UNSUNG HERO: MARK ADAMS

Ever since he teamed up with J. Craig Venter at the National Institutes of Health (NIH) in 1990, Adams has been one of the country's top sequencing gurus. After developing expressed sequence tags with Venter at NIH, Adams followed him to The Institute for Genomic Research (TIGR) in Rockville, Maryland, and then to Celera, also in Rockville, where he is refining methods for whole-genome shotgun sequencing.

NIH's deliberate approach won its spurs a year later, when an international consortium knocked off the yeast genome. Although still tiny, relative to humans, it was a major step up in size and complexity. By April 1996, Waterston and Sulston, who were well into sequencing *C. elegans*, were champing at the bit, urging Collins to let them plunge into all-out sequencing. In the right hands, they argued, the technology was good enough; the only stumbling block was money. "Just do it," Sulston urged at the time. The two also broached the heretical topic of dropping the accuracy goal to speed the process, from 99.99% to 99.9% (*Science*, 12 April 1996, p. 188).

Francis Collins. Favored a deliberate, methodical approach to mapping and sequencing.

But Collins would not be rushed. The goal was to assemble the definitive "book of life," and he insisted it be done to the highest possible quality. He decided to test the water with six pilot projects—a cautious style that earned him praise in some corners and criticism in others. The charge to the labs was to complete a major chunk of sequence while also demonstrating big improvements in cost and speed. After that, he said, the project would home in on its final strategy.

Collins soon abandoned his measured approach—not because of the persuasiveness of Waterston and Sulston's arguments, but because Venter threw down the gauntlet.

Venter redux

Showing a knack for impeccable timing, Venter dropped his bombshell on 9 May 1998, just days before the annual gathering of genome scientists at Cold Spring Harbor Laboratory. Venter announced that he had teamed up with Perkin-Elmer Corp., which was about to unveil an advanced, automated sequencing machine, to create a new company that would single-handedly sequence the entire human genome in just 3 years—and for a mere $300 million (*Science*, 15 May 1998, p. 994). What's more, said Venter, when he was done he would give the data away free to the community by posting it on his company's Web site. The company, soon to be named Celera Genomics and located in Rockville, Maryland, would make money not from the raw data, he explained, but from the analysis it would perform and sell to subscribers. Venter proposed to sequence the genome with the brute-force shotgun technique that had worked so well in *Haemophilus*—but this time, he would be shredding the entire 3-billion-base genome into zillions of fragments.

Leaders of the public project were angry and incredulous. After they had spent years laying the groundwork, could Venter really beat them to the finish and steal the glory? They were also deeply worried that if Congress fell for Venter's bravado, it might pull the plug on the public project. Venter's plan would never work, they countered—the sequence would be riddled with holes and impossible to reassemble.

Yet as they disparaged Venter's claim, they could not dismiss it. Venter had surprised them before. And this time, he had a hefty bankroll and 300 of Perkin-Elmer's sequencing machines, just then rolling off the assembly line at $300,000 a pop. And to reassemble his sequenced fragments, Venter would use one of the world's fastest supercomputers.

The leaders of the public program wasted no time in increasing the pace and reorienting the game plan in an attempt to beat him to the finish line. Collins announced new goals for the public project in September 1998, just 6 months after Venter's surprise announcement (*Science*, 18 September 1998, p. 1774). First, the consortium would complete the entire genome by 2003—2 years ahead of schedule, but also 2 years behind Venter. And, in a dramatic departure from previous philosophy,

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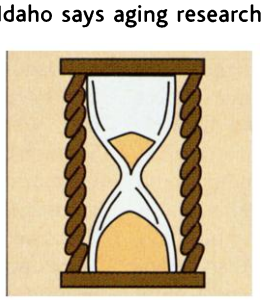
NEW SCIENCE:

A Parakeet Genome Project?

Researcher William Haseltine, head of Human Genome Sciences Inc. in Rockville, Maryland, likes to claim that knowledge from the human genome, combined with a few technology breakthroughs, will someday enable humans to live forever. Most researchers who study aging have more modest expectations—for example, trolling the genome for new insights into genes involved in so-called oxidative damage to cells and genes, which is thought to limit an organism's life-span.

A few in the field have another request: sequence the parakeet. One avian genome, the chicken's, is in progress, but George Martin of the University of Washington, Seattle, and Steven Austad of the University of Idaho says aging research could gain key insights from comparing the genome of a "real flier" with that of humans. "Good flying birds have remarkably long life spans for their size," he says: Some can live for 20 years or more. At the same time, they use an enormous amount of energy—a process that researchers believe is at the root of oxidative damage. Mice, for example, use much less energy but typically live only 2 years. A parakeet genome project, Martin says, could tell scientists "what the birds are doing that's so great"—and how humans might mimic their secrets.



–GRETCHEN VOGEL