tances to the Ia supernovae, the best standard candles. For one thing, Ia's are rare: Only eight have occurred in galaxies close enough to have visible Cepheids. Since 1992, Sandage's team has used HST—although not as a part of the Key Project—to observe those Cepheids and has calibrated the eight Ia's accordingly. Their most recent Hubble constant from Ia's is 61.

Freedman's team combined the same Cepheid observations with new data and analyzed them with the method used by the Sandage team and another, independent method—a procedure, says Abhijit Saha of the National Optical Astronomy Observatories, who is on both teams, that "reflects differences in philosophy." As a result, Freedman says, her team found that "the Ia distances based on Cepheids are systematically closer by 8%," leading to a somewhat higher Hubble constant.

Whether the number is 70 or 61 or somewhere in between, it won't provoke another age crisis. Astronomers now believe that the universe's density of matter is low and its expansion is speeded up by an energy, called the cosmological constant, that pervades empty space. Both factors would push up the age of the universe with a Hubble constant of between 60 and 70 to around 13 billion years (see p. 1503). The oldest stars are between 11 and 14 billion years old. Because of uncertainty in the stars' ages, says Freedman, "there's still some tension, but there's no crisis."

So we can go on with our lives, right? Not yet. The Key Project's results "are 90% of the answer," says Robert Kirshner of the Harvard-Smithsonian Center for Astrophysics in Cambridge, Massachusetts, "not the official end of the inquiry." Michael Turner of the University of Chicago agrees: "We're not quite done with this story. That last 10% is very important." Theorists' best model of the universe not only accommodates the mysterious energy of the cosmological constant, it actually requires it. "So we're on a roll," says Turner, who is himself a theorist. "But it could be snatched away by a more accurate measure of the Hubble constant." That's a matter of time: Satellites planned for the next decade should provide an accuracy of 1%.

If the final and exact value for the Hubble constant is well below 60, a cosmological constant could make the universe implausibly old, and theorists' favored cosmic model would be in trouble. "If a more precise value for the Hubble constant favors a universe with no cosmological constant," Turner says, "maybe we'll have another crisis—at least for the theorists."

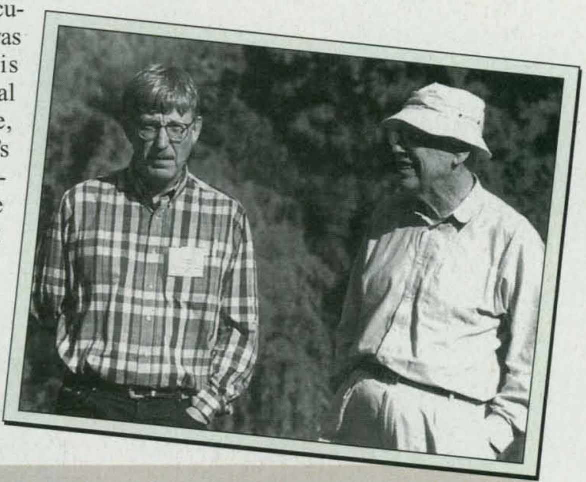
–ANN FINKBEINER

Ann Finkbeiner is a science writer in Baltimore.

HUMAN GENOME PROJECT

Sequencers Endorse Plan for a Draft in 1 Year

COLD SPRING HARBOR, NEW YORK—Meeting in a closed session here last week, leaders of a dozen scientific teams endorsed an international plan to complete a "working draft" of the human genome by the spring of 2000 and polish it into a "highly accurate" version by 2003. The decision was a vote of confidence for Francis Collins, director of the U.S. National Human Genome Research Institute, and for Michael Morgan of Britain's Wellcome Trust charity. As chief funders of the nonprofit human genome project, they have been pushing for several months for such a scheme. They say they're doing this to satisfy researchers who want sequence data as soon as possible. But there's another objective: to stay ahead of a commercial rival—Celera Genomics of Rockville, Maryland—which announced in 1998 that it intends to sequence the entire human genome by 2001 and patent many genes (*Science*, 15 May 1998, p. 994).



Strategizing. Francis Collins (*left*) and Cold Spring Harbor Lab chief James Watson confer.

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HUMAN CHROMOSOME ASSIGNMENTS REQUESTED BY MAJOR DNA SEQUENCING CENTERS

Baylor College of Medicine (R. Gibbs)	3, 12, X
MIT/Whitehead Center (E. Lander)	17, others*
Sanger Centre (J. Sulston)	1, 6, 9, 10, 13, 20, 22, X
U.S. Department of Energy (E. Branscomb)	5, 16, 19
Washington University (R. Waterston)	2, 3, 7, 11, 15, 18, Y
France (J. Weissenbach)	14
Germany (A. Rosenthal, H. Bloecker, H. Lehrach)	8, 21
Japan (Y. Sakaki, N. Shimizu)	8, 18, 21, 22

* Center director Eric Lander said MIT will sequence "whatever needs to be done."

When Collins and Morgan first floated the new plan in March, they embarked on a risky course: They essentially urged their own grantees to accept lower quality data—at least in the short term—to speed up production (*Science*, 19 March, p. 1822). Until then, the project aimed to produce a genome that is 99.99% complete, with most stretches of the genome sequenced 10 times over to reduce errors, by 2003. Now, they are asking grantees to produce a rough draft that will be at least 90% complete with fivefold redundancy. Some researchers were uneasy about this lowering of standards; had there been open dissent, the plan might have split the community.

That didn't happen, although some European members of the group were unhappy with the way the plan came about. They felt left out when Collins and Morgan switched gears in March. Andre Rosenthal of the Institute of Molecular Biotechnology in Jena, Germany, and Jean Weissenbach of Genoscope in Evry, France, made their objections known. The Anglo-U.S. leaders were "arrogant," Rosenthal says, to take this step without including everyone. And even U.S. scientists found the change tumultuous. It "made hamburger of all our plans," acknowledges Elbert Branscomb, director of the Department of Energy's Joint Genome

Institute in Walnut Creek, California.

Over the past few weeks, Collins and Morgan have tried to mend fences. Most foreign groups are satisfied that they have been included now, according to Rosenthal, and Collins announced at the meeting here that the international teams have given their support. The Europeans and at least one Japanese group—a team led by Yoshiyuki Sakaki of Tokyo University—have signed up for the "working draft" concept and agreed, like other participants, to daily release of the DNA sequence they generate.

Speaking as "operating manager and field marshal" of the U.S. and British sequencers, Collins said that the major centers' performance in 1998 indicated they had enough capacity to produce a fivefold-redundant working draft human genome by next year. He noted that about 10% of the human genome has now been sequenced in final form and 7% more in draft, and boasted that the collaboration has met all of its milestones, "without exception." The project, Collins added, will be "more important than the splitting of the atom or going to the moon."

Collins, Richard Gibbs, director of the genome center at Baylor College of Medicine in Houston, Texas, and Marco Marra of Washington University in St. Louis described the logistics of the new strategy in some detail for an audience of several hundred scientists gathered here. The new plan will require tight coordination to sustain the rapid pace of sequencing, Collins explained. The five largest human genome centers, calling themselves the G-5, have agreed to use as their source material a clone repository at Washington University managed by John McPherson; it will also serve as a method of allocating the work.

Teams have been invited to choose the chromosomes they prefer to analyze, but each choice includes performance goals. Gregory Schuler of the National Center for Biotechnology Information recorded an initial chromosome list last week (see table) and plans to track each center's progress. These assignment could change, though. Members of the G-5 confer by phone every week, and the full consortium will review progress every 3 months. If a member stumbles, assignments (and funding) may be reallocated.

Genome scientists have never attempted a collaboration of this scale or rigor before, and it's not clear how well it will go. As Collins said, he and others are watching with "white knuckles." Several problems still lurk at the edges. One open question is whether the new automated capillary electrophoresis sequencing machines that the centers are now installing will increase the rate of output, as the users are hoping. The MegaBACE capillary machines made by Molecular Dynamics performed reasonably well in tests at the Sanger Centre but did not get praise from others at last week's meeting. Nor did the new Perkin-Elmer 3700 capillary devices, which will form the core of Celera's sequencing operation. Three major labs (Massachusetts Institute of Technology, Washington University, and Sanger) reported that the new 3700 machines—although they demand less human tending—have proved not much more efficient than their predecessor, the 377, which they were meant to outperform dramatically. Even so, MIT has ordered 115 of the Perkin-Elmer machines and Washington University an initial batch of 27.

Two more important issues also remain unresolved: how to measure the quality of a lab's output and how to get from the draft sequence to the fully finished version in 2003. Gibbs said that the G-5 teams have settled on a "provisional" quality index that uses software called "Phred" to count the number of acceptable bases per unit of DNA sequence produced. A final index will be established this summer. But the decision on how to finish the genome is "still in flux," according to Gibbs. He said it may not make sense to try to fill all the gaps in the working draft by reanalyzing previously sequenced clones. It may be more efficient, Gibbs suggested, to start afresh with new clones. At this point, Gibbs said, "we're not really sure" what the best tactic will be.

That's a puzzle the sequencers hope to solve over the next year—in their spare time.

–ELIOT MARSHALL

PLANETARY SCIENCE

A New Look at the Martian Landscape

Mars is 100 million kilometers away, but in at least one respect, we now know it better than our own familiar Earth. On page 1495 of this issue, planetary scientists present a precise map of martian topography, accurate around the planet to within 13 meters of elevation; some parts of Earth are known only to 100 meters or more. "We now have a definitive picture of the shape of the whole planet," says David Smith of the Goddard Space Flight Center in Greenbelt, Maryland, principal investigator of the instrument, called the Mars Orbiter Laser Altimeter (MOLA), that gathered the data from its perch aboard the Mars Global Surveyor spacecraft.

Thanks to MOLA, a diverse array of martian features has now snapped into sharper focus, including the polar ice caps and the plateaus and lowlands that hint at the processes that shaped the planet. "MOLA's maps allow you to settle issues once and for all that have been contested in Mars geology for 25 years," says Jeff Moore, a planetary geologist with the

ScienceScope

Embryo Taboo Broken? President Bill Clinton may not be eager to receive it, but his National Bioethics Advisory Commission (NBAC) is ready to give him some provocative advice on human stem cell research. NBAC's draft recommendations—which hit the press last week—advise the government to end rules that now prevent federally funded researchers from deriving versatile stem cells from human embryos.

NBAC's opinion—likely to stir protest from antiabortionists—calls for a limited repeal of the current ban on embryonic stem cell research on grounds that it may be "unjust or unfair" in blocking potential medical benefits. NBAC aims to approve final recommendations in late June.


Cox

Spy Threat A new report has ratcheted up the pressure on programs that bring thousands of foreign scientists to the United States. This week, a House panel led by Christopher Cox (R–CA) released a long-awaited report concluding that China has used the exchanges to gather intelligence on U.S. nuclear weapons and supercomputers. It recommends that five agencies scrutinize the security risks and report to Congress by 1 July. Meanwhile, the National Academy of Sciences, the National Science Foundation, and the American Physical Society have warned against clamping down too tightly on exchanges, which some lawmakers want banned (*Science*, 7 May, p. 882).

Less Ravenous ITER Europe, Japan, and Russia continue to pursue a cheaper alternative to the moribund $10 billion International Thermonuclear Experimental Reactor (ITER). Last year, a U.S. pullout dashed hopes for the original fusion megaproject (*Science*, 9 October 1998, p. 209). This week, a new working group was to meet in Tokyo to begin mapping out a plan, sometimes called "ITER Light," that would run half the original cost or less.

Japanese officials say the ITER parties have ruled out the idea of scattering experiments among existing facilities. That means the panel will ponder a host of questions, such as a reactor's scale, cost, and location. It is not clear what combination will win out: "We don't know the positions of the other parties," says Hiroshi Kishimoto, director of Japan's Atomic Energy Research Institute and working group co-chair. The panel has until year's end to hammer out recommendations.

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