

LANDER: The Human Genome Project was an absolutely ludicrous notion proposed in about 1985, that we could determine the entire sequence of the human genome. And that this would provide incredibly useful information for all of biology. Both of those propositions were open to tremendous challenge.

The first, that we can do this. At the time DNA sequencing was less than a decade old. DNA sequencing was practiced with radioactive slab gels held up against film to detect sequences. It was stunningly inefficient. It was not that long before that point that people got whole graduate theses for sequencing of a couple of thousand letters and some plasmid. And here the field was talking about a million times more sequencing than that.

In addition, it was hotly debated whether this was worth anything at all. Everyone-- not everyone-- many people said, well, what would you do with that information, anyway? Who needs it? And the truth was, with regard to both of those propositions, the critics were right. We had no clue how in the world to do this. If anybody had gotten up in front of Congress and said, we know how to sequence the human genome, they would have been guilty of perjury.

It was a very interesting year from May of 1999 to May of 2000 when the amount of the genome that had been covered in draft form, not perfect form but draft form, grew from about 10% of the genome to about 90% of the genome in the course of one quite remarkable year. This involved a tremendous amount of coordination of 20 different groups around the world distributing clones, groups working in all different sizes.

Our group at the Whitehead Institute was, indeed, the largest single contributor to the effort. But in fact, there were major, major contributions from the Sanger center in England, from Washington University in St Louis, from the Department of Energy, from Baylor in Texas. And then a number of smaller groups, all of whom played, I think, incredibly important roles in keeping this an international project.

In fact, the project was so open that halfway through its scale up phase, the group in Beijing, China said they wanted to join. And we said, sure. And Beijing brought in 1 and 1/2 percent of the genome done there in China. The groups were all very different in how they approached this but they all shared one absolute commitment, which was that the data, however it was produced, would be freely released on the web every 24 hours without restrictions of any kind. That was the only condition for signing up to join the International Human Genome Project.