Structural basis of genome folding and its functions in gene regulation and epigenetic inheritance

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http://www.ibp.cas.cn/lighLab/lighLabkyjz/

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Zoom meeting

Registration → https://forms.office.com/r/Gvsz2t3UHX

Abstract

Dynamics of chromatin structures plays a critical role in transcriptional regulation and all other DNA related biological processes. Previously, we reported the 11 Å resolution cryo-electron microscopy (cryo-EM) structures of 30 nm chromatin fibers reconstituted in the presence of linker histone H1, which reveals a left-handed double helix twisted by the repeating tetra-nucleosomal structural units. Recently, we have determined the 3.6 Å resolution cryo-electron microscopy (cryo-EM) structures of 30 nm chromatin fibers with linker histone H5, uncovering that asymmetries and polarities of nucleosomes play important roles in the folding of chromatin fibers. In addition, we also demonstrated that formation of 30-nm chromatin fibers greatly facilitates the faithful propagation of H2AK119ub1 and H3K27me3 during cell divisions. In summary, our study demonstrates that the tetranucleosome is a novel regulatory structural unit of chromatin fibers beyond the nucleosome, and provides crucial mechanistic insights into functions of chromatin fibers in transcriptional regulation and epigenetic inheritance.

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