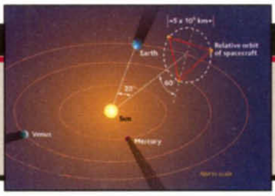


preserved in the 1.7-billion-year-old sediments, the two ancient ocean basins "simply look like the deep Black Sea," says Knoll. But these might have been restricted ocean basins such as the Baltic, not the open ocean, so Anbar is working on a molybdenum-isotope analysis that could gauge the oxidation 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.

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).

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

CREDIT: KAREN HUNTT MASON/CORBIS

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

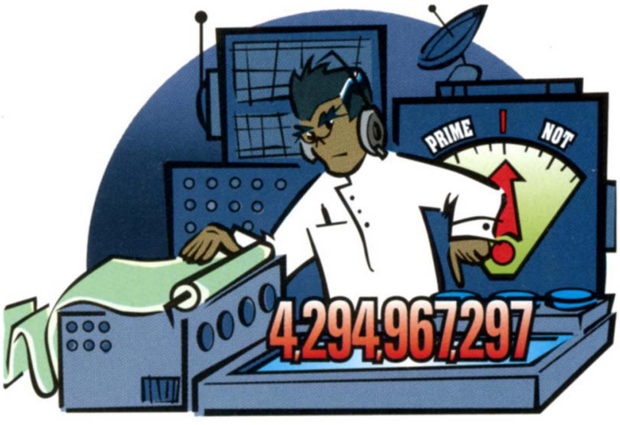
Simple Recipe Creates Acid Test for Primes

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 (whole numbers evenly divisible only by themselves and 1). Manindra Agrawal, a professor of computer science, and two students, Neeraj Kayal and Nitin Saxena, announced their result early this month, e-mailing copies of it to a number of experts in computational number theory.

"This is really fantastic, that we now know this to be true," says Hendrik Lenstra, one such expert at the University of California, Berkeley. The new result tidies up one of the corners of modern cryptography, which relies on hard-to-factor composite (nonprime) numbers to encrypt information. Although the algorithm is not practical at present, just knowing that it exists "simplifies our picture of what is going on," notes Andrew Odlyzko, a computational number theorist and director of the Digital Technology Center at the University of Minnesota, Twin Cities.



Prime suspect. A surprising new algorithm serves as a quick lie detector for positive integers.

What especially intrigues number theorists is that the algorithm and the proof of its efficiency are both very simple. Lenstra says he printed out the paper and discussed it with colleagues over dinner. "Before we had coffee we knew it was right," he says.

Put technically, the new result is a "polynomial time" algorithm for primality testing. That means it can take any N-digit number and return a yes-or-no answer in a run time bounded by a power of N—in this case, N^{12}. In computer science, polynomial time is the gold standard of efficiency. Any algorithm whose run time increases more steeply than that (as, say, 2^N does) quickly becomes time-consuming enough to bog down even the fastest computer.

Like other modern tests for primes, the new algorithm is based on a number-theoretic fact that Pierre de Fermat (of Last Theorem fame) discovered in the 17th century: If n is prime, then it evenly divides $a^n - a$ for any number a. Fermat's test makes it possible to prove that a number n is not prime without finding any of its factors. For example, $2^9 - 2 = 510$, which is not divisible evenly by 9. Hence, 9 cannot be a prime number.

Unfortunately, some composite numbers n also evenly divide $a^n - a$. To eliminate such "false positive" readings, the new algorithm runs a more elaborate but still elementary test, based on searching for pairs of numbers that fulfill a few simple conditions. If the search is successful, then n is declared composite; otherwise, it's prime. The key to the algorithm's efficiency is that the search can be restricted to a small range of numbers.

Constructing the primality test took a year of grueling work, Agrawal says. "There was nothing like an 'in a flash everything started making sense' feeling," he says. He and his students whittled away at the problem from various angles until July, when Agrawal hit on a substitution that made the last roadblock melt away.

"It's a bit of a surprise that such an easy algorithm had been missed all these years," says Carl Pomerance, a number theorist at Bell Labs in Murray Hill, New Jersey. "It's a delightful surprise—and perhaps also a bit of an embarrassment for those who have been working in the field, such as myself."

Cryptographers might well have more mixed feelings. They rely on now-difficult number theoretic computations, such as factoring large numbers, to safeguard cryptosystems that have become mainstays of the computer security business. If primality can be vanquished so easily, who's to say that a polynomial-time algorithm for factoring isn't just around the corner? Or, as Pomerance puts it, "What else have we overlooked?"

–**BARRY CIPRA**

ITALIAN REFORMS

Planned Mergers Raise Hue and Cry

NAPLES—Earlier this month Italian scientists were stunned to learn that their government is planning a major overhaul of the country's scientific establishment, including the axing of several institutes. Researchers are denouncing the plan, leaked to a prominent newspaper and denied by the government, as a ham-handed power grab drafted without their input.

According to a report in the 2 August edition of *la Repubblica*, the Ministry of University and Scientific Research intends to abolish eight publicly funded institutes and transfer the staff to the country's National Research Council (CNR). The institutes include the Anton Dohrn marine biology research station (Stazione Zoologica) in Naples, the National Institute of Applied Optics in Florence, and the National Institute for Experimental Oceanography and Geophysics in Trieste. Internal reforms would also be implemented at CNR, the Italian space agency, the National Institute of Geophysics and Volcanology, and the National Institute for Astrophysics.

"The Stazione Zoologica is a center of excellence," says Antonio Miralto, the institute's former director. "To have researchers of the Stazione Zoologica become part of the CNR would be a great error on the part of the government." William Speck, director of the Marine Biology Laboratory in Woods Hole, Massachusetts, says he was "shocked" by the news. "It is the oldest marine laboratory in the world."

CNR researchers are especially upset about a provision to choose institute directors through a top-down selection process, overseen by a president and an administrative council dominated by government appointees. Franco Pacini, an astronomer at the University of Florence and president of the International Astronomical Union, blasts this proposal as "obscene and unacceptable. It will basically put in the hands of politicians or administrators the choice for the best scientific leaders, even at the intermediate level."

The government's draft plan is close to its final form, says Claudia Di Giorgio, the journalist who received a leaked copy of the so-called "decree" after promising not to distribute it. However, a ministry spokesperson told *Science* that research minister Letizia Moratti is still working on the decree, which will be distributed to political bodies and the scientific community at the end of next month.

CNR is already moving to consolidate its 300 institutes into 100 larger units, and several scientists say it's ironic that the decree comes just as CNR has moved toward a more open selection process for its scientific directors. In addition, they are extremely unhappy that the proposed changes

Sinking feeling. The world's oldest marine biology research station at Naples is one of eight institutes slated for extinction.

CREDITS: (TOP TO BOTTOM) ILLUSTRATION: TIM SMITH; HISTORICAL ARCHIVES, STAZIONE ZOOLOGICA ANTON DOHRN