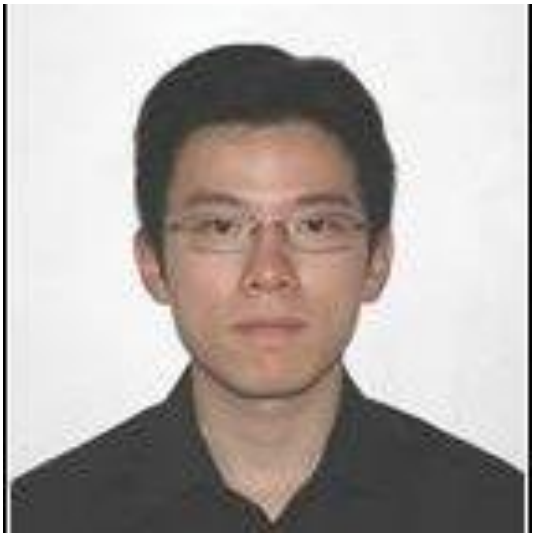
NUS National University of Singapore | Department of Biological Sciences
Faculty of Science

SEMINAR

Wed, 8 April 2015 | 3pm | DBS Conference Room 1

Hosted by Professor Prakash Kumar

A CLOSER LOOK AT THE LOCAL CHROMATIN PACKING IN PLANTS



By Liu Chang
Department of Molecular Biology
Max Planck Institute for Developmental Biology, Germany

The spatial organization of the genome in the nucleus is critical for many cellular processes such as transcription, DNA duplication, recombination and repair. It has been broadly recognized that the packing of chromatin inside the nucleus is not random, but structured at several hierarchical levels. The recently developed Hi-C technology is an efficacious method to investigate genome packing. From a high-resolution Hi-C map of a model dicot plant Arabidopsis thaliana, I have discovered that its local chromatin packing differs from the patterns seen in animals. At a genomic level, topologically associating domains (TADs), which are prominent in animals, are not an obvious structural feature of A. thaliana genome packing. Remarkably, there are many regions showing much higher intra-chromosomal interaction rates than neighboring regions. These regions are enriched with histone mark H3K27me3, suggesting that this epigenetic modification plays a role in organizing higher-order chromatin interaction in plants. In addition to chromosome-wide Hi-C maps, I have also developed computing pipelines to further examine the topological conformation of gene bodies. Interestingly, a large number of genes, including some showing very low or no transcriptional activities, adopt a gene looping structure, in which a gene's Transcription Start Site (TSS) interacts with its 3' end region. I will also discuss current trends in research related to plant chromatin folding, and several newly developed methods aiming to understand the molecular mechanisms underlying the interplay between chromatin structure and activity

Liu Chang is a Faculty Search Candidate

Artwork by Ann Nee, DBS, NUS