

responding, freely accessible complementary DNA (cDNA) clone repository. We believe that this initiative will have a great positive impact on human genome research and should significantly accelerate the pace at which genes responsible for human disease are identified by the basic biomedical research community.

The speed and scope of this exciting initiative are particularly noteworthy. Merck has finalized an agreement with the Genome Sequencing Center at Washington University to sequence 400,000 ESTs, each representing approximately 400 base pairs of "single pass" sequence, from the 5' and 3' ends of 200,000 human cDNA clones. The clones will be derived from various tissues and developmental stages and thus represent a large fraction of the human gene repertoire. The 3' end sequences will be highly suitable for generating polymerase chain reaction primer pairs for successfully probing genomic DNA and will therefore facilitate the mapping of specific cDNAs on human chromosomes. The 5' end sequences will be highly enriched for open reading frames and will therefore facilitate identification of human cDNA-based sequence similarity to proteins of known function in existing databases. New cDNA sequences will be submitted on a daily basis to dbEST (a division of GenBank at the U.S. National Center for Biotechnology Information) and made immediately available to the public through GenBank and its international collaborators, the European Bioinformatics Institute and the DNA database of Japan. Furthermore, the cDNA clones from which the ESTs are derived will be publicly available and distributed freely on request. The nonproprietary aspect of EST data and cDNA clone acquisition and use will maximize the enormous value offered to the biomedical community by this initiative.

The projected magnitude of the throughput for EST sequence generation is impressive and offers great promise for productive applications in the immediate future. Beginning in January 1995, 6000 to 8000 ESTs per week will be generated and deposited in the public databases. Thus, dbEST (which currently contains 32,208 human ESTs) will increase by more than 25,000 ESTs per month over the next 18 months. This rapid growth of data and clone resources, available to individual investigators within the biomedical research community (including industry and academia), will make repeated periodic homology searches for cDNAs of interest an increasingly productive strategy for elucidating basic biological processes and will accelerate progress in research laboratories throughout the world.

Public access to a comprehensive EST

database and corresponding cDNA clone repository is virtually guaranteed to make connections between basic biological research and mechanisms responsible for human disease and should do so at an enormous savings in time and resources. We thank Merck and Company, Inc. for providing the support and for adopting an open, nonproprietary policy that assures major advances in the study of human biology.

Maimon M. Cohen,

President,

*American Society of Human Genetics,
Department of Obstetrics and Gynecology,*

Division of Human Genetics,

University of Maryland,

Baltimore, MD 21201-1509, USA

Beverly S. Emanuel,

*Chair, Human Genome Committee,**

Department of Human Genetic

Molecular Biology,

Children's Hospital,

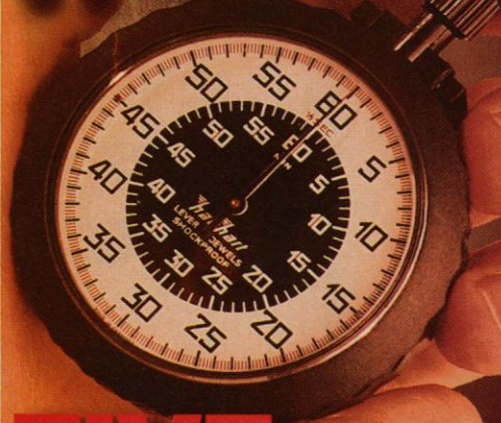
Philadelphia, PA 19104, USA

*Committee Members: **Anne Mary Bowcock**, Department of Pediatrics, University of Texas Southwest Medical Center, Dallas, TX 75235-8591, USA; **Judith G. Hall**, Department of Pediatrics, British Columbia Children's Hospital, Vancouver, BC, Canada V6H 3V4; **Philip A. Hieter**, Department of Molecular Biology and Genetics, Johns Hopkins Medical School, Baltimore, MD 21205-2185, USA; **David E. Housman**, Center for Cancer Research, Massachusetts Institute of Technology, Cambridge, MA 02139-4307, USA; **Julie R. Kornberg**, Division of Medical Genetics, Cedars-Sinai Medical Center, Los Angeles, CA 90048, USA; **Jeffrey C. Murray**, Department of Pediatrics, University of Iowa, Iowa City, IA 52245, USA; **Susan L. Naylor**, Department of Cellular and Structural Biology, University of Texas Health Science Center, San Antonio, TX 78284-7762, USA; **Robert L. Nussbaum**, Laboratory of Genetic Disease Research, National Institutes of Health/National Center for Human Genome Research, 9000 Rockville Pike, Bethesda, MD 20892, USA; **Patricia W. Ward**, Institute of Molecular Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030-3411, USA; **Stephen T. Warren**, 4035 Rollins Research Center, Howard Hughes Medical Institute, Emory University, Atlanta, GA 30322, USA.

Crystalline Polymorph Construction: Correction

In our report "Control of structure and growth of polymorphic crystalline thin films of amphiphilic molecules on liquid surfaces" (10 June, p. 1566) (1), we stated that over both 100% liquid formamide and 70% formamide in water, the amphiphile arachidamide without additive forms two major phases, both of which are multilayers. This is indeed the case over 100% formamide, but further analysis indicates that the phase of arachidamide without additive over 70% formamide in water, in which the molecular chains are aligned with their axes vertical with respect to the liquid surface and the carbon backbone planes of neighboring molecules are orthogonal to one another (\perp), is primarily a monolayer, contrary to

GET IT



FIVE TIMES FASTER

GET A GENOMIC CLONE WITH
A 75-100KB INSERT IN DAYS
FROM GENOME SYSTEMS'
P1 PLASMID LIBRARY
SCREENING SERVICE

[Human, Mouse(es), Rat, Drosophila]

We also provide a screening service
for human CEPH mega-YACs and
mouse YACs, or you can access these
libraries yourself for less than \$300

GenomeSystemsInc

7166 Manchester Road

St. Louis, Missouri 63143

800-430-0030

314-647-4696

Facsimile: 314-647-4134

France: Appel gratuit,
0590-2104

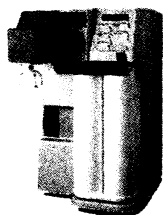
Germany: Rufen sie uns
an zum ortstarif,
0130-81-9081

UK: Call us free on,
0800-89-3733

Circle No. 12 on Readers' Service Card

Don't Drown Your Data.

Water from conventional ultrapure systems can contain trace levels of ions, pyrogens, and organics that mask peaks in today's sensitive chromatography methods. Protect your data from being swamped with the Milli-Q® TOC Plus. It provides 18 megohm-cm, organic-free (<3 ppb TOC) water and comes with an integral TOC monitor – so you'll know the level of organics in the water prior to running your chromatogram. Keep your data above water with the Milli-Q TOC Plus. For more information, call 1-800-MILLIPORE, ext. 8316. In Europe, fax us at our European headquarters in Paris at 33-1-30.12.71.83.



MILLIPORE

© 1994 Millipore Corporation Millipore Lab Catalogue on Internet: Access URL: menu and type: http://www.millipore.com

what we reported in (1). The phase in which the chains are tilted and have their backbone planes all parallel (\nearrow) is a multilayer, as we stated in (1). This conclusion is based on the intensity profiles of the Bragg rod data from the grazing incidence x-ray diffraction measurements (1, figure 1B, top). The full-width at half-maximum (fwhm) of the Bragg rod profiles along the vertical scattering vector q_z of the (11) and (02) reflections [yellow, not red, as stated in (1, figure 1B, top)] corresponding to the untilted (\perp) phase without additive are each 0.2 \AA^{-1} , indicating a monolayer. The fwhm's of the three reflections (11, 01, 10) of the tilted phase (\nearrow) [red, not yellow, as stated in (1, figure 1B, top)] without additive indicate a multilayer according to their fwhm of 0.1 \AA^{-1} . The fwhm's of the (11) and (02) Bragg rods of the untilted phase with additive (1, figure 1B, bottom) are almost the same as for the corresponding phase without additive.

This correction in no way contradicts the concluding statement in our abstract that auxiliary molecules designed to completely inhibit development of multilayer polymorphs lead primarily to a single phase monolayer. As stated above, the tilted multilayer phase for arachidamide on 70% formamide is completely inhibited in the presence of these additives. For 100% formamide subphase, the additive inhibits formation of the tilted and untilted multilayer phases, leading to the untilted monolayer phase, as clearly seen in (1, figure 2).

L. Leiserowitz

*Department of Materials and Interfaces,
Weizmann Institute of Science,
Rehovot 76100, Israel*

References

1. S. P. Weinbach *et al.*, *Science* **264**, 1566 (1994).



Malaria Vaccine Research

We disagree with the views expressed in the News article "Bumps on the vaccine road" (2 Sept., p. 1371) regarding a perceived lack of leadership in the field of malaria vaccine development.

Despite malaria's global importance, it is a low priority for the private sector. Public sector entities have therefore assumed leadership responsibilities, driving all aspects of research and development. Current funding levels are likely to prove insufficient to allow optimal progress. The required resources and capabilities are beyond those of any single agency, so scarce resources—distributed among different research groups—must be optimally used. Moreover, a coordinated, integrated, and open development process is instrumental to sustained progress.

In 1992, the Department of Defense's (DOD's) U.S. Army Medical Research and Development Command, the U.S. Agency for International Development (USAID), and the National Institute of Allergy and Infectious Diseases (NIAID) jointly put in place mechanisms to expedite the development and evaluation of promising malaria vaccine candidates. These collaborative efforts are being coordinated with the malaria vaccine development sponsored by the Commission of the European Communities (CEC), and the Special Programme for Training and Research in Tropical Diseases of the World Health Organization (WHO/TDR). Last year, the NIAID and USAID sponsored a meeting to acquaint investigators and scientific administrators with candidate vaccines and with the technical, regulatory, and clinical trial issues pertinent to accelerated development.

Today scientists can bring forward their most promising vaccine candidates for accelerated development and evaluation within this public sector framework. Most of the approaches discussed by R. S. Nussenzweig and C. A. Long in their Perspective "Malaria vaccines: Multiple targets" (2 Sept., p. 1381) are in fact being developed under the umbrella of the DOD/USAID/NIAID agreement. Among these are circumsporozoite (CS) protein-based and multiple antigen peptide vaccines, a CS protein-based vaccine to induce cytotoxic T cell responses, a live attenuated vaccinia vector (NYVAC) expressing seven key malaria genes, a recombinant transmission blocking vaccine (Pfs 25), both yeast- and *Escherichia coli*-expressed COOH-terminal regions of MSP-1 (a major malaria bloodstage antigen), alternative formations of the synthetic peptide bloodstage vaccine SPf66, and several nucleic acid vaccination strategies.

W. Ripley Ballou

*Department of Immunology,
Walter Reed Army Institute of Research,
Washington, DC 20307, USA*

Carter L. Diggs

Stephen Landry

*Malaria Vaccine Development Program,
United States Agency for International
Development,
Washington, DC 20523-1817, USA*

B. Fenton Hall

*National Institute of Allergy and
Infectious Diseases,
National Institutes of Health,
Bethesda, MD 20892, USA*



Correction

In our report "Activation of Raf as a result of recruitment to the plasma membrane" (3 June, p. 1463) (1), panels E and F of figure