members worry that the fellowship program might have to be scrapped altogether. Buys, the Dutch representative, warns that "further cuts will be disastrous."

Science committee members hope to convince Robertson of the value of science in strengthening the alliance. "If only they would forgo buying one F-16, you could use the money to transform NATO science," notes one member. At $25 million, such a financial transfer would more than double the science budget. On the other hand, a continued decline in the science program might leave it too poor to buy even spare parts for the fighter plane. **–RICHARD STONE**

DNA SEQUENCING

Venter's Next Goal: 1000 Human Genomes

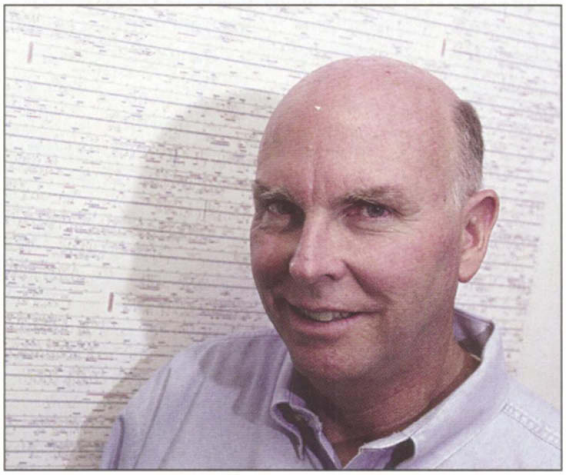
Fundraising campaigns often repay donors with mugs, buttons, or books as a token of thanks, but DNA sequencer J. Craig Venter is offering something more personal. People who donate $500,000 to his recently formed J. Craig Venter Science Foundation can have their genome analyzed and get the results on a disk.

Venter, who left the position of CEO at Celera Genomics in Rockville, Maryland, in January, is making this offer as he drums up support for several research projects that his nonprofit foundation will oversee. They include a scheme to develop hydrogen-producing organisms, a genetics policy shop, and a lab for high-speed DNA sequencing. The lab is a high priority, and Venter says he hopes to get it launched by January 2003; within 2 years, he expects it to sequence the genomes of 1000 individuals, including those of interested sponsors. It will also test new technologies, including an efficient DNA sequencing system patented last month by U.S. Genomics of Woburn, Massachusetts (*Science*, 25 October, p. 735).

Venter is steering $50 million of the funds he controls into the sequencing facility, much of it originating from the endowment of The Institute for Genomic Research (TIGR), also in Rockville. He founded TIGR in 1992; it is now run by his wife, biologist Claire Fraser, and it receives 95% of its funds from grants and contracts. Venter expects to find strong private support for human sequencing based on initial reactions, but he hasn't received any pledges as yet.

Donors to the project will have a chance to learn about their own DNA and at the same time contribute their genetic information to a pooled database for use in medical research, according to Venter. The data will be placed in the public domain, possibly in the National Institutes of Health's GenBank, he says. These human genomes will not be as complete as those produced last year by Celera and the public Human Genome Project led by the National Human Genome Research Institute, as the plan this time is to sequence only the "essential" gene-coding regions. Venter adds that he intends to publish his findings in a scientific journal.

Venter does not plan to collect medical data on donors, but he hopes to team up eventually with a health center that will be able to interpret the results and possibly even offer clients diagnostic information. He does not yet have such a medical partner. Venter believes that his new human DNA database will be more valuable than earlier ones containing "homogeneous genome sequence," because it will include many more individual genomes, making it easier to "identify associations between traits and genetics." Because this research involves human subjects, the project will follow "standard procedures," according to Venter, including securing informed consent from participants and approval by an institutional review board.



Premium offer. J. Craig Venter is proposing to analyze the genomes of interested major donors to his foundation.

Despite such assurances, Arthur Caplan, director of the University of Pennsylvania Center for Bioethics in Philadelphia, is concerned that volunteers who offer to donate DNA be told that they are unlikely to receive much benefit from participating. Caplan says that any genetic risk profile emerging from this effort is likely to be "loose, weak, and unreliable," because the field is so young. According to Caplan, proper informed consent should communicate "how poor the information is likely to be." This would not be a strong selling point for the foundation's fundraising efforts.

Richard Gibbs, director of Baylor College of Medicine's Human Genome Sequencing Center in Houston, Texas, also thinks that the plan to sequence the genomes of 1000 individuals is "flawed in some of its details," although he praises Venter for "pushing the envelope." The computer models used to identify genes in DNA data have not been fully validated, Gibbs says, suggesting that ramping up to do human genomes at high speed might yield unreliable results. He also is concerned that the road map for dealing with ethical issues is not clear, either, as there is no federal legislation in place to protect against genetic discrimination. In addition, he wonders whether Venter will find many people who are willing to participate in the project and can afford a $500,000 donation, the projected cost of a genome analysis.

Venter has faced skepticism before. He remains confident that his collection of 1000 human genomes will become a powerful tool for identifying the causes of disease, and that public fears about misuse of such data can be overcome. Venter explains that he donated his own DNA to the Celera genome sequencing project—and announced this fact—because he wanted to lead by example.

His new lab, in addition to probing human genomes, will test new high-throughput sequencing technologies available from a variety of companies such as U.S. Genomics and Solexa, a U.K.-based biotechnology company. The 3700-square-meter facility will also house biological energy research activities already under way at the Institute for Biological Energy Alternatives (IBEA)—established by Venter earlier this year—in addition to new microbial genome sequencing initiatives and environmental projects. "Researchers at TIGR and IBEA are simultaneously looking for new organisms and analyzing known organisms that metabolize carbon or create hydrogen," according to a TIGR statement.

TIGR will not be involved in the 1000-human-genomes sequencing effort, but Fraser hopes to use some of the new capacity for the 40 simultaneous sequencing projects it has under way, including genomes of *Plasmodium vivax*, a human malaria parasite, and other organisms. With TIGR's current backlog, Fraser says, "we could immediately make use of a 50% increase in sequencing capacity." The total capacity of the new sequencing lab will represent a fivefold increase over TIGR's current capability.

As Venter sees it, the critical challenge for scientists in his field is to connect with clinical medicine. "The most important thing now," he says, "is to make the human genome relevant to the general population."

–REBECCA SPIELER TRAGER

Rebecca Spieler Trager is an editor for *The Blue Sheet* in Chevy Chase, Maryland.

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