Seminar

"DDM1 a SNF2 chromatin remodeler controls nucleosome composition for heterochromatin silencing"

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- **Date: 2:00PM/May. 2(Thur.)/2019**
- **Place: Auditorium(1F), Postech Biotech Center**
- **Inquiry: Prof. Kyuha Choi (279-2361)**
- **Abstract:**

Heterochromatin is mostly comprised of transposons and repetitive sequences, which contain epigenetic signatures such as DNA methylation and histone modifications. DECREASED DNA METHYLATION 1 (DDM1) encodes a SNF2 chromatin remodeling protein in Arabidopsis, and its mutations cause loss of DNA methylation largely in transposon loci. LSH and HELLS are the mouse and human homologs that are crucial for DNA methylation as well as embryo development. LTR retrotransposons are transcriptionally activated in ddm1 mutants. We recently sequenced cDNA products using Illumina and Oxford Nanopore technologies from virus-like particles to identify functionally intact LTR retrotransposons in ddm1 background.

Previous studies showed that the accessibility of DNA methyltransferases to heterochromatin is determined by nucleosome positions. Therefore, we were interested in the exact functions of DDM1 in heterochromatin silencing as a SNF2 chromatin remodeling protein. There are two major H3 histone variants, H3.1 and H3.3, deposited in heterochromatin and euchromatin, respectively. Our microscopic results suggest that H3.1 deposition was markedly lost in ddm1, whereas H3.3 was ectopically accumulated in heterochromatin. Our ChIP-seq experiments strongly support that heterochromatic nucleosomes containing H3.1, H3K27me1 and H3K9me2 are lost in ddm1, whereas euchromatic nucleosomes with H3.3 and H3K27me3 were ectopically deposited in heterochromatic areas.

Surprisingly, DDM1 was mainly found in euchromatin areas, shown as dispersed subnuclear localization in the nuclei of dividing cells. We confirmed the localization of DDM1 in euchromatin using ChIP-seq of DDM1-FLAG. In agreement with our observation, previous studies showed that LSH/HELLS subnuclear localization was more enriched in euchromatin than in heterochromatin. The mutation in DDM1 ATPase domain caused markedly enhanced localization in heterochromatin, suggesting DDM1 is recruited to heterochromatin at first place and shifted to euchromatin after chromatin remodeling. Taken together, DDM1 play roles in removing H3.3 nucleosomes from heterochromatic areas so that proper deposition of H3.1 and DNA methylation can take place for heterochromatin silencing.

***This seminar will be given in English.**

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