pancreatic *Gck* promoter at various stages of development, as well as postnatally. This hypermethylation was associated with reduced *Gck* expression in pancreatic islets. Administration of the glucokinase activator dorzagliatin, an antidiabetic compound being tested in phase III clinical trials[9], enhanced glucose tolerance and increased insulin secretion from pancreatic islets. Together, these data identify the paternally derived *Gck* gene as an important target of maternal TET3 activity. The authors also reported two to three times more methylation at the *GCK* promoter in early-stage embryos from a woman who had diabetes than in equivalent embryos from two women who did not, suggesting that a similar mechanism is at work in humans.

Interestingly, *GCK* is part of a group of human genes that, when mutated, drive a disorder called maturity-onset diabetes of the young 2 (MODY2) (see go.nature.com/3owzrjm). Clinical data indicate that mutation of just one of the two copies of *GCK* is enough to cause disease — a phenomenon known as haploinsufficiency. Taking this knowledge together with Chen and colleagues' findings, we propose that hypermethylation of paternal-genome-derived DNA at the *GCK* promoter might have the same effect as *GCK* mutations, causing pancreatic *GCK* haploinsufficiency and MODY2 traits in progeny. This idea requires further investigation in clinical studies. In addition, more research is needed to identify the transcription factor(s) that would normally regulate expression of *GCK* but whose activity is impeded by hypermethylation.

Next, Chen *et al.* asked whether reduced *Tet3* expression was the only contributor to *Gck* hypermethylation and glucose intolerance in progeny from hyperglycaemic eggs. In support of this idea, genetically engineered eggs in which *Tet3* expression was abnormally low mimicked the effect of maternal hyperglycaemia, and deleting *Tet3* had even more-pronounced effects. Furthermore, injecting *Tet3* mRNA into embryos suppressed the effects of hyperglycaemia, whereas supplying catalytically inactive TET3 exacerbated them.

Together, these data suggest that sperm-borne DNA methylation — even from male mice that have healthy diets — can promote metabolic distress in progeny, and that TET3 activity in early embryos negates this risk. Such a function for TET3 might have evolved to accommodate the fact that DNA methylation levels are overall twice as high in the genome of sperm as in that of eggs[10]. We cannot, however, exclude the possibility that TET3 is also involved in demethylation of metabolic genes located on the maternal genome.

Finally, the authors provide evidence that eggs are very susceptible to hyperglycaemia when they are maturing. In line with this idea, exposure to high levels of glucose led to a drastic reduction in *Tet3* mRNA levels in mouse and human eggs that were undergoing maturation *in vitro*. Because no gene transcription occurs as eggs are maturing, this decrease is likely to reflect destabilization of *Tet3* mRNA that was transcribed before maturation. We note that genes controlling mRNA stability (such as *Ybx1*, *Ybx2* and *Zfp36*) are downregulated in hyperglycaemic eggs compared with controls (See Supplementary Table 1), possibly because of transcriptional misregulation during egg growth. It will be exciting to explore the mechanisms by which glucose signalling controls *Tet3* transcription and mRNA stability.

Obesity in reproducing couples often affects both partners, and it is known[2] that a high-fat diet primes eggs and sperm to transmit metabolic disorders to offspring in an additive manner. Chen and colleagues have identified a mechanism that can account for transmission from female mice, and a separate mechanism that involves small non-coding RNAs associated with sperm has been described for the inheritance of paternal metabolic disease in rodents[11–13]. Going forwards, it will be important to determine whether these two mechanisms are relevant to humans and, if so, how they intersect.

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1. Sales, V. M., Ferguson-Smith, A. C. & Patti, M.-E. *Cell Metab.* **25**, 559–571 (2017).
2. Huypens, P. *et al. Nature Genet.* **48**, 497–499 (2016).
3. Chen, B. *et al. Nature* **605**, 761–766 (2022).
4. Gu, T. P. *et al. Nature* **477**, 606–610 (2011).
5. Shen, L. *et al. Cell Stem Cell* **15**, 459–471 (2014).
6. Peat, J. R. *et al. Cell Rep.* **9**, 1990–2000 (2014).
7. Tsukada, Y. *et al. Sci. Rep.* **5**, 15876 (2015).
8. Amouroux, R. *et al. Nature Cell Biol.* **18**, 225–233 (2016).
9. Ren, Y., Li, L., Wan, L., Huang. Y. & Cao, S. *J. Enzyme Inhib. Med. Chem.* **37**, 606–661 (2022).
10. Kobayashi, H. *et al. PLoS Genet.* **8**, e1002440 (2012).
11. Chen, Q. *et al. Science* **351**, 397–400 (2016).
12. Sharma, U. *et al. Science* **351**, 391–396 (2016).
13. Zhang, Y. *et al. Nature Cell Biol.* **20**, 535–540 (2018).

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Biogeochemistry

Ocean acidification leads to silicon sequestration

David A. Hutchins

The seas are acidifying as a result of carbon dioxide emissions. It now emerges that this will alter the solubility of the shells of marine organisms called diatoms — and thereby change the distribution of nutrients and plankton in the ocean. **See p.696**

The ecologically dominant phytoplankton in much of the ocean are a group of unicellular organisms known as diatoms. On page 696, Taucher *et al.*[1] present a study that uses a combination of experimental, observational and modelling approaches to examine how the diatom-driven effects of ocean acidification — a consequence of rising carbon dioxide concentrations in seawater — will affect biogeochemical cycles. The separate lines of evidence suggest that ocean acidification will have far-reaching effects on the export of elements to the deep ocean.

Diatoms are highly efficient at converting dissolved CO_2 into organic carbon through photosynthesis, whereupon this organic carbon becomes incorporated into particles that sink rapidly to the deep ocean. Diatoms therefore serve as primary engines of a 'biological pump' that exports carbon to the deep ocean for sequestration[2]. Each diatom cell is enclosed in a shell of silica (SiO_2, where Si is silicon), and the solubility of the silicon in this biomineral is pH-sensitive — it becomes less soluble as seawater acidity rises[3,4]. Although these features of diatoms are familiar to marine scientists, their combined implications for future biogeochemical cycles in the context of ocean acidification had not been explored.

Enter Taucher and colleagues. They carried out a series of five experiments in various parts of the ocean in which natural phytoplankton communities were grown in large enclosures (with volumes of 35–75 cubic metres) known as mesocosms, which simulated future ocean acidification. When the authors measured the elemental composition of the diatom-derived debris at the bottom of the mesocosms, they observed much higher ratios of silicon to nitrogen than the ratios of particles suspended near the surface. This suggested that, at low seawater pH, diatom silica shells were dissolving much more slowly than nitrogen-containing compounds in the same sinking material. In other words, silicon was being exported from the surface to deeper waters preferentially to

nitrogen. The authors validated this finding using records of silicon-to-nitrogen ratios in sinking biological detritus in the open ocean, measured as a function of seawater pH, and obtained from particle-collecting sediment traps deployed by research vessels.

Oceanographers have long known that silicon in diatom shells has a deeper remineralization depth profile than those of elements such as carbon and nitrogen in sinking particles, meaning that silicon is converted more slowly to dissolved forms as particles sink. Silicon thus becomes progressively enriched in particles as they descend the water column, relative to the concentrations of other elements[5]. The advance in Taucher and colleagues' study is the finding that ocean acidification substantially magnifies the existing difference in the dissolution rates of elements in sinking diatom-cell debris.

The authors integrated their findings into a sophisticated biogeochemical model that extrapolated this differential remineralization to the year 2200. Their modelling suggests that widespread acidification could result in much of the marine silicon inventory becoming trapped in the deep ocean, as a result of the downward transport of highly silicon-enriched particles by the biological pump (Fig. 1). This implies that the amount of dissolved silicon returned to the upper ocean by large-scale, mid-depth ocean circulation patterns will decrease, thereby reducing the amount of this essential nutrient that is available to support diatom growth in sunlit surface waters. The model therefore predicts precipitous declines in worldwide diatom abundance in the future, because diatoms will be starved of the dissolved silicon required to build their shells.

One major question about Taucher and colleagues' predictions concerns the relative importance of two concurrent global-change processes that have opposing influences on silica dissolution: ocean acidification and warming. Although the authors show convincingly that increased ocean acidification will decrease the solubility of silica particles, seawater temperatures will also rise, and will increase dissolution rates[6]. The researchers calculate that the negative effects of acidification will probably outweigh the positive influences of warming. However, because silicon dissolution from sinking particles occurs throughout the water column, the overall outcome will depend on how well the authors' model captures the relative rates at which CO_2-derived acidity and heat will be transferred from the surface into the deeper ocean.

Another question to be clearly resolved is how acidification-mediated decreases in the rate at which silicon is lost from sinking particles will affect carbon sequestration by the biological pump. Silica produced by diatoms is denser than organic carbon, and so it is tempting to assume that increased silica retention will have a substantial ballasting effect[2,7] that will make particles sink faster, thereby increasing the efficiency of carbon export to the deep ocean.

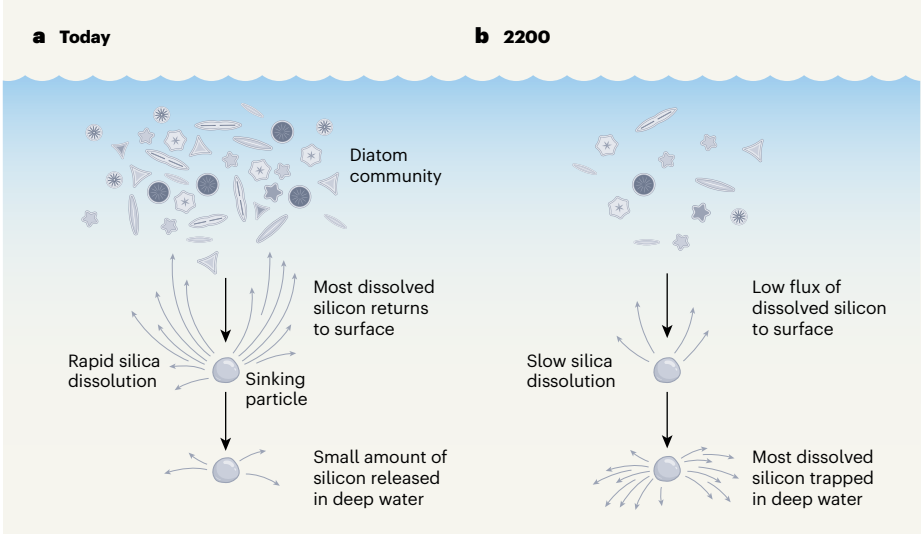

Figure 1 | Solubility of diatom shells in acidified oceans affects marine silicon fluxes. Unicellular phytoplankton known as diatoms have silica shells and produce organic carbon through photosynthesis at the ocean surface. This organic matter combines with silica from dead diatoms to form particles that sink to the sea floor. **a**, Currently, much of the silica dissolves relatively quickly as the particles sink. The resulting dissolved silicon is returned to the surface by upwelling waters, where it supports the growth of more diatoms. **b**, The ocean is acidifying as it takes up increased amounts of carbon dioxide from the atmosphere. Taucher *et al.*[1] report that, as the ocean becomes more acidic, less of the silica in particles will dissolve as they sink. The authors' models suggest that the flux of dissolved silicon returned to the ocean surface will be substantially reduced by the year 2200, because much of the marine silicon budget will become trapped in deep water. The net result is a precipitous fall in diatom abundance.

However, Taucher *et al.* found no obvious pH-related trends in the observed ratios of silicon to carbon for sinking particles in their mesocosms. They attribute the absence of such trends to variability in the effects of ocean acidification on the carbon-to-nitrogen ratios of particles produced by the different phytoplankton communities in their five experiments. If correct, this will make it extremely difficult to determine the net outcome of future changes in silica dissolution rates for diatom-mediated carbon export to the deep ocean.

"Ocean acidification substantially magnifies the difference in the dissolution rates of elements in sinking diatom-cell debris."

The questions raised by the new study about the direct influences of ocean environmental changes on the remineralization depth profiles of biologically essential elements could also be asked about other key nutrients. For instance, iron limits the photosynthetic production of organic compounds – especially by diatoms – across much of the ocean's surface[8]. Iron and silicon currently have similar remineralization depth profiles in the ocean[5], but acidification is likely to increase the solubility of iron in sinking particles[9]. Increases in ocean acidity should therefore release more iron from sinking particles in shallow waters, rather than less as is the case for silicon. This extra dissolved iron might then become readily available for reuse by diatoms and other phytoplankton growing near the ocean surface. An enduring contribution of Taucher and colleagues' study could be to encourage fresh scrutiny of the relative influences of global-change factors such as acidification, warming and deoxygenation on the remineralization of nutrient elements, and thus on their future export by the ocean's biological pump.

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1. Taucher, J. *et al. Nature* **605**, 696–700 (2022).
2. Tréguer, P. *et al. Nature Geosci.* **11**, 27–37 (2018).
3. Van Cappellen, P., Dixit, S. & van Beusekom, J. *Glob. Biogeochem. Cycles* **276**, 1075 (2002).
4. Milligan, A. J., Varela, D. E., Brzezinski, M. A. & Morel, F. M. M. *Limnol. Oceanogr.* **49**, 322–329 (2004).
5. Twining, B. S. *et al. Limnol. Oceanogr.* **59**, 689–704 (2014).
6. Kamatani, A. *Mar. Biol.* **68**, 91–96 (1982).
7. Petrou, K. *et al. Nature Clim. Change* **9**, 781–786 (2019).
8. Hutchins, D. A. & Boyd, P. W. *Nature Clim. Change* **6**, 1072–1079 (2016).
9. Lorenzo, M. R., Segovia, M., Cullen, J. T. & Maldonado, M. T. *Biogeosciences* **17**, 757–770 (2020).

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