two-prong approach: compilation and analysis of existing data and interpretation of high-resolution satellite data with standard protocols and definitions.

The success of the 1990 project required the cooperation of many institutions from developed and developing countries. Additional cooperation is required to improve global assessments and policy decisions with Forest Resources Assessment 2000.

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Reef Check: Complete Agreement

Because a sentence added in a revised version of the letter from Thomas J. Goreau *et al.* (11 July, p. 165) was not included in the printed letter, some readers may have formed the mistaken impression that the letter meant to criticize the purpose and value of the Reef Check 1997 project. That sentence read, "We support expanded citizens' monitoring efforts, which are important for public education and in identifying early warning signs, but we caution that the number of people able to correctly distinguish between coral diseases from bleaching and other forms of mortality is vastly less than that of certifiably accurate bird identifiers." The signatories of that letter and the letter from the organizer of Reef Check, Gregor Hodgson (11 July, p. 165), are in complete agreement that complementary efforts by professionals and trained amateurs, such as Reef Check, are urgently needed to assess the status of coral reefs around the world and protect them from rapidly increasing deterioration by widespread and multiple threats.

For those readers of the earlier article "Scientists launch survey of reef health" by Barbie Bischof (News & Comment, 6 June, p. 1494) who might have otherwise interpreted the photo and caption selected by *Science* to accompany the article, it should be clarified that the focus of Reef Check 1997 is to measure key indicators of human effects on coral reefs, such as numbers of edible high-value species, as stated in the article. Reef Check does not include a detailed survey of coral diseases.

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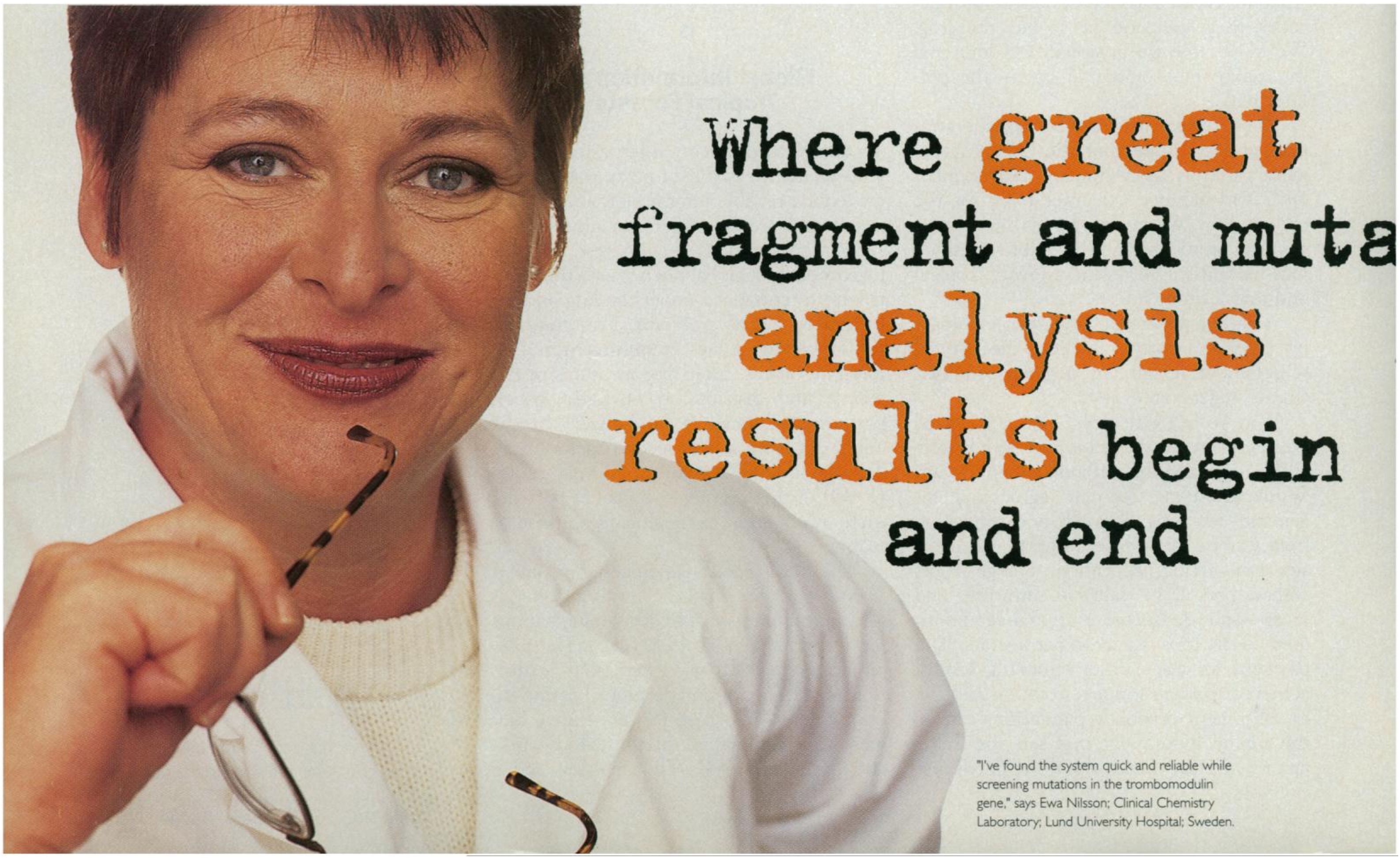
Corn Genome Initiative

In "Corn genome pops out of the pack" (News & Comment, 27 June, p. 1960), Jon Cohen summarizes the June 1997 National Academy of Sciences colloquium "Protect-



ing Our Food Supply: The Value of Plant Genome Initiatives." The National Corn Genome Initiative, proposing a $143-million, 5-year, federally funded research program, appears to emphasize basic biological research, but because corn is known largely as an agricultural crop, it is likely that the U.S. Department of Agriculture (USDA) would finance it. Even with successful legislation, it is unlikely that new money would become available; instead, it would likely be funded by diversions from other USDA programs, such as Hatch formula funds, the National Rice Institute competitive grants program, and the Agricultural Research Service (ARS) budget. We believe that there will be serious long-term consequences should a single-crop genome research initiative be supported at the expense of existing research infrastructure or mission-oriented research on many important U.S. food crops.

We support genomic research on important cereal crop plants, especially wheat, corn, and rice, the three main crops on Earth, in that order. We intend no discredit to a strong corn genome program, but without concurrent research on other species, comparative genome structure cannot be resolved. Transfer of research results from corn to other cereals will not be automatic. Each crop has unique gene complexes and characteristics and specific agricultural research needs.

We urge that a national multispecies cereal crop genome program be formulated and implemented. We suggest a tripartite program emphasizing basic genomic science in corn and other cereals, development of genetic resources and methodologies specific to each crop, and application of genomics to solve agricultural and consumer-based problems. With broad-based support, the development, financing, management, and implementation of such a program should reach beyond current modes. As genomic research is innovative, so also should be its facilitation. The Human Genome Project provides valuable lessons for a new plant genome effort.

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Cohen's 27 June article discusses dissatisfaction about the rate of release of *Arabidopsis* genome data from Japanese and European sequencing groups. The European Union (EU) *Arabidopsis* Sequencing Project integrates its work carefully with the U.S. and Japanese groups (for example, by providing clones for sequencing on the short arm of chromosome 4 to U.S. labs and by integrating the sequence efforts of U.S., Japanese, and European labs with respect to the short arm of chromosome 5, with the aim of rapidly generating a contiguous sequence). The third deposit of a European sequence, ten 200-kilobase contiguous units, was made to the European Bioinformatics Institute on 20 June, before Cohen's article appeared. The preparation of this contiguous sequence from individual components took some time, because it was generated from about 60 cosmid and bacterial artificial chromosome (BAC) clones and contained some difficult regions in terms of sequence complexity. Gene modeling revealed potential frameshifts, which were all resequenced.

Our goal of obtaining contiguous sequences may result in initial additional complexities, but it serves the important purpose of revealing larger-scale features that are needed for planning a sequencing strategy. We are now sequencing individual BACs that will not form a contiguous sequence until later this year, when another three will have been completed. The sequences of these individual BACs can be retrieved from the Martinsried Institute for Protein Sequences website while annotation is proceeding. This release policy is consistent with that described in a Memorandum of Understanding signed with our U.S. and Japanese partners last year. The agreement was put in place after the EU component of the *Arabidopsis* Genome Project began, and it has taken a little time to align our release policy more closely to that thought to be required by the *Arabidopsis* community.

The EU sequencing group knows that, although the release of sequences is a central aspect of a successful genome project, many of the more interesting features of plant chromosomes are only revealed by tackling the construction of contiguous sequences and dealing with complex regions as they occur.

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Response: My article reflected the criticisms of Bevan's U.S. collaborators, who had serious misgivings about what they contend are unnecessary delays in data release.

—**Jon Cohen**

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When Doors Are Closed at the NRC

Andrew Lawler's article of 9 May conveys the impression that the National Research Council (NRC) holds all of its study committee meetings behind closed doors. In fact, the information-gathering meetings that I organize on behalf of NRC committees are open to whomever wishes to attend.

Meetings are closed for only two reasons: to discuss committee members' personal financial information in order to determine whether they must be disqualified from service because of financial conflicts of interest, and to allow the committee to decide on its final conclusions and recommendations. These closed deliberations require about 20% of the total meeting time of the committees. It would be extremely damaging to the committee's work if deliberations about recommendations were made public before the committee has achieved a consensus on those recommendations.

The article reports that the National Academy of Sciences (NAS) is made up "primarily of elderly, white, and male scientists and engineers." While the NAS, the honorary body of scientists under which the NRC operates, has a long way to go in increasing its diversity, important efforts are being made by NRC staff to increase the diversity of study committees. NRC management strongly encourages study directors to appoint women and minority scientists to committees.