

David Garcia is in the Department of Politics and Public Administration and the Centre for Human | Data | Society, University of Konstanz, D-78457 Konstanz, Germany, and at the Complexity Science Hub Vienna, Vienna, Austria.
e-mail: david.garcia@uni-konstanz.de

1. Finkel, E. J. *et al. Science* **370**, 533–536 (2020).
2. Bruns, A. *Are Filter Bubbles Real?* (Wiley, 2019).
3. Nyhan, B. *et al. Nature* **620**, 137–144 (2023).
4. Guess, A. M. *et al. Science* **381**, 404–408 (2023).
5. Guess, A. M. *et al. Science* **381**, 398–404 (2023).
6. González-Bailón, S. *et al. Science* **381**, 392–398 (2023).

7. Bail, C. A. *et al. Proc. Natl Acad. Sci. USA* **115**, 9216–9221 (2018).
8. Bak-Coleman, J. B. *et al. Proc. Natl Acad. Sci. USA* **118**, e2025764118 (2021).
9. Bakshy, E., Messing, S. & Adamic, L. A. *Science* **348**, 1130–1132 (2015).
10. Robertson, R. E. *et al. Nature* **618**, 342–348 (2023).
11. Metzler, H. & Garcia, D. Preprint at PsyArXiv <https://doi.org/10.31234/osf.io/cxa9u> (2022).
12. Bail, C. *Breaking the Social Media Prism: How to Make Our Platforms Less Polarizing* (Princeton Univ. Press, 2022).
13. Lewandowsky, S. *et al. Technology and Democracy: Understanding the Influence of Online Technologies on Political Behaviour and Decision-making* (EU, 2020).

The author declares no competing interests.
This article was published online on 27 July 2023.

Biogeochemistry

An improved model of the ocean iron cycle

Brandy M. Toner

A revised conceptual model of the chemical and physical forms of iron in the ocean reconciles the mismatch between observations and simulations of the amount of dissolved iron in seawater – and might aid climate predictions. **See p.104**

Marine microorganisms known as phytoplankton use carbon dioxide to build their bodies, and the energy of sunlight to fuel their metabolisms. When they die, they sink to the ocean floor, carrying carbon with them. These organisms therefore act as the primary link between CO₂ in the atmosphere and carbon sequestered in ocean sediments. However, the scarcity of iron – a nutrient required for life – in seawater limits the growth of phytoplankton¹, and

therefore the quantity of carbon that can be sequestered. The amount and chemical forms of iron available to phytoplankton are key to how the ocean and atmosphere interact. On page 104, Tagliabue *et al.*² report a modelling framework and numerical tool that address some of the intricacies of marine iron chemistry and solve long-standing inconsistencies in simulations of the iron cycle.

Oceanographers have long struggled to

capture the complex processes that govern iron's chemical forms, bioavailability and transport in the ocean. Part of the problem is that iron concentrations in seawater are exceedingly low, yet iron is abundant in human environments. This means that specialized handling procedures, laboratory spaces and instruments are needed to prevent seawater samples from being contaminated by non-marine iron. The painstaking efforts involved mean that scientists cannot measure iron throughout the ocean at high enough spatial and temporal resolutions to understand the feedbacks between the ocean, atmosphere and biosphere. Robust conceptual and numerical models are therefore needed to describe the marine iron cycle.

Establishing such models requires knowledge of the chemical and physical forms that iron can take in the ocean. Unfortunately for phytoplankton, the modern ocean surface favours iron in its least water-soluble form – rusty minerals that carry the metal in its +III oxidation state³. However, dissolved organic molecules called ligands can bind to iron(III), increasing its solubility in water⁴, and therefore its bioavailability to phytoplankton.

For historical reasons, oceanographers group marine iron into different categories according to whether the iron can be separated from seawater using filters with 0.2-micrometre pores. Iron species that pass through such filters are considered to be dissolved, whereas retained iron is classified as particulate⁵. The concentration of dissolved iron is commonly measured and is an important parameter used to relate ocean chemistry to phytoplankton nutrition and the global element cycles in models⁶. More specifically, water-soluble ligand-bound iron is a key component of dissolved iron⁷ and a central feature

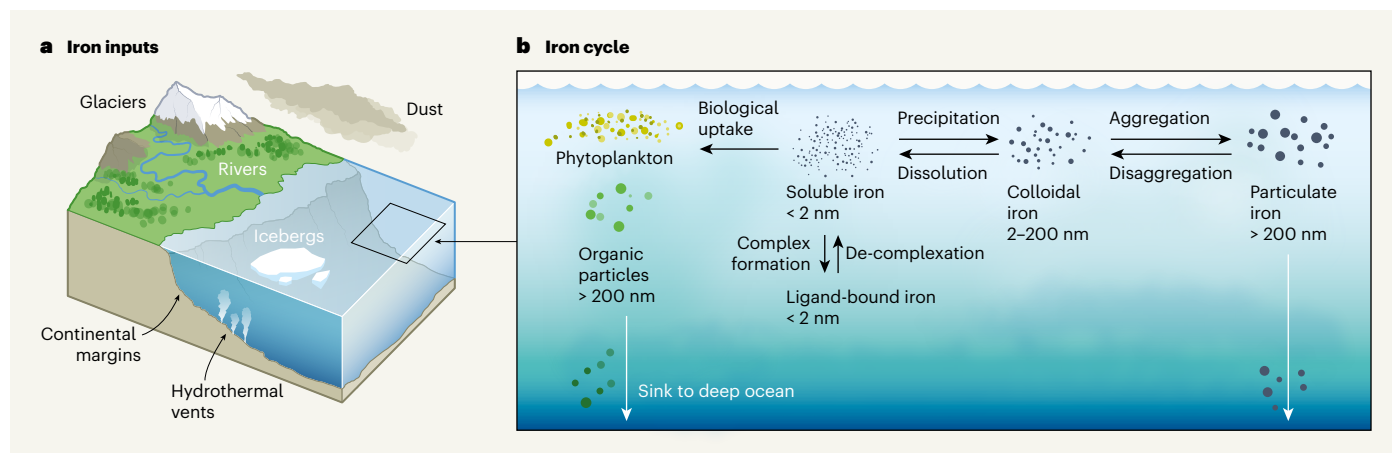


Figure 1 | A revised view of the iron cycle at the ocean surface. a, Iron inputs to the ocean include continental sources (such as rivers, glaciers and wind-blown dust) and hydrothermal vents. **b**, In sunlit seawater, soluble forms of iron are taken up by phytoplankton, which require the element for growth. Organic particles from dead phytoplankton sink to the deep ocean, taking some of the iron with them. The amount of iron available to phytoplankton is boosted by the presence of organic ligand molecules (not shown), which bind to iron in its +III oxidation

state, producing soluble complexes. Tagliabue *et al.*² propose that another pool of iron at the ocean surface – colloidal iron, which consists of particles about 2–200 nanometres in diameter – is key to describing the spatial and seasonal distribution of iron in seawater. These small particles can aggregate into ones that sink to the deep ocean. An advanced numerical model that includes this process accurately reproduces observed levels of dissolved iron around the globe, resolving a previously persistent mismatch between observations and models.

in models of iron chemistry in the surface ocean. The problem is that such models often fail to reproduce the observed distributions of dissolved iron in seawater⁶.

In fact, dissolved iron is a complex mixture of species that are aqueous and solid, organic and inorganic⁸. Dissolved iron is therefore now often subcategorized into soluble and colloidal fractions. Soluble iron is close to what is generally considered to be truly dissolved iron and is mainly thought to be dominated by iron-bound ligands, whereas colloidal iron consists of solids about 2–200 nanometres in diameter. This subcategorization has been a big step forward for research in marine systems, creating many opportunities for investigations of the poorly described colloidal-iron pool.

In this context, Tagliabue *et al.* now report new, accurate measurements of the concentrations of dissolved iron, ligands and particulate iron in a region of the Sargasso Sea in the Atlantic Ocean. Notably, the data provide the first record of seasonal patterns of variation for ligands and dissolved iron. This allowed the authors to represent the seasonal ligand variation accurately in a cutting-edge numerical model of the global ocean iron cycle (the PISCES–Quota model), to test whether this model could correctly simulate the observed variations of dissolved iron. The authors found that the depth and seasonal distributions of dissolved iron were poorly simulated, especially in the upper ocean, indicating that iron–ligand binding alone is insufficient to explain the observed levels of dissolved iron.

The team therefore developed a conceptual model of iron cycling that includes a pool of colloidal iron that is out of equilibrium with ligands (Fig. 1) – a change that means the concentration of dissolved iron is no longer controlled simply by ligand concentration. The new model allows colloidal iron to aggregate into particles that sink to the deep ocean, a mechanism that the authors call the colloidal shunt. When the colloidal shunt was incorporated into PISCES–Quota, the refined numerical model reproduced the authors' observational data better than did the original model, including the data for particulate iron.

Tagliabue *et al.* then applied this refined model to the global ocean, and again found that it reproduced observational data better than did the original PISCES–Quota model. Moreover, the simulations suggested that most ocean regions can be categorized into one of three groups, according to the dominant mode of iron cycling in seawater: areas characterized by high biological activity, which are dominated by biological cycling of iron; regions with low biological activity, dominated by the effects of iron–ligand binding; and areas that receive direct inputs of iron (such as windblown Saharan dust), which are dominated by the colloidal shunt. Moreover, the simulations indicate that iron cycling in

the upper water column through the colloidal shunt is important in about 40% of the ocean.

A limitation of the study is that the authors did not report the concentrations of colloidal iron in their fieldwork. This is ironic, because their findings provide a strong argument for colloidal iron to be analysed routinely along with dissolved and particulate fractions. The work also points to large gaps in our knowledge of the physical and chemical properties of colloidal iron: the mineralogy and aggregation–disaggregation mechanism (or mechanisms) are unknown. Direct observations of the properties of colloidal iron from field and laboratory studies are needed. Moreover, the fate of colloidal iron once it grows into larger particles is unclear – is it deposited in sediments, or does it undergo some form of recycling deeper in the water column?

Nevertheless, by reconciling the previously persistent mismatch between observations and models, and by determining the main iron-cycling processes that occur in different

ocean settings, Tagliabue and colleagues' work is a major advance for ocean biogeochemistry. The findings will aid our understanding of how modern climate change will progress, and of past feedbacks between the ocean, atmosphere and biosphere.

Brandy M. Toner is in the Department of Soil, Water, and Climate, University of Minnesota, St Paul, Minnesota 55108, USA.
e-mail: toner@umn.edu

1. Moore, C. M. *et al.* *Nature Geosci.* **6**, 701–710 (2013).
2. Tagliabue, A. *et al.* *Nature* **620**, 104–109 (2023).
3. Schwertmann, U. *Plant Soil* **130**, 1–25 (1991).
4. Kraemer, S. M. *et al.* *Rev. Mineral. Geochem.* **59**, 53–84 (2005).
5. Fitzsimmons, J. N. & Boyle, E. A. *Geochim. Cosmochim. Acta* **125**, 539–550 (2014).
6. Tagliabue, A. *et al.* *Glob. Biogeochem. Cycles* **30**, 149–174 (2016).
7. Gledhill, M. & Buck, K. N. *Front. Microbiol.* **3**, 69 (2012).
8. Fitzsimmons, J. N. & Conway, T. M. *Annu. Rev. Mar. Sci.* **15**, 383–406 (2023).

The author declares no competing interests.

Cell biology

Hotly awaited structures of the human protein UCP1

Michael J. Gaudry & Martin Jastroch

The protein UCP1 helps to release energy as heat in brown fat. Structures of human UCP1 provide crucial information about its mechanism of action, and might aid drug design for obesity and various metabolism-associated complications. **See p.226**

Organelles called mitochondria act as the powerhouses of our cells. Furthermore, through the action of the protein UCP1, mitochondria can be 'supercharged' to provide extra heat. On page 226, Kang and Chen shed light on the structure of human UCP1.

Mitochondria harvest the energy from food by means of cellular respiration, building up a gradient of hydrogen ions (protons) across the mitochondrial inner membrane. This gradient is harnessed to make the molecule ATP, the common energy currency of cells. In mammals, mitochondria are particularly abundant in a tissue called brown fat, in which their main role is to maintain a high body temperature in cold environments. Instead of helping to make ATP, these mitochondria uncouple respiration from ATP production through the 'proton leak' activity of the protein UCP1 (Fig. 1), which dissipates the proton gradient, and heat-releasing oxidation reactions are accelerated in an attempt to maintain the gradient².

Obesity and other metabolism-associated

complications, such as type 2 diabetes, are caused by the consumption of more calories than are burnt, increasing lipid deposition in white fat and other organs. The fact that excess calories can be burnt by increasing the mitochondrial energy turnover has sparked broad biomedical interest in exploiting this feature as a promising avenue for therapy.

Obese adult humans have limited amounts of brown fat, and so major efforts have been invested in trying to induce UCP1 expression in white fat³. To maximize energy consumption, however, UCP1 must be activated. It has long been known that natural UCP1 activators and inhibitors exist in the body – these are, respectively, molecules such as fatty acids and purine nucleotides (for example, ATP)². But there is little consensus about how these modulators interact with UCP1, or how protons are transported⁴ through it. A major bottleneck for study of the protein has been the absence of a structure for UCP1. This clouds interpretation of structure–function relationships, and hampers the design of