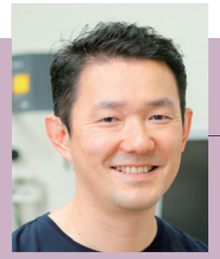

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Please replace [at sign] with @.

Research Interests

Epigenetics, Stem cell, chromatin, transcription

Education

2006	PhD, Department of Human Tumor Viruses, Graduate School of Biostudies, Kyoto University

Professional Career

2006 - 2009	Postdoc, National Institute of Genetics (NIG), JAPAN
2009 - 2014	Postdoc, Institute of Genetics and Molecular and Cellular Biology (IGBMC), Strasbourg, FRANCE
2014 - 2020	Associate Professor (PI), National Institute of Basic Biology (NIBB), JAPAN
2020 - present	Associate Professor (PI), NanoLSI, Kanazawa University.

Scientific Activities

2001 - 2006	Studies on Hepatitis C virus
2006 - present	Epigenetic regulation of cell lineage allocation

Honors

2015	The Young Scientists' Prize, The Commendation for Science and Technology by the MEXT
2015	Takenaka Promotion Prize

Publications

1. Miyanari Y, Torres-Padilla ME, Control of ground-state pluripotency by allelic regulation of Nanog, Nature, 483.470-473. 2012.
2. Miyanari Y*, Birling CZ. And Torres-Padilla ME*, Live visualization of chromatin dynamics using fluorescent TALEs, Nature Structural & Molecular Biology, 2013. *Corresponding authors
3. Kurihara M, Miyanari Y, et al., Genomic profiling of PML bodies reveals transcriptional regulation by PML bodies through the DNMT3A exclusion, Molecular Cell, 2020, Volume 78, Issue 3, 7 May 2020, Pages 493-505.e8.

Toward understanding transcriptional events deep inside the chromatin jungle

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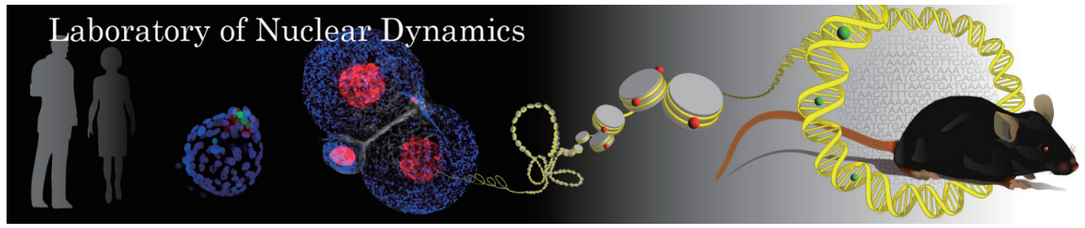
Chromatin is organized in a non-random fashion within 3D nuclear space. During developmental processes, the nuclear architecture is dramatically reconstructed, resulting in the establishment of cell-type specific nuclear organization. Defects in structural components of the nucleus are responsible for developmental aberrations and several human diseases. Remodeling of the nuclear architecture leads to spatial arrangement of genes, which could affect genome functions including gene expression. We aim to reveal the role of chromatin dynamics in cell lineage-allocation by deciphering the molecular mechanisms underlying the remodeling of nuclear organization and their effects on developmental gene expression, using mouse early embryos and embryonic stem (ES) cells as model systems. We uncovered allelic regulation of key gene for reprogramming, Nanog, is crucial for cell-lineage allocation in early mouse embryos [1,2]. We also studied a role of PML bodies in transcriptional regulation in ES cells [3]. In this seminar, I will present our recent studies to show you how we tackle our questions.

The promyelocytic leukemia (PML) body is a phase-separated nuclear structure physically associated with chromatin, implying its crucial roles in genome functions. However, its role in transcriptional regulation is largely unknown. We developed APEX-mediated chromatin labeling and purification (ALaP) to identify the genomic regions proximal to PML bodies. We found that PML bodies associate with active regulatory regions across the genome and with ~300 kb of the short arm of the Y chromosome (YS300) in mouse embryonic stem cells. The PML body association with YS300 is essential for the transcriptional activity of the neighboring Y-linked clustered genes. Mechanistically, PML bodies provide specific nuclear spaces that the de novo DNA methyltransferase DNMT3A cannot access, resulting in the steady maintenance of a hypo-methylated state at Y-linked gene promoters. Our study underscores a new mechanism for gene regulation in the 3D nuclear space and provides insights into the functional properties of nuclear structures for genome function.



References

[1] Miyanari Y, Torres-Padilla ME, Control of ground-state pluripotency by allelic regulation of Nanog, Nature, 483.470-473. 2012.

[2] Miyanari Y*, Birling CZ. And Torres-Padilla ME*, Live visualization of chromatin dynamics using fluorescent TALEs, Nature Structural & Molecular Biology, 2013. *Corresponding authors

[3] Kurihara M, Miyanari Y, et al., Genomic profiling of PML bodies reveals transcriptional regulation by PML bodies through the DNMT3A exclusion, Molecular Cell, 2020, Volume 78, Issue 3, 7 May 2020, Pages 493-505.e8.