



From a young BSJ member: advanced technologies encouraged me to dive into biophysics field

Kazuko Okamoto¹

Received: 15 January 2020 / Accepted: 11 February 2020 / Published online: 23 February 2020
© The Author(s) 2020

I am Kazuko Okamoto working as a researcher in RIKEN-Hiroshima University Collaboration Research Facility, which was opened in 2018. In the past 4 years, I have been working for single molecular imaging of transcription factors in living nuclei in order to understand the relationships between chromatin architecture and molecular dynamics of transcription factors. I have been fascinated by microscopy technology developing in biophysics field, including single molecular imaging; therefore, I started to study about the dynamics of transcription factors using such microscopes. Then, I joined The Biophysical Society of Japan (BSJ) 3 years ago, and they gave me a chance to write this commentary here as a young BSJ member.

I studied developmental biology in the early days of my scientific career; thus, I was estranged in the techniques and studies in the biophysics field. I have never thought that it is now possible to observe nucleoproteins including transcription factors at single molecular level and obtain spatio-temporal information inside living nuclei in the past.

The first trigger to get curious about the biological meaning of the relationship between chromatin architecture and transcription regulation was a CCCTC-binding factor (CTCF) protein which plays a role in the regulation of 3D architecture of chromatin and facilitates transcriptional insulation activity (Arzate-Mejía et al. 2018). When I was an undergraduate student, I used sea urchins

which are one of the common model organisms in the developmental biology field. I had observed fertilized sea urchin eggs with fluorescence-labeled CTCF in order to understand the relationships between transcriptional regulation and CTCF. At that time, my observation was just an analysis of the expression patterns during embryogenesis, and I had not reached the detailed behavior of CTCF inside living nuclei.

More than 10 years have passed since then; sequencing technology has greatly developed to detect the 3D chromatin architectures (Ohno et al. 2019), and single molecular imaging is now available inside living nuclei (Tokunaga et al. 2008, Coleman et al. 2015). My motivation to study the biological meaning of the relationship between chromatin architecture and transcription regulation revives, and I face the issue again.

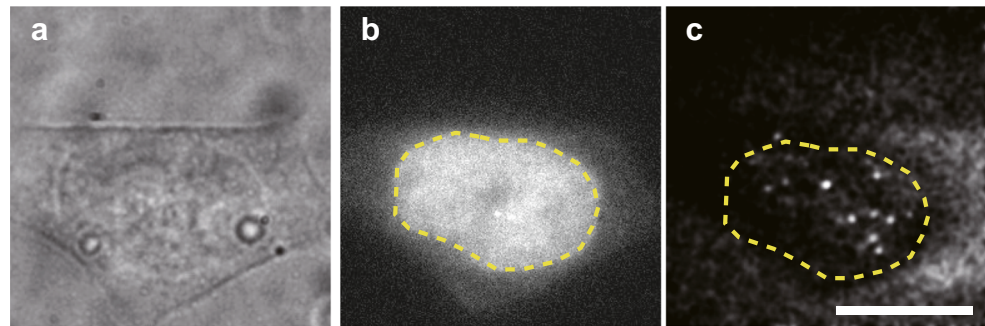
My question is very simple. Chromatin architectures control the transcription process by the binding of core transcriptional proteins, and then cellular states change. However, it is poorly understood how the chromatin architecture controls the binding of core transcriptional proteins. Now, I am enthusiastically involved in the observation of single molecular behavior of transcriptional proteins (Fig. 1).

In my case, advanced microscopic technology encouraged me to join biophysics field, and I am trying to understand the mechanisms of the interplay between chromatin architecture and transcription regulation again. The studies in transcription process will gain more attention in biophysical studies in Japan, and I am willing to contribute to the understanding of the transcription machinery by observing molecular behaviors of transcriptional proteins one by one. Finally, I would like to thank the BSJ for giving me the Early Career Presentation Award at the 57th Annual Meeting of BSJ in Miyazaki.

✉ Kazuko Okamoto
kazuko.okamoto@riken.jp

¹ Laboratory for Comprehensive Bioimaging, Center for Biosystems Dynamics Research, RIKEN, 3-10-23 Kagamiyama, The Research site in Hiroshima University, Higashi-Hiroshima, Hiroshima, Japan

Fig. 1 Example images of single molecular imaging of transcriptional proteins. **a** Bright-field image. **b** Epi-illumination of GFP-fused transcriptional proteins. **c** Single molecular image of GFP-fused transcriptional proteins. White dots indicate single molecules of transcriptional proteins. Scale bar, 5 μ m. Yellow dashed line indicates the nuclear membrane



Compliance with ethical standards

Conflict of interest The author declares that she has no conflict of interest.

Open Access This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>.

References

- Arzate-Mejia RG, Recillas-Targa F, Corces VG (2018) Developing in 3D: the role of CTCF in cell differentiation. *Development* 145: dev137729. <https://doi.org/10.1242/dev.137729>
- Coleman RA, Liu Z, Darzacq X, Tjian R, Singer RH, Lionnet T (2015) Imaging transcription: past, present, and future. *Cold Spring Harb Symp Quant Biol* 80:1–8. <https://doi.org/10.1101/sqb.2015.80.027201>
- Ohno M, Ando T, Priest DG, Kumar V, Yoshida Y, Taniguchi Y (2019) Sub-nucleosomal genome structure reveals distinct nucleosome folding motifs. *Cell* 176:520–534. <https://doi.org/10.1016/j.cell.2018.12.014>
- Tokunaga M, Imamoto N, Sakata-Sogawa K (2008) Highly inclined thin illumination enables clear single-molecule imaging in cells. *Nat Methods* 5:159–161. <https://doi.org/10.1038/nmeth1171>

Publisher's note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.