

might question the wisdom of such exploration. First, even the most repetitive and seemingly impenetrable stretches of the genome hold secrets that justify the effort. Second, each chromosome has its own story to tell, quite apart from the story of the genome as a whole. Although the sex chromosomes provide the strongest case for a special relationship between genome organization and the unique biology of a chromosome^{10,11}, the other chromosomes shouldn't feel left out. Each is the product of hundreds of millions of years of evolution, shaped by processes that have rearranged and exchanged sequences, contributed to the formation of new species, given birth to new genes and gene families, and provided the basis for a range of genetically determined or genomically influenced traits. Piecing together these events remains a

worthwhile challenge, for among the flotsam and jetsam of each chromosome lie clues to our history.

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Global change

Ups and downs in the Red Sea

Frank Sirocko

Changes in past conditions in the Red Sea have been exploited to provide a detailed record of sea-level variation over much of the last glacial period. That record might tie in with events in the far south and north.

On page 853 of this issue, Siddall *et al.*¹ present a new approach to reconstructing the history of sea-level change during the last glacial cycle. They provide a detailed record, with a resolution on the century scale, spanning the years between 70,000 and 25,000 years ago. This was a time of intense overall glaciation, punctuated by abrupt warmings and coolings. The last glacial cycle culminated some 18,000 years

ago with the so-called Last Glacial Maximum, before leading into our present interglacial condition, beginning about 10,000 years ago. The reason why past sea levels are of such interest is that they reflect global temperatures — during colder episodes, more of Earth's water becomes locked up in ice caps, with a consequent fall in sea levels.

The authors' approach involved analysing oxygen-isotope values of the calcite tests of

foraminifera from Red Sea sediment cores. Foraminifera are planktonic organisms that originally lived in the surface waters, and accumulated calcite in equilibrium with an oxygen-isotope measure ($\delta^{18}\text{O}$) of the water in which they lived. The $\delta^{18}\text{O}$ composition of the Red Sea is unlike that of the world ocean, because in this semi-enclosed basin the water is subject to especially strong evaporation. Strong evaporation favours release of the lighter ^{16}O isotope over that of ^{18}O — the water is thus enriched in ^{18}O , and is more saline.

This process is also typical for some other ocean basins at low latitude, such as the Persian Gulf or the Mediterranean. But the Red Sea is unique in the characteristics of its connection to the open ocean, through the Gulf of Aden. This connection, the Strait of Bab el Mandab, is only 18 km wide. It also has a 'sill', which at present lies 137 m below the surface. During the 'low stand' of sea level at the Last Glacial Maximum, however, it was at a depth of only about 15 m (Fig. 1). Accordingly, during glacial times, the amount of surface water flowing into the Red Sea was usually very restricted. The residence time of water in the basin was therefore much longer than now, leading to an even greater evaporative effect on the $\delta^{18}\text{O}$ and salinity characteristics. Put another way, compared with that of other records, the sea-level signal seen in the Red Sea sediments is greatly amplified.

Siddall *et al.*¹ have combined a hydraulic control model² of water flow with an algorithm to calculate the equilibrium $\delta^{18}\text{O}$ values; these are a function of the composition of the inflowing water, the surface-water temperature, evaporation and the amount of inflow. The authors then applied this model to interpret the record of a sediment core, known as KL11, from the central Red Sea. The overall result is a history of sea level that shows several prolonged maxima and minima, especially between 70,000 and 40,000 years ago (see Fig. 2b, overleaf).

The broader significance of this work lies in how it might be related to the ice-core records at high latitudes, both south and north. Thus, the calculated salinities and model-derived sea levels show a succession of highs and lows that are similar to the temperature variations inferred from two Antarctic ice cores, Byrd and Vostok. The KL11 record shows for the first time that the temperature variations documented for the Antarctic were probably paralleled by changes in sea level (Fig. 2a, b).

A few years ago, the Byrd ice core was synchronized in time to the Greenland ice core, GISP2. To do this, the authors concerned³ matched variations in levels of atmospheric methane, which must have occurred simultaneously worldwide. After carrying out this exercise, their most astonishing observation was that climate change in the Antarctic apparently occurred several millennia before

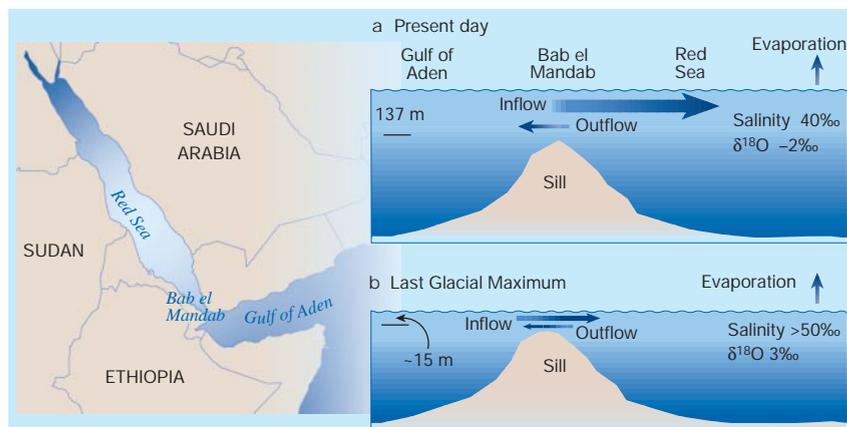


Figure 1 Now and then at the Strait of Bab el Mandab, which is connected to the Indian Ocean through the Gulf of Aden. **a**, Status at the present day, during an interglacial with a water depth of about 137 m at the sill. Typical water conditions are a salinity of 40 parts per thousand (‰) and a $\delta^{18}\text{O}$ value of -2‰ . In reality, the modern seasonal pattern of water flow is highly complex⁴. **b**, Status about 18,000 years ago, during a time of greatest cooling at the Last Glacial Maximum, with a water depth of approximately 15 m at the sill. The altered water-flow pattern and relatively stronger evaporative effect produced a salinity of more than 50‰, and a $\delta^{18}\text{O}$ value of 3‰. The size of the arrows is proportional to the strength of the processes indicated.

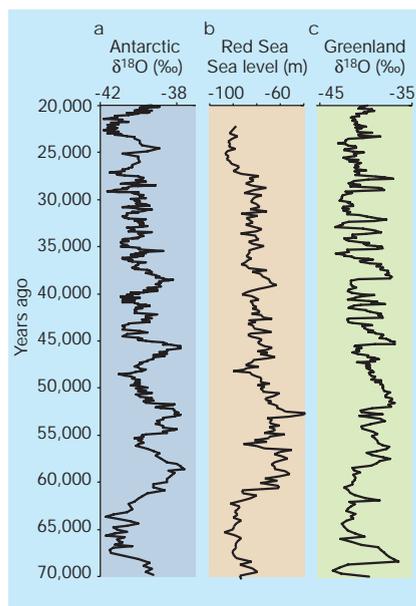


Figure 2 Comparison of records from the Antarctic, the Red Sea and Greenland. a, Data from the Byrd ice core from the Antarctic. These are $\delta^{18}\text{O}$ measurements in parts per thousand — the more negative the $\delta^{18}\text{O}$ figure, the cooler the climate. b, The Red Sea record of Siddall *et al.*¹, showing sea level in metres below today's level. c, Data from the GISP2 ice core from Greenland. These have the same units as a, with a and b having been brought into synchrony in earlier work³.

change in Greenland. If the sea-level record of Siddall *et al.* indeed follows that of temperature in the Antarctic, perhaps the chain of events was that Antarctic warming caused ice melting, and that the subsequent large rise in sea levels of several tens of metres in turn resulted in the collapse of continental ice sheets in the north. But however enticing this scheme may seem, there is an important caveat — in the Antarctic region itself, there

is no evidence as yet for melting of the Antarctic ice sheet during the interval of rapid climate changes between 70,000 and 25,000 years ago.

This view of events also assumes that the record inferred by Siddall *et al.* is robust — that is, for instance, that the $\delta^{18}\text{O}$ signal in the KL11 core has not been affected by environmental factors other than a sea-level-dependent basin-concentration effect, and that the Strait of Bab el Mandab has been stable over the period of time concerned. However, the range of 5‰ in the KL11 $\delta^{18}\text{O}$ curve (between -2‰ and 3‰ ; see Fig. 1) is a good indicator that the observed changes do indeed primarily represent the amplifying effect due to reduced exchange of water between the Red Sea and open ocean. Melting of the glacial continental ice would produce only a 1‰ change in the world ocean.

There are several methods for reconstructing sea levels, involving the measurement of oxygen-isotope variations of open-ocean water, lateral shifts in coastlines, and the height of shore terraces or drowned coral reefs. The beauty of Siddall and colleagues' approach compared with these other methods is that it can be applied to very high-resolution records as well as very long records. It promises to provide the data that will allow us to forge a firm link between events at low latitudes and those at high latitudes, and answer the fundamental question of whether the waxing and waning of the Antarctic ice sheet, and the consequent effects on sea level, have been the motor for abrupt climate change in the north. ■

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Gene regulation

Versatile assembler

Steven Henikoff

The protein machines that assemble and remodel chromosomal proteins often contain a common component. The role of this component in maintaining stability during development is now revealed.

No handyman would be without WD-40, the penetrating oil that stops squeaks, loosens rusted parts and protects against corrosion. The impressive versatility of WD-40 puts it in a class with the Swiss army knife; however, unlike the knife, which sports a collection of specialized modules, the oil is applied in a similar way to perform each different task. An analogous situation appears to hold for a member of the WD-40 protein family. The protein in

question resembles its household namesake in displaying a surprising amount of versatility: it is found in several protein machines that apparently act in different ways on chromatin, a packaged form of DNA. Researchers studying this WD-40 protein suspect that it too, like the oil, functions in the same way to carry out these different tasks — but just how it works and why it is found in such diverse complexes is a mystery. Hennig and colleagues' study of a mutant plant, described

in a recent issue of *Development*¹, could provide a crucial clue.

WD-40 proteins are so called because they contain a repeated segment, of some 40 amino acids, that includes a tryptophan–aspartate peptide ('WD' in the single-letter code for amino acids). A set of seven tandem WD-40 repeats folds into a propeller shape, in which each propeller blade can serve as a platform for binding a different protein². For instance, the particular WD-40 protein studied by Hennig *et al.*¹ — RbAp48 — was first identified in mammals as a ubiquitous binding partner for the retinoblastoma protein, and so is presumably involved in cell-growth suppression like this protein³. Subsequently, a biochemical role for RbAp48 was revealed when it was found to be part of the human chromatin-assembly factor-1 (CAF-1) complex. Chromatin somewhat resembles a string of beads; each bead is known as a nucleosome particle and is composed of DNA that is tightly wrapped around an octamer of four types of histone protein. The CAF-1 complex promotes the assembly of nucleosomes onto newly replicated DNA (Fig. 1)⁴.

RbAp48 is far more abundant in the cell than the other two CAF-1 subunits, p150 and p60, hinting that it also contributes to other complexes. Indeed, several further protein machines that act on chromatin include RbAp48 as an integral component⁵. For example, the fruitfly *Drosophila melanogaster* has an RbAp48-like protein that was first found in a chromatin-remodelling complex called NURF — which moves nucleosomes along DNA⁶ — and was later discovered in other complexes that affect chromatin. Among these are several complexes containing the E(Z) and ESC proteins⁷, implicated in maintaining the silent state of master regulatory genes during fruitfly development. One specific role of these complexes is to help remove acetyl groups from histones H3 and H4 (ref. 7); another involves adding methyl groups to a lysine amino acid in histone H3 (ref. 8). So, fruitfly RbAp48 is found in complexes that contribute to nearly every stage of chromatin metabolism, from nucleosome assembly and remodelling to histone modification. Moreover, RbAp48 relatives in other species are involved in yet more chromatin-associated processes: one is part of the major yeast histone acetyltransferase enzyme⁹.

The number of processes involving RbAp48, and the fact that its encoding gene is found only once in the *Drosophila* genome, might explain why researchers have been unable to isolate or engineer fruitflies containing RbAp48 mutations: the animals simply cannot survive. That in turn means that the role of this protein during development has remained obscure. But the model plant *Arabidopsis* has five genes encoding