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.

Michael W. Bevan
Coordinator, EU Arabidopsis
Genome Project,
John Innes Centre,
Norwich, United Kingdom
E-mail bevan@bbsrc.ac.uk

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***

■

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.

Jacqueline A. MacDonald
Senior Staff Officer,
Water Science and Technology Board,
National Research Council,
Washington, DC 20418, USA
E-mail: jmacdona@nas.edu

■

Telomerase Activity of Reverse Transcriptase

In their report "Reverse transcriptase motifs in the catalytic subunit of telomerase" (25 Apr., p. 561), Joachim Lingner *et al.* demonstrate that such motifs are present in the catalytic subunit of the telomerase that they purified and identified in *Euplotes aediculatus*. They show that similar motifs exist in a homologous yeast gene and that alteration of these motifs by classical yeast genetics affects telomere elongation. After mentioning that telomerases are frequently called "specialized reverse transcriptases," they stress that three main features distinguish them from other reverse transcriptases: (i) telomerase uses only a small portion of its RNA subunit as a template; (ii) during processive synthesis of telomeric repeats, the substrate translocates from one end of the template to the other by an as-yet-unknown mechanism; and (iii) the telomerase protein is stably associated with its RNA subunit (a feature also found in retrotransposon reverse transcriptase).

On the other hand, we have recently shown that, under specific in vitro conditions, human immunodeficiency virus–type 1 (HIV-1) reverse transcriptase uses a portion of its template RNA to perform a reiterative synthesis; the substrate then translocates from one end of the template motif to the other, and the enzyme maintains a stable association with its RNA (*1*). On specific template sequences, it is therefore sufficient to modify the cationic environment (from manganese chloride to magnesium chloride in the reaction buffer) in order to switch the HIV-1 reverse transcriptase mode of synthesis from a regular one to a telomerase-like reiterative synthesis (as described in figure 9 of the report by Lingner *et al.*).

Thus, HIV-1 reverse transcriptase can display an appreciable telomerase-like activity, indicating that these enzymes are biochemically closely related.

Miria Ricchetti
Henri Buc
Unité de Physicochimie des Macromolécules Biologiques, Institut Pasteur,
25 rue du Docteur Roux
75724 Paris Cédex 15, France
E-mail: mricch@pasteur.fr
E-mail: henribuc@pasteur.fr

References

1. M. Ricchetti and H. Buc, *Biochemistry* **35**, 14970 (1996).

Corrections and Clarifications

Because of an editing error, the tricarboxylic acid (TCA) cycle was incorrectly identified in Steven Sparks' letter "The purpose of glycosis" (27 July, p. 459).

Letters to the Editor

Letters may be submitted by e-mail (at science_letters@aaas.org), fax (202-789-4669), or regular mail (*Science*, 1200 New York Avenue, NW, Washington, DC 20005, USA). Letters are not routinely acknowledged. Full addresses, signatures, and daytime phone numbers should be included. Letters should be brief (300 words or less) and may be edited for reasons of clarity or space. They may appear in print and/or on the World Wide Web. Letter writers are not consulted before publication.