IGMセミナー

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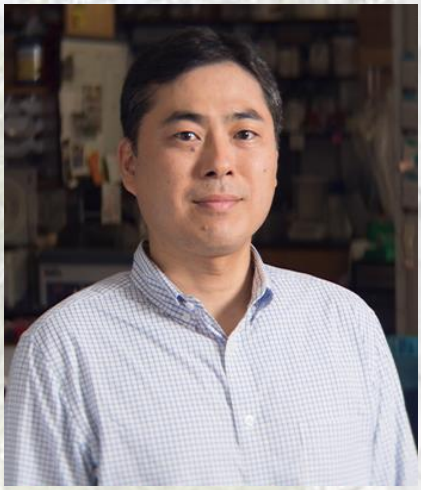
北海道大学遺伝子病制御研究所5Fセミナー室

Tidying Up the 3D Genome with Condensin and Cohesin

コンデンシンとコヒーシンによる3Dゲノム構造の組織化

Institute of Molecular Biology, University of Oregon

野間　健一　教授



［要旨］

How the structural maintenance of chromosomes (SMC) complexes, condensin and cohesin, govern the three-dimensional (3D) structure of the eukaryotic genome is an exciting research area. The condensin and cohesin complexes are highly conserved from simple systems, e.g., yeast cells, to the much more complex human system. Therefore, we have employed the fission yeast model and the latest 3D genomic approaches (in situ Hi-C and ChIA-PET), live cell imaging, and biochemistry to elucidate the 3D genome-organizing mechanisms. We have found that although condensin and cohesin often bind to the same loci, they mediate long- (100 kb – several Mb) and short–range contacts (< 100 kb), respectively, by bridging their binding sites, thereby forming the large and small domains (Kim et al. Nature Genetics 2016). The 300 kb – 1 Mb large domains are typically formed by condensin during mitosis. This mitotic domain organization does not suddenly dissolve, but rather diminishes gradually until the next mitosis (Tanizawa et al. Nature Structural & Molecular Biology 2017). Contrarily, the 50 kb small domains formed by cohesin are relatively stable across the cell cycle. Our study predicts that the condensin-mediated large domains serve as chromosomal compaction units. I will discuss how condensin and cohesin are recruited across the genome, how each mediates distinct genome-organizing events, and how they participate in nuclear activities such as transcriptional regulation and chromosomal dynamics. Moreover, we have recently shown that the human condensin complex functions in global 3D genome reorganization during the important process of cellular senescence. I will discuss our most recent findings of how condensin mediates cellular senescence in the human system.

世話人: 北海道大学遺伝子病制御研究所・大学院医学医学院　分子神経免疫学　村上正晃

共催: 日本生化学会北海道支部