National Center for Research Resources
NATIONAL INSTITUTES OF HEALTH

Genetic Tools for Optimizing the Use of Rhesus Macaques for Translational Research

Natcher Conference Center
National Institutes of Health

April 19-20, 2006

Final Workshop Report

September 2006

TABLE OF CONTENTS

I. EXECUTIVE SUMMARY

The workshop entitled, "Genetic Tools for Optimizing the Use of Rhesus Macaques for Translation Research," sponsored by the National Center For Research Resources (NCRR), took place on the NIH campus April 19 – 20, 2006. The objectives of the workshop were to discuss the current state-of-the-art regarding genetic analysis of the rhesus macaque and to identify the next generation of rhesus-based genetic tools and technologies needed by the research community. As primary output of the workshop, the NCRR requested that the attendees provide a consensus recommendation for those genetic technologies or tools that should be developed immediately in order to facilitate translational research using this important animal model.

The need for the workshop reflected three developments. First, the rhesus is the primary non human primate model used for many aspects of translational research. Second, various investigators, many funded by the NCRR, have developed first generation genetic technologies such as maps and microarrays, which are very useful for translational research using the rhesus. Third, a high quality draft assembly of the rhesus genomic sequence is available to researchers on the World Wide Web. The confluence of these three developments makes timely a consideration of the next generation of tools and technologies needed to further facilitate the use of the rhesus by the research community.

The workshop consisted of two parts. Part One comprised presentations summarizing the features and uses of currently available technologies and resources, including genetic and physical maps, microarrays, sequences and methods for sharing of data. As a forward-looking aspect of the presentation, this part of the workshop also included an overview of proteomics technologies.

Part Two of the workshop comprised panel discussions of many of the primary application areas in which the rhesus is used as an animal model: AIDS research, solid organ transplantation, emerging infectious diseases, aging, neurobiology, cardiovascular disease, metabolic syndrome, and respiratory disease. For each of the panels, the participants were asked to answer the following questions, specifically in regard to the use of the rhesus in translational research:

- Currently, what are the most frequently used genetic tools?
- What are the major barriers that new genetic tools could overcome?
- What new genetic and bioinformatics tools will be needed in the next 3 – 6 years?

Overall, there were 41 presenters, including members of specific application panels. There were a total of 80 participants, including extramural researchers, NIH intramural researchers and NIH program and review staff.

Commonalities across the application areas were identified. These are:

- The tools and technologies used most frequently are: 1) microarrays for gene expression analysis; 2) Major Histocompatability Complex (MHC) typing; and 3)

genotyping, including pedigree analysis. Microsatellite markers are currently used most often for genotyping.

- The most needed new or improved tools and technologies are: 1) single nucleotide polymorphism (SNP) discovery, typing and databases; 2) more extensive and uniform use of pedigree analysis; 3) improved and expanded MHC typing; 4) gene expression microarrays specific to certain application areas; and 5) better and easier access to bioinformatics tools for investigators of all levels of sophistication, including access to those tools already in common use by the genomics community.

- It was generally recognized that very user-friendly databases will be needed to fully make use of rhesus genome sequence data and that publication of a high quality genome sequence will potentially lead to many new opportunities and insights.

Recommendations for new tools useful across all application areas and for immediate consideration by the NIH were identified as development of:

- A database that will combine phenotypic and genotypic data, including pedigrees. Minimally, the database should include the rhesus housed at the National Primate Research Centers (NPRCs). The phenotypes should be as inclusive as possible, within the limits of practicality. The consensus list of phenotypes should be based on feedback from the research community, NPRC personnel and other relevant parties.

- A SNP map and database consisting of several hundred thousand polymorphisms and validated assays.

- A repository of blood samples and cell lines derived from many of the rhesus, for which phenotypes and genotypes are in the database in item 1, above.

II. PURPOSE AND OBJECTIVES OF THE WORKSHOP

Sponsor:

Division of Comparative Medicine, National Center for Research Resources (NCRR).

Purpose:

To summarize the current state-of-the-art regarding genetic tools that facilitate the use of the rhesus macaque for translational research. These available tools comprise: 1) genetic and physical maps of the rhesus genome; 2) microarrays for analysis of gene expression; 3) specific sequences; 4) the genomic sequence; and 5) databases.

To identify the next generation of genetic tools that will be needed to facilitate and optimize the use of rhesus for translational research.

To provide a list of specific tools or technologies that should be developed immediately to facilitate translational research using the rhesus.

Participants:

Current users and developers of rhesus-based genetic technologies and tools.

Current users of rhesus in the following specific application areas: AIDS research, solid organ transplantation, emerging infections, aging, neurobiology, cardiovascular disease, metabolic syndrome, and respiratory disease.

Altogether, there were 41 presenters and a total of 80 participants in the workshop. Participants and presenters included extramural scientists, NIH intramural scientists, and NIH program and review staff.

III. SUMMARY OF PRESENTATIONS AND DISCUSSION

PART 1. SUMMARIES OF CURRENT TECHNOLOGIES

INTRODUCTION AND OVERVIEW. In general, the currently available tools and data are being used for the following: 1) direct analysis of rhesus gene sequences; 2) genome-wide analyses of gene expression patterns, with an emphasis on understanding changes in gene expression in response to challenges of various types; 3) genetic linkage screens for quantitative trait loci (QTLs, which are genetic regions harboring a gene or genes that influence complex traits affected by more than one gene); and 4) analysis in related species such as cynomolgus and pigtail macaques and baboons.

These studies are used to examine two broad areas of inquiry. The first is genome diversity, studies of which are aimed at answering the question of how genetic differences among individual animals influence phenotypic or physiological differences among those individuals. Studies of genome diversity may involve one or more of the following: MHC and other immune genotyping, genome scans using linkage analysis, analysis of differences in gene expression patterns among individuals, and comparisons across species.

The second broad area of inquiry can be termed genome dynamics, which can involve, for example, changes in patterns of gene expression and/or epigenetic changes in genome structure. The two, interrelated, areas (genome diversity and genome dynamics) may require different tools and technologies.

GENETIC MAPPING. During the past several years, a rhesus genetic linkage map has been derived that, as of the date of the meeting, contains 368 microsatellite markers that have been mapped to unique locations in the rhesus genome. The current linkage map includes all 20 autosomes and the X chromosome; markers have an average spacing of 7.58 centiMorgans (cM). Current refinement of the map involves filling gaps that are larger than 10 cM in size, using microsatellites that are identified from the draft rhesus genomic sequence, with the objective of deriving a 5 cM map with no gap larger than 10 cM. The map is currently being used to identify QTLs related to anxiety and depressive behaviors, and it is anticipated that it soon will be applied to studies of phenotypes related to HIV/AIDS, and to other disease-related phenotypes. A parallel approach has been very successful in the baboon (using a baboon-specific linkage map), which has identified QTLs for physiological parameters such as estrogen levels, LDL and HDL cholesterol levels in response to diet, bone density, etc.

GENETIC ANALYSIS FOR COLONY MANAGEMENT AND DELINEATION OF POPULATION STRUCTURES. Analysis of mitochondrial DNA sequences has been very useful for understanding the differences in the population structures and relatedness of rhesus originating from India or China, respectively. The need for these investigations has been driven in large part by differences in the response of Indian *versus* Chinese rhesus to infection by the most commonly used Simian Immunodeficiency Virus (SIV) isolates. Mitochondrial variation has also been used to characterize differences among populations within China and has demonstrated that Nepalese rhesus are much more closely related to Indian than to Chinese rhesus.

PHYSICAL MAPPING USING SNPS. A pilot project, based on discovery and analysis of SNPs in the 3' terminal exons of specific genes, demonstrates that Chinese and Indian origin animals can be distinguished. SNP based assays can therefore be used for, among other purposes, identifying hybrid animals in captive breeding populations. Complementary to this approach will be the more general identification of SNPs throughout the genome that will result from the genomic sequencing effort. Taken together, these two approaches will help define SNP frequencies in the rhesus genome, leading to a more definitive strategy for deriving a high density SNP map for the rhesus. It was the general consensus of the workshop that development of a SNP map will

facilitate many aspects of translational research, colony management and experimental design.

SEQUENCING THE RHESUS GENOME. As of the workshop date, a high quality assembly of the rhesus genome is publically available. Twenty one thousand genes have been predicted and placed on the assembled rhesus sequence; these data are also publically available. Additional data on SNPs will also be obtained as the sequence is refined further. It was also pointed out in some of the presentations that new types of sequencing technologies could have a significant impact on the cost and speed of high throughput sequencing during the next five years. It was the consensus of the workshop that the published, annotated genome sequence will be of great use to the research community and that additional sequencing, for example, of individual animals from selected populations, is likely to inform many experimental paradigms in the future.

SPECIFIC SEQUENCES OF IMMUNOLOGICAL INTEREST. High resolution sequences of the MHC (major histocompatibility complex) and KIR (killer Ig-like receptor) loci have been determined using clone-based methods. These studies point out major differences between complex rhesus loci and their human counterparts and can perhaps be used to help explain experimental findings, for example, response to viral infection in the rhesus.

MICROARRAYS. Rhesus sequences for inclusion in microarrays have been derived from two different, but complementary methods. In a directed strategy, probe regions from the 3' ends of specific rhesus genes were isolated, based on the cognate regions in sequenced human genes. The second strategy involved random sequencing of rhesus cDNA libraries. Based on these sequences, two different microarrays are now available from commercial sources. One microarray contains probes for 47,000 transcripts, including 15,000 well-annotated genes. A second microarray contains probes for approximately 17,000 rhesus genes. It was the consensus of the workshop that these microarrays will be highly useful for a number of studies and that, for studies utilizing rhesus tissues, use of rhesus-specific microarrays will be preferable to use of human arrays. The workshop participants also recognized the potential use of the rhesus specific microarrays or new version thereof for genotyping. The potential application of the rhesus gene expression microarrays in studies of other macaque species, as well as other Old World monkey species, was also recognized as potentially quite significant.

DATABASES AND DATA SHARING. The workshop included presentations on models for data sharing that have been useful for some research communities. Not all of these models are used currently by the rhesus research community. Examples included the Genboree web site for collaborative work in genomics, GenBank as a centralized model for data access, the BIRN (Biomedical Informatics Research Network) for integrating complex data sets and the Genetics Management System (GeMS) for local data management in individual laboratories. In addition, the National Primate Research Centers are currently working on mechanisms for centralizing animal-related data across the entire Center network. The workshop participants recognized that rhesus-specific databases will become increasingly necessary as more genomic data are derived. One or

more of these models will likely be highly relevant to this issue. Over the near term, the most pressing needs will be for databases that build on the rhesus genomic sequence data and SNP data. In the longer term, it will be important that databases of information concerning rhesus are connected and integrated with databases containing information about other nonhuman primates.

PROTEOMICS. As a forward looking aspect, the workshop included an overview of high throughput proteomics technologies, although it was recognized that this is only beginning for the rhesus. High throughput proteomics is extremely information intensive and highly complementary to information obtained from genomic analyses.

PART 2. PANEL DISCUSSIONS ON SPECIFIC APPLICATION AREAS

Each panel was asked to provide an overview of the major experimental questions addressed in regard to the specific application area and to answer the following questions:

- Currently, what are the most frequently used genetic tools?
- What are the major barriers that new genetic tools can overcome?
- What new genetic and bioinformatics tools will be needed in the next 3 – 6 years?

The summaries below primarily contain the answers to these questions. Panelists also provided a considerable amount of information regarding specific experimental approaches and results that are not summarized here, but which were critical for answering the above questions.

AIDS RESEARCH. Fundamental questions addressed through the use of the SIV-rhesus model include obtaining enhanced understanding of: 1) effective methods of vaccine development; 2) correlates of immunity that are most important for understanding infection and AIDS-like disease in the rhesus; 3) mechanisms of pathogenesis; and 4) origin and pathogenesis of tissue-specific syndromes that may not be directly related to immune deficiency, such as HIV-associated dementia. The panel and other workshop participants also emphasized that many of the same questions and genetic tools are highly relevant to other disciplines, such as transplantation and studies of other infectious diseases.

Answers to the questions were as follows:

- Most frequently used tools:
  - MHC typing.
  - Microarrays.
  - Genetic databases.
- Major barriers: Lack of:
  - Some relevant markers in genotyping assays, including MHC markers.
  - Relevant databases.
- New tools needed:
  - More complete genotyping assays, including MHC typing.

- New genetic databases, including a SNP database.
- A database of animals across the NPRCs and other SIV testing sites that can facilitate understanding of the contribution of individual genetic polymorphisms to experimental outcomes. This database should include information on age, gender and pedigree as well as features such as MHC type that are directly related to AIDS research.
- A database of comparative genomic information among different species of non-human primates that are used for aspects of AIDS research.

TRANSPLANTATION. The participants in the panel discussed transplantation of solid organs using the rhesus. The transplantation community primarily uses genetic tools rather than develops them. Nevertheless, the use of genetic tools is very important to this community, with a large overlap with AIDS researchers, particularly in regard to the need for MHC typing and pedigree analysis.

Answers to the questions were as follows:

- Most frequently used tools:
  - MHC typing, this is paramount.
  - Microarrays.
- Major barriers: Lack of:
  - Accessibility to rhesus of optimal genetic composition.
  - More user-friendly, easily accessible bioinformatics tools.
- New tools needed:
  - More complete genotyping assays, including MHC typing and pedigree analysis.
  - Simplified microarrays containing immune response genes, preferably configured as microfluidic devices.

EMERGING INFECTIOUS DISEASES. Presentations were given on studies of avian flu virus and Ebola virus. These studies combine traditional approaches to virological issues with genomic approaches. Proteomic analysis of some of these infections in specific rhesus tissues and cell types have begun. In regard to the workshop questions, this area has the same response as the AIDS community (see above).

AGING. Most studies on aging in monkeys are physiological and normative, rather than genetic. The National Institute on Aging has funded aging monkeys colonies at the NPRCs, and these are the major source of experimental animals for non-invasive studies. A recent innovation is the development of the Primate Aging Database, which primarily contains information on physiological parameters in aging monkeys. This community has just begun to use genetic tools such as microarrays and genotyping to better understand aging in monkeys as it translates to issues in humans. Interestingly, the geographic origin of the animal (Indian versus Chinese) appears to be important for some studies, such as those involving caloric restriction.

Answers to the questions were as follows:

- Most frequently used tools:
    - Microarrays.
    - Genotyping.
- Major barriers: Lack of:
    - Cross-talk between physiologists and geneticists.
    - Facile mechanisms for sharing data.
- New tools needed:
    - More complete assays for genetic characterization, for example for characterizing polymorphisms in important immune loci such as the MHC and KIR.

NEUROBIOLOGY. This topic potentially covers a very wide array of studies. The panelists concentrated on studies of behavior, addiction and neurological diseases such as Alzheimer's disease. All of these conditions and diseases are likely polygenic, which complicates genetic studies. In addition, phenotypes are often physiological or behavioral, rather than based on specific biomarkers. The particular cells or tissues of interest are often imbedded among many other cell types, which further complicates analyses, for example, of global gene expression patterns. Unlike some of the other topics discussed in the workshop, anatomical imaging plays a particularly important role in neurobiology, thus emphasizing the need to study gene expression as a function of anatomy. Despite these potential difficulties, progress can be made with the existing genomic tools, for example, genotyping assays to identify QTLs related to behavior and microarray studies to characterize gene expression patterns related to responses to addictive drugs or development of disease.

Answers to the questions were as follows:

- Most frequently used tools:
    - Microarrays.
    - Genotyping.
- Major barriers: Lack of:
    - A high resolution physical map.
    - SNPs in specific genes of interest.
    - Database correlating genotypes with phenotypes of neurobiological interest.
- New tools needed:
    - SNP map, including SNPs in specific genes.
    - DNA from phenotyped animals.
    - A genotype / phenotype database of available animals.
    - Bioinformatics tools that will "turn data into knowledge." A BIRN-type structure may be essential for this.
    - Anatomical gene maps (e.g., a gene expression atlas for the nervous system).

COMPLEX DISEASES: CARDIOVASCULAR DISEASE, METABOLIC SYNDROME AND RESPIRATORY DISEASE. This panel had as its topic some of the most important complex diseases that are studied in the rhesus with likely translation to studies of human disease and morbidity. All of these conditions are expected to be influenced by multiple genes. Family studies based on pedigrees can be of particular use for some of these studies, as they reduce the "noise" inherent in large scale genotyping experiments. Although many studies of these types of diseases have been performed using rodents, the panelists pointed out that, in many cases, nonhuman primates are required because of their close anatomical similarity to humans. Examples cited were fat deposition, which, unlike humans and non human primates, takes place primarily in the reproductive system of rodents. Another example is airway branching, significantly different in primates than in rodents. Despite the inherent difficulties of studying complex diseases in the absence of having some of the tools very useful for studying rodents (for example, inbred lines of animals and their congenic and consomic derivatives), the panelists recognized that genetic analysis in non human primates has great potential.

Answers to the questions were as follows:

- Most frequently used tools:
  - Microarrays.
  - Genotyping.
  - SNP analysis of specific genes.
- Major barriers: Lack of:
  - Capabilities for high throughput genotyping, including lack of commercial platforms for non human primates.
  - SNPs in specific genes of interest.
  - Database correlating genotypes with phenotypes and family structures.
- New tools needed:
  - SNP map, including SNPs in specific genes.
  - A genotype / phenotype database.

IV. RECOMMENDATIONS

The participants of the workshop recognized that there was a high degree of commonality among the topics discussed in the various panel discussions. There were, of course, some needs that were more specific to some disciplines than others. All of the disciplines represented in the workshop were at least beginning to use the currently available tools, and some of these tools have been used extensively. The participants recognized that elucidation of the rhesus genome sequence and its comparison both with currently available high resolution sequences (for example, human and chimpanzee) as well as with other non human primate sequences in process, will open many new avenues of investigation. Finally, the need for databases to collect and disseminate both the existing genetic data and the vastly increased amounts of data expected to be generated in the near future was a pervasive theme of the discussions.

Given the many commonalities of needs among the various disciplines, the workshop participants recommended immediate development of the following:

- A database that will combine phenotypic and genotypic data, including pedigrees. Minimally the database should include the rhesus housed at the National Primate Research Centers (NPRCs). The phenotypes should be as inclusive as possible, within the limits of practicality. The consensus list of phenotypes should be based on feedback from the research community, NPRC personnel and other relevant parties. This will be facilitated by convening a workshop of relevant investigators and representatives of the funding agencies to produce a concrete plan for this database.

- A SNP map and database. Planning for this should follow completion of the preliminary SNP analyses discussed in the workshop.

- A repository of blood samples and cell lines derived from many of the rhesus, for which phenotypes and genotypes are in the database in item 1, above.

V. CONCLUSIONS

This workshop presented a rare opportunity for scientists from many different disciplines to discuss their use of genetic tools for the rhesus and to identify the many common problems and needs for genetic tools. The first generation of genetic tools and the genome sequence are already having a major impact on translational studies. Further development of genetic tools and the informatics infrastructure to fully utilize them is expected to greatly benefit translational research using the rhesus and thereby, to have a significant impact on human health.

VI. CONTACT INFORMATION

For more information about this meeting, please contact:

John D. Harding, PhD
Director, Primate Resources
Division of Comparative Medicine
National Center for Research Resources
National Institutes of Health
hardingj@mail.nih.gov
301-435-0744

For more information about NCRR, please visit www.ncrr.nih.gov.

AGENDA
NATIONAL INSTITUTES OF HEALTH (NIH) WORKSHOP: GENETIC TOOLS FOR OPTIMIZING THE USE OF RHESUS MACAQUES FOR TRANSLATIONAL RESEARCH
Natcher Conference Center, NIH Campus
April 19 – 20, 2006

April 19, 2006

7:30–8 a.m.	**Registration and Refreshments**
8:00–8:10 a.m.	**Welcome** *Dr. Louise Ramm, Ph.D., Deputy Director, National Center for Research Resources (NCRR)* *Dr. Franziska Grieder, D.V.M., Ph.D., Director of the Division of Comparative Medicine, NCRR*
8:10–8:20 a.m.	**Welcome and Charge to the Group** *Jack Harding, Ph.D., Director of Primate Resources, NCRR, Division of Comparative Medicine*
8:20–8:25 a.m.	**Questions**
SESSION 1	**FIRST GENERATION TECHNOLOGIES: MAPPING AND SEQUENCING** *Chair: Robert Norgren, M.D., Associate Professor, University of Nebraska Medical Center, Genetics, Cell Biology, and Anatomy*
8:25–8:55 a.m.	**Overview of rhesus-based genetic technologies and genetic mapping** *Jeffrey Rogers, Ph.D., Scientist, Southwest Foundation for Biomedical Research, Southwest National Primate Research Center*
8:55–9 a.m.	**Questions**
9–9:15 a.m.	**Physical Mapping, Colony Management** *David Glenn Smith, Ph.D., Professor, University of California, Davis, California National Primate Research Center*
9:15–9:20 a.m.	**Questions**
9:20–9:35 a.m.	**SNP Mapping** *Betsy Ferguson, Ph.D.,Research Professor, Oregon National Primate Research Center*
9:35–9:40 a.m.	**Questions**
9:40–9:55 a.m.	**BREAK**

April 19, 2006 (Continued)

9:55–10:25 a.m.	**Sequence of the Rhesus Genome** *George Weinstock, M.D., Professor & Co-Director, Baylor College of Medicine, Human Genome Sequencing Center*
10:25–10:45 a.m.	**Questions and Comments on Mapping and Sequencing**
10:45–11 a.m.	**Specific sequences: the MHC** *Daniel Geraghty, Ph.D., Member, Fred Hutchinson Cancer Research Center, Clinical Research Division*
11–11:05 a.m.	**Questions**
11:05–11:20 a.m.	**Specific sequences: KIR locus** *Mary Carrington, Ph.D., Principal Investigator, Laboratory of Genomic Diversity, NCI-Frederick*
11:20–11:25 a.m.	**Questions**
SESSION 2	**FIRST GENERATION TECHNOLOGIES 2: MICROARRAYS AND DATABASES** *Chair: Michael Katze, Ph.D., Professor, University of Washington, Department of Microbiology*
11:25–11:40 a.m.	**Microarrays 1** *Robert Norgren*
11:40–11:45 a.m.	**Questions**
11:45–Noon	**Microarrays 2** *Michael Katze*
Noon–12:15 p.m.	**Questions and Comments on Microarrays**
12:15–1 p.m.	**LUNCH**
1:00 – 1:15 p.m.	**Databases and Comparative Genomics 1** *Elaine Mardis, Ph.D., Associate Professor, Washington University, Genome Sequencing Center*
1:15–1:20 p.m.	**Questions**
1:20–1:35 p.m.	**Databases and Comparative Genomics 2** *Aleksandar Milosavljevic, Ph.D., Associate Professor, Baylor College of Medicine, Human Genome Sequencing Center*
1:35–1:40 p.m.	**Questions**

April 19, 2006 (Continued)

SESSION 3 **METHODS FOR DATASHARING**
Chair: Daniel Geraghty

1:40–2:40 p.m. **Panel Discussion**
Daniel Geraghty
Jeff Grethe, M.D., Scientific Coordinator, University of California, San Diego, BIRN Coordinating Center
Robert Robbins, Ph.D., Vice President, Fred Hutchinson Cancer Research Center
David Wheeler, Ph.D., National Center for Biotechnology Information

2:40–3 p.m. **Comments and Questions on Databases and Data Sharing**

3–3:15 p.m. **BREAK**

SESSION 4 **PROTEOMICS**

3:15–3:45 p.m. **Overview of Proteomics Technologies**
Richard Smith, Ph.D., Battelle Fellow and Chief Research Scientist, Pacific Northwest National Laboratory, Biological Sciences Division

3:45–3:55 p.m. **Questions**

SESSION 5 **AIDS PANEL**
Chair: Andrew Lackner, D.V.M., Ph.D., Professor and Director, Tulane National Primate Research Center

3:55–5 p.m. **Panel Discussion**
Andrew Lackner
Ronald Desrosiers, Ph.D., Professor and Director, New England Primate Research Center, Micro and Molecular Genetics, HMS
Howard Fox, M.D. Ph.D., Associate Professor, The Scripps Research Institute, Molecular and Integrative Neurosciences
Chris Miller, DVM, Ph.D., Professor, University of California, Davis, California National Primate Research Center
David O'Connor, Ph.D., Assistant Professor, University of Wisconsin-Madison
David Watkins, Ph.D., Professor, University of Wisconsin-Madison, Wisconsin National Primate Research Center

5–5:10 p.m. **Questions**

April 19, 2006 (Continued)

SESSION 6 **TRANSPLANTATION PANEL**
Chair: Chris Larsen, M.D., Ph.D., Director, Emory Transplant Center, Emory University

5:10–5:55 p.m. **Panel Discussion**
Chris Larsen
Amelia Bartholomew, M.D., Associate Professor, University of Illinois
Allan Kirk, M.D., Ph.D., Chief, Transplantation Branch, National Institute of Diabetes and Digestive and Kidney Diseases
Richard (Robin) Pierson, M.D., Associate Professor of Surgery, University of Maryland and Baltimore VAMC

5:55–6:05 p.m. **Questions**

6:05–6:20 p.m. **Final Questions and Comments**
Jack Harding

April 20, 2006

7:30–8 a.m. **Refreshments**

8–8:05 a.m. **Welcome to Day 2**
Jack Harding

SESSION 7 **EMERGING INFECTIOUS DISEASES, AVIAN INFLUENZA**

8:05–8:20 a.m. *Michael Katze*

8:20–8:35 a.m. *Steven Jones, Ph.D., Head of Immunopathology, and Head of Emerging Bacterial Diseases, Public Health Agency of Canada, National Laboratory for Zoonotic Diseases and Special Pathogens, Special Pathogensy Program*

8:35–8:45 a.m. **Questions**

SESSION 8 **AGING PANEL**
Chair: Joseph Kemnitz, Ph.D., Professor and Director,Wisconsin National Primate Research Center

8:45–9:30 a.m. **Panel Discussion**
Joseph Kemnitz
Julie Mattison, Ph.D., National Institute on Aging, Laboratory of Experimental Gerontology
Janko Nikolich-Zugich, M.D., Professor and Senior Scientist, Oregon Health & Science University, Oregon National Primate Research Center, Vaccine and Gene Therapy Institute
Mary Lou Voytko, Ph.D., Professor, Wake Forest University School of Medicine

9:30–9:40 a.m. **Questions**

9:40–9:55 a.m. **BREAK**

April 20, 2006 (Continued)

SESSION 9 **NEUROBIOLOGY PANEL**
Co-Chair: Stuart Zola, Ph.D., Professor and Director, Yerkes National Primate Research Center, Emory University
Co-Chair: Judy Cameron, Ph.D., Senior Scientist and Professor, Oregon Health Sciences University, Oregon National Primate Research Center

9:55–11:05 a.m. **Panel Discussion**
Stuart Zola
Judy Cameron
Willard Freeman, Ph.D., Assistant Professor, Penn State College of Medicine
Gregory Miller, Ph.D., Assistant Professor, Harvard Medical School, New England Primate Research Center
Cynthia Shannon-Weickert, Ph.D., Unit Chief, National Institute of Mental Health
Wei-Dong Yao, Ph.D., Assistant Professor, Harvard Medical School, New England Primate Research Center

11:05–11:15 a.m. **Questions**

SESSION 10 **CARDIOVASCULAR DISEASE, METABOLIC SYNDROME AND RESPIRATORY DISEASE PANEL**
Chair: Anthony Comuzzie, Ph.D.,Scientist, Southwest Foundation for Biomedical Research

11:15–12:10 p.m. **Panel Discussion**
Anthony Comuzzie
James Cheverud, Ph.D., Professor, Washington University School of Medicine
Dallas Hyde, Ph.D., Professor and Director, University of California, Davis, California National Primate Research Center
Jay Kaplan, Ph.D., Professor and Head of Comparative Medicine, Wake Forest University School of Medicine
Alice Tarantal, Ph.D., Professor, University of California, California National Primate Research Center

12:10–12:20 p.m. **Questions**

SESSION 11 **SUMMARY AND RECOMMENDATIONS**

12:20–1:15 p.m. *Jeffrey Rogers*

1:15 p.m. **Adjourn**

National Center for Research Resources

Genetic Tools for Optimizing the Use of Rhesus Macaques for Translational Research

April 19 - 20, 2006

Participants List

Kristin Abraham, Ph.D.
Program Director
National Institutes of Health
6707 Democracy Boulevard
Room 795
Bethesda, MD 20892
Phone: (301) 451-8048
Fax: (301) 480-0475
E-mail: abrahamk@extra.niddk.nih.gov

Agnes Azimzadeh, Ph.D.
Assistant Professor of Surgery
University of Maryland
10 South Pine Street
MSTF Building, Room 434C
Baltimore, MD 21201
Phone: (410) 706-0594
Fax: (410) 706-1200
E-mail: aazimzadeh@smail.umaryland.edu

Jeffrey Ahlers, Ph.D.
Program Officer
National Institutes of Health
6700B Rockledge Drive
Bethesda, MD 20852
Phone: (301) 435-3756
E-mail: jahlers@niaid.nih.gov

Christina Barr
Research Fellow
Laboratory of Clinical Studies
National Institues of Health
5625 Fishers Lane
Room 3S32
Rockville, MD 20852
Phone: (301) 443.3242
Fax: (301) 435.9278
E-mail: cbarr@mail.nih.gov

David Anderson, DVM
Director
Washington NPRC
1705 NE Pacific Street
Box 357330
Seattle, WA 98195
Phone: (206) 543-1430
Fax: (206) 616-6771
E-mail: danderso@u.washington.edu

Amelia Bartholomew
Associate Professor of Surgery
University of Illinois
840 South Wood Street
Suite 402CSB, M/C 958
Chicago, IL 60612
Phone: (312) 996-9891
E-mail: ambart@uic.edu

Michael Appel, Ph.D.
Program Director
Islet Cell Biology and Transplantation
National Institutes of Health
Democracy II - Room 792
6707 Democracy Blvd
Bethesda, MD 20892-5460
Phone: (301) 594-4740
Fax: (301) 480-0475
E-mail: appelm@niddk.nih.gov

Carol Bean, Ph.D.
Program Director
Division of Biomedical Technology
National Center for Research Resources
6701 Democracy Boulevard
Room 972
Bethesda, MD 20892
Phone: 301-435-0775
Fax: 301-480-3659
E-mail: cabean@mail.nih.gov

Participants List

Judy Cameron, Ph.D.
Senior Scientist and Professor
Oregon National Primate Research Center
505 NW 185th Avenue
Beaverton, OR 97006
Phone: (503) 690-5270
Fax: (503) 690-5519
E-mail: cameronj@ohsu.edu

Mary Carrington, Ph.D.
Senior Scientist
Laboratory of Genomic Diversity
SAIC-Frederick, National Cancer Instiute
Building 560, Room 21-89
P.O. Box B
Frederick, MD 21702
Phone: (301) 846-1390
Fax: (301) 846-6771
E-mail: carringt@ncifcrf.gov

James Cheverud, Ph.D.
Professor
Anatomy & Neurobiology
Washington University School of Medicine
Box 8108
660 South Euclid Avenue
St. Louis, MO 63110
Phone: (314) 362-4188
E-mail: cheverud@wustl.edu

Anthony Comuzzie, Ph.D.
Scientist
Genetics
Southwest Foundation for Biomedical Research
P.O. Box 760549
San Antonio, TX 78245-0549
Phone: (210) 258-9710
Fax: (210) 258-9686
E-mail: agcom@darwin.sfbr.org

Muriel Davisson, Ph.D.
Senior Staff Scientist
The Jackson Laboratory
600 Main Street
Bar Harbor, ME 04609
Phone: (207) 288-6223
Fax: (207) 288-6149
E-mail: muriel.davisson@jax.org

Ronald Desrosiers, Ph.D.
Professor
Microbiology and Molecular Genetics
New England Primate Research Center
One Pine Hill Drive, Box 9102
Southborough, MA 01772-9102
Phone: (508) 624-8002
Fax: (508) 460-0612
E-mail: ronald_desrosiers@hms.harvard.edu

Christopher Dubay, Ph.D.
Genetics Resource Director
Neuroscience
Oregon Health and Science University - OPRC
Mail Code: L584
505 NW 185th Avenue
Beaverton, OR 97006
Phone: (503) 533-2408
E-mail: dubayc@oshu.edu

Lynda Erinoff, Ph.D.
Associate Director
AIDS Research Program
National Institutes of Health
6001 Executive Boulevard
Room 5274
Bethesda, MD 20892
Phone: (301) 402-1872
E-mail: le30q@nih.gov

National Center for Research Resources

Genetic Tools for Optimizing the Use of Rhesus Macaques for Translational Research

April 19 - 20, 2006

Participants List

Betsy Ferguson, Ph.D.
Research Professor
Genetics Research & Informatics Program
Oregon National Primate Research Center
505 NW 185th Avenue
Beaverton, OR 97006
Phone: (503) 533-2403
Fax: (503) 690-5384
E-mail: fergusob@ohsu.edu

John Glowa, Ph.D.
Scientific Review Administrator
National Center for Research Resources
National Institutes of Health
6701 Democracy Boulevard
Bethesda, MD 20892
Phone: 301-435-0807
Fax: 301-480-3660
E-mail: glowaj@mail.nih.gov

Howard Fox, M.D., Ph.D.
Associate Professor
Molecular and Integrative Neurosciences
The Scripps Research Institute
10550 N. Torrey Pines Road
SP30-2030
La Jolla, CA 92037
Phone: (858) 784-7171
Fax: (858) 784-7296
E-mail: hsfox@scripps.edu

Jeffrey Grethe
Scientific Coordinator
BIRN Coordinating Center
University of California, San Diego
9500 Gilman Drive, MC 0715
La Jolla, CA 92093-0715
Phone: (858) 822-0703
Fax: (858) 822-0828
E-mail: jgrethe@ncmir.ucsd.edu

Willard Freeman, Ph.D.
Assistant Professor
Pharmacology
Penn State College of Medicine
500 University Drive
H078
Hershey, PA 17033
Phone: (717) 531-4037
E-mail: wfreeman@psu.edu

Franziska Grieder, DVM, Ph.D.
Director, DCM-NCRR
Division of Comparative Medicine
National Institutes of Health
6701 Democracy Boulevard
Bethesda, MD 20814
Phone: (301) 435-0744
E-mail: griederf@mail.nih.gov

Daniel Geraghty, Ph.D.
Full Member
Clinical Research Division
Fred Hutchinson Cancer Research Center
1100 Fairview Avenue, North
D4-100
Seattle, WA 98109
Phone: (206) 667-4668
Fax: (206) 667-6948
E-mail: geraghty@fhcrc.org

John Harding, Ph.D.
Director
Primate Resources
National Center for Research Resources
National Institutes of Health
6701 Democracy Boulevard
Bethesda, MD 20892
Phone: 301-435-0776
Fax: 301-480-3819
E-mail: hardingj@mail.nih.gov

Participants List

Anthony Hayward, M.D.
Director
Division for Clinical Research Resources
National Center for Research Resources
National Institutes of Health
6701 Democracy Boulevard
Bethesda, MD 20892
Phone: 301-435 0791
E-mail: haywarda@mail.nih.gov

Dallas Hyde, Ph.D.
Professor
University of California, Davis
One Shields Avenue
Davis, CA 95616
Phone: (530) 752-0420
Fax: (530) 754-6228
E-mail: dmhyde@primate.ucdavis.edu

Welkin Johnson, Ph.D.
Assistant Professor
Microbiology and Molecular Genetics
Harvard Medical School
One Pine Hill Drive
Southborough, MA 01772
Phone: (508) 624-8041
E-mail: welkin_johnson@hms.harvard.edu

Steven Jones, Ph. D.
Head of Immunopathology
National Microbiology Laboratory
Public Health Agency of Canada
1015 Arlington Street
Winnipeg, MB R3E 3R2
Phone: (204) 789-5065
Fax: (204) 789-2140
E-mail: steven_jones@phac-aspc.gc.ca

Sree Kanthaswamy, Ph.D.
Assistant Research Geneticist
Department of Anthropology
University of California, Davis
One Shields Avenue
209 Young Hall
Davis, CA 95616
Phone: (590) 219-2017
Fax: (530) 752-8885
E-mail: skanthaswamy@ucdavis.edu

Jay Kaplan, Ph.D.
Professor and Head of Comparative Medicine
Pathology/Comparative Medicine
Wake Forest University School of Medicine
Medical Center Boulevard
Winston-Salem, NC 27157-1040
Phone: (336) 716-1522
Fax: (336) 716-1515
E-mail: jkaplan@wfubmc.edu

Robert Karp, Ph.D.
Program Director, Genetics and Genomics
Digestive Diseases and Nutrition
National Institutes of Health
6707 Democracy Boulevard
Room 671, MSC 5450
Bethesda, MD 20892-5450
Phone: (301) 451-8875
E-mail: karpr@extra.niddk.nih.gov

Michael Katze, Ph.D.
Professor
Department of Microbiology
University of Washington
Box 358070
Katze Lab
Seattle, WA 98195-8070
Phone: (206) 732-6135
Fax: (206) 732-6056
E-mail: honey@u.washington.edu

Deepak Kaushal, Ph.D.
Research Assistant Professor
Division of Bacteriology and Parasitology
Tulane National Primate Research Center
18703 Three Rivers Road
Covington, LA 70433
Phone: (985) 871-6221
Fax: (985) 871-6390
E-mail: dkaushal@tulane.edu

Andrew Lackner, DVM, Ph.D.
Director
Tulane National Primate Research Center
18703 Three Rivers Road
Covington, LA 70433
Phone: (985) 871-6201
Fax: (985) 871-6569
E-mail: alackner@tulane.edu

Joseph Kemnitz, Ph.D.
Director and Professor
Wisconsin National Primate Research Center
1220 Capitol Court
Madison, WI 53715-1299
Phone: (608) 263-3500
Fax: (608) 265-2067
E-mail: kemnitz@primate.wisc.edu

Christian Larsen, M.D., Ph.D.
Director
Emory Transplant Center
Emory University
101 Woodruff Circle
Suite 5105-WMB
Atlanta, GA 30322
Phone: (404) 727-8466
Fax: (404) 727-3660
E-mail: clarsen@emoryhealthcare.org

Allan Kirk, M.D., Ph.D.
Chief
Transplantation Branch
National Institutes of Health
Building 10
Room 5-5752
Bethesda, MD 20854
Phone: (301) 496-3047
E-mail: allank@intra.niddk.nih.gov

Diane Lawrence, Ph.D.
Program Officer
National Institutes of Health
6001 Executive Boulevard
MSC 9555
Bethesda, MD 20892
Phone: (301) 594-3225
Fax: (301) 594-6043
E-mail: lawrencedi@mail.nih.gov

Kristy Kraemer, Ph.D.
Chief
Transplantation Basic Sciences Section
National Institute of Allergy and Infectious Diseases
6610 Rockledge Drive
Room 3043
Bethesda, MD 20892
Phone: (301) 496-5598
E-mail: kkraemer@niaid.nih.gov

Yen Li, Ph.D.
Program Officer
National Institutes of Health
6700B Rockledge Drive
Bethesda, MD 20892
Phone: (301) 496-3816
E-mail: yli@niaid.nih.gov

Yu-Hua Li, Ph.D.
Assistant Research Professor
Yerkes National Primate Research Center
Emory University
954 Gatewood Road
Atlanta, GA 30329
Phone: (404) 727-8520
E-mail: yuhuali@rmy.emory.edu

Guy Lingani, M.S.C.
System Administrator
Biochemistry
Howard University
520 W Street, NW
Washington, DC 20059
Phone: 202-806-9714
E-mail: gmlingani@howard.edu

Yanping Liu, M.D., Ph.D.
Health Scientist Administrator
Research Infrastructure
National Institues of Health
6701 Democracy Boulevard
Bethesda, MD 20817
Phone: (301) 451-4217
E-mail: liuyanp@mail.nih.gov

Francesca Macchiarini, Ph.D
Program Officer
National Institutes of Health
6610 Rockledge Drive
Room 3070
Bethesda, MD 20892
Phone: (301) 496-7551
E-mail: fmacchiarini@niaid.nih.gov

Elaine Mardis, Ph.D.
Associate Professor in Genetics and Molecular
Washington University
4444 Forest Park
Box 8501, Room 4127
Saint Louis, MO 63108
Phone: (314) 286-1807
Fax: (314) 286-1810
E-mail: sparrish@watson.wustl.edu

Julie Mattison, Ph.D.
Staff Scientist
Laboratory of Experimental Gerontology
National Institutes of Health
P.O. Box 56
Poolesville, MD 20837-0056
Phone: (301) 435-7637
E-mail: mattisonj@mail.nih.gov

Christopher Miller, DVM, Ph.D.
Professor
University of California, Davis
County Road 98 & Hutchison Drive
Davis, CA 95616
Phone: (530) 752-8584
Fax: (530) 754-4411
E-mail: cjmiller@ucdavis.edu

Gregory Miller, Ph.D.
Assistant Professor
Psychiatry
New England Primate Research Center
1 Pine Hill Drive
Southborough, MA 01772
Phone: (508) 624-8023
E-mail: gmiller@hms.harvard.edu

Participants List

Aleksandar Milosavljevic, Ph.D.
Associate Professor
Human Genome Sequencing Center
Baylor Collect of Medicine
One Baylor Plaza
Alkek 1619
Houston, TX 77030
Phone: (713) 798-4357
Fax: (713) 798-4373
E-mail: elken@bcm.tmc.edu

Lori Mulligan, M.P.H.
Director
Science Policy and Public Liaison
National Center for Research Resources
National Institutes of Health
6701 Democracy Blvd
Bethesda, MD 20892
Phone: (301) 435-0866
E-mail: mulligal@mail.nih.gov

Nancy Nadon, Ph.D.
Head
Office of Biological Resources
National Institutes of Health
7201 Wisconsin Avenue
GW 2C231
Bethesda, MD 20892
Phone: (301) 402-7744
Fax: (301) 402-5997
E-mail: nadonn@nia.nih.gov

Janko Nikolich-Zugich
Professor and Senior Scientist
Vaccine and Gene Therapy Institute
Oregon Health & Science University
505 NW 185th Avenue
Beaverton, OR 97006
Phone: (503) 418-2752
E-mail: nikolich@ohsu.edu

Robert Norgren
Associate Professor
Genetics, Cell Biology and Anatomy
University of Nebraska Medical Center
Omaha, NE 68198-5805
Phone: (402) 559-8891
E-mail: rnorgren@unmc.edu

David O'Connor, Ph.D.
Assistant Professor
University of Wisconsin-Madison
555 Science Drive
Madison, WI 53711
Phone: (608) 890-0845
Fax: (608) 265-8084
E-mail: doconnor@primate.wisc.edu

Ray O'Neill, Ph.D.
Health Scientist Administrator
National Institutes of Health
One Democracy Plaza
6701 Democracy Plaza, 9th Floor
Bethesda, MD 20892-4965
Phone: (301) 435-0749
E-mail: oneillr@mail.nih.gov

Richard Pierson, M.D.
Associate Professor of Surgery
University of Maryland
Cardiac Surgery, N4W94
22 South Greene Street
Baltimore, MD 21201
Phone: (410) 328-5842
Fax: (410) 328-2750
E-mail: rpierson@smail.umaryland.edu

Jonathan Pollock, Ph.D.
Chief
Institute for Defense Analysis
6001 Executive Boulevard
Bethesda, MD 20892
Phone: (301) 435-1309
E-mail: jpollock@mail.nih.gov

Jeffrey Pullen, Ph.D.
Project Officer
National Institutes of Health
6700B Rockledge
Room 5253
Bethesda, MD 20892
Phone: (301) 451-2774
E-mail: pillen@niaid.nih.gov

William Rall, Ph.D.
Health Scientist Administrator
National Institutes of Health
One Democracy Plaza, Room 946
6701 Democracy Boulevard
Bethesda, MD 20892
Phone: 301-434-0744
Fax: 301-480-3819
E-mail: rallw@mail.nih.gov

Louise Ramm, Ph.D.
Deputy Director
National Center for Research Resources
9000 Rockville Pike
Bethesda, MD 20892
Phone: 301-435-0879
E-mail: ramml@mail.nih.gov

Robert Robbins, Ph.D.
Vice President
Information Technology
Fred Hutchinson Cancer Research Center
1100 Fairview Avenue, North
J4-300
Seattle, WA 98109
Phone: (206) 667-4778
E-mail: rrobbins@fhcrc.org

Jeffrey Rogers, Ph.D.
Scientist
Genetics
Southwest Foundation for Biomedical Research
219 North Rolling View
San Antonio, TX 78253
Phone: (210) 258-9532
Fax: (210) 670-3344
E-mail: jrogers@darwin.sfbr.org

David Smith, Ph.D.
Professor
Anthropology
University of California, Davis
One Shields Avenue
209 Young Hall
Davis, CA 95616
Phone: (530) 752-6343
Fax: (530) 752-8885
E-mail: dgsmith@ucdavis.edu

Richard Smith, Ph.D.
Battelle Fellow and Chief Research Scientist
Pacific Northwest National Laboratory
902 Battelle Boulevard
Mail Stop K8-98
Richland, WA 99352
Phone: (509) 376-0723
Fax: (509) 376-7722
E-mail: rds@pnl.gov

Margaret Snyder, Ph.D.
Health Scientist Administrator
Office of Extramural Programs
National Institutes of Health
6705 Rockledge Drive
Room 4184
Bethesda, MD 20892
Phone: (301) 402-1058
Fax: (301) 480-3530
E-mail: snyderm@mail.nih.gov

Eliot Spindel, M.D., Ph.D.
Senior Scientist
Division of Neuroscience
Oregon Health & Science University
505 NW 185th Avenue
Beaverton, OR 97006
Phone: (503) 690-5512
E-mail: spindele@ohsu.edu

Danilo Tagle, Ph.D.
Program Director in Neurogenetics
Neurogenetics
National Institutes of Health
6001 Executive Boulevard
Neuorscience Center, Room 2133
Bethesda, MD 20892
Phone: (301) 496 5745
Fax: (301) 402 1501
E-mail: tagled@ninds.nih.gov

Alice Tarantal, Ph.D.
Professor
CA National Primate Research Center
University of California
Pedrick and Hutchison Roads
Davis, CA 95616-8542
Phone: (530) 752-6680
Fax: (530) 752-2880
E-mail: aftarantal@primate.ucdavis.edu

Walter Taylor, Ph.D.
Health Scientist Administrator
National Center for Research Resources
National Institutes of Health
6701 Democracy Boulevard
Room 936
Bethesda, MD 20892
Phone: (301) 435-0760
Fax: (301) 480-3770
E-mail: taylorwf@mail.nih.gov

Melanie Veirs, M.S.
University of Maryland
655 West Baltimore Street
BRB 7-047
Baltimore, MD 21201
Phone: (410) 328-5328
Fax: (410) 328-5488
E-mail: mveirs@som.umaryland.edu

Mary Lou Voytko, Ph.D.
Professor
Neurobiology & Anatomy
Wake Forest University School of Medicine
Medical Center Boulevard
Winston-Salem, NC 27157
Phone: (336) 713-7174
Fax: (336) 713-7168
E-mail: mlvoytko@wfubmc.edu

David Watkins, Ph.D.
Professor
Pathology and Laboratory Medicine
University of Wisconsin-Madison
UW AIDS Vaccine Research Lab
555 Science Drive
Madison, WI 53711
Phone: (608) 265-3380
Fax: (608) 265-8084
E-mail: watkins@primate.wisc.edu

National Center for Research Resources

Genetic Tools for Optimizing the Use of Rhesus Macaques for Translational Research

April 19 - 20, 2006

Participants List

Harold Watson, Ph.D.
Program Officer
National Center for Research Resources
National Institutes of Health
6701 Democracy Boulevard
Room 944
Bethesda, MD 20892
Phone: 301-435-0884
Fax: 301-480-3819
E-mail: watsonh@mail.nih.gov

Cynthia Weickert, Ph. D.
Unit Chief
MiNDS, CBDB
National Institutes of Health
10 Center Drive
Bethesda, MD 20892
Phone: (301) 496-9776
E-mail: shannowc@mail.nih.gov

George Weinstock
Professor & Co-Director
Human Genome Sequencing Center
Baylor College of Medicine
One Baylor Plaza
Alkek 1619
Houston, TX 77030
Phone: (713) 798-4357
Fax: (713) 798-4373
E-mail: elken@bcm.tmc.edu

David Wheeler, Ph.D.
Staff Scientist
National Center for Biotechnology Information
8600 Rockville Pike
Bethesda, MD 20892
Phone: (301) 435-5950
E-mail: wheeler@ncbi.nlm.nih.gov

Wei-Dong Yao, Ph.D.
Assistant Professor
Psychiatry
Harvard Medical School
One Pine Hill Drive
Box 9102
Southborough, MA 01772
Phone: (508) 624-8106
Fax: (508) 786-3317
E-mail: wei-dong_yao@hms.harvard.edu

Jane Ye, Ph.D
Health Scientist Administrator
National Institutes of Health
6701 Rockledge Drive
Bethesda, MD 20892
Phone: (301) 435-0513
E-mail: yej@nhlbi.nih.gov

Stuart Zola, Ph.D.
Director
Yerkes National Primate Research Center
Emory University
954 Gatewood Road, ND
Atlanta, GA 30329
Phone: (404) 727-7707
Fax: (404) 727-0623
E-mail: szola@rmy.emory.edu

Joanne Zurlo, Ph.D.
Director
Institute for Laboratory Animal Research
The National Academies
500 Fifth Street, NW
Washington, DC 20001
Phone: (202) 334-2486
E-mail: jzurlo@nas.edu