

plant disease. I could add that the first discoveries of host gene polymorphisms affecting disease outcome ensued from the earliest applications of mendelian analysis to wheat (1). In a brief essay, it was impossible to do justice to every worthy milestone.

I would indeed be sorry if, as pointed out by Silvergleid, my remarks about hepatitis C might leave some confusion about the safety of the blood supply. At least since 1992, the advent of improved screening methods has essentially erased that threat. According to the Center for Disease Control and Prevention, the incidence of hepatitis C infection has fallen from 230,000 to 36,000 per year since the advent of that screening (2), and as Silvergleid notes, intravenous self-inoculation accounts for most new cases today.

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References

1. R. H. Biffen. *J. Agric. Sci.* 1, 4 (1905).
2. *Morb. Mortal. Wkly. Rep. Suppl.* 47, no. RR-19 (16 October 1998).

Still Havens for Coral Reefs

In her Letter "Confounding factors in coral reef recovery" (21 July, p. 391), Caroline S. Rogers says that "the recovery of coral

reefs from hurricanes is almost invariably confounded by anthropogenic stresses, most notably fishing... Humans have now degraded tropical marine ecosystems to the point where our ability to evaluate ecological theories about succession and effects of disturbance has been compromised."

Although true for many locales, this statement should not be overgeneralized. The Great Barrier Reef of Australia comprises almost one-third of global reef and lagoon area. Fishing pressure is very low, and other anthropogenic effects are negligible. The total fishing catch of reef species is less than that of Florida, which has a reef area less than 1% that of the Great Barrier Reef. Elsewhere in the Pacific and Indian oceans, numerous oceanic reefs remain relatively pristine, with little or no noticeable anthropogenic stress.

A realistic estimate of negatively impacted reefs would probably be about 50%. They are, of course, where there are the most people and hence receive the most attention, but there is still ample opportunity "to evaluate ecological theories about succession and effects of disturbance" where there is little or no anthropogenic stress.

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CORRECTIONS AND CLARIFICATIONS

News Focus: "Will Livermore laser ever burn brightly?" by Charles Seife and David Malakoff (18 Aug., p. 1126). Information about the work-sites of two scientists was incorrect. Steve Haan works at Lawrence Livermore National Laboratory, not at the Los Alamos National Laboratory. In addition, Bedros Afeyan works at Polymath Research Inc. in Pleasanton, California.

Policy Forum: "China's forest policy for the 21st century" by R. Zhang *et al.* (23 June, p. 2135). On the map of China, two provinces were labeled "Jiangxi." The more northern province should have been labeled "Jiangsu."

Pathways of Discovery: "Cloning: Pathways to a pluripotent future" by Anne McLaren (9 June, p. 1775). The lamb at the bottom of the figure on page 1780 should have been dark to indicate the origin of its genetic material.

News Focus: Sidebar piece "Decoding a mouse name" by David Malakoff (14 Apr., p. 250). The acronym used by the Charles River Laboratories for the mice they breed is CrI, not Cr as stated in the article. And 1297/SvEvBrd-Hprt^{b-m2} mice have a white-bellied agouti coat color, not a steel-colored coat. [E. M. Simpson *et al.*, *Nature Genet.* 16, 19 (1997)].

Program Announcement

Cystic Fibrosis National Bioinformatics Center

Cystic Fibrosis Foundation Therapeutics, Inc., an affiliate of the Cystic Fibrosis Foundation, in cooperation with InforMax, Inc. and the University of North Carolina-Chapel Hill announces the creation of a Cystic Fibrosis National Bioinformatics Center.

In its effort to apply cutting edge technology to cystic fibrosis research, Cystic Fibrosis Foundation Therapeutics, Inc. has licensed the GenoMax enterprise bioinformatics software from InforMax, Inc., and will provide this powerful gene analysis software tool free of charge to a limited number of CF researchers. In addition, Cystic Fibrosis Foundation Therapeutics, Inc. has established a contract with University of North Carolina-Chapel Hill's Center for Bioinformatics to house and support the use of the software by participating CF researchers. The software will be accessible to researchers via the internet, in particular for analysis of data generated during gene expression studies using microarray platforms. Participating researchers will be asked to contribute their data to a centralized database that will also be housed and maintained at the University of North Carolina-Chapel Hill, so that results from many laboratories can be mined together by the participants.

This centralized informatics solution for CF investigators, made possible by an unprecedented relationship among academia, industry and a non-profit voluntary health organization, is another measure of the Cystic Fibrosis Foundation's continuing commitment to assure the progress of cystic fibrosis research.

By providing this informatics solution to members of the cystic fibrosis research community, the Cystic Fibrosis Foundation hopes that scientists will use the tools of functional genomics to identify new and novel targets for future CF drug development.

Scientists wishing to use this resource to address important cystic fibrosis-related questions are invited to visit the Cystic Fibrosis Foundation web site (www.cff.org) or contact Dr. Christopher Penland, Director of Research at the Cystic Fibrosis Foundation, at (301) 907-2520 for more information about the program and application forms.



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