PRESS RELEASE

DNA COMPACTION AND ITS ASSOCIATION WITH DISEASES

10 Jul 2014, Singapore – Scientists at TLL have identified a specific type of protein which is responsible for the compaction of DNA. This compaction affects the way information flows from genomic DNA and has an impact on evolution, life and certain diseases.

Irregular compaction of DNA plays a role in disease and is commonly associated with cancer. In a normal cell, DNA is compacted in well-defined areas, whereas in a cancer cell, the degree and structure of DNA compaction is abnormal.

Using *Arabidopsis thaliana* as a simple model system, a team led by Dr Frederic Berger uses molecular engineering and biochemistry to study the compaction of DNA and its impact on plants. The findings have been published as a research article in the prestigious international journal *Cell*, and provide valuable insight to understanding similar mechanisms that are related to human diseases.

The genetic information of all living organisms is kept within the DNA. The typical length of a human's DNA is about three meters. In order for the DNA to fit into the nucleus of a cell, which is a few micrometers in diameter, a group of five proteins ("histones") are responsible for the packaging of DNA. These histones assemble into nucleosomes forming bead-like structure around which the DNA is wrapped ("histone beads") and thus, occupying less space. However, this process only provides a limited degree of compaction and the mechanisms that cause higher degree of genome compaction remain unknown.

Dr Frederic Berger and Dr Ramesh Yelagandula, former TLL Junior Research Fellow, have identified a specific type of histone, H2A.W, which is able to configure the DNA into three dimensional structures. The team discovered that H2A.W has a special domain at its tail that enables histone beads to pack into higher order assemblies. This compaction of DNA affects the way information from genomic DNA is transmitted.

“This research findings pave the way for unraveling the origin of DNA compaction into the limited space of the nucleus and provide insights into understanding how higher order structure of DNA causes gene silencing,” said Dr Berger. “Moving forward, our research will focus on understanding the origin of H2A.W and its equivalent in humans.”

Dr Berger also foresees that this new knowledge will provide a more in-depth understanding of the origin of abnormal organization of compacted DNA in diseased cells and its impact. On a longer term, this insight will contribute to pharmacological research in the development of agents that remediate deregulation of DNA organization in cancer cells.

“Basic research is the fundamental building block for innovation. By utilizing simple model organisms such as Arabidopsis to study biology, it contributes to the understanding of other more complex mechanisms and helps create impactful application,” said Prof Chan Soh Ha, Executive Director of TLL. “I congratulate Dr Berger and his team for this significant finding and look forward to future developments from this research.”

Dr Berger led a research team at the Ecole Normale Superieure de Lyon focusing on endosperm development in Arabidopsis before joining TLL in 2004 as a Senior Principal Investigator. His current research interests focus on the areas of epigenetics and histone variants.

About Temasek Life Sciences Laboratory (TLL)

TLL, established in 2002, is a beneficiary of Temasek Trust and is affiliated to the National University of Singapore and Nanyang Technological University. The research institute focuses primarily on understanding the cellular mechanisms that underlie the development and physiology of plants, fungi and animals. Such research provides new understanding of how organisms function, and also provides foundation for biotechnology innovation.

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