# Seattle International Conference on Primate Genomics 2005

## University of Washington National Primate Research Center (NPRC)
## Illumigen Biosciences, Inc.

**Bell Harbor Conference Center**
**Seattle, Washington**
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# Meeting Report

The Seattle International Conference on Primate Genomics 2005 was organized by the University of Washington National Primate Research Center (NPRC) and Illumigen Biosciences, Inc. and involved approximately 150 attendees. The meeting was held over a three-day period from May 20 – 23, 2005. Members of the evolutionary biology, primate research, genome sciences, HIV and immunology, and infectious disease and biodefense communities were well represented. The meeting provided a rare opportunity for suppliers of primate genomics information and resources to interact with their consumer counterparts. Attendance at the conference was driven by advertising on the *Science* magazine Web site, targeted e-mail to more than 1,000 investigators of National Institutes of Health (NIH)-funded, primate-related grants, and through the National Center for Research Resources (NCRR)-funded NPRCs. NCRR's Division of Comparative Medicine and the Office of AIDS Research (Office of the Director, NIH) were represented at the meeting, which was supported by grant funding from NCRR and financial sponsorship from thirteen corporations.

The first session of the meeting (*Technology, Informatics, and Primate Genomics Resources*) was principally focused on primate genome sequence information and clone resources, with a particular emphasis on the creation of bacterial artificial chromosome (BAC) libraries and large-scale, genome-wide sequencing of the rhesus macaque and chimpanzee genomes. The second session of the meeting (*Primate Evolution*) focused on comparative primate evolution and was heavily influenced by the many recently published chimpanzee-human comparative studies. The third (*Primate Genomics, Immune Function, and HIV/SIV Disease*) and fourth (*Primate Genomics and Biodefense*) sessions were principally focused on the rhesus macaque model of HIV/AIDS and primate models of emerging infectious disease, including those related to biodefense. The final session of the meeting (*Functional Genomics and Primates*) encompassed numerous functional genomics and quantitative trait genetics applications of primate models including brain development, behavior, neuropsychiatric disorders, and metabolic syndrome.

The meeting included a roundtable discussion at the end of each of the first and second days. Audience participation was encouraged during both roundtable discussions. The first roundtable focused on outstanding primate genomics resource needs and recommendations for future funding. Conclusions from this first roundtable discussion generally fell into two categories:

1) Adequacy of existing and proposed primate genome assemblies. Participants generally felt that the proposed and ongoing shotgun sequencing and assembly of nonhuman primate genomes would be adequate for most user applications. However, it was agreed that for specific applications, finished genomic sequence is preferred. One such application involves comparative analysis among primate genomes in order to identify genes and sequences specific to one or a few species. Shotgun assemblies are sometimes inadequate for comparative analyses, as they collapse local regions of duplication, and make identification of species-specific sequences or sequence families more challenging.

2) Additional primate genomic resources. Several members of the panel and audience emphasized the need for the development of more nonhuman primate resources and encouraged the funding of applications to develop these resources. Among the suggested resources were: (A) cell lines from diverse animal populations and/or primate families for genetic and population diversity studies; (B) cDNA resources from additional biomedically important primate species; (C) bioinformatics resources and Web portals for the organization and dissemination of genomic information and analyses from primate species; (D) resources of phenotypic information from animals in captivity; and (E) resources for the collection and dissemination of genetic information for animals in captivity, including HLA and mitochondrial DNA typing, family organizations and parentages, and immortalized cell lines.

In particular, several members of the audience expressed an interest in having access to primate tissues at necropsy for experimental studies. Methods for expanding existing NPRC-focused tissue distribution programs to accommodate a larger community of researchers were also discussed and the need emphasized.

A topic of particular emphasis was the need to establish cDNA libraries, lymphoblastoid and fibroblast cell cultures, and tissue banks for the chimpanzee, focusing initially on those animals scheduled for transfer to sanctuary. The group also emphasized the value of additional chimpanzee phenotypic studies for those animals that are not transferred to sanctuary and that remain available as research subjects.

The second roundtable discussion focused on primate models of infectious disease and quantitative human traits. Recommendations from the group focused on three key areas: ongoing development of rhesus macaque-specific microarrays, development of additional small primate models of human disease, and characterization of the genetic diversity among macaque species.

**1. Recommendations Related to Rhesus Macaque Microarray Resources**

There was considerable discussion of the newly developed rhesus macaque-specific microarrays. One type of array each from the University of Washington/Agilent Technologies, Inc. and the University of Nebraska/Affymetrix, Inc. has been developed, and both are commercially available. Discussion centered on the content of the first-generation arrays and proposed future array development, with several attendees expressing an interest in providing input into the design of second generation arrays. Participants proposed exploratory studies to measure the impact of interspecies diversity on the use of the array in other Old World monkey species. Additional bioinformatics and data analysis resources will be needed to accommodate continued use of the new array resources. Various participants emphasized the importance of researchers transitioning array experiments in macaques to the new macaque arrays and the importance of continued development of the array resource to the HIV/AIDS research community.

## 2. Recommendations Related to the Characterization of Genetic Diversity Among Macaque Species

Several attendees emphasized the importance of programs to characterize the genetic and immunological diversity of macaques used in biomedical research. Participants generally felt that there was inadequate characterization of the genetic diversity among captive animals, as well as among related macaque species (*fascicularis* vs. *mulatta* vs. *nemestrina*) and animals of divergent geographic origin (Indian vs. Nepalese vs. Chinese). There was consensus that additional genetic and immunological characterization of at least captive rhesus macaques is needed.

## 3. Development of Additional Small Primate Models of Human Disease

Several participants expressed concern that there is still no small primate model of HIV infection; rather, there are only models that rely on surrogate viruses. These participants noted a need for additional primate models of HIV/AIDS and other critical human diseases. Considerable discussion was devoted to the current paucity of Indian-origin rhesus macaques for experimental work. While it was noted that NCRR has funded Specific Pathogen Free (SPF) colonies to provide much needed additional captive rhesus animals, considerable discussion was devoted to alternative models. Several possible alternative animal resources were discussed including rhesus from Nepal and China and other macaque and New World monkey species. The consensus of the group was that no animal resource other than the rhesus was sufficiently genetically characterized to support confident use by the research community. No consensus was reached regarding the development of alternatives to rhesus macaques of Indian origin.

## Future Working Group Proposed

It was agreed at the close of the meeting that a smaller working group should be organized to formulate specific recommendations for additional NIH-funded primate genomics efforts with an emphasis on meeting the critical current needs of the research community.