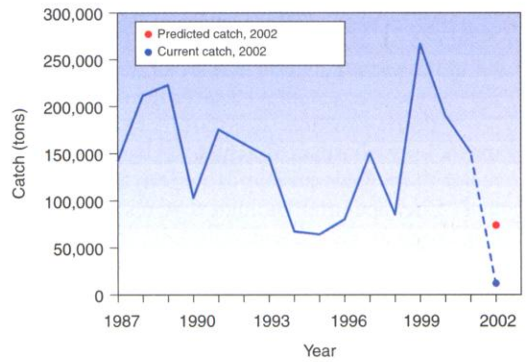

Here today ... Researchers can now predict the ups and downs of the Argentinean flying squid.

aficionados but no surprise to a team here at the British Antarctic Survey (BAS). Using a model based on ocean temperatures and currents, BAS researchers predicted the dearth of squid off the Falkland Islands.

In contrast to many other fish stocks that are reeling, overfishing is not to blame for this year's pathetic catch of the Argentinean flying squid. The culprit is poor hatching and nursery conditions last year, says BAS biologist Paul Rodhouse, who developed the model with BAS's Claire Waluda. The model's success may help gird the industry for future off years, and it may serve as a template for predicting catches of other short-lived species, such as anchovies, in the South Atlantic and elsewhere.

A key hurdle the researchers had to overcome in modeling the flying squid is its short life-span: only 1 year. The larvae hatch near the River Plate estuary off the coast of Argentina in July and then, after maturing, swim several hundred kilometers south to cooler, plankton-rich waters near the Falkland Islands. There they are caught by international fishing vessels using lines between February and June. Those that elude capture attempt to return to their breeding grounds, where they spawn and die. The fact that the population goes from larvae—"no squid at all"—to fully grown adults in only a few months makes sampling and predictions based on the previous year's catch difficult, says Robin Cook, a modeling expert at the Fisheries Research Services in Aberdeen, U.K. Indeed, last year's catch is mostly irrelevant, says Rodhouse, who compares the squid to the desert locust: "It doesn't make any difference how many you kill. When the environmental conditions are right, they return as a plague."

Rodhouse and Waluda zeroed in on sea temperature in the nursery area in July to predict the catch 8 months later. Last July, temperatures were 1.5° Celsius warmer than average, driving a shift in currents that swept larvae into the open ocean. "While they are small, they are at the mercy of the currents," says Waluda.

The duo predicted a catch of 73,000 tons this year, near the bottom of an annual catch that fluctuates wildly between 60,000 and 290,000 tons a year. With only a few weeks to go this season, the haul has barely reached 10,000 tons—a severe economic loss considering that the squid fetches $3000 per ton.

The model's success may help fishery managers cope with future disastrous years by suggesting, for example, how many vessels should be licensed. In addition, this type of model could work for other fisheries—such as a squid fishery off the coast of South Africa—that are susceptible to the vagaries of currents, says Jean-Paul Robin, an expert on cephalopod fisheries at the University of Caen, France. In the meantime, managers at the South Atlantic squid fisheries are steeling themselves to this coming July's readings—and the omen they will offer.

–**ADAM BOSTANCI**

SCIENTIFIC COMMUNITY

U.S. Science Academy Elects New Members

The U.S. National Academy of Sciences last week elected 72 new members—11 women and 61 men. Among them was J. Craig Venter, the controversial leader of a private venture that last year completed a rough draft of the human genome. Some members were prepared for a challenge to Venter's election, but none materialized. The new members and their affiliations at the time of election* are:

Harvey J. Alter, National Institutes of Health (NIH); **Boris L. Altshuler**, NEC Research Institute and Princeton University; **Kathryn V. Anderson**, Cornell University and Sloan-Kettering Institute; **Barry C. Barish**, California Institute of Technology (Caltech); **Jacqueline K. Barton**, Caltech; **Adriaan Bax**, NIH; **Zdenek P. Bazant**, Northwestern University; **Philip A. Beachy**, Howard Hughes Medical Institute (HHMI) and Johns Hopkins University School of Medicine; **Manuel Blum**, Carnegie Mellon University; **John Bongaarts**, The Population Council; **Patrick O. Brown**, HHMI and Stanford University School of Medicine; **Carlos J. Bustamante**, HHMI and University of California (UC), Berkeley; **William C. Campbell**, Drew University; **Harvey**

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* For more details, go to www.national-academies.org.

ScienceScope

Neutron Plans Unveiled European researchers will make their case next week for a powerful accelerator designed to produce neutrons to probe the structure of proteins and designer materials. On 16 and 17 May, leaders of the European Spallation Source (ESS) project will meet in Bonn, Germany, to unveil their plan to the research community, the media, and—most importantly—politicians who will decide whether to fund the long-discussed facility. "It's like a motor show where we'll pull the sheet off our wonderful new model, and we want to hear the audience gasp," says Robert Cywinski, a physicist at the University of Leeds, U.K., and chair of the European Neutron Scattering Association.

An expert commission gave ESS its blessing in 1996 (*Science*, 9 May 1997, p. 891), but political support was slow to follow. Since then, planners have redesigned the machine so that it would leapfrog over two sources under construction in the United States and Japan. ESS "would allow [Europe] to keep [its] position on the world stage for 30 to 40 years," Cywinski says.

But ESS backers first need to find an estimated $1.5 billion. Construction could begin in 2004, with completion set for 2011. Five sites are competing for the project: Yorkshire and the Rutherford-Appleton site near Oxford, U.K., Lund in Sweden, and Jülich and Halle in Germany.

Mouse Tale at End? It's official: Mice, rats, and birds used in laboratory research are no longer animals—at least according to a major federal animal welfare law. In a big win for the biomedical research community, Congress this week approved a massive farm bill that includes language exempting the animals from regulation under the Animal Welfare Act. President George W. Bush is expected to sign the bill, ending a decade-old struggle by animal activists to force the U.S. Department of Agriculture to regulate the use of the most common laboratory animals (*Science*, 22 February, p. 1439). The bill also orders the National Academy of Sciences to conduct a 1-year study of the use and regulation of mice, rats, and birds in research.

Animal advocates, however, say they will carry the fight to a new arena: the states. John McArdle of the Alternatives Research and Development Foundation in Eden Prairie, Minnesota, says activists will work to pass state laws that require researchers to consider alternatives to animals in experiments and to treat all animals humanely.

CREDITS: (TOP TO BOTTOM) SOURCE: BAS; C. GILBERT/BAS; ROBERT F. BUKATY/AP

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