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A house divided

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Avian neighborhood watch

EVOLUTION

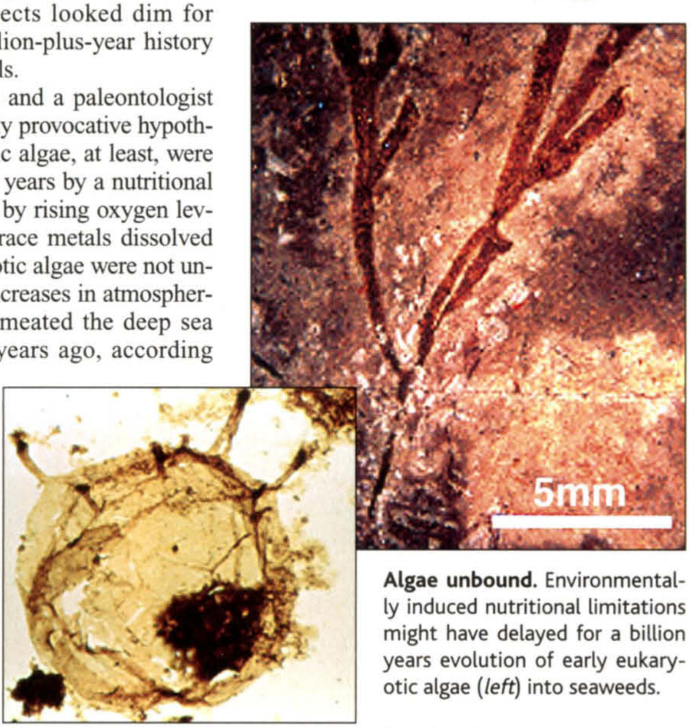
Could Poor Nutrition Have Held Life Back?

Our planet's middle age was "the dullest time in Earth's history," as one wag put it. From about 2 billion to 1 billion years ago, in the middle of the Proterozoic Eon, the green scum of cyanobacteria and their ilk reigned supreme, changing little from eon to eon. During that long hegemony, our cellular ancestors, the eukaryotes, went nowhere evolutionarily. Prospects looked dim for them despite their billion-plus-year history and rising oxygen levels.

Now a geochemist and a paleontologist propose an intentionally provocative hypothesis: that the eukaryotic algae, at least, were held back for a billion years by a nutritional deficiency brought on by rising oxygen levels and mediated by trace metals dissolved in the sea. The eukaryotic algae were not unleashed until further increases in atmospheric oxygen finally permeated the deep sea fewer than a billion years ago, according to the hypothesis, which is presented on page 1137 of this issue of *Science* by geochemist Ariel Anbar of the University of Rochester in New York state and paleontologist Andrew Knoll of Harvard University. The idea "is elegant," says geochemist Timothy Lyons of the University of Missouri, Columbia. "It explains a lot, but we really need to have more data. This paper will define research for years to come."

What might be called the Malnourished Earth hypothesis is founded on a 1998 proposal by geochemist Donald Canfield of Odense University in Denmark. With the exception of the near-surface, he suggested, the world ocean remained oxygen-free, or anoxic, after oxygen first appeared in the atmosphere about 2.2 billion years ago. That was when the great banded iron formations now mined for their metal ceased growing from the anoxic, iron-rich seawater that typified Earth's oceans since its beginnings. In the conventional view, oxygen had ended the age of banded iron formations by penetrating throughout the ocean and removing the iron in the form of insoluble iron oxides.

But Canfield, drawing on new measurements of the sulfur-isotope composition of Proterozoic ocean sediments, suggested that banded iron formation had been turned off by rising sulfide levels, not by oxygen. Below the uppermost waters the ocean remained anoxic, he argued, while the newly oxygenated atmosphere weathered large amounts of sulfur off the land and into the ocean. There it took the form of sulfides (including hydrogen sulfide). By forming insoluble compounds with the iron, these sulfides removed most of the iron from the sea. The ocean in the Mesoproterozoic, from 1800 million to 800 million years ago, would thus have been like neither Earth's primordial ocean—anoxic and iron-rich—nor the modern ocean—oxygen-rich and iron-poor. Chemically, it would have been like today's Black Sea.



Algae unbound. Environmentally induced nutritional limitations might have delayed for a billion years evolution of early eukaryotic algae (*left*) into seaweeds.

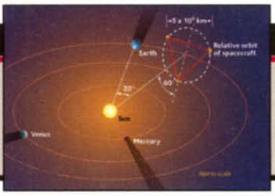
SOURCE: A. KNOLL

In such an ocean, iron would be removed to low concentrations, as would other metals, including molybdenum, copper, zinc, vanadium, and cadmium. The eukaryotic algae, in particular, would have missed some of those metals sorely. Their enzymes for taking up essential nitrogen in the form of nitrate are built around an iron atom and a molybdenum atom. The less of each of these metals in seawater, the harder it is for eukaryotic algae to get their nitrogen from nitrates. They have no way to fix nitrogen—convert the nitrogen gas of the atmosphere into usable nitrogen—as cyanobacteria do. Even bacteria's nitrogen fixation requires iron-based enzymes, the most efficient of which requires molybdenum as well. And eukaryotes generally lack bacteria's ability to ingest nitrogen-containing particles.

All in all, the Mesoproterozoic could have meant nutritionally hard times for ocean life, Anbar and Knoll conclude. The dearth of fixed nitrogen induced by scarce iron and molybdenum could have caused the generally low ocean productivity of the Mesoproterozoic, they say. And eukaryotic algae would have been at an evolutionary disadvantage. Multicellular algae, in particular, compete best when there are high levels of nitrate, not just the bare minimum. That could explain the steady and persistently low diversity of relatively simple eukaryotic algae through the Mesoproterozoic, Anbar and Knoll say, until 2 billion years after their first appearance. Only after mountain-building wrenched North America, sending more weathered metals into the sea, and atmospheric oxygen levels increased further, converting sulfides to sulfates and freeing up the trace metals, could the eukaryotes end their "profoundly boring" period and diversify toward larger, multicellular plants.

"They've put together a nice working hypothesis," says geochemist Louis Derry of Cornell University in Ithaca, New York. "It could be true, … [but] the literature on [Proterozoic] environments is full of interesting ideas. There's not as much data, so it is easy to carry out thought experiments. The trick to doing good science on these old materials is finding things you can test."

Geochemist Yanan Shen of Harvard, Canfield, and Knoll have in fact recently tested the foundation of the working hypothesis using Mesoproterozoic rocks from two former ocean basins in northern Australia. To judge by indicators of anoxia such as iron pyrite



preserved in the 1.7-billion-year-old sediments, the two ancient ocean basins "simply look like the deep Black Sea," says Knoll. But these might have been restricted ocean basins such as the Baltic, not the open ocean, so Anbar is working on a molybdenum-isotope analysis that could gauge the oxidation state of the world ocean from a few samples. Even then, many geophysiological links would remain to be proven between ancient ocean chemistry and the rise of well-fed eukaryotes. **–RICHARD A. KERR**

LANGUAGE EVOLUTION

'Speech Gene' Tied to Modern Humans

The ability to communicate through spoken language is the trait that best sets humans apart from other animals, most human origins researchers say. Last year the community was abuzz over the identification of the first gene implicated in the ability to speak. This week, a research group shows that the human version of this so-called speech gene appears to date back no more than 200,000 years—about the time that anatomically modern humans emerged. The authors argue that their findings are consistent with previous speculations that the worldwide expansion of modern humans was driven by the emergence of full-blown language abilities.

"This is the best candidate yet for a gene that enabled us to become human," says geneticist Mary-Claire King of the University of Washington, Seattle. But other researchers caution that uncertainties underlying the team's mathematical analysis, as well as debate about the gene's function, make dramatic conclusions premature. The case that the gene is closely linked with language ability "can only be said to be circumstantial," comments geneticist David Goldstein of University College London.

The gene, called *FOXP2*, was identified last fall by geneticist Anthony Monaco's group at Oxford University, in collaboration with cognitive neuroscientist Faraneh Vargha-Khadem and colleagues at the Institute of Child Health in London (*Science*, 5 October 2001, p. 32). They showed that *FOXP2* mutations cause a wide range of speech and language disabilities. Geneticist Svante Pääbo's group at the Max Planck Institute for Evolutionary Anthropology in Leipzig, Germany, in collaboration with Monaco's team, then set about tracing the gene's evolutionary history.

The Leipzig team, with graduate student Wolfgang Enard taking the lead, sequenced the *FOXP2* genes of several primates—chimpanzee, gorilla, orangutan, and rhesus macaque—as well as that of the mouse and compared them with the human sequence. The gene encodes a protein with 715 amino acids; it resembles other members of a family of regulatory genes implicated in embryonic development. Since the last common ancestor of humans and mice, which lived some 70 million years ago, there have been only three changes in the protein's amino acid sequence, the team reported online in *Nature* on 14 August. And two of these changes have occurred in the human lineage since it split with that of chimps roughly 6 million years ago.

Evolutionary leap. One of these primates is able to talk about what he's seeing; the other isn't.

CREDIT: KAREN HUNT MASON/CORBIS

These amino acid changes might have given some evolutionary advantage to the hominids who harbored them, the researchers surmised. This hypothesis gained support from calculation of a parameter known as Tajima's D statistic, an estimate of how much selection pressure has been exerted on a particular gene over the course of evolution. In general, the more negative this D value, the more selection has occurred. *FOXP2* had a highly negative D value—in fact, out of 313 well-characterized human genes recently analyzed, only one outscored *FOXP2* (*Science*, 20 July 2001, p. 489).

The team estimated how recently the human version of *FOXP2* became "fixed" in human populations—that is, when all humans harbored the last amino acid substitution. Although the date cannot be pinpointed, the team concluded that the fixation was 95% likely to have occurred no more than 120,000 years ago and was virtually certain to have occurred no earlier than 200,000 years ago.

Most of the researchers who spoke with *Science* agree that the authors make a strong argument that the human version of *FOXP2* has been favored by natural selection. "Overall, [that] case has been made," says Goldstein. But he and others were less eager to accept the dating of the gene: "Dating analyses [such as these] are fraught with uncertainty."

Now that the human version of *FOXP2* has been found to be advantageous to human evolution, the debate over the gene's role in language has become even more relevant. Some scientists caution against overstating the importance of *FOXP2* in the evolution of language ability. "It would be foolish to talk about *FOXP2* as the gene that evolved to permit the emergence of speech and language," says Elizabeth Bates, a neuroscientist at the University of California, San Diego, although it is clearly "one of the genes" that did so. Indeed, Pääbo suggests that this gene, which may be implicated in the ability to make the mouth and facial movements essential to speech, might have been selected for precisely because it improved vocal communication once language had already evolved.

–MICHAEL BALTER

NUMBER THEORY

Simple Recipe Creates Acid Test for Primes

Quick, now: Is 341 a prime number? That one's pretty easy to answer. How about 4,294,967,297? That's still a snap if you use a computer. But what if the number you're interested in has thousands of digits? Then things get murky, because the obvious way to settle the issue—systematically checking whether smaller numbers divide it—takes far too long. In recent decades, theorists have devised clever algorithms for telling whether a large number is prime, but none that could be proven to work quickly.

Until now.

Three computer scientists at the Indian Institute of Technology in Kanpur have found what researchers have long sought: a provably efficient algorithm for testing primes