

ASHBi SEMINAR

Molecular organization of the genome

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Date: Monday, 9th December 2019

Time: 16:00–17:00

Venue: Seminar Room 103&107, Faculty of Medicine Bldg. A

Since the discovery of the DNA double helix by Dr. Watson and Crick in 1953, a long-standing question is how the DNA molecule is higher-order structured in the cell as the genome. Recently we developed a method to analyze 3D structure of genomic DNA in cells at the resolution of its basic structural unit, the nucleosome, composed of DNA wrapping around histone octamers [1]. This method, named Hi-CO, can analyze 3D positions and orientations of every nucleosomes across the genome, based on next generation sequencing and super-computer analyses. The data revealed that nucleosomes in yeast genome are irregularly folded with reflecting epigenetic status at each genomic locus, and its arrangement comprises two basic folding motifs: α -tetrahedron and β -rhombus analogous to α -helix and β -sheet motifs in protein folding. In this seminar, I will present molecular-level organizational principles of the genome revealed by Hi-CO, as well as our recent challenges on super-sensitive disease diagnoses based on a 3D single molecule imaging technology [2] [3].

[1] Ohno, M., Ando, T., Priest, D. G., Kumar, V., Yoshida, Y., Taniguchi, Y. “Sub-nucleosomal genome structure reveals distinct nucleosome folding motifs”, *Cell* 176, 520-534 (2019)

[2] Taniguchi, Y., Choi, P. J., Li, G., Chen, H., Hearn, J., Babu, M., Emili, A. & Xie, X. S. Quantifying E. coli proteome and transcriptome with single-molecule sensitivity in single cells. *Science* 329, 533-538 (2010)

[3] Taniguchi, Y., Nishimura, K. Microscope, focusing unit, fluid holding unit, and optical unit. Patent #6086366 (JP), #9880378 (US), #2983029 (EP)

Organizer: Prof. Mitinori Saitou

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