More recent numerical analyses (2) have arrived at volcanic probabilities that are different from the estimates obtained in DOE's study. DOE's panel of experts arrived at an aggregate mean that is essentially the same as the minimum reported in the recent literature, and some estimates by individual members of the expert panel are one to two orders of magnitude lower. Because volcanism has a low probability, but is potentially a high-consequence event, such differences may affect estimated risk (3). Although a factor of 10 difference in probability is often of little concern in risk assessments, environmental standards for the proposed geologic repository have not, to date, required consideration of potentially disruptive events with probabilities less than 10^{-4} in 10^4 years.

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Risks in Collaboration?

If fraudulent work is published (Letters, 3 Jan., p. 14), all co-authors must take some measure of responsibility, not for the fraudulent acts, but because author responsibility is implicit in the process of scientific publishing. Risks of fraud in collaborations outlined by the correspondents should not reduce collaboration: surely they should strengthen collaboration by reminding us to understand that which is attributed to us. Nor should they require the banning of all but single-author papers: collaboration often strengthens work because it requires frequent and critical discussion of all facets of the problem. Nor should they limit the number of authors: all significant contributors must receive recognition and take the responsibilities of authorship. Nor should they be comparable to acts of individuals in a marriage that are not inherently essential to the relationship.

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Funding Sequencing Efforts

In "Life with 6000 genes" (Articles, 25 Oct., p. 546), André Goffeau *et al.* note that, despite the potential gain of sequencing a number of human pathogenic organisms, only limited funds have been made available for such projects. The Burroughs Wellcome Fund and the National Institute of Dental Research, part of the National Institutes of Health (NIH), have recently co-funded a project at Stanford University to use "sample-sequencing" to identify genes in *Candida albicans*, a major pathogenic fungus. The researchers' strategy will reveal at least a portion of about 95% of all *Candida* genes that can be identified by their similarity to genes in other species. Information

about the project will be announced on the C. *albicans* World Wide Web at server http://alces.med.umn.edu/Candida.html.

The authors also make a bold and intriguing policy recommendation.

> While we await the completion of the human genome sequence sometime around the year 2005, there is danger of dispersing sequencing power among too many model genomes. Instead, it may be desirable to direct sequencing capacity toward eukaryotic parasites (such as *Plasmodium falciparum*, *Trypanosoma cruzei*, *Schistosoma mansoni*, and *Leishmania donovani*) that plague millions of people in developing countries.

Because of the intermediate size of these genomes, this would be a more readily achievable task, the authors maintain, "provided that funding is increased from its present modest levels." We strongly affirm this recommendation.

A good start in this direction was made several years ago, when the Wellcome Trust, a United Kingdom–based medical charity, initiated a project to map the genome of *P. falciparum*, the parasite that causes malaria. Independently, the World Health Organization provided seed grants to establish Parasite Genome Networks for five other pathogenic organisms: *Filaria*, *Schistosoma*, *Leishmania*, *Trypanosoma brucei*, and *T. cruzi*. The malaria genome effort recently has received a significant boost: the Wellcome Trust, the Burroughs Wellcome Fund, NIH's National Institute of Allergy and Infectious Diseases, and the U.S. Department of Defense formed a funding consortium to begin sequencing the *P. falciparum* genome. However, other parasite networks are still struggling to secure the necessary funding to move forward rapidly, despite their great progress in developing international collaborative links and proving the feasibility of sequencing.

In order to secure funding for this historically underserved research community, it will probably be necessary to seek funds from a variety of government and private sources interested in genomics as well as parasitology. The successful establishment of the *P. falciparum* consortium—an international working group of multiple private and public funding agencies—demonstrates the plausibility of this approach. What is now needed is the will to dedicate the funds.

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Response: I am pleased to learn that a project has been started on sample sequencing of C. *albicans* and that the Wellcome Trust has made a laudable start toward the sequencing of the Plasmodium genome. To my knowledge, the funding provided by Wellcome is significant, but far from being sufficient to ensure the rapid completion of the sequencing of this genome. The funds provided by the World Health Organization appear to barely make it possible to proceed toward the construction of sequence-ready libraries of five pathogens and are by no means sufficient to sequence these genomes. The Commission of the European Community does not seem to be getting involved in the sequencing of parasite genomes. But whatever happens, I believe that laboratories in developing countries should be involved in an organized way, rather than having the sequencing work done in only a few large Western sequencing centers.

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Doppler *What*?

In "Iron in Io" (This Week in Science, 3 May 1996, p. 625), there was mention of "Doppler waves generated by the Galileo orbiter." "Doppler waves," per se, do not exist, but the relative motion of the Galileo orbiter with respect to the Earth can, indeed, generate a "Doppler effect." Exploring this effect, J. D. Anderson *et al.* came to the conclusion that Io may have a large metallic core composed of iron.

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"Ecological Footprint"

The News piece "Ecologists look at the big picture" (13 Sept., p. 1490) by Anne Simon Moffat mentions a fascinating model of how living standards and presumably personal choices result in an "ecological footprint." If the developer of that model, population biologist William Rees of the University of British Columbia, could develop a version, possibly for export to the home computer, that would enable an individual (and perhaps communities) to estimate his or her own footprint, then by manipulating the input (for example, by becoming a vegetarian, reducing gasoline consumption, or recycling waste) one