Challenging an Ice-Core Paleothermometer

Doug MacAyeal

The temperature-depth profile near Earth's surface has long been recognized as an inventory of environmental history. In 1864 for example, Lord Kelvin used such a profile to argue that the age of Earth's crust since a presumed molten "birth" was inconsistent with prevailing notions of geologic time (*1*). Kelvin's age estimate turned out to be low because it did not account for radioactive heating within rocks and mantle connection which were discovered after the time of Kelvin's analysis. Nevertheless, an important lesson is appreciated from Kelvin's work (*2*): Environmental history (such as annual average surface air temperature) produces a unique effect on near-surface Earth temperatures.

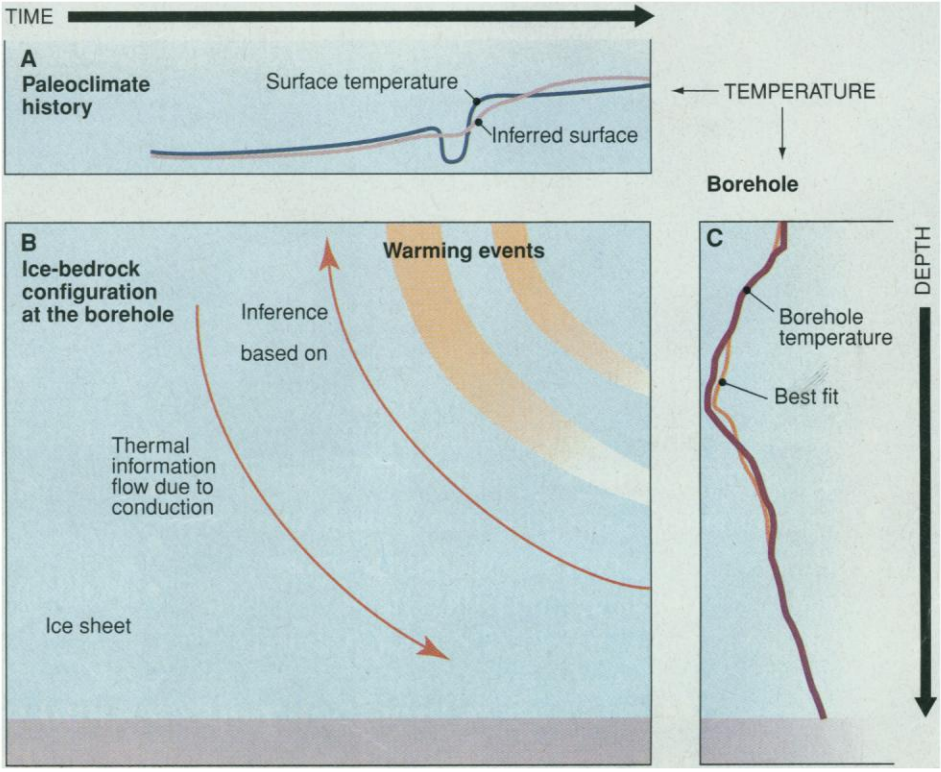
A fitting demonstration of Kelvin's lesson appears on page 455 of this issue, where Cuffey *et al.* report an analysis of temperature in the 3044-m-deep borehole at the GISP2 Greenland ice-core site (*3*). The first aim of their analysis is to challenge the fidelity of the surface-temperature history deduced previously from the ice-core oxygen-isotope stratigraphy of the GISP2 ice core. This oxygen-isotope derived history and a companion history derived by similar means from the GRIP ice-core site are very much on the minds of paleoclimatologists. They reveal an enigmatic climate-change pattern noted for its severity and abruptness (*4*). The challenge Cuffey *et al.* mount is fair because oxygen-isotope variation of ice is not strictly a function of local surface temperature alone, but is rather a compound function of the hydrologic process which delivers snow to the ice sheet. The second aim, pending the outcome of the first, is to calibrate the oxygen-isotope paleothermometer of the GISP2 ice core; that is, to quantify the relation between oxygen-isotope ratio shifts in the ice and temperature shifts at the time the ice was deposited.

The essence of the analysis of Cuffey *et al.* is a solution of the borehole-temperature paleothermometry problem for the GISP2 ice-core site. This problem is solved by estimating a 40,000-year surface-temperature history that successfully predicts the present-day temperature profile measured in the borehole. A solution to this problem is not easy to produce, nor is it easy to trust. The author of a recently published text on geophysical inverse theory refers to solutions of the borehole-temperature paleothermometry problem as "worthless for practical purposes" (*5*, p. 87).

The cause for this disclaimer is easily appreciated even without knowing much about the physics of heat flow in ice sheets or the mathematics of inverse methods. A surface temperature change penetrates an ice sheet by the combined effects of heat conduction and continual downward ice movement associated with snow accumulation (see figure). In the absence of heat conduction, downward movement would create an ideal one-to-one relation between borehole temperature at a given depth and surface temperature at a corresponding time.

Solution of the borehole-temperature paleothermometry problem would be a snap (much like what we desire ice-core oxygen-isotope paleothermometry to be) if this ideal, chronologically ordered thermal stratigraphy could be preserved. In actuality, the ideal thermal stratigraphy is not preserved because heat conduction erases temperature contrasts that are the signal of ancient surface-temperature change.

This "thermal memory" loss is a grave practical obstacle for the inference of a trustworthy temperature history. A flawed, untrustworthy solution (*6*) can display excessive, unrealistic oscillations that are constrained by nothing more than the minute, random errors in the borehole temperature measurements. Even adequate solutions have problems and can be trusted only to a limited extent because they can lack valid and interesting features, such as the Younger Dryas or Dansgaard-Oeschger events, that are too short-lived or too an-



A deeper look. The problem solved by Cuffey *et al.* (*3*) is illustrated by **B** (the ice configuration at the borehole site over time) showing how thermal information propagates through the ice sheet by downward ice movement and heat conduction. Surface temperature perturbations, such as the warming events shown **A**, penetrate the ice sheet and move down and to the right through the box with the passage of time. At the present day (right edge of **A**), the ice-sheet temperature is measured, yielding the profile shown in **C**. A backward-time calculation, or a series of trial forward-time calculations, are used to infer a surface temperature history that best predicts the borehole temperature data. The problem is difficult because heat conduction limits thermal memory. The result of this obstacle is that the inferred surface temperature history is not unique. Short-lived or ancient surface temperature events do not have sufficient influence on present-day borehole temperature to be resolved. Cuffey *et al.* overcome the nonuniqueness difficulty by selecting the history that most closely resembles the low-pass filtered (broad time-scale smoothed) ice-core oxygen-isotope chronology.

The author is in the Department of Geophysical Sciences, University of Chicago, Chicago, IL 60637, USA. E-mail: drm7@midway.uchicago.edu

cient to be preserved in the borehole temperature profile.

Practitioners of borehole-temperature paleothermometry cope with the obstacle of limited thermal memory by striking a balance between opposing goals. One goal is fidelity between borehole-temperature observations and the predicted borehole temperature profile based on the inferred surface temperature history. The other goal is simplicity of the inferred surface-temperature history, namely, sufficient simplicity to suppress the wild oscillations that would otherwise be introduced by random error in temperature measurement. These two goals are opposing, because improvements in satisfying one goal (say, simplicity of the temperature history) will detract from the satisfaction of the other (fitting borehole-temperature data).

Cuffey *et al.* strike the balance between the opposing goals in a remarkably adept manner that reflects their aim to challenge the ice-core isotopic paleothermometer (*3*). For the goal of simplicity, Cuffey *et al.* demand that the inferred surface-temperature history be linearly related to only the broadest time-scale patterns of the oxygen-isotope record. For the goal of fidelity, they minimize a least-square measure of misfit between the observed borehole temperature log and the temperature profile predicted by the inferred surface-temperature history. (This prediction involves a sophisticated ice-sheet temperature model, which is one of the technical highlights of their analysis.) The adjustable parameters, which are tuned to achieve this minimization, are simply the slope and intercept of the linear relation defining the ice-core oxygen-isotope paleothermometer. As can be appreciated from figure 2 of the report by Cuffey *et al.*, the twin opposing goals are achieved, and the ice-core oxygen-isotope paleothermometer is both confirmed and calibrated.

This success is qualified, however, by its applicability to only the broadest time-scale feature of the surface-temperature history of the GISP2 site, that is, the glacial to interglacial warm-up. Other interesting climate features implied by the ice-core isotopic record, such as the 10,000-year-old Younger Dryas event or the presence or lack of the controversial Eem/Sangamon cold spells, may never be confirmed. These ancient and short-lived features fall below the resolution threshold of borehole-temperature paleothermometry (*7*).

For scientists who generate and interpret ice-core paleoclimate data, the success of the analysis by Cuffey *et al.* is satisfying because it culminates several decades of effort to use borehole-temperature paleothermometry as a check on other techniques for deriving environmental histories. Of more general interest, their work implies that past estimates of the glacial to interglacial warm-up derived from the ice-core isotope records have been too conservative (that is, were 8°C when they should have been 16°C) (*8*). This deduction is in accord with similar conclusions drawn recently about glacial-period temperatures in the tropics (*9*) and confirms that polar amplification of climate change (for instance, the poles respond with greater amplitude than the tropics) is a central characteristic of Earth's climate.

References and Notes

1. Lord Kelvin, *Trans. R. Soc. Edinburgh* **23**, 157 (1864).
2. F. M. Richter, *J. Geol.* **94**, 395 (1986).
3. K. M. Cuffey *et al.*, *Science* **270**, 455 (1995).
4. R. A. Kerr, *ibid.* **260**, 890 (1993).
5. See exercise 2.06(iii) of R. L. Parker, *Geophysical Inverse Theory* (Princeton Univ. Press, Princeton, NJ, 1994).
6. For example, see D. R. MacAyeal, J. Firestone, E. D. Waddington, *J. Glaciol.* **37**, 326 (1991). See also, D. Dahl-Jensen, S. J. Johnsen, W. S. B. Paterson, C. Ritz, *ibid.* **39**, 421 (1993).
7. J. Firestone, *ibid.* **41**, 39 (1995).
8. This conclusion, that the glacial to interglacial warm-up was much greater than previous interpretations of Greenland ice-core isotopic records indicated, was also achieved in a similar analysis by Cuffey's predecessor at the Geophysics Program of the University of Washington, J. Firestone. Firestone's study involved data from a Greenland ice-core site that was not as well suited for borehole-temperature paleothermometry as the GISP2 site. See (*7*).
9. L. G. Thompson *et al.*, *Science* **269**, 46 (1995). See also W. S. Broecker, *Nature* **376**, 212 (1995).

Life With 482 Genes

André Goffeau

For many years we believed that the first genome to be sequenced entirely would be that of the bacterium *Escherichia coli*, estimated to be 4720 kilobases long (*1*). More recently, the prospect of completing the much longer genome of the yeast *Saccharomyces cerevisiae* (12,500 kilobases) before the end of 1995 has been entertained (*2*). But to everyone's surprise, an outsider won the race for the first complete genome sequence—that of the bacterium *Haemophilus influenzae*, a 1830-kb sequence, recently reported by a team from the Institute for Genomic Research (TIGR) headed by Craig Venter (*3*). This "premiere" was performed on a very small bacterial genome, and not on the long mammalian fragment on which one might have expected TIGR to have concentrated its powerful resources. Now, Venter and his colleagues have focused on an even smaller genome, that of *Mycoplasma genitalium*, the complete sequence of which is reported in the paper by Fraser *et al.* in this issue of *Science* (*4*). This parasite (but not necessarily a pathogen) of human genital and respiratory tracts has a genome of only 580-kb long.

Sequencing of the *M. genitalium* genome was the product of a collaboration among three teams. Foremost among these is TIGR, a nonprofit institute with large-scale, high-throughput DNA sequencing facilities that has given the rights to commercialize its findings to an allied company, Human Genome Sciences, Inc. TIGR and its director Craig Venter are known mainly for their mass production of sequence tags for human genes (ESTs) expressed in different tissues (*5*). The second team is led by Hamilton Smith from the Johns Hopkins University School of Medicine, who is best known for his pioneering work on restriction enzymes in bacteria, work that opened the field of molecular genetics and for which he won the Nobel Prize in 1978. The third team is that of Clyde Hutchison from the University of North Carolina, who is an internationally recognized expert in the study of *Mycoplasma* species.

One of the most impressive features of the sequencing effort for the *M. genitalium* genome is its efficiency, a testament to the power of the TIGR sequencing and informatics facilities. The first DNA extraction from *M. genitalium* was carried out in early January 1995, and the manuscript was submitted on 11 August 1995.

On the technical side, the most spectacular aspect of the work is the application of random ("shotgun") sequencing and assembly of the 8650 needed sequencing reactions in a single contig (that is, a collection of overlapping clones that collectively cover the target region). This accomplishment was made possible by the development of a series of highly performing informatics tools already tested during the sequencing of the *H. influenzae* genome. On the scientific front, the originality of the work stems from the fact that the *M. genitalium* genome has one of the smallest known genomes of any free-living organism. It is therefore reasonable to assume that its genome sequence reveals the near-

---

The author is at the Université Catholique de Louvain, Unité de Biochimie Physiologique, Place Croix du Sud, 2-20, B 1348 Louvain-la-Neuve, Belgium.