colleagues discover is that the Nernst signal persists well above T_c, up to a temperature (T_{onset}) of 150 K. Furthermore, whereas T_c decreases with decreasing doping, T_{onset} increases, with the same trend as the T^* associated with the pseudogap. This is taken as evidence that vortex-like objects exist up to a temperature of 150 K, in samples where T_c ranges from 30 K to essentially zero.

The data are so striking and unexpected that the results need to be interpreted carefully. According to previous a.c. conductivity measurements[7], vortices rapidly multiply above T_c. But eventually their cores start to overlap and the notion of vortices loses its meaning. This appears to happen about 30 K above T_c and seems at odds with the conclusion of Xu and colleagues. Admittedly, the two experiments look at different families of copper oxides, and the apparent discrepancy needs to be resolved by performing both experiments on similar samples. The Nernst measurement is possibly more sensitive to vortices than the a.c. method, but the measurement of T_{onset} relies on the assumption that the normal-state Nernst effect is small and temperature independent. Although this is well established for conventional metals, it is worth recalling that all charge-transport properties are unusual in the underdoped copper oxides. So the meaning of T_{onset} must be viewed with some caution.

Nonetheless, these data clearly indicate strong vortex-like behaviour up to 100 K when the superconducting T_c is less than 30 K. Despite 100 K being much lower than the temperature scale associated with the pseudogap, the existence of such a large region of fluctuating superconductivity is a surprising finding that adds to the mystery of the high-T_c superconductors. ■

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Global change

Iron uncertainty

Adina Paytan

In these pages last week, there was an account[1] of a new explanation[2] for the lower levels of CO_2 in the atmosphere during the last glaciation (about 130,000 to 20,000 years ago) compared with the ensuing interglacial[3]. Given that CO_2 remains one of the main determinants of global warming, the matter is of obvious interest. The explanation held that it was the high availability of silica, rather than of iron[4], that induced phytoplankton growth during the last glaciation. Results described by Loubere (page 497 of this issue[5]) show a different picture again, at least for the eastern equatorial Pacific Ocean (EEP); see the map on page 498. The EEP is an important area in terms of the high levels of both new ocean biological productivity (up to half of the global total) and ocean–atmosphere exchange of CO_2.

Here I will concentrate on the iron-fertilization hypothesis, which for several years has been at the centre of debate among those studying climate change. The idea is that during glacial periods the land was drier and the winds stronger, meaning that more iron-containing dust was blown over the oceans. Iron is a limiting nutrient for phytoplankton photosynthesis, so its greater availability increases productivity in the ocean surface[4]. Increased productivity results in greater incorporation of CO_2 into organic matter through photosynthesis. When the phytoplankton die or get eaten, some of their remains sink to the ocean bottom, effectively removing CO_2 from contact with the atmosphere for a long time. The result, during glacial times, was lower concentrations of CO_2 in the atmosphere.

Over the past 50 years, oceanographers have used a whole range of indicators (proxies) to try to determine the difference in surface biological productivity between glacial and interglacial periods. Data reported so far for the EEP have produced equivocal results, and there is no consensus as to the direction or degree of any productivity change[6]. In an attempt to resolve the question, Loubere[5] has analysed assemblages of bottom-dwelling organisms known as foraminifera in sediment cores from different regions of the EEP. He then used these assemblages to infer surface productivity at different times in the past.

For the most part, organisms dwelling at the bottom of the sea depend entirely on the rain of organic matter — food particles — falling from above. So it is likely that the abundance and distribution of such organisms will be controlled by the amount of organic material they receive. Other variables such as substrate type, oxygen availability and currents will also have an influence. But in the ocean today, bottom-living foraminifera do indeed provide a highly sensitive record of environmental changes associated with the amount of food available[7]. This productivity proxy is independent of variation in the rates of sediment accumulation, which is the weak point of many other productivity proxies.

Loubere concludes that the EEP has not responded uniformly to climate factors: one region (the Southern Equatorial Current area) exhibited lower productivity and another (the equatorial area) higher productivity during the last glacial. Because local winds would probably deposit iron uniformly throughout the whole EEP region, he suggests that iron fertilization is unlikely to be the primary control on productivity.

The productivity reconstruction implied by the foraminiferal analysis is straightforward and consistent with some (though not all) studies in this region[8,9]. So Loubere has staged an impressive attack on the idea that iron has a global role in regulating marine productivity. But there are questions to be answered before accepting the death of the iron hypothesis.

Iron might indeed increase productivity in the sunlit surface waters, but that will not necessarily augment the amount of carbon removed to depth. Moreover, iron will increase primary productivity only when it is the ultimate limiting nutrient. If the supply of other nutrients (such as phosphate, nitrate or silica) is low, or other processes (such as water circulation and mixing patterns, or food-web dynamics) limit productivity, then extra iron will not help much. In the specific area of the Southern Equatorial Current, within the EEP, iron might not be limiting, so other processes or nutrients might be more important in regulating productivity.

On the other hand, iron could still be the key nutrient in other regions within the equatorial Pacific, including the south tropical Pacific[6], the Panama Basin[10] and the central[11] and western[12] equatorial Pacific, as well as in other oceans (the Atlantic and possibly the Southern Ocean). So the regional variability might indicate that, although iron was added to the EEP region during glacial times, the ultimate processes controlling productivity in each sub-zone were different.

A striking point brought out by Loubere's results is the evidence for small-scale variability in productivity, and thus nutrient distribution, in the EEP during the last glacial. This suggests that data obtained from a few sediment cores cannot be easily interpolated and used to interpret global or even regional environmental change — as Herguera[12] has pointed out, looking at a few tiles of a mosaic leaves us far from able to say what it looked like.

The underlying assumption with palaeoceanographic data obtained from only a few sites (cores) is that they represent regional conditions and can be extrapolated laterally. Yet high-resolution time series of regional oceanographic observations indicate that mesoscale variability in both space (tens of kilometres) and time (interannual and

decadal) is considerable (J. A. McGowan, personal communication). Reliable, high-resolution historical maps of productivity, similar to those derived from present-day satellite imaging data, would help a great deal in understanding the distribution of, and controls on, past productivity. Unfortunately such maps are unlikely to be available for some time.

The work by Loubere[5] adds important information about palaeoproductivity in the EEP. But the apparent conflict in glacial productivity reconstruction using different proxies remains, and it will have to be settled. Because several processes affect each of these proxies, the signals obtained may reflect a complex interaction between those processes, rather than productivity alone. At any given place, a multi-proxy approach is required, as is a thorough examination of all the assumptions underlying, and processes affecting, each of the proxies used. Moreover, independent proxies for iron availability or lack of it — such as the composition of specific organic compounds, the ratios of silicate to nitrate and phosphate, or some iron-concentration proxy preserved in mineral phases — are needed to get a true understanding of iron's role in regulating productivity. ■

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Bacterial genomics

Treasure trove for cholera research

Matthew K. Waldor and Debabrata RayChaudhuri

Cholera has afflicted human beings and shaped human history for over two millennia. The causative infectious agent of this diarrhoeal disease, the comma-shaped bacterium *Vibrio cholerae* (Fig. 1), colonizes the mucosal surface of the human small intestine and secretes cholera toxin. The toxin stimulates secretion of water and electrolytes by the cells of the small intestine, leading to the severe watery diarrhoea that is characteristic of cholera[1]. Unlike most bacterial agents of diarrhoea, *V. cholerae* tends to survive in aquatic environments during periods between epidemics, can give rise to dramatic outbreaks of disease, and has spread from its endemic focus in Asia, causing seven global 'pandemics' so far.

The study of this disease has a remarkable history, having spawned central tenets in the fields of epidemiology (starting with John Snow's famous tracing of an outbreak to a water pump in Broad Street, London, in 1854), treatment for diarrhoeal disease, microbial ecology and pathogenesis, and mucosal immunology. The complete genome sequence of a representative isolate from the ongoing seventh pandemic of cholera is described by Heidelberg *et al.*[2] on page 477 of this issue, and promises to usher in an exciting era of post-genomic investigation of this organism.

The *V. cholerae* genome consists of two circular chromosomes (Fig. 2), the larger comprising some 2.96 million base pairs (megabases) and the smaller being of roughly 1.07 megabases[2]. Both chromosomes have roughly the same amount of guanine plus cytosine nucleotides, constituting about 47% of the genome. This suggests to us that these two units of replication (replicons) have existed together for a long period, even though Heidelberg *et al.*[2] suggest disparate evolutionary origins for these chromosomes.

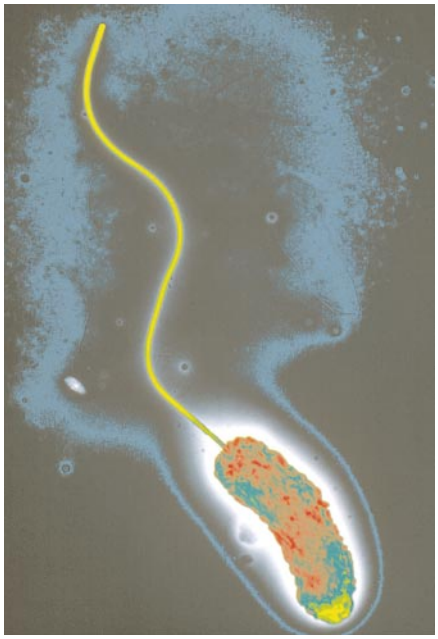

Figure 1 ***Vibrio cholerae*, the bacterium that causes cholera. The epidemiology and biology of cholera infections have been studied for centuries. Now, with the publication of the bacterium's genome sequence[2], comes the opportunity for post-genomic analyses. Magnification approximately ×10,000.**

The larger chromosome, chromosome I, contains a preponderance of genes dedicated to essential cell functions such as DNA replication, cell division, gene transcription, protein translation and cell-wall biosynthesis. It also has most of the genetic loci that are associated with virulence (Fig. 2), many of which have been acquired from other species. For example, a major determinant of pathogenicity, cholera toxin[3], is encoded in the genome of a virus that integrates into the *V. cholerae* genome[4] on chromosome I. A factor essential for colonization of the intestine, toxin-coregulated pilus[5], is encoded on chromosome I in a '*Vibrio* pathogenicity island' found in *V. cholerae* strains that cause pandemics[6]. The expression of genes involved in virulence is regulated by proteins such as ToxR and ToxT[7,8], both of which, along with several other such regulators, are also encoded on the larger chromosome (Fig. 2).

A longstanding view, based on studies of *Escherichia coli*, held that bacterial cells each contain a single circle of chromosomal DNA. But this view has changed with the discovery of an increasing number of microorganisms that contain more than one chromosome, in circular and linear configurations[9,10]. The presence of essential genes is thought to be a defining feature of chromosomes[9]. Several essential genes, including those encoding the ribosomal proteins L20 and L35, are present only on chromosome II, confirming its status as a bona fide chromosome. The presence of essential genes on chromosome II also indicates that it is probably inherently stable — it is unlikely that essential functions would be delegated to an unstable replicon during the course of evolution. Genes from all 16 categories used to subdivide cellular functions[2] occur on chromosome II, although, for eight of these classes, it contains significantly fewer genes than chromosome I. Represented prominently on chromosome II are genes involved in the transport of sugars, metal ions and anions, in the metabolism of sugars and energy, in two-component signal transduction, and in DNA repair.

Why and how does genetic information become distributed onto separate replicons? Heidelberg *et al.*[2] argue that chromosome II of *V. cholerae* was acquired as a plasmid, a circular piece of DNA that replicates autonomously. But we cannot rule out the possibility that the small chromosome arose by excision from a single large ancestral genome. One would imagine that, by distributing the genome content among more than one chromosome, a bacterium could achieve faster genome duplication and cell division, with the possible upshot being a growth advantage and an increased ability to survive in a competitive environment. Heidelberg *et al.* found 105 genes with copies on both