

Research from the Batzer laboratory featured on the cover of *Science*

In the 13 April 2007/today's issue of *Science*, the genome sequence of the rhesus macaque (*Macaca mulatta*) is unveiled. The rhesus macaque genome will enhance its significance as a model for biomedical research and for studies on primate evolution. A team of more than 170 scientists from around the world was involved in the sequencing and analysis of the genome. Here at LSU, the Batzer laboratory played a key role in the analysis of the mobile element composition of the rhesus macaque genome. The research of Mark Batzer's group, in collaboration with Brygg Ullmer (CS+CCT), yielded two publications in the journal *Science*. The publications are accompanied by an interactive poster, online videos, interviews, and educational tools.



COVER: A rhesus **macaque** in the NIH Animal Center, Poolesville, MD. Photo: Joshua Moglia.

The rhesus macaque (*Macaca mulatta*) is an abundant primate species that diverged from the ancestors of *Homo sapiens* about 25 million years ago. Because they are genetically and physiologically similar to humans, rhesus monkeys are the most widely used nonhuman primate in basic and applied biomedical research. We determined the genome sequence of an Indian-origin *Macaca mulatta* female and compared the data with chimpanzees and humans to reveal the structure of ancestral primate genomes and to identify evidence for positive selection and lineage-specific expansions and contractions of gene families. A comparison of sequences from individual animals was used to investigate their underlying genetic diversity.

We studied the genomic composition and evolution of transposable elements in the rhesus macaque, a representative of the Old World monkey lineage. The L1 family of long interspersed

elements appears to have evolved as a single lineage, and Alu elements have evolved into four currently active lineages. We also found evidence of elevated horizontal transmissions of retroviruses and the absence of DNA transposon activity in the Old World monkey lineage. In addition, ~100 precursors of composite SVA (short interspersed element, variable number of tandem repeat, and Alu) elements were identified, with the majority being shared by the common ancestor of humans and rhesus macaques. Mobile elements compose roughly 50% of primate genomes, and our findings illustrate their diversity and strong influence on genome evolution between closely related species.

The complete description of the macaque genome blueprint enhances the utility of this animal model for biomedical research and improves our understanding of the basic biology of the species.

Han K.*, M. K. Konkel*, J. Xing*, H. Wang*, J. Lee, T. J. Meyer, C. T. Huang, E. Sandifer, K. Hebert, E. W. Barnes, R. Hubley, W. Miller, A. F. A. Smit, B. Ullmer and M. A. Batzer (2007) *Mobile DNA in Old World monkeys: a glimpse through the rhesus macaque genome*. Science 316: 238-240

* These authors contributed equally to this work.

Rhesus Macaque Genome Sequencing and Analysis Consortium (2007) *Evolutionary and biomedical insights from the rhesus macaque genome*. Science 316: 222-234

Link to interactive poster:

<http://www.sciencemag.org/sciext/macaqueposter/>

Link to educational tools:

<http://www.sciencemag.org/cgi/data/316/5822/246a/DC1/1>