which would have blotted out the star-forming signature of Hu's more distant galaxy.

But Hu says both observations may be right. Seeing the signature of star formation in the newly discovered galaxy suggests that enough galaxies already existed to see off the neutral hydrogen around it, in turn implying a largely transparent universe. By contrast, a quasar is so brilliant—about 1000 times brighter than an ordinary galaxy—that it clears away the neutral hydrogen fog around itself. So although the quasar itself may shine through, this says little about the condition of other parts of the universe. And the neutral hydrogen that Fan sees may well be due to cold, dark clouds of neutral hydrogen between us and the quasar, says Hu, rather than evidence of the widespread pre-reionization fog.

Spinrad is confident that Hu's faint source is a true early galaxy. "I think the result is right," he says. "The idea that the universe was dark … at that kind of redshift, it can't be a completely correct statement any longer." Loeb, however, would prefer to wait for more results: "It would be much more convincing if there were more objects of this type."

–ANDREW WATSON

Andrew Watson is a writer in Norwich, U.K.

CHEMISTRY

Whisper of Magnetism Tells Molecules Apart

High-energy physicists aren't the only scientists with a lust for power. For decades, chemists have built ever stronger magnets to improve nuclear magnetic resonance (NMR) spectroscopy, a technique that gleans the structure of molecules from the unique magnetic signatures of their component atoms. But generating those high magnetic fields is expensive, which drives up the cost of those probes and related medical imaging scanners.

A team led by researchers at Lawrence Berkeley National Laboratory (LBNL) and the University of California (UC), Berkeley, is bucking the trend with a strategy that could pay off for physicians and their patients. On page 2247, the group describes a new way to get detailed chemical information at ultralow magnetic fields. Because NMR forms the basis of magnetic resonance imaging (MRI), the new technique might someday eliminate the massive and costly magnets used in today's medical imaging systems.

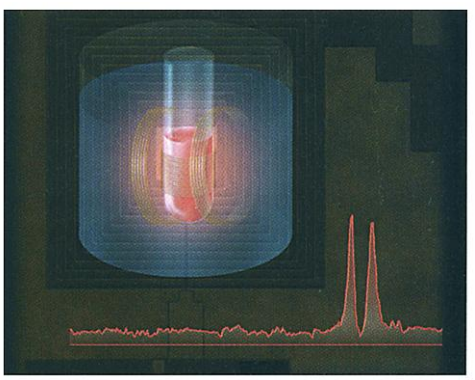
"It's a very elegant piece of work," says Warren S. Warren, who heads the center for molecular and biomolecular imaging at Princeton University in New Jersey. Allen Garroway, a physicist at the Naval Research Laboratory in Washington, D.C., says that the prospect of low-field medical imaging is "tantalizing" because of the "huge market" for low-cost MRI. But all agree that extending this technique to medical MRI machines still faces significant hurdles.

In traditional NMR, bigger magnets make it easier to track atoms. Some atomic nuclei behave like tiny bar magnets and align when placed in a magnetic field. In NMR, researchers disrupt that alignment slightly and use the telltale oscillation, or precession, of nuclei around the magnetic axes to identify particular atoms and their positions. The more powerful the external magnetic field is, the more pronounced this "chemical shift" signal becomes. That makes it possible to work out the structure of larger molecules and make use of smaller samples.

But NMR spots other telltale magnetic signatures beyond the chemical shift. In a related effect, called "J-coupling," for example, electrons around different atoms in a molecule influence one another in ways that split the atoms' spectral signatures from one line into two or more. "It tells you which atoms are bonded to which," says Alexander Pines, a chemist at UC Berkeley, who led the new study along with physicist John Clarke of UC Berkeley and LBNL. The signal for this effect, it turns out, remains constant as the applied magnetic field drops.

Pines and his colleagues decided to see whether they could use this effect to identify compounds using only a very small magnet and a simple two-part test. In a test tube, they placed a solution of water and two different test molecules: methanol and phosphoric acid. They then used an ultrasensitive magnetic field detector, called a SQUID, to try to pick up the characteristic spectral-line splitting signature of a phosphorus atom bound to an oxygen that is, in turn, bonded to a hydrogen. Phosphoric acid has this phosphorus-oxygen-hydrogen configuration. But when it's mixed with water, hydrogen atoms quickly drop off and reattach themselves to the acid molecules. The NMR detector didn't see this as a three-atom configuration and registered just a single spectral line.

Next, the researchers reacted the methanol and phosphoric acid to form trimethylphosphate, a compound that also has the three-part phosphorus-oxygen-hydrogen configuration, but with the hydrogens fixed in place. In this case, the SQUID spotted a phosphorus-oxygen-hydrogen configuration and registered it as a split in the spectral line.



CREDIT: ROBERT MCDERMOTT

Power-less. A sensitive detector (background) picks up molecular fingerprints in NMR spectra without high-field magnets.

Pines hopes the work will lead to a low–magnetic-field approach to MRI imaging. But that effort faces at least one very difficult challenge, says Warren. MRI builds images piece by piece, detecting the magnetic spins of hydrogen nuclei in small volumes of a material. Reducing the applied magnetic field makes it harder to pick the spins out of random background noise and could degrade the resolution of a scan. Warren says alternative advanced imaging techniques may solve the problem. If so, J-coupling could revolutionize medical imaging by making the machines, now housed in specialized centers at hospitals, cheap enough for the doctor's office.

–ROBERT F. SERVICE

FORENSIC SCIENCE

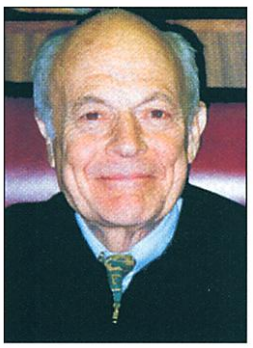
Judge Reverses Decision On Fingerprint Evidence

A federal judge in Philadelphia has changed his mind and decided that fingerprint examiners should have their say in court—even if what they do isn't science.

In January, Judge Louis H. Pollak of the U.S. District Court for the Eastern District of Pennsylvania found that fingerprint identification didn't meet the U.S. Supreme Court's standards for scientific evidence (*Science*, 18 January, p. 418). Pollak ruled that fingerprint identification failed three of four criteria set by the high court in its 1993 decision, *Daubert* v. *Merrell Dow Pharmaceuticals*. He said that the technique hadn't been scientifically tested, wasn't subject to scientific peer review, and didn't possess a known rate of error. Fingerprinting was "generally accepted" among forensic scientists, he found, but that did not establish its reliability. Pollak said fingerprint examiners could testify in an impending murder trial, but he forbade them from stating whether prints found at the crime scene matched those taken by authorities.

Worried that the ruling would undermine one of their most powerful tools, federal prosecutors persuaded Pollak to reconsider the issue. On 13 March, he ruled that his interpretation of *Daubert* had been too narrow. Fingerprinting is a form of technical expertise akin to accident reconstruction or art appraisal, he said, so it need not meet the scientific peer-review requirement. And although the method's error rate is unknown, he writes, there is no evidence that it is unacceptably

high. In the absence of rigorous testing, he said, limiting the testimony of fingerprint examiners would "make the best the enemy of the good."



On second thought. Fingerprint identification can continue, Judge Pollak ruled.

The new decision is a mixed blessing for practitioners, allowing them to declare matches but implying that they are technicians, not scientists, says James Starrs, a forensic scientist and law professor at George Washington University in Washington, D.C. "It's a blow to their status in the scientific community," he says. However, Pat Wertheim, a forensic scientist at the Arizona Department of Public Safety in Tucson, says the distinction between scientists and technicians makes little difference in a trial. "For all practical purposes," Wertheim says, "the 12 people on the jury couldn't care less."

–ADRIAN CHO

Adrian Cho is a freelance writer in Boone, North Carolina.

EVOLUTIONARY BIOLOGY

Ancient DNA Untangles Evolutionary Paths

Analyzing ancient DNA for clues into the deep past has had a bad rap: Too many false reports of recovered dinosaur DNA have sullied the field's reputation. Now, that's about to change. Two independent research groups have shown that, when studied correctly, genetic material preserved in cold environments can reveal quite a bit about the past.

Alan Cooper, a molecular evolutionist at the University of Oxford, United Kingdom, and his colleagues used ancient DNA to reconstruct the migration patterns of subarctic brown bears living up to 60,000 years ago. Similarly, David Lambert's group at Massey University in Palmerston North, New Zealand, examined 6000-year-old DNA from Antarctic penguins to determine the rate at which the birds' genomes evolved.

The two teams report their findings on pages 2267 and 2270, respectively. "Both these papers begin to chart a new course in ancient DNA studies," comments Robert Wayne, an evolutionary biologist at the University of California, Los Angeles.

Researchers first began extracting sequence information from DNA in museum specimens about 15 years ago, gradually moving on to ever older material. Much progress has been made using antique DNA to study genetic variation and to place extinct species in their family trees, but supposed extractions of DNA from dinosaur fossils or million-year-old insects in amber casts proved to be studies in modern contamination.

Cooper avoided some common technical pitfalls by studying bones from northern Alaska, the Yukon, and Siberia, where DNA was kept on ice for thousands of years in the permanently frozen soil. In addition to these fresh-frozen samples, he and his colleagues had access to hundreds of bones in museums with their DNA still in intact fragments. To check the work, a second lab reanalyzed the DNA samples.

Cooper's team used the samples to look at the history of an intriguing geographic region. Until 11,000 years ago, the area called Beringia had a land bridge between the Asian and American continents, enabling species to cross back and forth—including humans about 13,000 years ago. The bones "provided an amazing opportunity to look at the genetic record" of several species, such as bears, bison, and lions, at what was "a biological crossroads," Cooper explains.

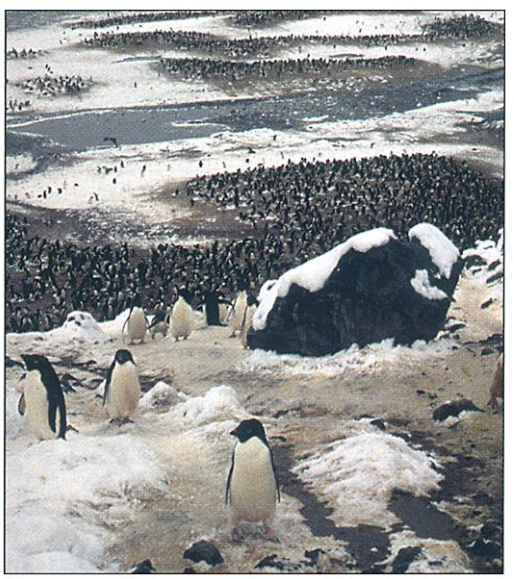
The researchers analyzed DNA from bones of 36 brown bears, using radiocarbon dating to verify the ages of 30 bones. They sequenced two pieces—one 135 and the other 60 bases long—of the mitochondrial genome and grouped the bears according to the degree of similarity in the sequences. The work indicates that the distributions of these ancient genetic groups did not correspond to those of modern populations. This finding serves as a caution to researchers that "what we see in present-day [distributions] is not necessarily true about the past," says Rob Fleischer, an evolutionary biologist at the Smithsonian Institution in Washington, D.C.

The data further indicate that brown bears may have disappeared from much of Alaska and the Yukon 35,000 years ago, only to reappear 14,000 years later. Because this reappearance corresponds with the disappearance of a larger animal called the short-faced bear, Cooper suggests that competition between the two species influenced the changes in their distributions.

Meanwhile, Lambert and colleagues took advantage of frozen remains from a species at the other end of the globe. Adélie penguins' large colonies have existed for thousands of years, with the same birds and their descendents returning to the sites year after year. As a result, "here you have [layers of bones] in colonies that are beautiful" and ripe for DNA studies, says Axel Meyer, an evolutionary biologist at the University of Konstanz, Germany.

Lambert's team members collected and dated 96 bones from various layers and gathered 300 blood samples from living birds. They and a lab at the University of Auckland, New Zealand, analyzed a rapidly evolving 352-base sequence from the mitochondrial genome, cataloging changes between the ancient and modern samples. From that, they calculated the rate of evolutionary change.

In the past, studies estimating mutation rates have obtained just a few data points over very short (one or two generations) or very long (perhaps millions of years) time scales. But in this study, the researchers were able to "use the whole history of the past 6000 years and the genealogy of the genes to extrapolate the mutation rate," says Wayne. Lambert's group puts that rate at about two to seven times faster than were previous estimates for other species.



Homebodies. Antarctic penguins that have historically stuck to the same breeding sites proved perfect for studies of ancient DNA.

Questions remain about both studies, however. Lambert says more bones were needed for Cooper's group to draw its conclusions. And Cooper wishes the DNA for the penguin study went back farther than 6000 years, so the variation would better reflect long-term rates of evolution. Others, including Fleischer, applaud the amount of DNA that Lambert collected but still worry that ancient changes in the penquins' distribution could have distorted the results.

Nonetheless, says Svante Pääbo, an evolutionary biologist at the Max Planck Institute for Evolutionary Anthropology in Leipzig, Germany, "the study of ancient DNA has now advanced to a point where one can study genetic variation within species over thousands of years and [obtain] data that can be trusted." Lambert's and Cooper's studies may thus push the use of ancient DNA farther along the path to redemption.

–ELIZABETH PENNISI

CREDITS: (TOP TO BOTTOM) PHILADELPHIA LEGAL INTELLIGENCER; D. LAMBERT ET AL.