

## Hiroshi Ochiai

The Division of Gene Expression Dynamics, Medical Research Center Initiative for High Depth Omics, Medical Institute of Bioregulation, Kyushu University

**Wednesday, January 17, 2024**

16:00-17:00

1F Auditorium, DB Building C, Kobe / Broadcast online via Zoom

Zoom meeting URL will be announced on the event day by e-mail.

※This seminar is open only to BDR members

## Regulation of gene expression dynamics in pluripotent stem cells revealed by imaging analysis

### Summary

Our bodies are composed of a variety of cell types, each fulfilling unique functions through the specific expression of particular groups of genes. These gene expressions are precisely regulated by the interaction between the gene promoters and distal enhancers. This regulatory mechanism involves cell type-specific binding sites for transcription factors, playing a crucial role in the recruitment of RNA Polymerase II and transcription co-factors.

Furthermore, these transcription regulatory factors possess numerous intrinsically disordered regions, promoting the formation of condensates within the cell nucleus. It is believed that the formation of these condensates facilitates the physical proximity of enhancers and promoters, thereby promoting continuous transcriptional activation. Recent imaging analyses and single-cell RNA sequencing have confirmed dynamic transcriptional activation in various species, cell types, including mouse embryonic stem cells. Dynamic transcriptional activation, or transcriptional bursting, refers to the phenomenon where genes switch between a transcriptionally active state, continuously synthesizing RNA, and a transcriptionally inactive state, where little to no synthesis occurs. This transcriptional bursting is understood to gene expression levels and the heterogeneity in gene expression among cells. However, the specifics of how the condensate formation of transcription-related factors and the stability of enhancer-promoter interactions control transcriptional bursting remain unclear.

In this seminar, I will introduce transcriptional dynamics control mechanisms in mouse embryonic stem cells elucidated using state-of-the-art imaging techniques, including live single-gene imaging and sequential fluorescent in situ hybridization (FISH). In particular, I will provide the latest insights into the transcriptional bursting and their regulatory mechanisms, discussing how transcriptional bursting controls gene expression levels.

### References:

1. Ochiai, H., Ohishi, H., Sato, Y. & Kimura, H. Organization of transcription and 3D genome as revealed by live-cell imaging. *Curr Opin Struc Biol* 81, 102615 (2023).
2. Ohishi, H. et al. Transcription-coupled changes in higher-order genomic structure and transcription hub viscosity prolong enhancer-promoter connectivity. *bioRxiv* 2023.11.27.568629 (2023) doi:10.1101/2023.11.27.568629.
3. Ohishi, H. et al. STREAMING-tag system reveals spatiotemporal relationships between transcriptional regulatory factors and transcriptional activity. *Nat Commun* 13, 7672 (2022).
4. Ochiai, H. et al. Genome-wide kinetic properties of transcriptional bursting in mouse embryonic stem cells. *Sci Adv* 6, eaaz6699 (2020).
5. Ochiai, H., Sugawara, T. & Yamamoto, T. Simultaneous live imaging of the transcription and nuclear position of specific genes. *Nucleic Acids Res* 43, e127–e127 (2015).