

Into an ice age

Kurt M. Cuffey

Analyses of a new ice core from Greenland yield the first high-resolution picture of the start of the last ice age in the Northern Hemisphere, and of the onset of climate instability as our planet cooled.

The relatively warm and stable climate that humanity has enjoyed for the past 10,000 years will inevitably give way to a new ice age — a tremendous environmental transformation that is destined to bury the sites of Boston, Edinburgh and Stockholm under glacial ice. In *The Day After Tomorrow*, the Hollywood movie most notable for its public abuse of thermodynamics, a new ice age starts in only one week. What does such a transition look like in reality?

A new ice core¹ that samples the entire 3-km thickness of the north-central Greenland ice sheet (Fig. 1) provides us with an unprecedentedly rich and precise view of the onset of the most recent ice age, some 120,000 years ago. And it is from the location of greatest interest — the North Atlantic region, where rapid climate changes have been most dramatic in the past. This achievement, reported on page 147 of this issue¹, is the result of the efforts of the multinational North Greenland Ice Core Project (NGRIP). Remarkably, individual years of snow deposition are distinguishable for events as far back as 123,000 years in the past — a few years ago, such a resolution was thought to be unattainable.

The story of how the impossible became possible would itself make a fine movie, complete with dramatic scenes of enlightenment in the mass spectrometry lab as isotope analyses reveal past climatic changes. In the early 1990s, two deep ice cores recovered from central Greenland yielded a detailed environmental history extending 100,000 years back in time, through the entirety of the last glacial climate². These showed that climate was frightfully unstable. Within the space of a few decades, the North Atlantic region could evidently warm by 10 °C, while smaller changes of temperature and moisture occurred over wide areas of the planet³.

Unfortunately, structural disturbance of the deepest ices⁴ prevented these cores from revealing either the onset of the glacial period or events during the preceding warm interglacial period, known as the Eemian, about 130,000 to 120,000 years ago. Initial

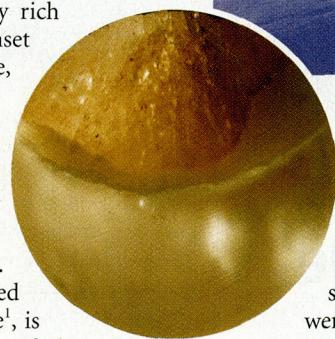


Figure 1 Core territory — the Greenland ice cap, which holds a climate record going back to the last interglacial, the Eemian. Inset, cross-section of an ice core that resulted from drilling slightly offset from the main bore hole; the half-moon shape is composed of Eemian ice.

reports to the contrary⁵, highlighting apparent climate instabilities within the Eemian, were clearly mistaken, as the new report demonstrates¹. Yet the degree of climate stability during the Eemian is of intense interest: the Eemian was slightly warmer than the world is now, providing an analogue for a possible future climate warmed by atmospheric pollution.

Further to the north of central Greenland (see the map on page 147), the climate is drier. It should therefore be possible to find ice from this last interglacial period safely above the disturbed basal zone. Thus the NGRIP project was born. It seemed likely that this new core would recover a record of the entire last interglacial climate and the start of the ice age. There was little hope for high temporal resolution, however; ice layers are cumulatively thinned as the regional flow compresses them downwards against the subglacial bedrock topography and stretches them horizontally. The vertical compression causing thinning is strongest if there is no melt at the ice sheet bed. And this was precisely the situation expected for the NGRIP site, given that basal temperatures are generally well below the melting point throughout northern and central Greenland.

But the beds of ice sheets, hidden beneath kilometres of opaque ice, contain surprises. The new NGRIP core proved to be located on

something like a volcanic centre — a highly unusual, localized zone of high heat flow from the underlying crust⁶. This heat is melting the basal ice, eliminating the oldest ice layers, and creating a relatively warm and wet environment — which, as the authors point out, merits further investigation for signs of microbial life. This melt also significantly reduces the thinning of deep ice layers, allowing the extraordinary annual resolution of the glacial-onset record reported by the NGRIP team.

The melt has eliminated much of the Eemian ice. Fortunately, however, enough remains to provide a clear record of its latter few millennia, in which the climate was rather stable but warmer than the present by at least 5 °C. The persistence of stable climate under such warm conditions is a key observation. But the loss of the older ice precludes an answer to the even more important question of whether climate was stable in the five or so millennia following the onset of warmth, from about 130,000 years ago, when meltwater runoff from Greenland would probably have been greatest⁷. It has been suggested that increased freshwater flux to the North Atlantic might have the capacity to induce climate change by affecting the ocean's density structure and circulation⁸.

The start of the glacial period was characterized by a mostly gradual cooling, lasting about five millennia¹. The growth of ice

sheets is necessarily a slow process, limited by the transfer of moisture through the atmosphere, and it appears likely that this process initially limited the rate of climatic cooling. Then, approximately 114,000 years ago, with temperatures having dropped less than halfway to typical full glacial values, the first rapid climate changes began — as documented here for the first time. The timing and characteristics of these events offer an invaluable subject for climate modellers; the mechanisms underlying rapid climate change are still being debated, and climate models have not yet convincingly predicted them.

There is much work yet to be done on the NGRIP core, especially examining the high-resolution characteristics of the record, quantifying the temperature history, and investigating the biogeochemical changes that accompanied the transition to glacial climate. The overview presented in this issue¹ is sufficient to demonstrate that it is a valuable and remarkable core. Yet the NGRIP project has not achieved its primary goal: a reasonably complete record of climate during the last interglacial. How warm did this period get? Were any parts of it climatically unstable? Such information is crucial for evaluating climate models of a warmer world, and for understanding sea-level changes induced by melting of the Greenland

ice sheet. Analysis of basal ices gives direct and compelling evidence that the ice sheet retreated significantly during this period⁹.

There is only one way to fill this gap. A new ice core will have to be extracted from the dry regions of north-central Greenland, but at a safe distance from the heat-flow anomaly discovered at the NGRIP site. The cost and effort of such a project are trivial compared with the possible impact of a rise in sea level, and maybe even rapid climate change, induced by warming of the Arctic region.

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Evolutionary biology

Early evolution comes full circle

William Martin and T. Martin Embley

Biologists use phylogenetic trees to depict the history of life. But according to a new and roundabout view, such trees are not the best way to summarize life's deepest evolutionary relationships.

Charles Darwin described the evolutionary process in terms of trees, with natural variation producing diversity among progeny and natural selection shaping that diversity along a series of branches over time. But in the microbial world things are different, and various schemes have been devised to take both traditional and molecular approaches to microbial evolution into account. Rivera and Lake (page 152 of this issue¹) provide the latest such scheme, based on analysing whole-genome sequences, and they call for a radical departure from conventional thinking.

Unknown to Darwin, microbes use two mechanisms of natural variation that disobey the rules of tree-like evolution: lateral gene transfer and endosymbiosis. Lateral gene transfer involves the passage of genes among distantly related groups, causing branches in the tree of life to exchange bits of their fabric. Endosymbiosis — one cell living within another — gave rise to the double-membrane-bounded organelles of

eukaryotic cells: mitochondria (the powerhouses of the cell) and chloroplasts (of no further importance here). At the endosymbiotic origin of mitochondria, a free-living proteobacterium came to reside within an archaebacterially related host — see Fig. 1 for terminology. This event involved the genetic union of two highly divergent cell lineages, causing two deep branches in the tree of life to merge outright. To this day, biologists cannot agree on how often lateral gene transfer and endosymbiosis have occurred in life's history; how significant either is for genome evolution; or how to deal with them mathematically in the process of reconstructing evolutionary trees. The report by Rivera and Lake¹ bears on all three issues. And instead of a tree linking life's three deepest branches (eubacteria, archaebacteria and eukaryotes), they uncover a ring.

The ring comes to rest on evolution's sorest spot — the origin of eukaryotes. Biologists fiercely debate the relationships between eukaryotes (complex cells that have a nucleus

Prokaryotes Cells lacking a true nucleus. Gene transcription occurs in the cytoplasm.

Archaeabacteria Prokaryotes with a plasma membrane of isoprene ether lipids. Protein synthesis occurs on distinctive, archaeabacterial-type ribosomes. Synonymous with Archaea.

Eubacteria Prokaryotes with a plasma membrane of fatty acid ester lipids. Protein synthesis occurs on distinctive, eubacterial-type ribosomes. Synonymous with Bacteria.

Eukaryotes Cells possessing a true nucleus (lacking in prokaryotes), separated from the cytoplasm by a membrane contiguous with the endoplasmic reticulum (also lacking in prokaryotes). Include double-membrane-bounded cytoplasmic organelles derived from eubacterial endosymbionts^{11–13}. The plasma membrane consists of fatty acid ester lipids. Protein synthesis occurs on ribosomes related to the archaeabacterial type. Synonymous with Eucarya.

Proteobacteria A name introduced for the group that includes the purple bacteria and relatives¹⁸. The endosymbiotic ancestor of mitochondria was a member of the proteobacteria as they existed more than 1.4 billion years ago.

Figure 1 Who's who among microbes. In 1938, Edouard Chatton coined the terms prokaryotes and eukaryotes for the organisms that biologists still recognize as such³. In 1977 came the report of a deep dichotomy among prokaryotes¹⁹ and designation of the newly discovered groups as eubacteria and archaeabacteria. In 1990, it was proposed² to rename the eukaryotes, eubacteria and archaeabacteria as eucarya, bacteria and archaea. Although widely used, the latter names left the memberships of these groups unchanged, so the older terms have priority.

and organelles) and prokaryotes (cells that lack both). For a decade, the dominant approach has involved another intracellular structure called the ribosome, which consists of complexes of RNA and protein, and is present in all living organisms. The genes encoding an organism's ribosomal RNA (rRNA) are sequenced, and the results compared with those for rRNAs from other organisms. The ensuing tree² divides life into three groups called domains (Fig. 2a). The usefulness of rRNA in exploring biodiversity within the three domains is unparalleled, but the proposal for a natural system of all life based on rRNA alone has come increasingly under fire.

Ernst Mayr³, for example, argued forcefully that the rRNA tree errs by showing eukaryotes as sisters to archaeabacteria, thereby obscuring the obvious natural division between eukaryotes and prokaryotes at the level of cell organization (Fig. 2b). A central concept here is that of a tree's 'root', which defines its most ancient branch and hence the relationships among the deepest-diverging