

Genomic sequence and comparison of two macaques reveal new insights into biomedical research

October 17 2011

The South China Center for Innovative Pharmaceuticals, Sun Yat-Sen University, and BGI, the world's largest genomic organization, announced that they were among the research organizations from China, US and UK comprising an international research group that completed the genome sequence and comparison of two non-human primate animal models - Chinese rhesus macaque and cynomolgus. The study is published today online in the journal *Nature Biotechnology*.

This study marks an important milestone in [macaque](#) genome research and plays an important role in the better understanding of genetic differences among [macaque monkeys](#). It also reveals new insights into the [evolutionary history](#) of the macaque genome, human disease research and [drug discovery](#). "We believe these insights will generate great interest among geneticists, medical scientists and clinical researchers worldwide and facilitate the effective use of non-human primate models in medical research." said Prof. Guangmei Yan, the co-leading author of the study and Senior Consultant of The South China Center for Innovative Pharmaceuticals.

Macaques are the most extensively used non-human primates in biomedical research. They have contributed to pre-clinical studies all over the world, including the discovery of vaccines, drug development and behavioral research. Indian rhesus macaque, in particular, has been used for more than half century in pre-clinical research. However, India

banned the export of all macaques in 1978, leading to the current shortage of resource for pre-clinical research.

Facing this problem, scientists have been gradually paying more attention on other macaque species/subspecies for a suitable alternative [animal model](#), particularly on the Chinese rhesus macaque (*Macaca mulatta lasiota*) and the cynomolgus/crab-eating macaque (*Macaca fascicularis*). "In order to select the most relevant non-human primate model in a study, it is important for researchers to understand the [genetic variation](#) and inter-species differences among macaque species as well as the genetic diversity between macaques and human." said Dr. Guojie Zhang, the co-leading author of the study and Director of Genomic Evolution and Comparison Centre at BGI..

In this study, the team sequenced the genomes of a female Chinese rhesus macaque (CR) and a female cynomolgus (CE) by the whole-genome shotgun strategy on BGI's next-generations sequencing platform. The genome size of CR and CE is about 2.84 Gb and 2.85 Gb, respectively. Using the genomic data, the researchers also compared the two genomes with the previously sequenced Indian [rhesus macaque](#) (IR) and explored the abundant genetic heterogeneity among the three macaques. They found there were over 20 million single-nucleotide differences and 740,827 indel events in the three macaque species, which will provide abundant genetic heterogeneity for use in future biomedical analysis and application. It is important to note that a large number of [genetic differences](#) were shared between at least two macaques. The divergence rate of CE/IR (40%) was higher than that of CR/IR (31%) and CR/CE (34%).

In addition, the divergence pattern between CR, CE and IR also suggested the occurrence of ancient introgression from CR to CE over an extended period of evolutionary time. 217 strong selective sweep regions were identified with reduced variability between the three

macaque species, implying that some genes in macaques may experience positive selection in evolution. "Genome sequence and comparison of CR and CE confirmed that introgressive hybridization probably played an important role in the formation of the genome of the extant mainland-origin cynomolgus macaque. Thus, the CE could be a useful model for exploring gene interchanges between primate species, and the consequent role of this process in primate evolution and speciation." added Dr. Zhang

Another interesting finding is that some specific genes in macaques display a high degree of sequence similarity with human disease gene orthologues and drug targets. This demonstrated the prominent use of macaques in biomedical research. To study the orthologues of human druggable protein domains in macaques and to create a resource for the therapeutic exploitation of the 'druggable genome'; the team screened the macaque orthologues for currently known drug domains. Almost all of the druggable orthologues can be detected in the three-macaque species/subspecies, indicating that these animal models are likely to be functionally equivalent. However, in very few cases, macaques exhibit differences with respect to human.

"We are excited about all the findings in the study, especially those with great biomedical interests. For instance, macaques have protective immunity against human retrovirus, HIV-1 virus, but are easily infected by SIV virus. TRIM5 α protein in macaques can lead to anti-infection of HIV-1, whereas TRIM5 α in human does not have the same effect. Variations of TRIM5, a gene encoding TRIM5 α were observed at different frequency in the macaque population, and this may be the key hereditary factor for the ability to protect against HIV-1 infection among individual macaques." added Dr. Zhang.

Adding to the efforts in the genomic studies of macaques, earlier this month BGI has released the first monkey exome sequencing platform

based on next-generation sequencing technology and the monkey exome capturing array (MECA)

(<http://www.physorg.com/news237552855.html>). MECA is a proprietary exome capture array designed by BGI for capturing the entire monkey exome. The combination of this revolutionary array and BGI's high-throughput sequencing technology not only can simplify the workflow of exome sequencing experiments, but also improve cost-effectiveness and turnaround time.

Provided by Beijing Genomics Institute

Citation: Genomic sequence and comparison of two macaques reveal new insights into biomedical research (2011, October 17) retrieved 2 May 2024 from <https://phys.org/news/2011-10-genomic-sequence-comparison-macaques-reveal.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.