Genome Planners Fear Avalanche of Red Tape

The complexities of organizing national and international efforts to map and sequence the human genome could be made worse by unnecessary bureaucracy

THE GENE MAPPERS and sequencers whose job it is to nurture the National Institute's of Health part of the U.S. Human Genome Initiative met last week in Bethesda to assess progress in biology's megaproject. This, the second meeting of the institute's program advisory committee, set the initiative onto its last lap toward home, a National Plan to be presented to Congress next spring. Although protagonists have known from the start that there is an ever-present danger of becoming deluged by an avalanche of data stemming from the venture, they apparently were less aware of the dangers of voluminous bureaucratic red tape. They are unaware no longer.

"If the governments will leave us alone, we will be all right," says Rockefeller University's Norton Zinder, chairman of the NIH committee. "But if we are forced to act as delegates of our countries, rather than as scientists engaged in an exciting international project, then it won't work." Zinder steered the committee through its discussions last week, at which the potential organizational problems of what inevitably will be a world-wide effort became all too apparent.

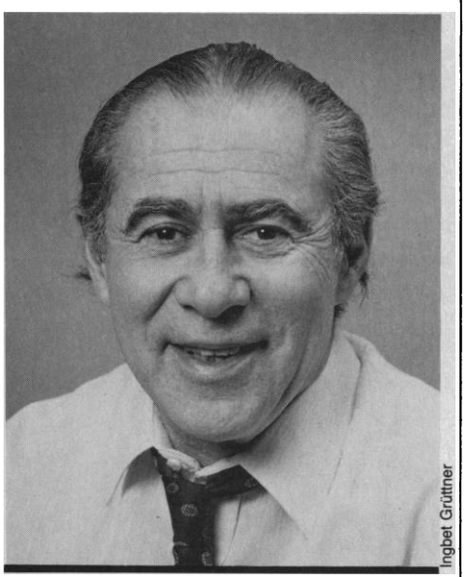
Said James Watson, associate director of Human Genome Research at NIH, referring to the all-important establishment databases: "The prospects of having an international committee that would make decisions on this are unrealistic, because there are so many tensions in Europe." In addition, he added, "there is very little money for this kind of thing in Europe at present."

Watson later told *Science* that "Our immediate concern is to establish U.S. policy, which should be in place next spring. Of course we want to cooperate internationally, but all we can say is that we will cooperate when there is something to cooperate with."

Questions of international cooperation aside, the national plan will focus on overall goals of the program, its administrative and scientific organization, data handling, and ethical issues. Effectively an argument for spending upwards of $200 million a year the next 15 years, the plan needs congressional friends. "Already we are finding there is a lot of support, a lot of enthusiasm for the project," says Mark Guyer, special assistant to the director of NIH's Office of Genome Research.

That support is manifested in the $27.5 million for the genome project in this year's NIH budget, a figure that will probably be almost quadrupled for fiscal year 1990. Such is the scale of the project.

It was partly because of the enormous scale of the venture that Watson suggested earlier this year that perhaps different chromosomes should be assigned to different countries, thus preventing overlapping effort. Watson, who by now should be getting



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"If the governments will leave us alone, we will be all right." —Norton Zinder

used to ruffling feathers with his often unrestrained imagination, was immediately accused of trying to control the activities of scientists both here and in other countries. "I was misunderstood," Watson told the NIH committee last week. "I see the chromosome—or perhaps part of a chromosome—as the logical unit of management. I certainly would not wish to exclude people from working on what they want to. But I am concerned with trying to reduce the cost for the United States."

Obviously nervous about how decisions would be made on which research group would work on which chromosomes, the committee nevertheless agreed that the chromosome was indeed the logical "unit of management," at least for the collection of data. Watson acknowledged the potential for stirring ill-will—at home and abroad—if this coordination function is mishandled. In any case, said Watson, "It is premature for making decisions on this. But this kind of coordination will be essential in a couple of years, and more particularly as we reach closure."

By contrast with the jumpiness engendered by the notion of parceling out chromosomes, a second bold Watson proposal drew unanimous approval: to fund a collaborative U.S./U.K. project to sequence the entire sequence of the roundworm, *Caenorhabditis elegans*. "A wonderful idea," said Phillip Sharp, of the Massachusetts Institute of Technology. "I'm all for it," added Nancy Wexler, of Columbia Presbyterian Medical Center, New York. And so it went around the table.

For two decades this little worm has been under the combined molecular and genetic microscope of Sydney Brenner and his team at the Medical Research Council's Laboratory of Molecular Biology in Cambridge, England, plus various spin-off teams in the United States, particularly at MIT. As a result, *C. elegans* is about as closely scrutinized as an organism of its size—a couple of millimeters—can possibly be.

"Recently the Cambridge people have been mapping the *C. elegans* genome, and have cut it into about 100 [pieces], each about the size of the *E. coli* genome," said Watson. "The Cambridge people would like to sequence the genome, but they are afraid there won't be funds available in the U.K." Watson proposed a collaborative sequencing project, with Maynard Olson and his colleagues at Washington University, St. Louis, that would cost each country about $600,000 a year for 3 years, as a feasibility study in the first instance. If it works, the venture would require 50 people churning out a 1000 base pairs a day for 6 years.

"It would be a wonderful end to the *C. elegans* project," said Watson. "It would also be a wonderful beginning to the genome project as a whole," says Zinder. "The *C. elegans* genome is about as big as a single human chromosome. If this can be done it will help us find out if we can do the big one."

Ironic, given the tenor of the rest of last week's meeting, that the single most concrete proposal to emerge was an instance of international collaboration.

■ ROGER LEWIN