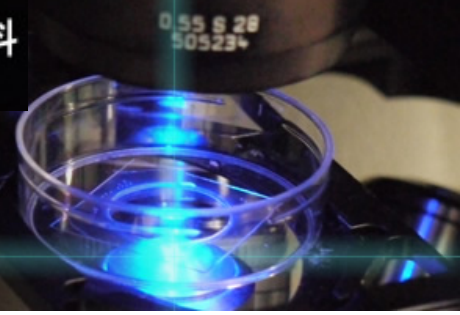
奈良先端科学技術大学院大学 バイオサイエンス研究科

NARA INSTITUTE of SCIENCE and TECHNOLOGY GRADUATE SCHOOLof BIOLOGICAL SCIENCES

研究科セミナー



Tidying Up the 3D Genome: From Epiginetics to 3D Genomics

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日時：1月24日（水）午後4時00分～午後5時00分

会場：研究科 大セミナー室

要旨

How eukaryotic genomes are organized into a 3D structure is an emerging and exciting research area. Disorganization of this structure is correlated with human disease, including cancer. Despite the clear importance of 3D genome organization to basic and medical research fields, genome-organizing mechanisms and their functions in distinct nuclear processes are poorly understood. Recent studies indicate that the structural maintenance of chromosomes (SMC) complexes, condensin and cohesin, are involved in gene contacts including enhancer-promoter interactions and topological domain organization, although how they establish the 3D genome structure and contribute to nuclear activities remains largely unclear. 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 large and small domains (Kim et al. 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. 2017). 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 (Iwasaki et al. 2015; Noma 2017). Furthermore, our recent study indicates that the human condensin complex functions in the global genome reorganization during the important process of cellular senescence (Yokoyama et al. 2015). I will also share our preliminary data showing how 3D genomic approaches can be sucssessfuly applied to the different systems to study virus latency and T cell regulation.

参考文献

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Iwasaki O, Tanizawa H, Kim KD, Yokoyama Y, Corcoran CJ, Tanaka A, Skordalakes E, Showe LC, Noma K. 2015. Interaction between TBP and condensin drives the organization and faithful segregation of mitotic chromosomes. *Molecular Cell* 59: 755-767.

Noma K. 2017. The yeast genomes in 3D: Mechanisms and Functions. *Annual Review of Genetics*. Vol. 51: 23-44.

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