



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

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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 Histocompatibility 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:

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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
Pathogens Program*

8:35–8:45 a.m.

Questions

SESSION 8

AGING PANEL

*Chair: Joseph Kernnitz, Ph.D., Professor and Director, Wisconsin
National Primate Research Center*

8:45–9:30 a.m.

Panel Discussion

Joseph Kernnitz

*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

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