Institute, who has asked her to serve on many panels. Collins adds: "She will be a great champion for science and for women in science." Princeton graduate and genome researcher Eric Lander of the Massachusetts Institute of Technology in Cambridge describes Tilghman as a "great scientist, a true humanist, and a wonderful person," as well as "a spectacular choice for Princeton."

Tilghman was on the search committee until 6 weeks ago, according to the chair of the trustees' executive committee and head of the search committee, Robert H. Rawson Jr. She left a meeting early to teach, and in her absence, the other members decided they wanted her to become a candidate. She agreed and withdrew from the search committee. The remaining members chose her unanimously.

Tilghman—like Shapiro—was born in Canada. She joined Princeton's faculty in 1986, became a Howard Hughes Medical Institute investigator in 1988, and was elected to the National Academy of Sciences and the Institute of Medicine less than a decade later. She received Princeton's top teaching award in 1996. Since its founding in 1998, she has run Princeton's Lewis-Sigler Institute for Integrative Genomics; no successor has yet been named. **–ELIOT MARSHALL**

THE 1918 PANDEMIC

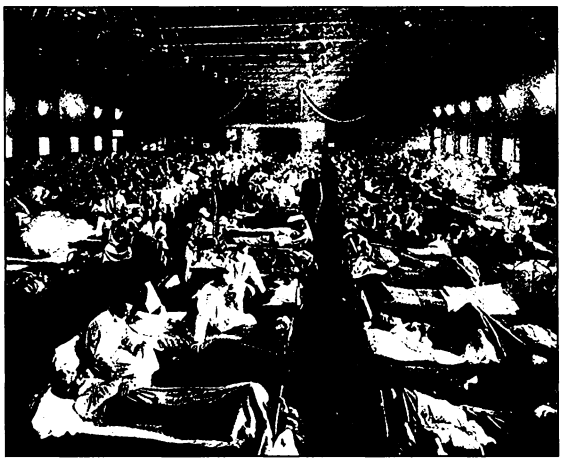
Killer Flu With a Human-Pig Pedigree?

LONDON—Scientists have come up with a new explanation for what made the Spanish flu the biggest killer of the 20th century. The deadly influenza did not jump from birds into humans, they argue, but rather was the unfortunate result of an unprecedented recombination of pig and human flu genes. "This is a great step away from the existing theories of the origin of 1918 flu," says virologist Mark Gibbs of the Australian National University in Canberra, whose team presented its findings at a symposium here on 25 April at the Royal Society.

Reassuringly, such genetic recombination appears to be an exceedingly rare event, suggesting that the odds of a reprise of the Spanish flu pandemic—which killed 40 million people around the world in 1918 and 1919—are vanishingly low. Some experts, however, argue that this proposed explanation for the Spanish flu's virulence is flawed: Recombination among flu strains, they assert, does not happen at all.

Four years ago in *Science*, a team led by virologist Jeffery Taubenberger of the Armed Forces Institute of Pathology in Washington, D.C., published the initial RNA sequences of the 1918 flu strain after isolating it from the preserved tissue of victims (21 March 1997, p. 1793). Poring over these data, Gibbs's team homed in on the gene for hemagglutinin (HA), a viral protein used to gain entry into target cells. Novel HA configurations are harder for the immune system to recognize, making the protein a key determinant of a strain's virulence.

The researchers used standard software to compare the sequence of the 1918 HA gene to those from 30 closely related influenza strains from birds, pigs, and humans. "Within a few hours we had a preliminary signal," says Gibbs. Pursing this further, they discovered that the 1918 version appeared to be a chimera of sorts: One end bore a marked resemblance to human flu sequences, the middle was strikingly similar to pig, while the other end again was human. The "simplest scenario," says Gibbs, is that the HA gene (which, researchers concur, originated in bird flu strains) slipped into mammals sometime before 1918 and diverged into two lineages, human and pig.



CREDIT: AP/NATIONAL MUSEUM OF HEALTH

Spanish flu victims. New work suggests that the 1918 strain derived its lethal powers from an unprecedented genetic recombination.

Then in a bad twist of fate, these HA genes recombined to form the version that made the Spanish flu so much harder for the immune system to recognize—and therefore more virulent. "It looks for all the world like the signature of recombination, and I can't see how to explain it otherwise," says Eddie Holmes, who studies viral evolution at the University of Oxford. "We are talking about a rare event, but evolution is all about rare events."

The idea has met with skepticism from some top flu researchers, however. Taubenberger, for one, argues that the Gibbs group has misinterpreted the 1918 sequence. He believes that an influenza virus with an avian HA gene had started circulating in humans just before the start of the pandemic. In the fall of 1918, this virus infected humans and swine simultaneously and split into two lineages, and disparity in the rate of evolution between the two strains since then has confused the picture, says Taubenberger. "Human flu viruses are subject to huge immunological pressure and are forced to mutate rapidly," as humans are so long-lived and develop immunity to many strains, he says, while pig strains mutate slowly because their hosts don't live long enough to develop such broad immunity. Thus, Taubenberger argues, the HA gene in the 1918 human samples resembled that of the avian ancestor of both pig and human strains. But by the 1930s—the date of the earliest strains that can be directly compared—the human gene had changed dramatically, while the pig gene had changed little. That, he says, would explain why sections of the 1918 human virus look similar to those of later pig viruses.

Taubenberger does not believe that flu strains—like other negative strand RNA viruses—are capable of recombination, in which new genes are patched together from sections of other genes. Not that flu strains are limited to evolution through mutation: A kind of whole-gene swapping between strains, called reassortment, is thought to have spawned the virulent avian flu strains that jumped into mammals in 1957 and 1968.

Gibbs acknowledges that it will be an uphill battle to convince some of his colleagues that influenza strains are capable of recombining. "One of the paradigms," he says, "is that flu goes in for reassortment but not for recombination." But, he argues, recombination provides the best explanation for the genetic data. **–JOHN PICKRELL**

U.S. SCIENCE POLICY

Former Advisers Fret Over OSTP Vacancy

CAMBRIDGE, MASSACHUSETTS—Although billed as a celebration, the largest gathering of U.S. presidential science advisers had more the air of a wake. Meeting here last week, the former government officials were all too aware that a new Administration is busy making critical decisions without benefit of the kind of scientific advice that has guided most presidents in the past half-century. "Nobody is celebrating the future here," says Neal Lane, former science adviser to President Bill Clinton and now a professor at Houston's Rice University.

Lane was one of eight former science advisers who gathered on 1 May at the Massachusetts Institute of Technology (MIT) to celebrate the 25th anniversary of the Office of Science and Technology Policy (OSTP).

Advice meisters. Past science advisers include, from left: D. Allan Bromley; Ed David; MIT president Charles Vest, who hosted the affair; Neal Lane; Guyford Stever; George Keyworth; Donald Hornig; Jack Gibbons; and William Golden.

(Eight of the 18 formal or informal advisers made it to the meeting; only two of the living advisers did not show.) In addition to discussing their role in shaping U.S. policies on basic research, defense, health, and the environment, the officials worried that the Bush Administration may not be interested in giving the same opportunities to their successor. "There are too many litmus tests," complained D. Allan Bromley, who advised the current president's father, George H. W. Bush.

Some advisers and senior scientists see the empty office in the Old Executive Office Building as an ominous sign that the White House prefers not to hear advice that may conflict with its ideological goals. "It's clear that science policy is not one of the Administration's priorities," says William Golden, who advised President Harry Truman. But Administration officials insist that the delay is due to the truncated transition following the contested election and onerous paperwork requirements. "We are behind the curve, and this is only one of many positions," says Sean O'Keefe, deputy director of the Office of Management and Budget.

The former advisers ticked off several recent actions by the new president that they feel could have benefited from input from a science adviser. They include the decision to abandon the process spelled out in the Kyoto Treaty to limit greenhouse gases, reduce spending on energy R&D, reverse water-quality standards, and move ahead with a new missile defense system (see p. 1035). Decisions on the use of stem cells in research and oil drilling in the Arctic loom on the horizon, they added. "These are all issues with a strong R&D component," says MIT President Charles Vest. "But I don't know with whom they are consulting."

Although he declined comment, Vest is believed to be one of several persons approached who have asked not to be considered for the science adviser's job. And the post may become less appealing with every passing day. Any nominee is likely to face detailed questions at a Senate confirmation hearing about the candidate's stance on global warming, stem cell research, and other controversial topics, notes Bromley. Proposed tight budgets for all research agencies except the National Institutes of Health also diminish the attractiveness of the job. Even so, Bromley says he believes that the White House may be ready to announce a candidate within a few weeks. **–ANDREW LAWLER**

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MICROBIOLOGY

Shale-Eating Microbes Recycle Global Carbon

Once again, microbes are proving just how versatile they can be. Key players nearly everywhere—from deep-sea vents to termite guts, and perhaps even on the Red Planet—microbes carry out biochemical reactions that help recycle the elements of life, such as carbon, nitrogen, and oxygen. On page 1127, geochemist Steven Petsch and his colleagues at the Woods Hole Oceanographic Institution (WHOI) in Massachusetts now describe a new role for microbes: promoting the release of organic material locked up in sedimentary rocks. "It has never before been demonstrated that the organisms are involved [in this process]," says Don Canfield, a biogeochemist at Odense University in Denmark. "And what [Petsch and colleagues] have done is pretty neat." The work also fills a gap in the global carbon and oxygen cycles.

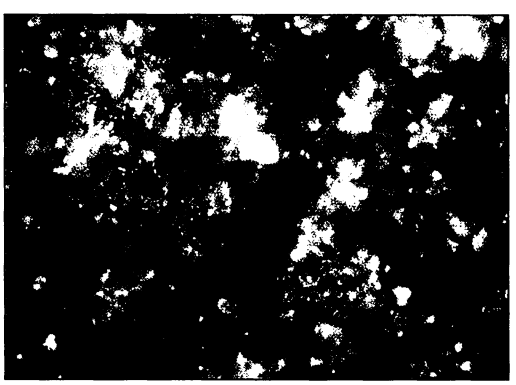
The researchers worked on the common sedimentary rock shale. As shale forms, it traps carbon in a complex material called kerogen, which is held in microscopic pores in the rock—thus holding the carbon out of the carbon cycle. In shale exposed to air, however, the carbon is slowly oxidized to carbon dioxide and released. Indeed, says John Hedges, a marine organic geochemist at the University of Washington, Seattle, the weathering of shales "is one of the big sinks for oxygen." Even so, because kerogen is insoluble and hard to work with, few researchers had tried to figure out how kerogen is oxidized.

For his experiments, Petsch, working with WHOI colleagues geomicrobiologist Katrina Edwards and organic geochemist Tim Eglinton, collected samples of shale in various states of degradation from an outcrop in Kentucky. Back in the lab, he ground up and sterilized some of the collected shale, and extracted any remaining accessible carbon. He then inoculated samples of the ground-up shale sediment with material taken from deep within cores dug out from each of six depths along the outcrop. In theory, any microbial life those cores contained would have had "no energy source except shale" in the treated rock, Edwards points out.

After several months of culturing these samples, the researchers detected signs of microbial life under the microscope. They also searched for phospholipids, fatty molecules found in cell membranes. "The lipids tell us that, yes, these are bacteria," Petsch explains. In addition, he and his colleagues used accelerator mass spectrometry to determine the relative amounts of two unusual forms of carbon, carbon-13 and carbon-14, in the cultured samples. The ratio of the two indicates the age of the microbes' food source as carbon-14 decays over time.

The researchers found six types of phospholipids in the cultures and 41 in the samples from the weathered outcrop, suggesting that microbes lived in both, but that only a subset thrived in the lab tests. Because the phospholipids from the cultures contained almost no carbon-14, Petsch knew that the microbes were consuming the shale's kerogen—formed with the shale about 365 million years ago—and not sneaking much nourishment from a younger food source, which would still have contained carbon-14. "[The work] is a beautiful combination of an established technique and the right experimental question," comments Hedges. "It's going to bring a focus of more biology on this aspect of geochemistry."

Even so, Cynthia Riediger, a petroleum geochemist at the University of Calgary in Canada, cautions that it remains to be seen just how important this newly unearthed microbial contribution is to the carbon and oxygen cycle. To find out, researchers will need to quantify the amount of shale as well as the relative role of the microbes in weathering. But "the next big question that looms out of this study is who are these organisms," Hedges notes. Petsch may soon have that answer. He says he has already isolated DNA from the cultures and is well on his way to finding out just who's been eating the shale all these millions of years. **–ELIZABETH PENNISI**



Shale diet. Microbes (blue) found among shale particles degrade carbon compounds in the rock pores.