Barbara Alving Named Director of NCRR

On April 2, 2007, NIH Director Elias A. Zerhouni, M.D., named Barbara Alving, M.D., as the Director of the National Center for Research Resources (NCRR). As Acting Director of NCRR, Alving oversaw the launch of the Clinical and Translational Science Awards (CTSA) program—a new national consortium of academic health centers that will transform the conduct of clinical and translational research. The goal of the consortium is to ensure that biomedical discoveries are rapidly translated into prevention strategies and clinical treatments for both rare and common diseases.

"Dr. Alving has demonstrated exceptional leadership in the recent efforts of the NIH to energize the discipline of clinical and translational research across the nation," said Zerhouni. "The CTSA program marks the first systemic change in clinical research in 50 years and is a critical component of how we will effectively re-engineer the clinical research enterprise, including training the next generation of researchers. It will be with Dr. Alving's vision, creativity, and leadership that we will be able to maximize our investment in the CTSA consortium, ensure that benefits extend to the greater research community, and that new medical advances are delivered to the people who need them."

A native of Indiana and a graduate of Purdue University, Alving earned her medical degree *cum laude* from Georgetown University School of Medicine, where she also served as an intern in internal medicine. She completed her residency training, followed by a research fellowship in hematology, at the Johns Hopkins Hospital in Baltimore. She began her research career as a Public Health Officer in the Division of Blood and Blood Products at the U.S. Food and Drug Administration (FDA) on the NIH campus. Alving then joined the Walter Reed Army Institute of Research, where she served at the rank of colonel as the Chief of the Department of Hematology and Vascular Biology. In 1997, Alving became the Chief of the Section of Hematology and Oncology at the Washington Hospital Center in Washington, D.C. In 1999, she joined the National Heart, Lung, and Blood Institute (NHLBI) as the Director of the Division of Blood Diseases and Resources. She then became the NHLBI Deputy Director and Acting Director while also serving as the Director of the Women's Health Initiative (2002–2006). In 2005, Zerhouni tapped her to be the Acting Director of NCRR.

A Professor of Medicine at the Uniformed Services University of the Health Sciences in Bethesda, Alving is also a Master in the American College of Physicians. She currently serves the NIH Director as the official NIH liaison for the Centers for Medicare and Medicaid Services and is a member of the Advisory Board for Clinical Research at the NIH Clinical Center.

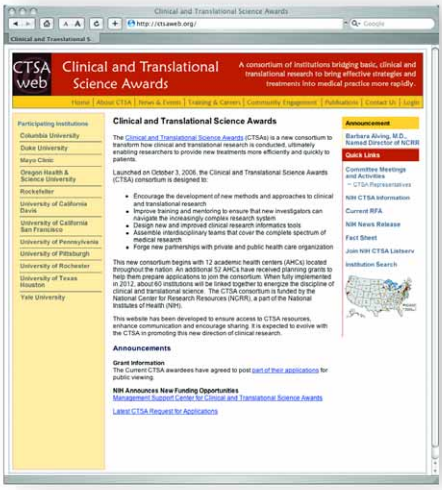
She is a recipient of the American Society of Hematology Award for outstanding service and also received a Commendable Service Award from the FDA for her work on hypotensive agents in albumin products. Her military honors include the U.S. Legion of Merit, awarded by the U.S. Army, for work that improved the care of soldiers in combat. She is a co-inventor on two patents, has edited three books, and has published more than 100 papers in the areas of thrombosis and hemostasis.

CTSA Web Site Launched

The recently unveiled Clinical and Translational Science Award (CTSA) program Web site (http://ctsaweb.org) features resources, news, and general information about the CTSA consortium. It aims to enhance communication and encourage sharing of resources provided by CTSA members.

The site includes detailed information on each CTSA, training activities sponsored by the CTSAs, publications, upcoming meetings, community engagement activities, and a fact sheet about the CTSAs. The site also links to the current CTSA Request for Applications, which was issued on March 22, 2007.

The CTSA consortium currently consists of 12 academic health centers around the nation, which are linked to energize clinical and translational science nationwide. In all, 60 institutions are expected to be part of the CTSA consortium by 2012. The CTSA initiative grew out of the NIH commitment to reengineer the clinical research enterprise, one of the key objectives of the NIH Roadmap for Medical Research.



■ **The newly launched CTSA Web site at http://ctsaweb.org.**

[CONTINUED FROM PAGE 13]

2007 Conferences Lineup

NCRR is sponsoring several conferences this year covering a broad range of topics, from the implementation of translational research in underserved communities, to the analysis of genes in the rhesus macaque, to the use of nonhuman primate models for developing AIDS treatments and embryonic stem cell lines. These conferences not only inform scientists of key developments in different areas of research, but they also serve to ensure that members of the NCRR community are aware of long-term goals and progress on different initiatives.

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FOSTERING COLLABORATIVE COMMUNITY-BASED CLINICAL AND TRANSLATIONAL RESEARCH

May 15 and September 21, 2007

The May 15 workshop will identify key factors that prevent and enable effective academic-community research partnerships. Participants will develop and disseminate guidelines and best practices for conducting community-based clinical and translational research in minority and other medically underserved groups. Key areas of focus will include the development and maintenance of core research infrastructure to enable and encourage community participation, the development of research protocols that work effectively in community settings, and the establishment of community buy-in and trust to enhance recruitment and retention of research participants.

This one-day workshop will be held in the DoubleTree Hotel, Bethesda, Md., in conjunction with the 2007 National Research Conference (May 16–18) of the Agency for Healthcare Research and Quality's (AHRQ) Practice-Based Research Networks. A second regional workshop will be held in Los Angeles, Calif., on September 21. The two events are intended to develop specific recommendations to support the implementation of planned NCRR initiatives to enhance clinical and translational research in underserved communities. They will also help leverage related efforts of sister agencies, including AHRQ, the Health Resources and Services Administration, the U.S. Centers for Disease Control and Prevention, and the Indian Health Service.

Individuals interested in attending either workshop may contact Michael Sayre at sayrem@mail.nih.gov, Shelia McClure at mcclursh@mail.nih.gov, or Fred Taylor at taylorwf@mail.nih.gov.

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IMPROVING GENETIC RESOURCES FOR THE RHESUS MACAQUE

May 23, 2007
Natcher Conference Center, Building 45
NIH Campus, Bethesda, Md.

This workshop will identify enhanced genetic resources for optimizing the use of the rhesus macaque as a model animal in biomedical and translational research. In particular, participants will define the resolution, approach, and resources needed to generate a single nucleotide polymorphism (SNP) map of the rhesus macaque genome.

The workshop was conceived, in part, during the 2006 NCRR-sponsored "Genetic Tools for Optimizing the Use of Rhesus Macaques for Translational Research" workshop in which participants identified the development of an SNP map for the rhesus as a major goal. Grantees funded by NCRR have so far identified SNPs that distinguish between macaques of Chinese and Indian origin. In addition, as part of the project to sequence the rhesus genome, scientists at the Human Genome Sequencing Center, Baylor College of Medicine, have identified several thousand SNPs from a subset of the rhesus genomic sequence.

Individuals interested in attending the workshop may contact Jack Harding at hardingj@mail.nih.gov.

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THE 25TH ANNUAL SYMPOSIUM FOR NONHUMAN PRIMATE MODELS FOR AIDS

September 10–13, 2007
Monterey Conference Center
Monterey, Calif.

This symposium will serve as a scientific forum for disseminating and exchanging the new research findings, ideas, and directions of an international group of scientists whose research focuses on the study of experimental immunodeficiency virus infections. These include human immunodeficiency virus (HIV), simian immunodeficiency virus (SIV), and recombinant SIV/HIV in nonhuman primate models. The knowledge gained from nonhuman primate studies will help scientists better understand how HIV and SIV cause disease and will facilitate the development of new methods for the treatment, control, and prevention of AIDS in human populations.

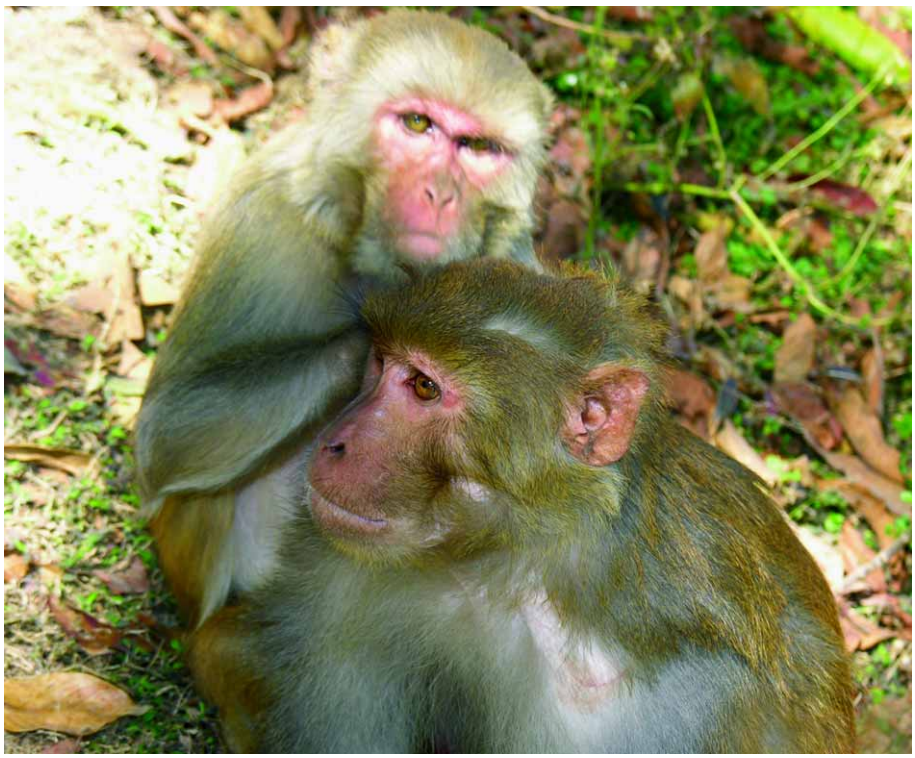
Previous meetings of the Annual Symposium have had a significant impact on understanding viral pathogenesis in primate models and the development of AIDS drugs and potential vaccines. This year's meeting will focus on the biology of primate lentivirus infection and the use of nonhuman primate models for the study of viral pathogenesis, vaccines, and therapeutic approaches against primate lentivirus infection and disease; primate genomics; viral agents associated with simian acquired immunodeficiency syndrome; and the mechanisms of natural resistance to endemic primate lentiviral infection in several primate species.

Scientists interested in attending the meeting should visit www.cnprc.ucdavis.edu/NHPM2007.

DEVELOPMENT AND USE OF NONHUMAN PRIMATE EMBRYONIC STEM CELL LINES
Fall/Winter 2007

The workshop will review the status of derivation, availability, and characterization of nonhuman primate embryonic stem cells (NHP ESCs) and define their potential uses, specifically in regard to translational research. Another goal will be to provide advice to NIH administrators on new initiatives needed to fully realize the potential of NHP ESCs to help advance the goals of regenerative medicine. Participants will include researchers with experience in NHP ESC derivation and experts in the areas of human ESC research and regenerative medicine.

Individuals interested in attending the workshop may contact Jack Harding at hardingj@mail.nih.gov.



The effort to sequence the rhesus macaque genome was supported by several NCRR-funded National Primate Research Centers.

Genome of the Rhesus Macaque Unveiled

Scientists had already laid bare the complete genetic codes of humans and chimpanzees. They have now added a third primate to the list of sequenced genomes: the rhesus macaque or, by its Latin name, *Macaca mulatta.* This old-world monkey is the nonhuman primate most widely used in biomedical studies focusing on major diseases, such as AIDS and diabetes. Its genome sequence is reported in the April 13, 2007, issue of *Science* magazine.

The sequencing, funded by NIH's National Human Genome Research Institute, was performed at the Baylor College of Medicine Human Genome Sequencing Center in Houston, Texas; the Genome Sequencing Center at Washington University in St. Louis, Missouri; and the J. Craig Venter Institute in Rockville, Maryland.

It was based on the DNA from a single individual—a female rhesus macaque housed at the NCRR-funded National Primate Research Center (NPRC) at the Southwest Foundation for Biomedical Research in San Antonio, Texas. The California, Oregon, and Yerkes NPRCs, also funded by NCRR, contributed additional biological samples used in the study.

The human genome was sequenced in 2001. With the sequencing of the chimpanzee *(Pan troglodytes)* genome in 2005, scientists were able to investigate which genes humans share with this close relative, from which they diverged about 6 million years ago. Macaques are more distant in the evolutionary timescale, as they are believed to have diverged from humans 25 million years ago.

But this distance is actually useful for studying evolution. By comparing rhesus macaque and human DNA, which are about 7 percent different from one another, scientists can see which genes have been conserved in primates over time and which ones have not. Compared to the human genome, the chimp genome is only about 1.5 percent different.

The *Science* article describes about 200 genes that probably play a key part in determining differences among primate species, including genes involved in hair formation, immune response, membrane-protein generation, and sperm-egg fusion. Also, researchers found some intriguing examples where a normal form of a macaque gene looks like a diseased human gene.

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