CDB SEMINAR

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~~Tuesday, March 8, 2016~~ **Tuesday, March 15, 2016**

16:00~17:00   A7F Seminar Room   ↑ updated on Jan. 29.

Biochemical analysis of genome functions using the locus-specific chromatin immunoprecipitation technologies: key tools to elucidate 4D Nucleome

* This seminar is a part of the Epigenetics Seminar Series 2015.

Summary
Elucidation of molecular mechanisms of genome functions such as transcription and epigenetic regulation requires identification of components mediating the genome functions. To this end, we developed the locus-specific chromatin immunoprecipitation (locus-specific ChIP) technologies, consisting of insertional ChIP (iChIP) and engineered DNA-binding molecule-mediated ChIP (enChIP) using transcription activator-like (TAL) proteins and the clustered regularly interspaced short palindromic repeats (CRISPR) system. Locus-specific ChIP consists of locus tagging and affinity purification and can be combined with down-stream analyses such as mass spectrometry (MS), RNA sequencing (RNA-Seq), or next-generation sequencing to identify proteins, RNAs, or other genomic regions associated with the target genomic region. I will present our recent analyses of genome functions using locus-specific ChIP. We have successfully identified proteins associated with even a single copy locus of multicellular higher eukaryotes using locus-specific ChIP combined with MS. Furthermore, using enChIP-RNA-Seq, we identified RNAs associated with telomeres. To our knowledge, this is the first non-biased identification of RNAs associated with specific genomic regions. Finally, we've successfully identified interactions between genomic regions using iChIP-Seq and enChIP-Seq analyses, showing that these technologies would be key tools for elucidation of "4D Nucleome", dynamics of the three-dimensional structure of the nucleus.

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