report also presents a cautionary tale to the rest of the world: "BSE could have arisen anywhere and spread wherever animal protein is recycled," says Ferguson-Smith. "Other countries should ponder our experience."

–HELEN GAVAGHAN

Helen Gavaghan writes from Hebden Bridge, West Yorkshire, U.K.

GENE SEQUENCING

China, Denmark Team Up to Tackle the Pig

BEIJING—China and Denmark have formed a consortium to sequence the pig genome. The project, expected to take several years, is the first to tackle livestock; when completed, it would be the fourth to tackle a mammalian genome, after the human, mouse, and rat. The partners hope that information from the project will benefit pig-breeding industries in both countries as well as basic science and medicine.

The project links the Danish Institute of Animal Sciences, the Royal Veterinary and Agricultural University (KVL), and representatives from Denmark's pig industry with the Beijing Genomics Institute (BGI) of the Chinese Academy of Sciences (CAS). Leaders of the four groups struck a deal on 20 October during a visit here by a Danish delegation. The partnership is a "perfect match" between China's powerful sequencing capacity and Denmark's expertise in pig breeding and experience in comparative and functional genomics research, says BGI Director Yang Huanming. "We came here with the intention of signing an agreement, and we are satisfied with the result," notes KVL pro-rector Torben Greve, who is head of the Danish Pig Genome Consortium.

The two sides have agreed to split the $15 million cost of the first phase of the project, a 3-year effort to identify valuable genes, develop markers for physical and genetic mapping, and provide research tools for xenotransplantation. A second phase, taking several more years and costing up to $60 million, would aim for a working draft covering 90% of the sequence and 95% of the genes. The pig genome is estimated to contain 3 billion base pairs.

BGI will do the sequencing and sequence analysis using a supercomputer and more than 100 of the latest capillary sequencing machines. BGI plans to redirect its current roster of 45 machines from work on the international human genome project to the pig project, says BGI deputy director Yu Jun. Denmark will be responsible for developing genetic markers for valuable traits such as disease resistance, growth, and litter size. Its scientists will also build about 100 libraries of cDNA clones containing partial gene sequences that will help the teams identify the full-length genes.

Each side has agreed to put up $2 million for the initial phase. CAS has already provided the Beijing institute with money. The Danish ministries of research and of food, agriculture, and fisheries are expected to fund work in Denmark, while the National Committee for Pig Production and the Danish Bacon and Meat Council support the BGI sequencing team.

Researchers had hoped to make the sequencing data available to the scientific community immediately, as has been the case under the so-called Bermuda rules used in the human genome project. But industry contributors asked for release to be delayed several months. "Both sides have agreed to create a balance between the Bermuda rules, which require immediate release within 24 hours, and the present data-release policies by other private sectors to protect commercial applications," says Yang.

Even so, the partners say that they remain committed to the concept of sharing. "This project is just like any other international collaboration project, and there will be no new restrictions," says Orla Gron Pederson of Denmark's national committee. The final terms of data release are still being hashed out, Yang says, along with provisions for scientific procedures, intellectual property rights, and future partners. Yang says that institutes in Singapore and France have expressed an interest in the project but so far lack funding.

Gene partners. Beijing's Wang Jian explains the genomics institute's capabilities to Danish delegation led by, at left, Torben Greve and Orla Gron Pedersen.

CREDIT: (BOTTOM) *CHINA FEATURES*

The project marks "an important step" for China toward sequencing the country's resource

ScienceScope

Moving On? Apparently disgusted by this year's uglier than usual budget fight, Senator Arlen Specter (R–PA) (below), head of the appropriations subcommittee that oversees the budget of the National Institutes of Health (NIH), says he may move on to other leadership responsibilities. The hint, dropped in several press interviews last week, has alarmed biomedical research advocates, who count Specter among the handful of key lawmakers who have successfully pushed to double NIH's budget by 2003.

According to the *Washington Fax* newsletter, Specter said that "I don't expect to be on this subcommittee next year because of the futility of what we've done here." The comment came amid highly partisan political wrangling that has stalled approval of this year's NIH bill, which reportedly includes a 15% increase for the $17.9 billion agency.

Specter's departure would leave NIH spending panels in both the House and Senate leaderless, because Representative John Porter (R–IL), a major NIH booster, is retiring this year. Few of the potential replacements share either man's zeal for the cause, lobbyists say. But some caution against reading too much into Specter's comments, saying they could be designed to motivate supporters to lobby him to stay. Says one: It may be his " 'Tell me you love me' dance."

Reform Light More than 3 years after Claude Allègre, France's former research minister, launched his ill-fated campaign to radically overhaul the basic research agency CNRS, the French government has approved a scaled-down version of his reform package (*Science*, 31 March, p. 2387). The Council of Ministers approved a decree on 25 October giving the 26,000-researcher organization greater scientific autonomy, especially by removing government appointees from its scientific advisory council. On the other hand, the minister strengthened the powers of the CNRS executive board, which answers to the government and decides broad-based research strategy. And for the first time, foreign scientists will be asked to join the CNRS's external scientific evaluation committee.

Physicist Edouard Brézin, president of the executive board—whom Allègre had charged with carrying out the reform effort—announced that he will step down now that his work is done.

genomes, notes Wang Guihai, director of the CAS Bureau of Life Sciences. It is the second project of the China Biological Resource Genomes Project, following a decision to sequence China's superhybrid rice (*Science*, 5 May, p. 795). Danish officials hope to use the knowledge to stimulate work in bioinformatics as well as to strengthen the country's pork industry. A better understanding of pig genomics would also promote the use of transgenic animals as sources of transplant organs, as disease models, and for the production of medical treatments. **–LI HUI**

Li Hui writes for *China Features* in Beijing.
With reporting by Lone Frank in Denmark.

ARCHAEOLOGY

New Site Suggests Anasazi Exodus

High in the cliffs of Mesa Verde in southwestern Colorado lie some of the world's most beautiful and mysterious ruins. For decades, scientists have puzzled over the fate of the people who once lived there, the Anasazi. Whereas conventional wisdom has them dying off or leaving slowly, archaeologist Stephen Lekson of the University of Colorado, Boulder, has now proposed a more dramatic and large-scale exodus to the south for at least some Anasazi. That effort, he argues, would have required a higher degree of social cohesion than has been attributed to the Anasazi culture.

Lekson's work involves pottery and masonry styles from three pueblo ruins in southern New Mexico, up to 470 kilometers from Mesa Verde. "These sites are significantly farther south than the Anasazi are supposed to have gone," says Lekson, who has been invited to present a paper on his finds at the Society for American Archaeology annual meeting next April. "Meanwhile, the size involved suggests whole villages picked up and moved as units. This is different from the usual picture of just individual families wandering off." Comments Jefferson Reid, an anthropologist at the University of Arizona in Tucson who has heard Lekson's presentations: "This is a highly plausible idea that can now be evaluated."

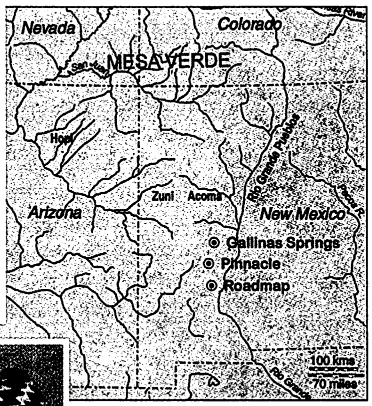
The traditional view of the Anasazi's disappearance suggests that a killer drought or large-scale political or social stresses set off a slow trickle of émigrés. Rarely are large groups imagined in motion. And rarely are the emigrants said to have moved farther than the areas that became today's pueblos in northern Arizona and New Mexico, ranging from the northern Rio Grande country in the east to the Hopi lands to the west. Lekson, in contrast, found Anasazi-like artifacts 420 kilometers south of Mesa Verde, at Pinnacle Ruin (see map), during work this summer with graduate students Brian Yunker and Curtis Nepstad-Thornberry. He says the far-south pueblo-style ruin, like two others in the region, exhibits key characteristics of Mesa Verdean culture that "stick out like a sore thumb" in their locale, he says.

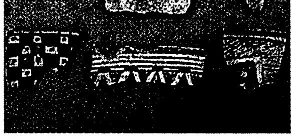
Half of the pottery sherds collected at the site look very much like the Mesa Verde black-on-white style, Lekson argues. The neatly coursed masonry and layout of the multistoried room-blocks look more like the massive defensive pueblos of Mesa Verde than like the region's less organized Mogollon culture sites. And an excavated midden shows that Pinnacle's dwellers piled their trash thickly like Mesa Verdeans instead of following the local practice of spreading it thinly around habitations. Such evidence, along with the sheer size of the three southern ruins—which between them may have contained 800 rooms—"pretty strongly" argues that a sizable stream of well organized Anasazis trekked deep into southern New Mexico around 1300, Lekson says.

Several researchers who have heard Lekson's presentations are attracted to his ideas but say that more data are needed. Archaeologist Harry Shafer of Texas A&M University in College Station, for example, chided Lekson for drawing "premature" conclusions without further excavations and chemical trace analyses of the ceramics. Nevertheless, John Kantner, an archaeologist at Georgia State University in Atlanta, says that "a huge, systematic move could add another element to the picture" of greater mobility.

Lekson, for his part, says that the small amount of trash at the site suggests that his wayfarers' wanderings did not end in southern New Mexico. Moreover, the oral traditions of several pueblo peoples possibly descended from Anasazi emigrants tell of long, convoluted migrations that wended far to the south, then turned back north. "It could be these folks came here for 100 years, then headed north again," Lekson says. "Quite a trip, huh?" **–MARK MURO**

Mark Muro writes from Tucson, Arizona.





Long march. Potsherds *(top)* found at the Pinnacle site in New Mexico resemble typical Anasazi pottery from the Mesa Verde region *(left)*, suggesting a long trip south.

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MICROBIOLOGY

Listeria Enlists Host In Its Attack

It was just a small innovation—a 27–amino acid addition to a protein some 500 amino acids long. But that change likely made all the difference for a food-borne pathogenic bacterium called *Listeria monocytogenes*. As described on page 992 by microbiologists Amy Decatur and Daniel Portnoy of the University of California, Berkeley, this innovation enables *Listeria*, which can cause meningitis and death in people with compromised immune systems, to deploy a toxic protein without killing its host cell. As a result, the microbe remains comfortably ensconced within the cell and can avoid confronting antibodies, the immune system's foot soldiers.

Many bacterial pathogens are extracellular, frequently doing their dirty work by injecting toxins into cells. But not *Listeria*. When consumed, say, in a contaminated cheese, it enters the body and hunkers down in a nearby macrophage—even though this type of immune cell usually helps fend off infections.

As a macrophage first engulfs *Listeria*, it traps the microbe in a vacuole called a phagosome, supposedly out of harm's way and targeted for eventual destruction by the cell. But once inside, *Listeria* makes a pore-forming protein called listeriolysin O that tunnels into the phagosome membrane, dissolving it and setting the microbe free within the macrophage, where it can replicate before conquering other cells.

Microbiologists had long wondered why *Listeria*'s pore-forming protein doesn't bore through the macrophage's outer membrane as well and destroy the host cell. That's how a family of 19 related proteins deployed by extracellular pathogens usually work. Although these bore in from the outside, there seemed to be no reason why listeriolysin O couldn't punch holes in the membrane from within. Indeed, 6 years ago, Portnoy made a *Listeria* strain in which he replaced the