater than the previous likelihood ratio, we will replace the parameter set with the newly generated ones, and we repeat the procedure (more detailed description of the overall process is in Inomura et al., 2020). In our parameterization, the number of iterations was 10,000, which was sufficient in getting a visually decent model-data fit (Figure 2). Optimized values for a_{Fe} and A_{Pho}^{Fe} can be found in the Supplementary Information (Supplementary Table S1).

After finding parameter values that yield the closest fit to the observed data, we ran simulations under increasing iron concentrations (ranging from 0 to 8 nM, with increments of 1e-3 nM), in order to observe the effect of iron concentration on the cellular carbon allocation to four categories of macromolecular pools: molecules involved in biosynthesis, photosynthesis, essential cellular structure, and storage. For each species, the model was run using optimized parameters, as well as constant irradiance and temperature values reflective of those used in each culture study (Table 1).

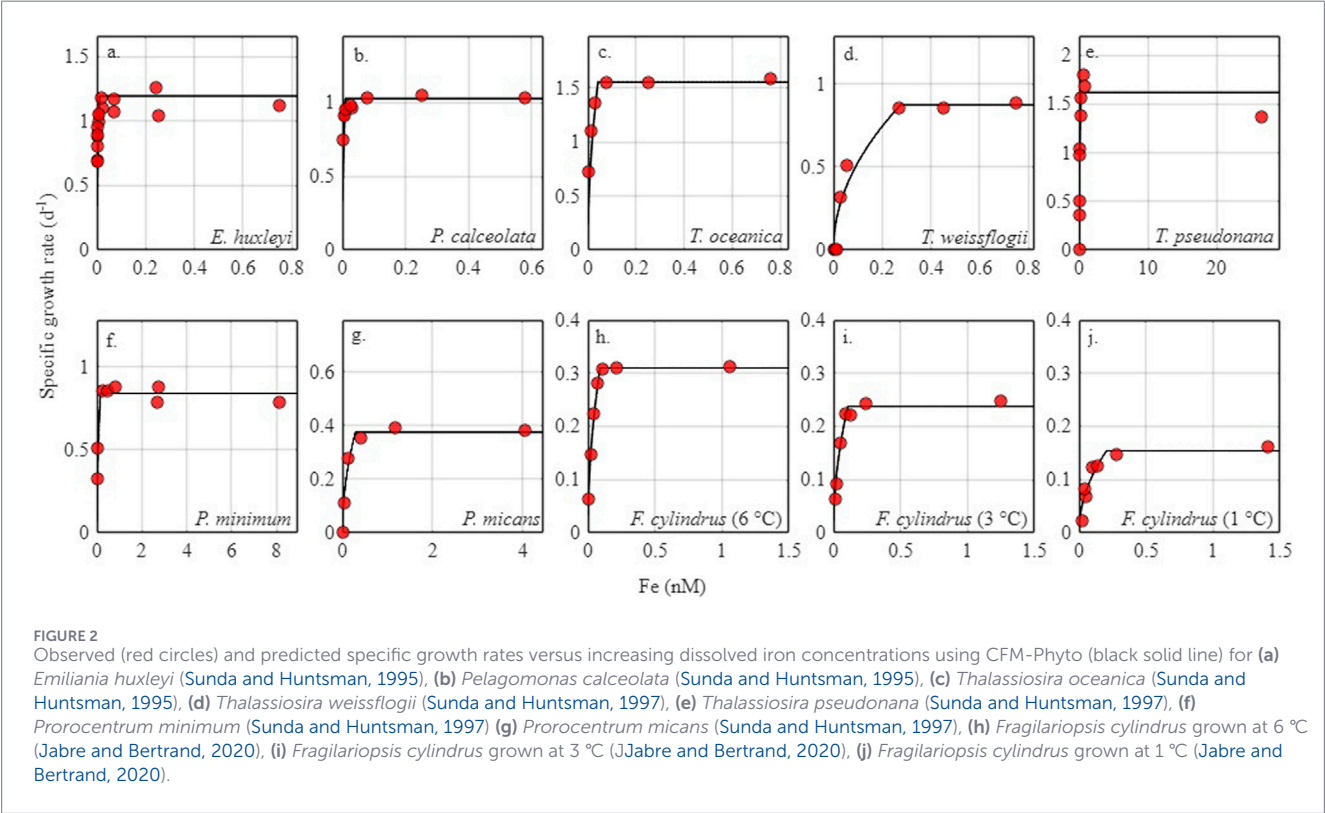
2.4 Functional macromolecular allocation

After calculating the growth rate (Section 2.2), CFM-Phyto was extended to resolve the interacting effects of iron limitation, temperature, and light intensity on functional carbon-based allocation (Inomura et al., 2020). This iteration of the model takes in the growth rate (Equation 8), light intensity (Equation 6), and temperature (Equation 9), using these factors to predict functional macromolecular allocation. Key assumptions include: (1) A saturating relationship between light intensity and C fixation rate (Equation 6), (2) Fixed composition of photosystems, (3) Linear relationship between the growth rate and biosynthetic proteins, and (4) Linear relationship between RNA, growth rate, and the quantity of proteins (Inomura et al., 2020).

Assumption (1) follows a commonly used formula based on target theory (Geider et al., 1998; Cullen, 1990). Assumption (2) indicates that the composition of chloroplasts is constant due to a lack of data needed to constrain their molecular variation. Whereas this assumption may not strictly reflect reality, it simplifies the model while providing a close fit for the overall elemental stoichiometry of the cell (Inomura et al., 2020). Assumption (3) follows a simple idea: biosynthetic protein is required to create biomass for new cells. Thus, to grow faster, the cells need more biosynthetic protein. This assumption is based on the observed relationship in heterotrophic bacteria (Scott et al., 2010; Bremer and Dennis, 1996). This relationship can also be inferred from the generally observed pattern of phytoplankton growth: increasing

TABLE 1 List of phytoplankton taxa used in this study.

Author(s)	Year	Species used	Light ($\mu\text{mol m}^{-2}\text{s}^{-1}$)	Temperature ($^{\circ}\text{C}$)	Isolate
Sunda and Huntsman, 1995	1995	<i>E. huxleyi</i>	500	20	Oceanic
Sunda and Huntsman, 1995	1995	<i>P. calceolata</i>	500	20	Oceanic
Sunda and Huntsman, 1995	1995	<i>T. oceanica</i>	500	20	Oceanic
Sunda and Huntsman, 1997	1997	<i>T. weissflogii</i>	500	20	Neritic
Sunda and Huntsman, 1997	1997	<i>T. pseudonana</i>	500	20	Neritic
Sunda and Huntsman, 1997	1997	<i>P. minimum</i>	50	20	Neritic
Sunda and Huntsman, 1997	1997	<i>P. micans</i>	50	20	Neritic
Jabre and Bertrand (2020)	2020	<i>F. cylindrus</i>	50	6	Neritic
Jabre and Bertrand (2020)	2020	<i>F. cylindrus</i>	50	3	Neritic
Jabre and Bertrand (2020)	2020	<i>F. cylindrus</i>	50	1	Neritic



growth rates require increased protein content and, as a result, an increase in the cell's overall N:C ratio (Rhee, 1978; Chalup and Laws, 1990). This assumption is also supported by a recent proteomics study that shows linearly increasing levels of proteins related to biomass synthesis (Jahn et al., 2018). Assumption (4) is based on the observed linear relationship between the ratio of RNA to protein with the growth rate in heterotrophic bacteria and in phytoplankton (Scott et al., 2010; Nicklisch and Steinberg, 2009). We used previously defined parameters based on the culture of *Synechococcus linearis*, which were previously represented in regional and global patterns of observed elemental stoichiometry (Healey, 1985; Inomura et al., 2022; Liefer et al., 2024).

We also incorporate the effects of temperature on cellular functional allocation. The Arrhenius rate constant is used to relate the ambient temperature on the rate of biosynthesis associated with cellular respiration and growth (Armin and Inomura, 2021):

$$Arr = e^{\frac{E_a}{R} \left(\frac{1}{T} - \frac{1}{T_{ref}} \right)}$$

(9)

where the activation energy (E_a) is equal to 70,000 J (mol)⁻¹, the universal gas constant R is set to 8.3 J mol⁻¹ K⁻¹, and the reference temperature (T_{ref}) is set to 293 K (Taylor et al., 1997; Armin and Inomura, 2021). This rate constant is applied to the allocation of carbon to biosynthetic proteins through the

following equation (Armin and Inomura, 2021):

$$Q_C^{Pro-Bio} = \frac{A_{Bio}}{Arr} \times \mu \quad (10)$$

The rate constant is also applied to the allocation of phosphorus to RNA through the following equation:

$$Q_P^{RNA} = \frac{A_P^{RNA}}{Arr} \times \mu \times Q_C^{Pro} + Q_{P,min}^{RNA} \quad (11)$$

2.5 Global gridded light, temperature, and dissolved iron data

To implement CFM-Phyto on a global scale, we obtain global gridded satellite output of surface PAR and k_{dPAR} (obtained from the Suomi National Polar-orbiting Partnership's Visible Infrared Imaging Radiometer Suite) in order to calculate the 3D climatological average of light intensity in the upper ~100 m of the ocean (Son and Wang, 2015). To calculate the light intensity at depth z (I_z , in $\mu\text{mol m}^{-2}\text{s}^{-1}$) given surface PAR (I_0), we use the following formulation Equation 10 (Morel, 1988):

$$I_z = I_0 e^{-k_{dPAR}z} \quad (12)$$

where k_{dPAR} represents the diffuse attenuation coefficient of PAR (in m^{-1}).

The upper ~100 m grid boxes of ocean temperature were obtained from the Reagan et al., 2024 product and averaged over depth (Reagan et al., 2024). The climatological values of temperature and light used as input for CFM-Phyto are located in the Supplementary Information (Supplementary Figure S4). Global gridded dissolved iron concentrations were obtained from a data-driven dissolved iron climatology and averaged over the upper 100 m (Huang et al., 2022) (Supplementary Figure S3).

3 Results and discussion

3.1 Model validation

Two major growth phases are inferred from the model output: a rapidly increasing growth rate, where growth is limited by iron availability, and a carbon-limited growth phase, where additional iron input does not stimulate growth. Under low iron concentrations, the increase in cellular demand for iron is attributed to an increase in iron uptake, driving an inferred nonlinear relationship between μ and iron as seen in the iron-limited phase of growth (Figure 3C).

Under severe iron limitation, cells allocate a large fraction of carbon to storage molecules (Supplementary Figure S1). As iron availability increases, storage carbon declines while photosynthetic and biosynthetic allocation increases to support faster growth. Once cells enter the carbon-limited phase, storage is depleted and carbon is primarily directed toward growth-supporting machinery. This pattern is consistent with proteomic evidence (Jahn et al., 2018; Zavřel et al., 2019; Faizi et al., 2018).

CFM-Phyto appears to reproduce the observed growth rates in phytoplankton across different Fe concentrations (Figure 3). Maximum specific growth rates, as well as the concentration of

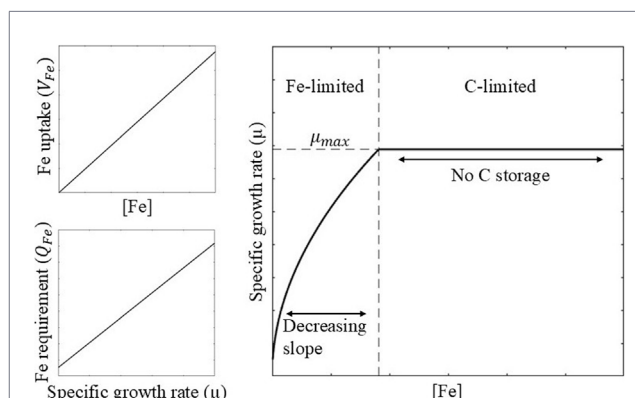


FIGURE 3
Schematic showing two major growth phases of phytoplankton under increasing iron concentration: iron-limited growth, where the slope of growth rate versus iron decreases until it reaches a maximum growth rate (μ_{max}), and carbon-limited growth, where all of the cellular carbon is allocated to biosynthetic and photosynthetic molecules in order to support the maximum growth rate.

Fe required to reach them, vary among species and size classes, reflecting the physiological diversity between phytoplankton taxa. The open ocean isolates *Emiliania huxleyi*, *P. calceolata*, and *Thalassiosira oceanica* saturate at the lowest iron concentrations, reflecting their adaptation to iron-limiting conditions (Sunda and Huntsman, 1995).

3.2 Macromolecular allocation and elemental stoichiometry

Carbon-based macromolecular allocation provides a physiological explanation for the changes in elemental stoichiometry. The overall elemental stoichiometry of the cell is dependent upon the relative abundance of each macromolecular pool and its respective stoichiometric makeup. Under iron limitation, the cell allocates a significant portion of its cellular carbon to storage, lowering its total N:C ratio (Figure 4a–4c). In contrast, the cell allocates more carbon to biosynthesis when iron is replete, increasing its total protein content and, as a result, its overall N:C ratio (Figure 4b–4d).

In CFM, cellular nitrogen is allocated to essential molecules, which represent a constant pool of non-photosynthetic phospholipids, DNA, ATP, and ADP (molecules essential for maintenance and growth), photosynthesis, and biosynthesis (Inomura et al., 2020). The photosynthetic apparatus, which consists of proteins, chlorophyll, and lipid-rich thylakoid membranes, has a relatively high N:C ratio (Geider and La Roche, 2002). Increasing growth rates are accompanied by higher fixed C requirements, leading to increased photosynthetic molecules and higher overall N:C ratios within the cell (Inomura et al., 2020). Under iron limitation, CFM output suggests that oceanic species (e.g., *Emiliania huxleyi*, *P. calceolata*, and *Thalassiosira oceanica*) have higher N:C ratios than their neritic counterparts (Figure 4c). This physiological difference, as suggested by CFM and supported by culture studies, is the result of their relatively low iron requirements, which allow

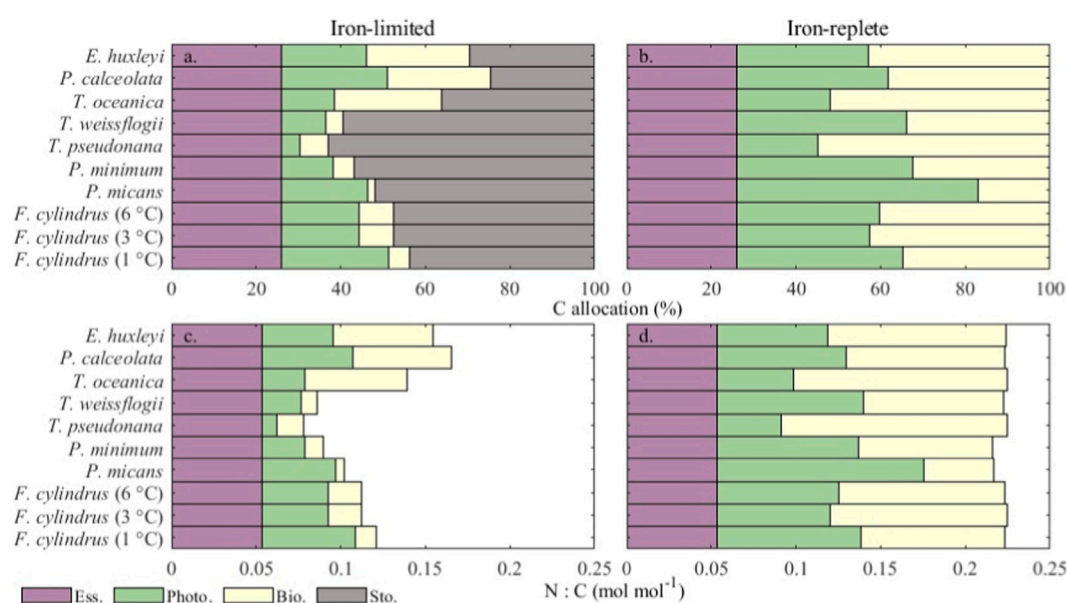


FIGURE 4
Carbon-based (a,b) and nitrogen-based (per cellular C; (c,d)) functional allocation under iron-limited (left [dFe] = 0.001 nM) and iron-replete (right; [dFe] = 1 nM) conditions.

them to survive in the iron-depleted open ocean (Sunda and Huntsman, 1995).

3.3 Interactions between iron concentration, light, and temperature

Light and temperature impose constraints on phytoplankton growth and physiology: the former through limiting photosynthetic activity, and the latter through limiting biosynthetic processes (Schoffman et al., 2016; Armin and Inomura, 2021). Increasing temperatures have been demonstrated to increase the metabolic efficiency of biosynthetic processes within phytoplankton (Regaudie-de-Gioux & Duarte, 2012). In a previous iteration of CFM-Phyto that incorporates temperature into calculations of carbon-based allocation, it was found that the number of biosynthetic molecules needed to maintain a specific, constant growth rate is inversely related to temperature (Armin and Inomura, 2021). Here, we examine the response of phytoplankton to the interacting effects of iron limitation, light, and temperature by focusing on *T. oceanica*, an open ocean diatom isolate (Figure 5; Sunda and Huntsman, 1995).

In this iteration of CFM-Phyto, increasing temperature increases the maximum growth rate of *T. oceanica*, driving a higher fixed carbon requirement from photosynthetic processes, leading to higher Fe:C ratios (and higher iron requirements) within the cell (Supplementary Figure S2).

Iron limitation is associated with insufficient carriers within the photosynthetic electron transport chain. At high latitudes, phytoplankton acclimate to low light levels by increasing their PSU numbers, leading to higher Fe requirements (Raven, 1990). It follows that phytoplankton in low-light, iron-limited environments (i.e., the Southern Ocean) exhibit iron and light co-limitation

(Buitenhuis and Geider, 2010; Schoffman et al., 2016). Under low light, *T. oceanica* is predicted to allocate more of its resources to photosynthetic processes (Figure 5c,d). As observed with temperature, high light conditions support higher growth rates and thus require the synthesis of molecules that support growth.

3.4 Prediction of global *Thalassiosira oceanica* growth rate and elemental stoichiometry

In an effort to predict the biogeography and elemental stoichiometry of the oceanic phytoplankton *T. oceanica*, we evaluate CFM-Phyto output using the climatological average values of dissolved iron, light, and temperature. We also compare the growth and allocation of *T. oceanica* to its neritic relative, *Thalassiosira weissflogii* (Figure 6). In iron-replete open ocean regions, such as the subtropical North Atlantic Gyre, *T. oceanica* experiences a maximum growth rate exceeding 2 d^{-1} (Figure 6a).

It is worth noting that in coastal regions, including the coastal Indian Ocean, along the Benguela and Canary currents in the South Atlantic, and along the Peru current in the South Pacific, lower specific growth rates contrast with relatively high Fe:C ratios. This coincides with more carbon being allocated to photosynthetic processes in these regions (Supplementary Figure S5). This is a result of high K_{dPAR} and lower PAR values in coastal upwelling regions, where high chlorophyll-a concentrations serve as a major attenuator of light (Kirk, 1994). Conversely, low Fe:C ratios are observed in high latitudes. In these regions, cells tend to store carbon due to excess carbon fixation relative to iron uptake. Such carbon storage may be utilized for quick growth when they experience sudden input of iron. Thus, despite there being more iron available in coastal upwelling regions, *T. oceanica* is better able to compete in

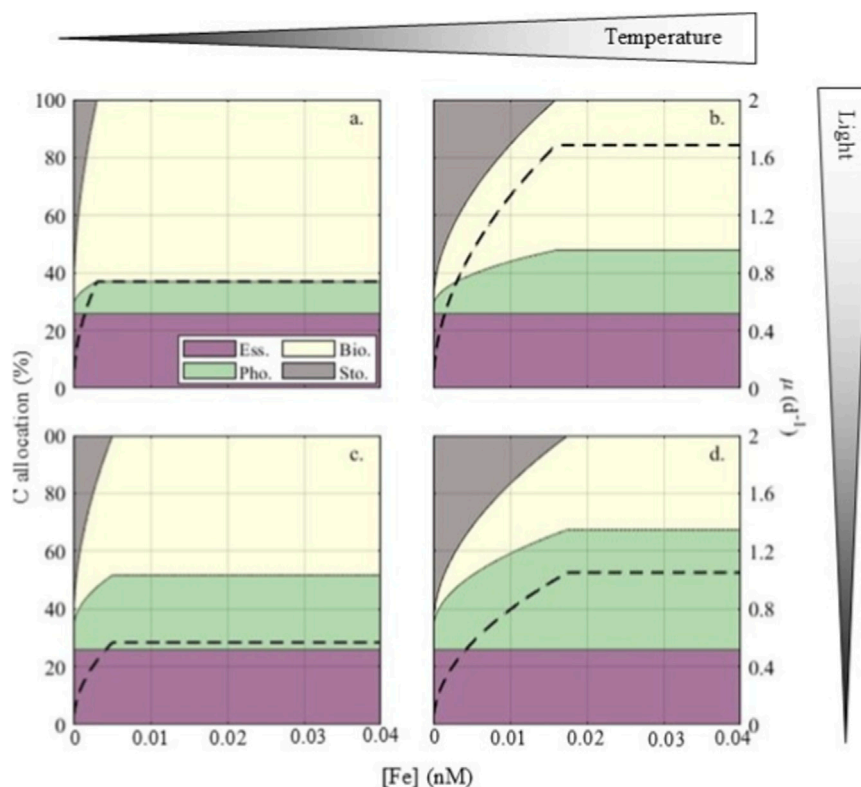


FIGURE 5

Carbon-based macromolecular allocation of *Thalassiosira oceanica* under high light (a,b) $I = 500 \mu\text{mol m}^{-2}\text{s}^{-1}$, low light (c,d) $I = 50 \mu\text{mol m}^{-2}\text{s}^{-1}$, high temperature (b,d) $T = 30^\circ\text{C}$, and low temperature (a,c) $T = 10^\circ\text{C}$ conditions. Dotted line represents the specific growth rate.

open ocean regions, where ample light availability encourages high growth rates in species with low iron requirements.

3.5 Comparison to other cellular level models

Our macromolecular model occupies a unique niche in the spectrum of currently available models (Inomura et al., 2020). Developed upon previous versions of the Cell Flux Model (Inomura et al., 2020; Armin and Inomura, 2021), this model resolves macromolecular allocation explicitly and relates it to the cell's overall elemental stoichiometry.

Recent studies show a close relationship between elemental stoichiometry and macromolecular allocation; this model is developed to mechanistically bridge such relationships (Liefer et al., 2019; Liefer et al., 2024). The idea is similar to one of Shuter's classic models (Shuter, 1979), as well as to other more recent models, including those from Geider et al. (1998), Flynn (2001), Pahlow and Oschlies (2009), Bonachela et al. (2013), and Clark et al. (2013); however, there are substantial differences. For example, whereas the model developed by Geider et al. focuses on C:N ratios and functional molecular allocation, our model resolves C:N:P:Fe and the allocation of specific macromolecules, such as proteins and RNA. This aspect of resolving macromolecules in order to group them into functional roles also differentiates our model from those listed above, which solely focus on those

larger, functional groups. Furthermore, our model is highly empirical, which also makes it distinctive from some models that are not rigorously tested with experimental data. A comparison of CFM-Phyto to other cellular-level models is provided in the Supplementary Material of Inomura et al. (2020).

3.6 Contribution to earth system models

Current earth system models often represent marine microbes as static stoichiometric reactions. Those that incorporate variable stoichiometry fail to constrain the physiological mechanisms that drive it (Follows et al., 2007; Henson et al., 2022). For example, the Marine Biogeochemistry Library (MARBL), a component of the Community Earth System Model (CESM), relies on coarse-grained relationships between cellular stoichiometry and environmental conditions (Long et al., 2021). In this model, P:C uptake rates of phytoplankton functional types increase linearly with ambient phosphate concentrations until a maximum P:C value is reached. Similarly, Fe:C uptake varies linearly as a function of dissolved iron concentration. This formulation, while more flexible than implicitly modeling microbial growth with fixed stoichiometric ratios, does not provide a mechanistic link to the processes that control their stoichiometric ratios, thus limiting its predictive power. Other recent global models have applied variable stoichiometry without explicitly resolving macromolecules, which are important indicators of cellular functionality (Séférian et al., 2020).

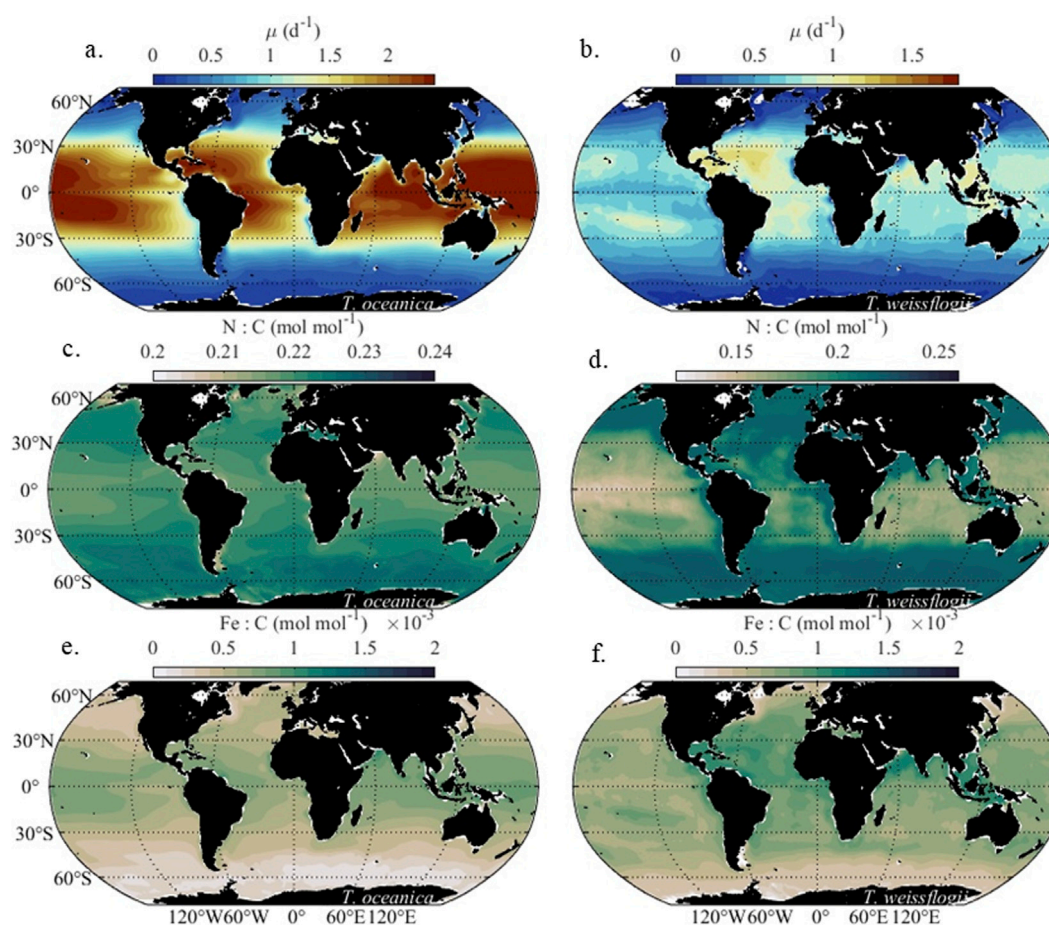


FIGURE 6

Global specific growth rate (a, b), N:C ratios (c, d), and Fe:C ratios (e, f) *Thalassiosira oceanica* (left) and *Thalassiosira weissflogii* (right), averaged over the upper 100 m of the water column.

This model provides an additional dimension of phytoplankton physiology, building upon previous efforts. Macromolecular allocation in phytoplankton has been included in a recent simulation on MITgcm (Inomura et al., 2022). The limitation of the MIT-GCM simulation is that it includes only two functional taxa: small and large phytoplankton. This present study brings a more comprehensive empirical relationship to constrain macromolecular allocation under iron limitation across various phytoplankton taxa. In addition, it incorporates the interacting effects of temperature (Equations 9, 10) and light on the allocation and elemental makeup of these taxa. This effort will connect laboratory studies and earth system models more strongly than previous works, facilitating efforts toward simulating the ecophysiology of diverse microorganisms in the global ocean.

4 Conclusion

The Cell Flux Model of Phytoplankton quantifies the impact of dissolved iron concentration on the distribution of macromolecules and elemental ratios within phytoplankton cells. Model output captures the taxon-specific relationship between iron concentration,

light levels, temperature, as well as their co-related influences on carbon-based macromolecular allocation. The implementation of iron limitation into a coarse-grained cellular physiology model allows for better characterization of marine microbial distribution and better representation of nutrient cycling for interpretive and predictive models. Future iterations of the model that include luxury iron uptake and storage, as well as nitrogen and iron co-limitation will further improve our understanding of the ecophysiology of various phytoplankton taxa on a global scale.

5 Importance

Despite the importance of iron limitation on phytoplankton growth and physiology within high-latitude marine environments, there exists a gap between observed patterns and their representation in global ecosystem and biogeochemical models. In this paper, we model the effects of dissolved iron on the elemental makeup of various phytoplankton taxa. This research seeks to improve the predictive power of global ocean models through providing a mechanistic understanding of the effects of iron, light,

and temperature co-limitation on phytoplankton physiology and elemental stoichiometry.

Data availability statement

The datasets presented in this study can be found in online repositories. The names of the repository/repositories and accession number(s) can be found in the article/[Supplementary Material](#). The model code used for this study can be found on GitHub at: https://github.com/mkbernish/CFM_Phyto_Iron.

Author contributions

MB: Formal Analysis, Software, Visualization, Writing – original draft, Writing – review and editing. MG: Conceptualization, Data curation, Investigation, Writing – review and editing. JK: Conceptualization, Data curation, Supervision, Writing – review and editing. BP: Data curation, Methodology, Writing – review and editing. KI: Conceptualization, Funding acquisition, Investigation, Methodology, Project administration, Supervision, Writing – review and editing.

Funding

The author(s) declared that financial support was received for this work and/or its publication. This study was supported by the National Science Foundation (OCE-2048373, subaward SUB0000525 from Princeton University, and OCE-2227425 to KI), Rhode Island Science and Technology Advisory Council (AWD14107 to KI) and the Simons Foundation (LS-ECIAMEE-00001549 to KI). We thank these foundations for their support.

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