1C4b Cell cycle dependent change in chromatin architecture of fission yeast revealed by chromatin live dynamics analysis.

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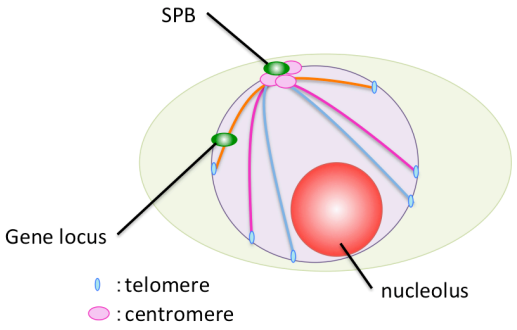
In eukaryotic cells, DNA is tightly packed in a higher order architecture, chromatin. The gene regulations should require rearranging the chromatin architecture to allow for the protein complexes to access the target genes. Recent biochemical analysis have successfully detected genome-wide chromatin interaction, but they cannot evaluate chromatin structural variability.

We have started to grasp how the chromatin architecture changes in nucleus directly by using live cell imaging with fluorescence microscopy. In collaboration with Prof. Hiraoka (Osaka Univ.) and Da-Qiao Ding (NICT), we made a series of yeast cells harboring the fluorescence protein labeling at specific target gene positions.

A set of time laps images for the dynamics of 15 gene positions were collected to see their average locations and dynamic properties inside nucleus. With the collected image data, we analyzed the chromatin dynamics of each chromosome in different cell cycle phases, which demonstrated that each chromatin changes its global architecture according to the cell phase.



In the presentation, we are going to discuss how the global chromosome architecture is related to gene regulations.