



CDB SEMINAR

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Monday, December 21, 2009

16:00~17:00 A7F CDB Seminar Room

Understanding the epigenetical functions of histone H3-lysine 56 modification in DNA repair, transcription, and chromatin structural regulation.

Summary

Histone modification plays important roles in a variety of DNA metabolisms. Acetylation of histone H3 on lysine 56 (H3-K56) is originally discovered in *S. cerevisiae* and is required for DNA repair, transcription, and histone deposition. This residue is located near the entry/exit point of DNA in the nucleosome suggesting a modification could affect nucleosome and chromatin structure. H3-K56 acetylation is also found in mammalian cells for DNA damage response. Importantly, this modification is also connected to core transcriptional network in human embryonic stem cells.

We identified the enzyme that catalyzes K56 acetylation in *S. cerevisiae*. The catalytic subunit, Rtt109, does not share primary sequence homology with the previously known histone acetyltransferase (HAT) enzymes, but revealed as the structural homolog of metazoan HAT, p300/CBP. Recently, it was reported that p300/CBP catalyzes K56 acetylation in human cells. Rtt109 alone is an inherently weak catalyst, however, Rtt109 can be dramatically stimulated by either of two highly conserved proteins, Asf1 or Vps75 that binds histones and facilitates their deposition onto DNA. Despite their shared ability to stimulate Rtt109 in vitro, Asf1 and Vps75 have different, rather, opposite roles in vivo. Together, multiple functions in chromatin regulation of K56 acetylation and its-related factors will be discussed.

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