



## INTRODUCTION

# A Barrel of Monkey Genes

THE RHESUS MACAQUE, *MACACA MULATTA*, HAS LONG BEEN USED AS AN important research tool in medicine, from the discovery of the Rh factor to modern-day trials of AIDS vaccines and investigations of neurological and behavioral disorders. As an Old World monkey, it is one of our closest relatives outside of the great apes—chimpanzees, gorillas, and orangutans—making it highly informative on many levels. Today, we unveil the genome of this magnificent Old World monkey and, in doing so, open ourselves to further investigation.

Nonhuman primates have been critically important in developing medical advances that have saved human lives. The availability of this genome sequence will enable new and better experiments that will speed up the pace of research and reduce the number of animals needed for biomedical research in the long run. Analysis of the sequence is stimulating studies on population structure (Hernandez *et al.*, p. 240) that will help researchers interpret differences between experimental groups when they occur and to investigate species-specific effects. Researchers have developed microarray chips of macaque-specific genes so that changes in gene expression in response to perturbations, such as viral infection or hormone treatment, can be followed sensitively through time (see the News article by Pennisi on p. 216). Differences and similarities in the expression of genes related to immune response between macaque and human are already apparent.

Before the rhesus macaque sequencing effort, the human and chimpanzee genomes were available, but these tools could not be used to their fullest potential in studies of evolution. When we look at humans and chimpanzees, we are gazing through a very narrow window, because they diverged so recently in evolutionary history. The rhesus macaque, as our next closest relative, is an ideal outgroup for human/chimpanzee comparisons. We now can step back and examine the past 25 million years of primate evolution, identifying genomic similarities and differences between each species. As shown by the Rhesus Macaque Genome Sequencing and Analysis Consortium (p. 222) and discussed in a second News article by Pennisi (p. 218), the addition of genomic information from macaques is resulting in a much clearer understanding of primate biology and evolution. Within the special section, we also present investigations broadening our understanding of the dynamic nature of primate chromosomes and examining the differences among primate genomes, including the duplications, rearrangements, mobile elements, and evolutionarily new centromeres (Han *et al.*, p. 238; Harris *et al.*, p. 235; and Ventura *et al.*, p. 243). Genes or regions that show evidence of selection among primates may yet provide the Rosetta stone that will allow us to read our own history in the genomes.

—LAURA M. ZAHN, BARBARA R. JASNY, ELIZABETH CULOTTA, ELIZABETH PENNISI

## The Rhesus Macaque Genome

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