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Research Interests

biophysics, molecular motors, cytoskeletons, atomic force microscopy

Education

2001. Mar	B. Sci., Dept. of Phys, Fac. of Sci., Kanazawa Univ.
2003. Mar	M. Sci., Div. of Math. & Phys. Sci., Grad. Sch. Nat. Sci. & Tech., Kanazawa Univ.
2005. Sep	Ph.D., Div. of Basic Sci., Grad. Sch. Nat. Sci. & Tech., Kanazawa Univ.

Professional Career

2005 - 2010	Research Fellow (DC2 & PD), JSPS and Postdoctoral Fellow, CREST, JST
2010 - 2018	Assistant Professor & Associate Professor, Bio-AFM Frontier Research Center, Institute of Science and Engineering, Kanazawa University
2013 - 2017	PRESTO Researcher, JST
2018 - present	Professor, WPI-NanoLSI, Kanazawa University

Scientific Activities

2000 - 2008	Development of high-speed atomic force microscopy (HS-AFM)
2008- present	Biological application studies using HS-AFM and improvement of HS-AFM

Honors

2017	JSPS Prize
2013	Prize for Science and Technology (Development Category), The Commendation for Science and Technology by the Minister of Education, Culture, Sports, Science and Technology
2012	Young Researcher's Nanoprobe Technology Prize (JSPS Nanoprobe Technology 167)

Publications

1. **Kodera N**, Noshiro D, Dora SK, …, Longhi S, Ando T, "Structural and dynamics analysis of intrinsically disordered proteins by high-speed atomic force microscopy", ***Nat. Nanotech***. (in press).

2. Ngo KX, **Kodera N**, Katayama E, Ando T, Uyeda TQ, "Cofilin-induced unidirectional cooperative conformational changes in actin filaments revealed by high-speed atomic force microscopy", ***eLife 4***, 04806 (2015).

3. **Kodera N**, Yamamoto D, Ishikawa R, Ando T, "Video imaging of walking myosin V by high-speed atomic force microscopy", ***Nature 468***, 72-76 (2010).

Single-molecule visualization of intrinsically disordered Rett syndrome protein, MeCP2 by high-speed Atomic Force Microscopy

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High-speed atomic force microscopy (HS-AFM) directly visualizes biological molecules in action at nanometer spatial and sub-second temporal resolution. The unique performance of HS-AFM has been demonstrated by direct observations of many protein systems [1]. Importantly, HS-AFM can even resolve thin and flexible features of intrinsically disordered regions (IDRs), single polypeptide chains with height of ~0.5 nm, in a protein that could not be analyzed by any techniques at single molecule level. In some cases, dynamic structural transitions in IDRs between ordered- and disordered-conformations can be directly visualized [2-4].

Here, we applied HS-AFM to Methyl-CpG binding protein 2 (MeCP2). MeCP2 is a chromatin regulatory protein essential for brain development and activity in vertebrates. Specific missense and nonsense mutations in MeCP2 lead to the neurodevelopmental disorder, Rett syndrome (RTT). HS-AFM demonstrated that MeCP2 transitions between a fully extended dumbbell-like structure with the methyl DNA binding domain (MBD) and C-terminal domain (CTD) at the extremities, and a compact structure where the MBD and CTD interact in cis. The MBD within the full length protein equilibrates between unfolded and well folded states. MBD–CTD interactions stabilize the MBD in its folded state and are essential for MeCp2 plasticity (Fig. 1). The R106W, R133C, F155S and T158M RTT mutations all showed aberrant MBD dynamics compared to wild type. Furthermore, we observed sliding movements of MeCP2 along dsDNA, bridging two adjacent dsDNAs and DNA condensations by MeCp2. These results would gain insight into the molecular basis of RTT [5].

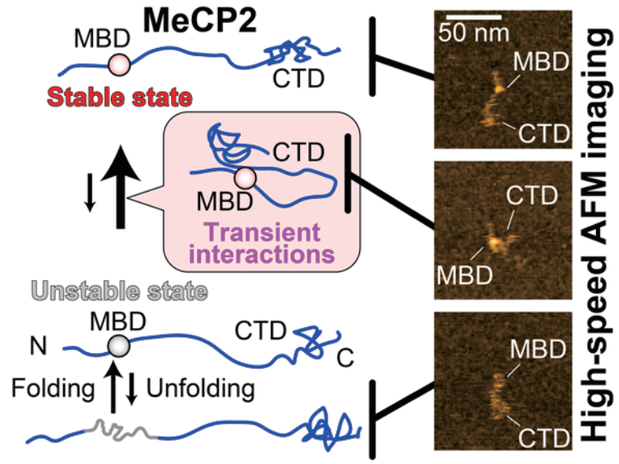

Fig.1 HS-AFM images and schematics showing that MBD-CTD interactions stabilize the MBD in its folded state.

References

[1] T. Ando, Curr. Opin. Chem. Biol., 2019, 51, 105-112.

[2] M. Hashimoto, N. Kodera, Y. Tsunaka, M. Oda, M. Tanimoto, T. Ando, K. Morikawa, and S. Tate, Biophys. J., 2013, 104, 2222-2234.

[3] N. Terahara, N. Kodera, T. Uchihashi, T. Ando, K. Namba, and T Minamino, Sci. Adv., 2017, 3, eaao4119.

[4] N. Kodera, D. Noshiro, SK. Dora, …, S. Longhi, and T. Ando, Nat. Nanotech. (in press).

[5] N. Kodera, AA. Kalashnikova, …, T. Ando, and JC. Hansen, (in revision).