



National Center for Research Resources
NATIONAL INSTITUTES OF HEALTH

Genetic Tools for Optimizing the Use of Rhesus Macaques for Translational Research
Bethesda, MD
April 19 – 20, 2006

Workshop Summary

On April 19 – 20, 2006, the National Center for Research Resources (NCRR) sponsored a workshop entitled, *Genetic Tools for Optimizing the Use of Rhesus Macaques for Translational Research* at the Natcher Conference Center in Bethesda, Maryland. The purpose of the workshop was to define the next generation of genetic tools needed to optimize the use of rhesus macaques in translational research. This topic is timely since the rhesus is the most widely used nonhuman primate for translational studies directly related to human health. A set of first-generation genetic tools have been developed, and the rhesus genome sequence has now been determined. Thus, there is a need to define the next generation of genetic tools.

The workshop was comprised of two parts. The first part consisted of 10 short presentations summarizing the status of existing studies, including genetic and physical maps, discovery of single nucleotide polymorphisms (SNPs), sequence of the rhesus genome, specific sequences of immunological interest, microarrays, databases, and an overview of proteomic technologies. The second part of the meeting consisted of panel discussions on specific application areas, including data sharing, AIDS, transplantation, emerging infectious diseases, aging, neurobiology and behavior, cardiovascular disease, metabolic syndrome, and respiratory disease. Altogether, combining both parts of the meeting, 41 scientists gave presentations or participated in the panels. The agenda also included ample time for general discussion and input from the entire group that participated in the workshop (approximately 80 people, including NIH extramural staff).

Each application panel was asked to address the following:

1. For the particular discipline under discussion, which genetic tools are used most frequently at the current time?
2. What are the major barriers in the field that could be overcome by development of new genetic tools or refinement/expansion of existing tools?
3. What new (or expanded) bioinformatics tools are needed?
4. Provide a prioritized list of the major tools needed (or refined/expanded) in the next 3 years and the next 6 years, respectively.

Based on the answers to these questions, as well as on the information provided about the current technologies, the participants identified common needs across the application areas and provided recommendations for development of the next generation of genetic tools for the rhesus macaque. These conclusions will be summarized in the complete meeting report in the near future and will be made available on the NCRR web site at <http://www.ncrr.nih.gov>.

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