er causes of mortality, and thus would not provide the kind of accurate data that researchers on coral diseases could use. Support is urgently needed for field monitoring efforts to document the spread of new and old diseases, and for laboratory work to identify them and their causes, before the significance of this rapidly intensifying threat to coral reefs can be understood. A workshop is scheduled to evaluate all current Caribbean coral reef diseases and produce a common classification scheme and nomenclature at the Association of Marine Laboratories of the Caribbean Annual Meeting, hosted by the University of Costa Rica in San Jose, Costa Rica, from 21 to 25 July 1997.

Thomas J. Goreau\*
Global Coral Reef Alliance,
324 Bedford Road,
Chappaqua, NY 10514, USA
E-mail: goreau@earthlink.net

\*Cosigners: A. W. Bruckner, Department of Marine Sciences, University of Puerto Rico, Lajas, PR 00667-0908; J. Cervino, Global Coral Reef Alliance; R. L. Hayes, Howard University College of Medicine, Washington, DC 20059, USA; I. Nagelkerken, Caribbean Marine Biological Laboratory, Piscadera Baai, Curacao, Netherlands Antilles; J. W. Porter, K. G. Porter, Institute of Ecology, University of Georgia Athens, GA 30602-2202, USA; L. L. Richardson, Department of Biological Sciences, Florida Interna-

tional University, Miami, FL 33199, USA; **D. L. Santavy**, U.S. Environmental Protection Agency, Gulf Ecology Division, 1 Sabine Drive, Gulf Breeze, FL 32561–5299, USA; **G. W. Smith**, Biology Department, University of South Carolina, Aiken, SC 29801, USA; **E. H. Williams**, Department of Marine Sciences, University of Puerto Rico.

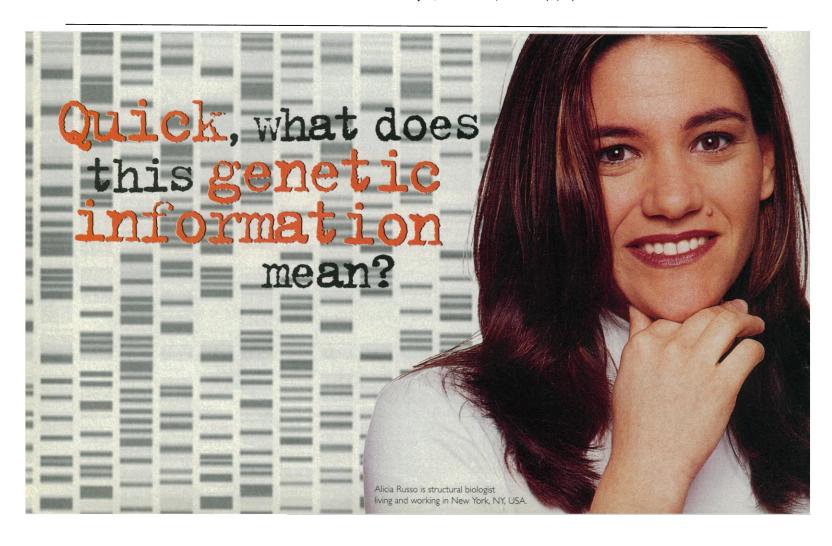
The photograph on page 1494 depicting a coral "beset by white plague disease" shows no evidence of white plague (or of any other known disease of scleractinian corals) on the *Montastraea* species, as shown. Numerous fish grazing scars, however, including some recovering lesions, appear to be present. It is also possible that these are bleached spots. White plague is characterized by the loss of tissue from the base of the colony progressing upward. While *Montastraea* is a known host, white plague is more common on other scleractinian species.

Erich Mueller
Director
Pigeon Key Marine Research Center,
Mote Marine Laboratory,
Post Office Box 500895,
Marathon, FL 33050, USA
E-mail: emueller@mote.org
Esther C. Peters,
Tetra Tech, Inc.,
10306 Eaton Place,
Suite 340,
Fairfax, VA 22030, USA

## Photosystem I Measurements in Mutants B4 and F8 of Chlamydomonas

In the report "Oxygenic photoautotrophic growth without photosystem I" by J. W. Lee et al. (19 July 1996, p. 364) (1) and elsewhere (2), it is said that mutants of the green alga Chlamydomonas that lacked detectable levels of functional Photosystem I (PSI) were capable of photoreduction of atmospheric carbon dioxide, autotrophic growth, and sustained simultaneous photoevolution of H<sub>2</sub> and O<sub>2</sub>. The absence of PSI in the mutant strains B4 and F8 used in our work (1, 2) was confirmed by physical, biochemical, and genetic techniques.

Subsequent analyses in our own laboratories, however, as well as those of colleagues to whom we have sent the mutants, indicate that there is variability in the PSI content of the cultures that depends on growth conditions. While some strains retain undetectable amounts of P700, others contain variable (0 to 20%) amounts of wild-type P700. We stand by our original measurements, which showed a lack of detectable P700 in strains F8 and B4 at the time of these studies (1, 2).



Elias Greenbaum James Weifu Lee Carol V. Tevault Stephen L. Blankinship Oak Ridge National Laboratory, Post Office Box 2008, Oak Ridge, TN 37831-6194, USA Thomas G. Owens Cornell University, Ithaca, NY 14853, USA Laurens J. Mets University of Chicago, Chicago, IL 60637 USA

#### References and Notes

- 1. J. W. Lee, C. V. Tevault, T. G. Owens, E. Greenbaum, Science 273, 364 (1996); see also J. M. Olson, ibid. 275, 996 (1997); T. G. Owens, J. W. Lee, C. V. Tevault, E. Greenbaum, ibid., p. 996.
- 2. E. Greenbaum, J. W. Lee, C. V. Tevault, S. L. Blankinship, L. J. Mets. Nature 376, 438 (1995).

### **Corrections and Clarifications**

In the letter by Charles A. Zeigler in the issue of 27 June (p. 1955), several errors were introduced during editing. The book Higher Superstition, referred to in the last line of column one, is by P. R. Gross and N. Levitt only. Reference 1, The Flight from Science and Reason, should have identified P. R. Gross, N. Levitt, and M. W. Lewis as "Eds.," and the publication date should have been "1997," not "1994."

In the Table of Contents for the issue of 13 June, the last name of the first author of the report appearing on page 1719, "HSV-TK gene transfer into donor lymphocytes for control of allogeneic graft-versus-leukemia," was spelled incorrectly. It should have been, "Bonini."

An article by Charles Seife about the upgrade of the Arecibo telescope in Puerto Rico (News & Comment, 20 June, p. 1785) erroneously referred to the dish being in the crater of a dead volcano. It is in a limestone sinkhole.

In Jocelyn Kaiser's News & Comment article "When a habitat is not a home" (13 June, p. 1636), the caption for the photographs of a red-cockaded woodpecker and a pine forest on page 1636 should not have read, "[a] rare red-cockaded woodpecker and the loblolly pine habitat it prefers," but rather, "[a] rare red-cockaded woodpecker and the loblolly pine, one of the habitats it prefers.'

In reference 27 (p. 1533) of the report "The source of green light emission determined from a heavy-ion storage ring experiment" by D. Kella et al. (6 June, p. 1530), the year was incorrect. The reference should have read, "S. L. Guberman, paper presented at the American Physical Society Meeting, Washington, DC, 18 to 21 April 1997.'

The ScienceScope item "Lawmakers target biosphere program" (30 May, p. 1323) mischaracterized a bill in the U.S. House of Representatives concerning the U.S. Man in the Biosphere Program (USMAB). The proposed legislation would kill the program only if Congress failed to authorize USMAB and would remove existing biosphere reserves only if each did not obtain congressional approval within 3 years.

In the report "Burst conditions of explosive volcanic eruptions recorded on microbarographs' by M. M. Morrissey and B. A. Chouet (28 Feb., p. 1290), the label on curve A in figure 1 (p. 1291), which read "5 kPa", was incorrect. It should have read, "0.8 kPa".

The end of note 11 (p. 539) in the report "DCP-1, a Drosophila cell death protease essential for development" by Z. Song et al. (24 Jan., p. 536) should have stated, "The GenBank accession number for dcp-1 is AF001464."

#### 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.

Accumulating raw genetic information is just the beginning of what automated DNA sequencing can offer you. Deciphering that data and generating accurate results to specific applications-

# Our dedicated, automated DNA analysis Software can tell Alicia in seconds

Nobody can offer you more dedicated software products for sequencing applications than Pharmacia Biotech—including three new automated DNA analysis application software called AlleleLinks™, HLA SequiTyper™ and Mutation Analyser. All three let you go from evaluation to results in seconds. All three significantly reduce your analysis time by transforming large amounts of raw data into results. As they only operate with ALF® automated DNA sequencers, with all three you'll get the type of extremely reproducible and accurate results only single dye chemistry can deliver.

HLA SequiTyper: quickly determines subtypes of HLA Class I and Class II genes by comparing your results against a data base built on the findings of HLA typing communities. AlleleLinks: this fully-automated genotyping software automatically scores alleles utilizing locus data bases. Supporting X-linkage and large pedigrees, it provides simultaneous analysis of multiple gels. Mutation Analyser: simultaneously analyzes entire genes while giving you direct access to raw data. Ideal for confirmatory sequencing—you can link your results to others' findings (i.e. clinical records)—Mutation Analyser offers convenience, fast analysis and accurate results.

Go to http://www.biotech.pharmacia.se/seq/seq.htm#seq6 for more information on these software; look within our home page for details about ALFexpress®. And start getting the most from automated DNA analysis products—like quick, accurate, and reproducible genetic results.



