Cantor, Harvard Medical School (HMS); **Susan E. Carey**, Harvard University; **John E. Carlstrom**, University of Chicago; **Constance L. Cepko**, HHMI and HMS; **Vicki L. Chandler**, University of Arizona; **Francis V. Chisari**, Scripps Research Institute; **William C. Clark**, Harvard University; **George H. Denton**, University of Maine, Orono; **John Francis Doebley**, University of Wisconsin, Madison; **W. Ford Doolittle**, Dalhousie University; **Jennifer A. Doudna**, HHMI and Yale University; **Donald N. Duvick**, Iowa State University; **Richard A. Easterlin**, University of Southern California;

Charles T. Esmon, HHMI and University of Oklahoma Health Sciences Center; **Richard Anthony Flavell**, HHMI and Yale University School of Medicine; **Joseph F. Fraumeni**, NIH; **Charles R. Gallistel**, Rutgers University; **Laurie H. Glimcher**, HMS and Harvard School of Public Health; **Michael F. Goodchild**, UC Santa Barbara; **Morris Goodman**, Wayne State University School of Medicine; **Richard H. Goodman**, Oregon Health Sciences University; **John P. Grotzinger**, Massachusetts Institute of Technology (MIT); **Willy R. G. Haeberli**, University of Wisconsin, Madison; **Charles B. Harris**, UC Berkeley; **Kristen Hawkes**, University of Utah; **John L. Hennessy**, Stanford University; **Vernon Martin Ingram**, MIT; **H. Jeffrey Kimble**, Caltech; **Eric I. Knudsen**, Stanford University School of Medicine; **Michael Levitt**, Stanford University School of Medicine; **Tom C. Lubensky**, University of Pennsylvania; **Alan G. MacDiarmid**, University of Pennsylvania; **Geoffrey W. Marcy**, UC Berkeley; **Gail Roberta Martin**, UC San Francisco; **Rowena G. Matthews**, University of Michigan; **David W. McLaughlin**, New York University; **James C. McWilliams**, National Center for Atmospheric Research and UC Los Angeles; **Richard E. Nisbett**, University of Michigan; **Saul Perlmutter**, Lawrence Berkeley National Laboratory; **Veerabhadran Ramanathan**, UC San Diego;

Mark A. Ratner, Northwestern University; **Anatol Roshko**, Caltech; **Joshua R. Sanes**, Washington University School of Medicine; **Peter Sarnak**, New York University; **Stephen H. Schneider**, Stanford University; **Gerald Schubert**, UC Los Angeles; **Peter W. Shor**, AT&T Laboratories Research; **David O. Siegmund**, Stanford University; **Yum-Tong Siu**, Harvard University; **Patricia Gail Spear**, Northwestern University Medical School; **Bruce M. Spiegelman**, HMS; **Thomas Südhof**, HHMI and University of Texas Southwestern Medical Center; **Lawrence H. Summers**, Harvard University; **G. David Tilman**, University of Minnesota, Twin Cities; **Scott D. Tremaine**, Princeton University; **J. Craig Venter**, The Institute for Genomic Research; **Sheldon Weinbaum**, City University of New York; **Richard V. Wolfenden**, University of North Carolina, Chapel Hill; **Chi-Huey Wong**, Scripps Research Institute.

The following foreign associates were also elected last week:

Juan Luis Arsuaga, Universidad Complutense de Madrid (Spain); **Francisco De la Cruz**, Instituto Balseiro (Argentina); **Gerhard Ertl**, Fritz Haber Institute, Max Planck Society for the Advancement of Science, Berlin (Germany); **Lajos Ferenczy**, University of Szeged (Hungary); **Sergio Henrique Ferreira**, University of São Paulo (Brazil); **Jan-Åke Gustafsson**, Karolinska Institute (Sweden); **Brian John Hoskins**, Reading University (U.K.); **Thomas M. Jessell**, HHMI and Columbia University College of Physicians and Surgeons (U.K.); **Wolfgang Ketterle**, University of Heidelberg and MIT (Germany); **Ho Wang Lee**, National Academy of Sciences of the Republic of Korea (Republic of Korea); **Tak Wah Mak**, University of Toronto (Canada); **Gopinath Balakrish Nair**, National Institute of Cholera and Enteric Diseases, Bangladesh (India); **Tomoko Ohta**, National Institute of Genetics, Mishima (Japan); **David P. Ruelle**, Institut des Hautes Études Scientifiques, France (Belgium); **David Schindler**, University of Alberta (Canada).

ANTHRAX SEQUENCE

Useful Data But No Smoking Gun

Seven months after anthrax letters hit U.S. media and government offices, investigators still haven't nabbed a suspect—and the genome project launched in part to help them seems unlikely to provide a break either. An analysis of the genome of the strain used in the attacks, published online this week by *Science* (www.sciencexpress.org), has yielded extra tools for fingerprinting the hundreds of different anthrax strains, but little in the paper suggests that it can help the FBI tie the attack strain to a specific lab.

"I don't see how this could help us much," says Barbara Hatch Rosenberg, director of the Federation of American Scientists' Chemical and Biological Arms Control Program, who has closely watched the federal investigation. But even without an immediate payoff, researchers at The Institute for Genomic Research (TIGR) in Rockville, Maryland, who conducted the research, say it provided experience in comparing microbial genomes that could be useful in future outbreaks.

Last fall's letters contained spores of a *Bacillus anthracis* strain called Ames, which was collected from a dead cow in Texas in 1981, sent to the U.S. Army Medical Research Institute of Infectious Diseases in Fort Detrick, Maryland, and later forwarded for experiments to some 14 other labs.

Because microbes mutate whenever they grow, it's possible that the current strain at each lab is a little different from the rest. And if one of them happens to match the attack strain, now dubbed Florida, it might lead to the bioterrorists. But until recently, genetic fingerprinting studies by Paul Keim's lab at Northern Arizona University in Flagstaff had looked at diversity at just several dozen markers, rather than the entire genome, and these had failed to discriminate among different Ames isolates.

Now, TIGR's Timothy Read, Keim, and others have sequenced the entire Florida strain and compared it with the so-called Porton strain, whose genome TIGR had already sequenced. (A paper describing that genome is due out later this year.) Like most strains, the Florida strain contains two extra rings of DNA, called plasmids, that the Porton strain lacks, so the researchers compared their sequences with the plasmids from two other strains. In all, the team found 53 places where the Florida genome differed from the Porton strain and the two previously sequenced plasmids.

Criminal code. The DNA of the anthrax strain sent to a Florida publishing company has been sequenced.

CREDIT: LUIS M. ALVAREZ/AP

But could these apparent genetic hotspots also help tell apart other, previously indistinguishable anthrax strains? To find out, the researchers took four Ames isolates collected from various labs; another Ames strain from a dead goat in Texas; and two non-Ames strains found in cattle. For each strain, they determined the exact sequence at each of the 53 markers.

Although the markers could clearly distinguish the samples from dead animals, they did a poor job of discriminating

among the four lab strains. One had 36 copies of the nucleotide A where others had only 35—an almost meaningless difference. Another had 37 copies at that same spot; but that strain also lacked one of the plasmids, making it easy to tell apart anyway. At all the other markers, the four lab strains and the Florida strain were identical.

Theoretically, more variation may emerge when the Ames strains from all 15 labs are put through the same 53-marker test. But the scant differences found so far "offer only slim hope that something useful will come out," says Rosenberg. Still, says Keim, the study shows that full-genome sequencing could be a useful forensic tool. And in cases such as bioterror crimes, the price tag—some $125,000 for a bug's genome—is hardly an issue: "A lawyer's sneeze costs more than that."

–MARTIN ENSERINK

ARCTIC RESEARCH

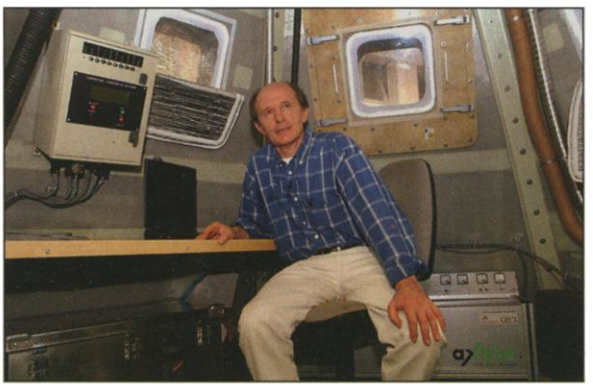
A Man and His Dog, Adrift But Equipped

PARIS—An aimless wanderer usually can't be expected to produce good science. But French physician Jean-Louis Etienne—who in 1986 was the first person to reach the North Pole alone on foot—is wandering with a purpose. He's drifting on the Arctic ice, collecting a wealth of hard-to-obtain data for a half-dozen research teams across France.

On 11 April, a helicopter dropped off the adventurer and his dog Lynet at the North Pole, along with what they will call home until July: The 9-cubic-meter Polar Observer, which resembles the Mercury space capsules from the 1960s. The gas-heated, hydrogen- and solar-powered capsule, fitted with a range of scientific instruments, is perched on an ice floe that wind and marine currents are driving across the Arctic Ocean.

For the researchers lucky enough to have equipment along for the $1 million ride—financed by the Midi Pyrénées regional council, Gaz de France, Unilever, and several other public and private sponsors—the mission is a unique opportunity to corroborate satellite data and fill holes in their knowledge. For example, Gérard Brogniez, an expert on atmospheric optics at the University of Lille, and his colleagues have outfitted the capsule with photometers for measuring visible, infrared, and ultraviolet (UV) light. Part of the data will allow them to determine the concentration of aerosols such as nitrous oxides and water vapor in the lower atmosphere that absorb infrared rays and contribute to the greenhouse effect. And data on how much energy the ice soaks up will help researchers predict global climate changes that are influenced by energy gains or losses at Earth's surface. The intensity of UV light that reaches the surface, meanwhile, serves as a proxy for the ozone layer's thickness. Normally these measurements are made by satellite and verified by ground stations—something that is not generally feasible in the Arctic Ocean. "The ice pack is always moving, and you can't put expensive equipment there," says Brogniez.

Etienne's polar peregrinations are also a boon to paleoclimatologist Denis-Didier Rousseau's team at the University of Montpellier. The group has tracked pollen from Mediterranean plants such as grapes and olive trees several thousand kilometers to Greenland. But "there are no data on the transport of pollen over the Arctic Ocean," says Rousseau, who has provided the Polar Observer with a device resembling a weathervane equipped with pollen-trapping filters. Filling this gap, he says, should help refine models of global wind patterns. It also should aid work on the distribution of fossil pollen in sediments and at archaeological sites. "We must have a good knowledge of the present if we want to study the past," he says.



Catch his drift? Explorer Jean-Louis Etienne will collect valuable data from the comfort of this high-tech igloo.

CREDIT: CHRISTOPHE ENA/AP

As *Science* went to press, Etienne and his canine companion were drifting south-southeast of the North Pole, having covered nearly a quarter of the estimated 500-kilometer journey. In a recent Web dispatch (www.jeanlouisetienne.fr, in French), Etienne describes a typical evening inside the cozy capsule: "The blizzard is blowing this evening at 30 kilometers per hour. It plays the evacuation vents and air intakes of the Polar Observer like an organ. Nice and warm, I am going to be able to sleep peacefully." If their nights and days continue uneventfully, in July Etienne and Lynet should end up near the coast of Greenland, where a Russian icebreaker plans to pick them up.

–MICHAEL BALTER

ScienceScope

Case Closed U.S. prosecutors have dropped most of their charges against one of two Japanese researchers accused of scientific espionage—leaving him with hefty legal bills. Biologist Hiroaki Serizawa last week pleaded guilty to giving false information to FBI agents. But prosecutors in Akron, Ohio, dropped charges that he had conspired in 1999 with a friend, Takashi Okamoto, to smuggle Alzheimer's disease research materials out of the United States (*Science*, 18 May 2001, p. 1274).

Serizawa's troubles began after Okamoto gave him vials containing "DNA constructs" and other "trade secrets" taken from Okamoto's former lab at the Cleveland Clinic in Ohio. Some vials were shipped to Japan, sparking the charges. Japanese officials have found no trace of the vials, but the United States has asked them to extradite Okamoto to Ohio to stand trial.

Serizawa has said that he never knew what was in the vials, and the government conceded that the material did not constitute trade secrets. But rather than face an expensive trial, Serizawa pleaded guilty to the lesser charge, which carries a maximum 5-year jail term. Prosecutors let Serizawa, who lives in Kansas City, Kansas, retain his green card and continue as a permanent U.S. resident. However, he was denied tenure last month at the University of Kansas Medical Center in Kansas City. Friends and colleagues, meanwhile, are raising funds to help him pay an estimated $250,000 in legal bills.

Genomics for All The World Health Organization (WHO) could become a broker between the genome haves and have-nots. A new report surveys the genetic research landscape internationally and calls for WHO to help developing nations benefit from genomics. It concludes that WHO could carve a useful niche by setting up ethics guidelines to protect research volunteers, building research and training programs in poor nations, and examining new gene-based therapies for developing-world diseases. Such steps would help developing nations "be ready" to exploit future advances, says lead author David Weatherall, a geneticist at Oxford University, U.K.

WHO's General Assembly is expected to consider the ideas at its 13 May meeting in Geneva, Switzerland. Even if approved, however, donors—including governments, drug firms, and philanthropies—will have to be convinced that the plan is worth the estimated $20-million-a-year price tag.

Contributors: David Malakoff, Philipp Weiss, Gretchen Vogel, Eliot Marshall, Melissa Mertl