Eisenstein acknowledges that tight funding and a focus on large facilities have resulted in "a big squeeze on grants." But he says that accepting unsolicited proposals from academics for new facilities, rather than holding open competitions, has served astronomy well by encouraging creative ideas.

However, both Eisenstein and Miller agree that the academy report could be a boon to a long-discussed proposal for NSF to pay for additional instrumentation at private observatories in exchange for blocks of time on those telescopes, which NSF would then dole out to researchers. "We need to start with practical things, and I have high hopes for this," says Miller. Eisenstein says he hopes to find enough money in NSF's 2002 budget, now under review by Congress, to begin funding the exchange program, assuming that both sides can agree on how to structure the arrangement. "The burden of proof is on us—with the full cooperation of the community—to figure out a way to implement this [program]," says Eisenstein.

Miller and a group of directors of private observatories say that such an agreement would be a welcome sign that NSF is listening to them. And they hope that the Augustine report will foster a new era of greater cooperation. "At least this gives us a mandate to make the best use of funds in a coordinated way," says Paul Goldsmith, director of the National Astronomy and Ionosphere Center in Arecibo, Puerto Rico.

–ANDREW LAWLER

GENOMICS

Painting a Picture of Genome Evolution

Normally, we associate evolution with organisms growing more complex as they acquire new genes over time. But as a new analysis of the genome sequences of two bacteria shows, genes can be lost as well as gained during evolution. Even more intriguingly, the work provides snapshots capturing gene decay in the act and thus illuminates the actual genomic changes that occurred over tens of millions of years of evolution.

The research, which is described on page 2093 by microbiologist Didier Raoult of the Marseilles School of Medicine in southern France and his colleagues, focuses on two pathogenic bacteria: *Rickettsia conorii*, the culprit in Mediterranean spotted fever, and *R. prowazekii*, which causes typhus. These organisms diverged from a common ancestor 40 million to 80 million years ago, and evidence of accumulated mutations in a gene shared by the two indicates that *R. prowazekii* is evolving more rapidly. To explore how the two grew apart, the Raoult team sequenced the complete 1.3-billion-base-pair genome sequence of *R. conorii* and then compared it to *R. prowazekii*'s genome sequence, which was determined 3 years ago by Charles Kurland of the University of Uppsala in Sweden and his colleagues.

The two *Rickettsia* are good subjects for this analysis partly because both are obligate intracellular parasites, which means they can survive only in the cells of their insect vectors or in the cells of animals they infect, such as humans. Thus, they rarely encounter other species with which they can exchange genetic material, making it easier to trace how their individual genomes change over time.

Evolution clue. The newly sequenced genome of *Rickettsia conorii*, shown here inside a host cell, is providing insights into evolution.

Scientists have long predicted that, for a minute bacterium trapped in an animal's cell, shrinking the genome can preserve energy and improve efficiency. The new analysis by the Raoult team gives a stamp of approval to this theory. It shows that *R. prowazekii*'s genome is smaller overall—1.1 billion bases compared to its cousin's 1.3 billion. It also has one-tenth as much repeated DNA and far fewer active genes; whereas *R. conorii* has 1374 such genes, *R. prowazekii* has only 834.

What's more, remnants of nearly half the genes that no longer function in *R. prowazekii* remain in its genome. The arrangement of this "junk" DNA even mirrors the configuration of the active genes in *R. conorii*. "It was like having one of the two being the ancestor of the other one and then seeing what has happened during all these years," says Raoult.

"This [sequence] is telling us something about evolution that maybe we already should have known," says David Walker, a pathologist at the University of Texas Medical Branch in Galveston, referring to the fact that bacterial genes decay. Because remnants of many of the genes lost by *R. prowazekii* stay behind in the pathogen's genome, he adds, the new sequence could shed light on why genes degrade and how their functions change as they do.

CREDITS: (LEFT TO RIGHT) COURTESY VSEVOLOD POPOV/UNIVERSITY OF TEXAS MEDICAL BRANCH IN GALVESTON; CHIP CLARK/NATIONAL MUSEUM OF NATURAL HISTORY, SMITHSONIAN INSTITUTION

ScienceScope

Strength in Numbers Biomedical researchers will now have to demonstrate that they—and not an industry or government funder—control data from a study in order to get the results published in some of the world's most prominent medical journals.

The editors of 11 major journals this week issued a joint vow to reject studies in which the sponsor was allowed to manipulate or withhold results. Researchers say that the move will help discourage drug companies from trying to tweak or cover up results that don't support their financial interests.

The journals will now "routinely require authors to disclose details of their own and the sponsor's role in the study." The guidelines do allow sponsors to ask for time—30 to 60 days—to review a manuscript before it is submitted. Signers included the editors of *The New England Journal of Medicine*, *The Lancet*, *The Journal of the American Medical Association*, and leading journals in Denmark, Canada, Australia, the Netherlands, and New Zealand.

The Washington, D.C.–based Pharmaceutical Research and Manufacturers of America endorsed the move. Sheldon Krimsky, a public health professor at Tufts University in Medford, Massachusetts, who has sounded the alarm about conflicts of interest in science, calls it "a bold step forward by a small but important group of journals."

Going Slow A panel asked to plot the future of science at the Smithsonian Institution met last week for the first time—and speed was not on the agenda.

The 18-member commission was appointed in the wake of Smithsonian Secretary Lawrence Small's controversial reorganization proposals made earlier this year (*Science*, 20 July, p. 408). But the panel's report may take a year or more to complete. "Given the importance and enormity of the task before us, we will take as long as it takes to do it right," says chair Jeremy Sabloff, director of the University of Pennsylvania Museum in Philadelphia.

The panel has already received a proposal from an ad hoc group of seven scientists at the National Museum of Natural History to divide the Smithsonian into three research institutes while keeping close ties between research and public programs. Smithsonian officials also submitted charts outlining their own reorganization proposals.

Indeed, the work already offers a remarkably clear view of the stages of gene decay. As the *R. prowazekii* genome sequence shows, first genes are interrupted by a stop codon, a sequence of three nucleotides that tells the protein-synthesis machinery that it has reached the end of the gene and should stop. Occasionally, these interrupted genes continue to make incomplete proteins of their own. But as degradation progresses, genes lose the ability to produce proteins and eventually stop being copied into messenger RNA altogether, although they remain identifiable.

The decay is likely the combined result of random mutations and adaptation. Struck by a mutation that disables a gene, individual *Rickettsia* microbes either die or pass the altered genes on to their offspring. Raoult points out that some of the genes lost make enzymes needed to produce amino acids also generated by the host—meaning that the bug can abandon these genes without losing access to the amino acids. "If you don't have some positive benefit from that gene, you lose it," says Nancy Moran, an evolutionary biologist at the University of Arizona in Tucson.

Having painted the outline of *Rickettsia* evolution with broad brush strokes, scientists now hope to focus on the details of how gene inactivation occurs. Moran notes that many of the genes lost perform basic functions such as DNA repair. Thus, it's possible that the loss of, say, one specific DNA repair gene instead of another affects which mutations stick. By clarifying how genes lost may guide the bacterium's evolution, scientists can perhaps grasp how its existing design came to be. **–JENNIFER COUZIN**

Jennifer Couzin is a writer in San Francisco.

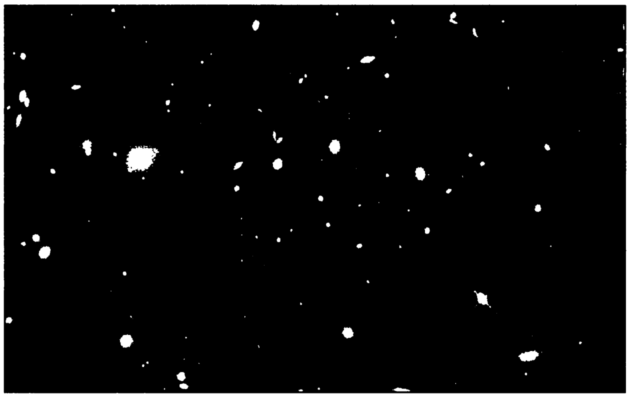
ASTROPHYSICS

Orbiting Observatories Tally Dark Matter

WASHINGTON, D.C.—As galaxy clusters belch x-rays in all directions, they reveal the hidden mass in the universe. At a meeting here celebrating 2 years of observations with the Chandra X-ray Observatory,* astronomers claimed that Chandra observations, along with pictures from the Hubble Space Telescope, enabled them to calculate the amount of dark matter in the cosmos—and seriously damage one theory about its nature.

One of the biggest puzzles in astrophysics is the nature of dark matter, the invisible substance whose gravitational pull holds galaxies together. "It's been about 25 years since we appreciated that dark matter is the dominant form of matter in the universe," says Joel Bregman, an astrophysicist at the University of Michigan, Ann Arbor.

In the past few months, astronomers have measured the amount of dark matter by looking at wiggles in the cosmic background radiation (*Science*, 4 May, p. 823) and by analyzing the distribution of galaxies in space (*Science*, 13 April, p. 188). They've concluded that ordinary matter makes up only about 5% of the mass needed to give space the shape that cosmologists prefer, while dark matter makes up another 25% or so. (The mysterious "dark energy" or "quintessence" seems to make up the remainder.) At the symposium, Steven Allen, an astronomer at the Institute of Astronomy in Cambridge, U.K., presented new evidence that those figures are correct.



Weighty matters. Warped images of galaxies in cluster Abell 2390 helped reveal the mass in intervening space.

With the Chandra satellite, Allen and his colleagues observed the x-rays emitted by gas inside massive galaxy clusters. "For the very first time, we're able to accurately measure the temperature of this gas," Allen says. From the temperature profile and density of the gas, the team figured out how much mass is holding the cluster together. "It's very straightforward," he says.

Meanwhile, pictures from the Hubble Space Telescope and ground-based observatories gave an independent measurement, based on how much the extreme mass of the cluster bends light, a phenomenon called gravitational lensing. The more lensing, the more mass is concentrated in the cluster. Although the two methods are very different, their results agree. "With the optical data and the x-ray data, you get the same answer," says Allen. The values for the amounts of matter and dark matter in the universe match what the cosmic background and galaxy-distribution data imply. "It's the most accurate determination to date of the amount of dark matter in galaxy clusters," he says.

John Arabadjis of the Massachusetts Institute of Technology has used Chandra x-ray data to draw an even stronger conclusion about dark matter. Some theorists postulate that dark matter is self-interacting—that is, particles of it are fairly likely to collide with one another. In that case, the collisions should force the dark matter to spread out more than it would otherwise. This hypothesis seemed to explain the distribution of matter in the centers of dwarf galaxies, but according to Arabadjis, Chandra's x-ray measurements show that dark matter in galaxy clusters doesn't spread out as one would expect if the particles collided easily. Thus, the model that succeeds in dwarf galaxies seems to fail in larger structures. "We can more or less say that self-interacting dark matter is dead now," Bregman says.

Paul Steinhardt of Princeton University is less sure. "The model's been declared dead many times," he says. Steinhardt thinks the study's assumptions are too crude to give definitive answers yet. And even if Arabadjis is right, he says, "there's plenty of room left in the self-interacting picture. But the simplest version might be in trouble." **–CHARLES SEIFE**

GEOLOGY

Swiss Scientists Trace 645-Year-Old Quake

At dinnertime on 18 October 1356, residents of Basel, Switzerland, felt the jolt of an earthquake that toppled churches and castles 200 kilometers away and triggered weeklong fires. The ground seemed to slumber after that. Although a few obscure accounts tell of periodic tremors in the area up to 1721, the nature of the 1356 earthquake—the largest historical seismic event in central Europe—remained a mystery. Now, on page 2070, researchers re-

Ravaged. A 1544 woodcut shows the earthquake that leveled Basel 2 centuries earlier.

CREDITS: (TOP TO BOTTOM) HUBBLE SPACE TELESCOPE; NISEE/EERC

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* "Two Years of Science With Chandra," 5–7 September.