

3D mapping of human genome to help understand diseases

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Genome Institute of Singapore's (GIS) Associate Director of Genomic Technologies, Dr. Yijun RUAN, led a continuing study on the human genome spatial/structural configuration, revealing how genes interact/communicate and influence each other, even when they are located far away from each other. This discovery is crucial in understanding how human genes work together, and will re-write textbooks on how transcription regulation and coordination takes place in human cells.

The discovery was published in *Cell*, on 19 January 2012. The GIS is a research institute under the umbrella of the Agency for Science, Technology and Research (A*STAR).

Using a genomic technology invented by Dr. Ruan and his team, called ChIA-PET, the Singapore-led international group, which is part of the ENCODE (ENCyclopedia Of DNA Elements) consortium, uncovered some of the fundamental mechanisms that regulate the gene expression in human cells.

“Scientists have always tried to understand how the large number of genes in an organism is regulated and coordinated to carry out the genetic programs encoded in the genome for cellular functions in our cells. It had been viewed that genes in higher organisms were individually expressed, while multiple related genes in low organisms like bacteria were arranged linearly together as operon and transcribed in single unit,” Dr. Ruan explained. “The new findings in this study

revealed that although genes in human genomes are located far away from each other, related genes are in fact organised through long-range chromatin interactions and higher-order chromosomal conformations. This suggests a topological basis akin to the bacteria operon system for coordinated transcription regulation. This topological mechanism for transcription regulation and coordination also provides insights to understand genetic elements that are involved in human diseases.”

GIS’ executive director Prof Huck Hui NG said: "This is an important study that sheds light on the complex regulation of gene expression. Yijun's team continues to use the novel method of Chromatin Interaction Analysis with Paired-End-Tag sequencing to probe the higher order interactions of chromatin to discover new regulatory interactions between genes."

“This publication describes ground-breaking work by Dr. Yijun Ruan and his team at Genome Institute o Singapore,” added Dr. Edward Rubin, Director of the Joint Genome Institute in US. “They address the fundamental question of how communication occurs between genes and their on and off switches in the human genome. Using a long range DNA mapping technology called ChIA-PET, the study reveals in three dimensional space that genes separated linearly by enormous distances in the human genome can come to lie next to each other in the cell when it is time for them to become active. I expect this study to move rapidly from primary scientific literature to textbooks describing for future students the operating principles of the human genome. The ChIA-PET technology, that is the telescope used in this exploration of the human genome, is an innovative and powerful molecular technology invented by Dr. Ruan and his collaborators.”

The ENCODE is an ongoing project which was awarded to Dr. Ruan’s team by the National Human Genome Research Institute (NHGRI), an institute belonging to the National Institutes of Health (NIH, USA). The

project was set up in 2003 with the aim of discovering all functional elements in the [human genome](#) to gain a deeper understanding of human biology and develop new strategies for preventing and treating diseases. So far Dr. Ruan's team has received over US\$2 million towards this project.

More information: The research findings described in the press release can be found in the 19 January 2011 advanced online issue of *Cell* under the title “Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation”.

Provided by Agency for Science Technology and Research (A*STAR)

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