usual. ... In this period there are hundreds of known cemeteries, but they are all out there in the landscape."

Moreover, most Iron Age graves consisted of burial mounds sheltering only one individual. But not at Boussac—the two groups appear to have been chosen for a single subterranean burial. So not only were there apparent status differences between the two groups, but also between all the buried people and the rest of society. The big question, says Wells, "is why did these individuals get this unusual burial? Is there a social status difference or ritual religious difference between [different] groups in society?" Richard Osgood of the Institute of Archaeology at Oxford University draws an analogy to burials of "the Zulu chiefs of the 19th century. ... Once the chiefs died, their entire entourage was killed and buried with them." Although it's sheer speculation, he says, a similar relationship could be behind the Boussac interments.

If scientists could determine the family relationships between the individuals in the cave, they might be able to bolster some of these theories or rule them out. To get a handle on genetic relations, Vidal's group of regional archaeologists is teaming up with anthropologists at the University of Bordeaux to extract DNA from the skeletons. They also plan to examine arm, shoulder, and other bones for marks made where muscles were attached. The severity of such marks can reveal whether or not the people were habitually engaged in hard labor. Activity differences might, for instance, provide support for the servant hypothesis. And artifacts on the cave floor near the burials might yield clues about lifestyle.

Archaeologists have been hunting for evidence of social complexity in this region for some time, says Wells. Although the first urban centers, complete with divisions of labor and status among the population, emerged in the Near East during the Bronze Age, about 3500 B.C., the rise of towns in temperate Europe is thought to be an independent development, which begins to show up in the archaeological record at about 600 B.C. "These finds [at Boussac] from a century or two before," Wells says, "might tell us something about the process of social and economic change leading to the formation of these more complex communities."

The first step will be radiocarbon dating of the two groups of skeletons, as well as other organic material—such as bits of wood—that may eventually be found, to confirm that they were buried simultaneously. Vidal expects these tests, the DNA work, and the other studies to be completed later this year. If they do support the notion of social distance between the adorned and unadorned bodies, it would be a discovery to ornament any archaeologist's career.

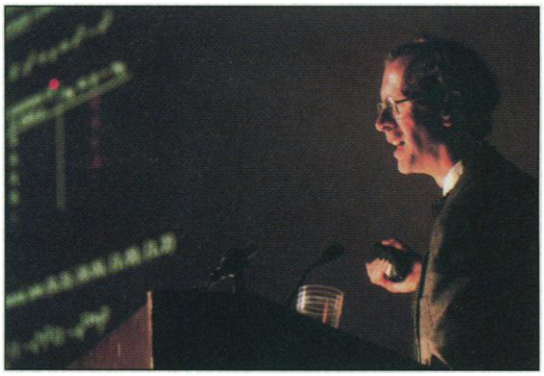
–**Michael Balter**

MATHEMATICS

# Princeton Mathematician Looks Back on Fermat Proof

It's official: Fermat's Last Theorem has been proved. Less than 2 years after the first announcement of a proof, and within 7 months of the release of a revised manuscript correcting a mistake in the original, Princeton University mathematician Andrew Wiles's solution of the famous 350-year-old problem has passed scholarly muster and is slated to appear in the May issue of *Annals of Mathematics*. The impending publication was celebrated at a special presentation at Princeton last week, where Wiles gave a personal account of his 7-year pursuit of a childhood dream.

It was a tortuous journey toward a goal that sounds deceptively simple: Proving that the equation $x^n + y^n = z^n$ has no solutions in positive integers $x$, $y$, and $z$ if the exponent $n$ is greater than 2. The French mathematician Pierre de Fermat made this claim in the late 1630s in the margin of a mathematics text, tantalizing future generations of mathematicians by noting (in Latin) that he had "a remarkable proof which the margin is too small to contain." Recalled Wiles, "I spent some of my childhood trying to solve it on the assumption that Fermat had had a solution and ... I didn't know too much less than he would have known."



NEW JERSEY NEWSPHOTOS

**QED.** Andrew Wiles reviews his 7-year struggle.

In fact, the proof took far more than Fermat could have known, but the final version still fits his comment to a tee. It is both remarkable and larger than a margin could contain, occupying an entire issue of the *Annals*, which is doubling its normal print run for what is sure to be a collector's item. The proof consists of two papers. The first is substantially the theory offered by Wiles in 1993. The second, written with Richard Taylor of Cambridge University (a former Wiles student), corrects—or rather circumvents—the notorious "gap" experts identified near the end of Wiles's original argument.

Even with the gap, Wiles's original exposition had qualified as an important and powerful contribution to number theory, but this time there's little doubt he has completed the proof. Because of their historic significance, the two papers have been through an unusually thorough review. One reviewer reportedly went so far as to double-check some of the work by other people on which Wiles's proof depends.

The significance of the feat isn't just historical, though. When the young Wiles was beguiled by Fermat's Last Theorem, it was widely seen as a mathematical curiosity. Wiles himself eventually put it aside to pursue more mainstream mathematics. But in 1986, Ken Ribet at the University of California, Berkeley, proved that Fermat's Last Theorem actually was part of mainstream mathematics. "What Ribet [did] was to link Fermat's Last Theorem with a problem in mathematics that would never go away," Wiles explained.

The newer problem, known as the Taniyama-Shimura conjecture, is an assertion about objects in number theory known as elliptic curves—the solutions to particular classes of equations. Since it was formulated in the 1960s, number theorists had struggled to make any progress in proving the conjecture. When Ribet linked it to Fermat's Last Theorem—still unproven after 350 years—many mathematicians saw confirmation of their fears that the conjecture was profoundly difficult. But not Wiles, who saw a "wonderful excuse" to return to his boyhood dream. He set out to prove the Taniyama-Shimura conjecture for the class of elliptic curves linked to Fermat's Last Theorem.

"He [Ribet] had finally given me the excuse to put my professional expertise to work against my childhood passion," Wiles recalled. "Immediately when I heard about it in the summer of '86, I knew I would never let it go."

Even so, Wiles said, "I started without any idea how to proceed." He likens the experience to "entering a darkened mansion. You enter a room, and you stumble months, even years, bumping into the furniture. Slowly you learn where all the pieces of furniture are, and you're looking for the light switch. You turn it on, and the whole room is illuminated. Then you go on to the next room and repeat the process."

The project would have been discouraging, he notes, but for the fact that he could tell he was getting good mathematical results along the way: Even if he hadn't found the master switch, he had lit up room after room. "If I'd spent 7 years and had nothing to show for it, then I might have reacted differently, but at any period during that time, I knew I was making progress," he recalled. Eventually he had explored enough of the mansion to formulate a blueprint for the proof. A key breakthrough in 1991 convinced him that "the proof was just around the corner." It was, "but the corner was a bit longer than I anticipated," he said in an oblique reference to the gap that threatened to thwart his quest.

The gap lay in Wiles's use of a relatively new and sophisticated mathematical tool called an Euler system, which promised to be more powerful than the original method. Unable to fix the gap in the Euler system, he enlisted Taylor's help to give the earlier approach another try, but he ran into the same difficulties that had prompted his detour into Euler systems. "I was beginning to be resigned at that point to a long haul," he told *Science*. In the end, though, it was his struggle with Euler systems that provided the missing insight for the original method.

"I was taking one last look at the Euler system and tried to formulate exactly what was wrong with it," he recalled. "Suddenly, on September 19 last year, I had this wonderful revelation." He "saw in a flash" the key to his original approach. "My problems were over. I was so amazed by this that for several hours I put it down and did some administrative chore, and then returned to it to check that it was still there. It was so simple and elegant that at first it seemed too good to be true." Actually, says Wiles, "it was too good to be false." Not only did the insight complete the proof, but it also simplified the parts he had laid out more than a year earlier.

The finished proof is still rough going even for the experts, but number theorists are eager to latch onto the methods Wiles has introduced. Fred Diamond, a former student of Wiles who is now at Cambridge University, has already extended Wiles's proof of the Taniyama-Shimura conjecture to a larger class of elliptic curves, and many are optimistic that the full conjecture may fall within a few years. Wiles won't say whether he will take on the task himself. "I'll have to take my time to think about what to work on next," he told *Science*.

For mathematics as a whole, the next task may be finding a suitable replacement for Fermat's Last Theorem: a new problem to tantalize future generations and draw youngsters to the profession. It's not clear how significant Fermat himself thought the problem was, Wiles says, but "I think he would be amazed at what his marginal note has done for the history of mathematics."

–**Barry Cipra**

MEETING BRIEFS

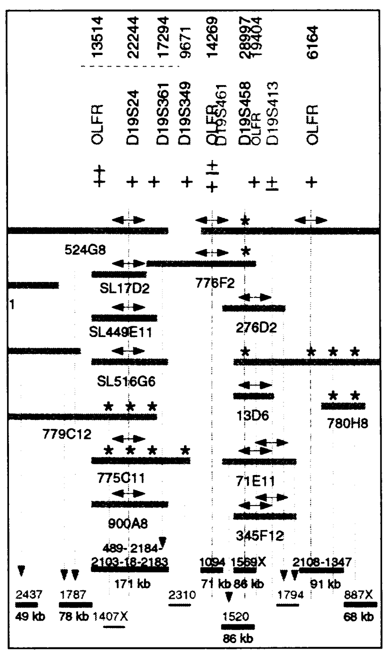
# Genome Mappers Have a Hot Time at Cold Spring Harbor

**COLD SPRING HARBOR, NEW YORK**—The "Genome Mapping & Sequencing" meeting held here from 10 to 14 May was electrifying. Huddles of geneticists debated how to start the final stage of the Human Genome Project (HGP)—large-scale sequencing. Then the outside world intruded as Francis Collins, director of the National Center for Human Genome Research at the National Institutes of Health (NIH), in an unscheduled address, asked the attendees to urge members of Congress to vote against budget cuts that could shrink the NIH budget by 20%. But even as conference attendees looked to the future with mixed elation and trepidation, they already have a sense of accomplishment, as the following samples attest.

## A La Carte

One of the HGP's major goals has been to produce detailed maps of the human genome. Those maps, it is hoped, will lead to disease genes and provide guideposts for the ultimate sequencing effort. In mapping there has been plenty of progress, as the buzzwords bandied around at Cold Spring Harbor indicated. New terms such as "sequence-ready map," "integrated map," and "ultimate map" were on everybody's lips, while old ones such as "high-resolution" had taken on new meanings.

Last year, a genomic map counted as high-resolution if it contained one genetic landmark per 100 kilobases (100,000 bases) of DNA. "Now 'high-resolution' means ready to stick in the ABI [sequencing] machine," said mapping expert Ken Krauter of Albert Einstein College of Medicine. That means a new criterion has been added: The segments between landmarks must also be broken into overlapping fragments that by some people's estimates should be as short as 10 kilobases. That's an onerous task. But maps of at least two chromosomes, 16 and 19, have reached that stage, and they are expected to be the first chromosomes to be completely sequenced.




ANNE OLSEN/LAWRENCE LIVERMORE NATIONAL LABORATORY

**Full of facts.** A portion of the detailed chromosome 19 map is shown here.

Once sequence information starts pouring off the production line, geneticists will need reams of additional data to work out what it all means—where the genes are hidden among the masses of noncoding DNA, for example, and which genes are likely to be involved in causing disease. Consequently, the information-rich "integrated maps" of human chromosomes 3, 11, 12, 13, 16, 19, 21, and 22 that were on display at Cold Spring Harbor attracted intense interest.

To make integrated maps, researchers first establish the gross topography, the positions along the chromosomes of segments of human DNA that, for ease of manipulation, have been cloned in bacterial and yeast cells. Layered on top of these ordered DNA segments, which cover up to 98% of some chromosomes, are the specific addresses of hundreds of genes and DNA markers as determined by genetic linkage studies, which give their relative positions, or by physical mapping, which provides their actual sites on the genome. "A truly impressive accomplishment" is how genome scientist Maynard Olson of the University of Washington, Seattle, described the integrated maps.

While some attendees pored over maps of individual human chromosomes, others followed global interests. From France came Jean Morissette of Généthon, a private research institute in Evry, who offered the close-to-final version of Généthon's human genetic linkage map. That map now covers the entire human genome and is packed with 5300 markers—two-and-one-half times the number available 18 months ago.

And Isabelle Le Gall of the Centre d'Étude du Polymorphisme Humain (CEPH) in Paris presented a new and improved version of CEPH's physical map that comprises aligned,