Molecular Origin of 24 Hour Period in Cyanobacterial Protein Clock

Department of Life and Coordination-Complex Molecular Science
Division of Biomolecular Sensing

AKIYAMA, Shuji — Professor (April, 2012–)
ABE, Hitomi — Secretary

Circadian (approximately 24 h) clocks are endogenous time-keeping systems encapsulated in living cells, enabling organisms to adapt to daily fluctuation of exogenous environments on the Earth. These time-keeping systems, found ubiquitously from prokaryotes to eukaryotes, share the three characteristics. First, the circadian rhythmicity of the clocks persists even without any external cues (self-sustainability). Second, the period is little dependent on ambient temperature (temperature compensation). Third, the phase of the clock can be reset by external stimuli such as lightning, humidity, or temperature so as to be synchronized to the external phase (synchronization).

KaiC, a core protein of the circadian clock in cyanobacteria, undergoes rhythmic structural changes over approximately 24 h in the presence of KaiA and KaiB (Kai oscillator). This slow dynamics spanning a wide range of both temporal and spatial scales is not well understood, and is central to a fundamental question: what determines the temperature-compensated 24 h period?[1,2] The Kai oscillator reconstitutable *in vitro* is advantageous for studying its dynamic structure through a complementary usage of both X-ray crystallography and solution scattering, its transient response by using physicochemical techniques, and its molecular motion through a collaborative work with computational groups.

Our mission is to explore the frontier in molecular science of the cyanobacterial circadian clock from many perspectives. This Annual Report summarizes our recent activities from April 1, 2012 through August 31, 2012.

1. Tracking the Ticking of Cyanobacterial Clock Protein KaiC in Solution[3)]

The ATPase activity of KaiC *alone* is strongly correlated with the oscillatory period of the Kai oscillator. This correlation suggests that the ATPase activity of KaiC is one of the period-determining factors of the Kai oscillator. Hence, the determination of the structural change of KaiC interlocked with the ATPase activity is of great of importance.

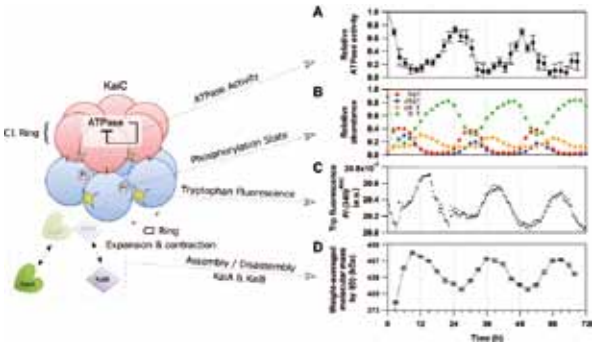

Figure 1. Circadian dynamics of cyanobacterial clock protein KaiC. The C1 and C2 domains in each protomer of KaiC are drawn as red and blue spheres, respectively. Expansion and contraction motions of the C2 ring (B, C) in solution serves as a timing cue for assembly/disassembly of KaiA and KaiB (D), and is interlocked with its C1 ATPase udder a control of negative-feedback regulation (A).

To track the dynamic transition of KaiC in real-time, we recorded the time evolution of intrinsic tryptophan (Trp) fluorescence from KaiC contained in the Kai oscillator. KaiC is a dumbbell-shaped molecule composed of tandemly duplicated N-terminal (C1) and C-terminal (C2) domains. Six protomers are assembled into a hexamer to attain a double-doughnut shape. Two tryptophan (Trp) residues located in the protomer-protomer interface of the C2 domain can serve as a sensitive probe to monitor the potential structural transition of the C2 ring. The intensity of the Trp fluorescence from KaiC revealed a rhythmic fluctuation with the period of approximately 24 h (Figure 1, panel C). So far as we know, this is the first experimental evidence that demonstrated a dynamic

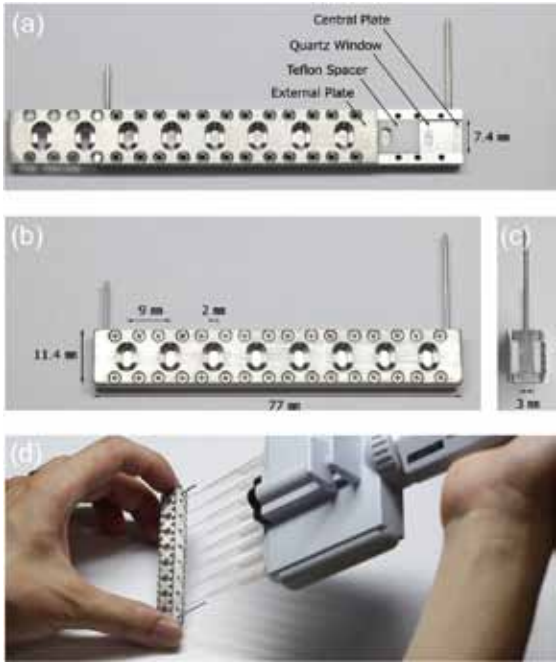

Figure 2. Octuple cuvette. (a) Photograph of the central plate covered by the quartz window, Teflon spacer and external plate, in that order. (b) Front view of the assembly. (c) Side view of the assembly. (d) Filling and removal of solutions using a commercially available eight-channel pipette. The sample volume of each chamber is 25 µl.

structural transition of the C2 ring of KaiC in solution.

Concomitantly with the Trp-fluorescence dynamics, KaiC underwent a periodic change in its phosphorylation state (Figure 1, panel B). KaiC has the two phosphorylation sites, *i.e.*, Ser431 and Thr432, in the C2 domain, and both residues are phosphorylated and then dephosphorylated in a programmed sequence during the phosphorylation cycle as follows: KaiCS/pT → KaiCpS/pT → KaiCpS/T → KaiCS/T (where 'S' represents Ser431, 'pS' represents phosphorylated Ser431, 'T' represents Thr432, and 'pT' represents phosphorylated Thr432). Interestingly, the Trp fluorescence was maximized at the timing when the KaiCpS/T state was populated (Figure 1, panels B and C). The result suggests the Trp fluorescence is an excellent measure of the phosphor-coupled transition of the C2 ring in KaiC.

2. Visualization of Dynamic Structural Changes of KaiC Using Small-Angle X-Ray Solution Scattering Technique[3,4)]

To visualize the C2-ring dynamics confirmed by tracking Trp fluorescence, we measured the small-angle x-ray scattering (SAXS) from KaiC in solution. To obtain the SAXS data of biological samples in solution, one must first record the scattering intensity of the sample (biomacromolecules in solution) and then that of the matching buffer in the separate

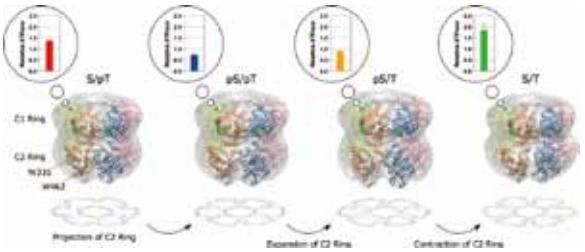

Figure 3. Expansion and contraction motions of C2 ring of KaiC interlocked with ATPase activity.

experiment, and finally find the difference between two intensities. The cuvette used for conventional SAXS experiments has only a single observation chamber in order to ensure the qualitative subtraction of the scattering contributed by the solvent molecules. On the other hand, the use of the single-chamber cuvette makes both the experiment and analysis time-consuming.

To record the SAXS pattern of KaiC both efficiently and qualitatively, we designed and constructed an eight-chamber cuvette (octuplet cuvette), each chamber of which was fabricated so uniformly to ensure the inter-chamber subtraction (Figure 2). The developed cuvette enabled us to acquire SAXS dataset of KaiC roughly 10 times faster without any significant degradation of data quality.

On the basis of the obtained SAXS data, we built low-resolution models of the KaiC hexamer as shown in Figure 3. The overall shape is almost unchanged in the transition from KaiCS/pT to KaiCpS/pT, whereas the radius of the C2 ring is dramatically enlarged in the subsequent transition from KaiCpS/pT to KaiCpS/T. The expanded C2 ring is partly contracted in the transition from KaiCpS/T to KaiCS/T, and is further contracted in the subsequent transition from KaiCS/T to KaiCS/pT. The present model suggests that KaiC ticks through expanding and contracting motions of the C2 ring.

The dynamic motion of the C2 ring uncovered throughout our study is chronobiologically meaningful, we believe, in terms of the elucidation of the key conformational change tightly coupled to the period-determining ATPase of KaiC. Our group is trying to improve spatio-temporal resolution of the experiments so as to draw a more dynamic and detailed picture of KaiC ATPase.

References

1) S. Akiyama, *Cell. Mol. Life Sci.* **69**, 2147–2160 (2012).
2) A. Mukaiyama, T. Kondo and S. Akiyama, *SPring-8 Research Frontiers 2011* 47–48 (2012).
3) Y. Murayama, A. Mukaiyama, K. Imai, Y. Onoue, A. Tsunoda, A. Nohara, T. Ishida, Y. Maéda, T. Kondo and S. Akiyama, *EMBO J.* **30**, 68–78 (2011).
4) S. Akiyama and T. Hikima, *J. Appl. Crystallogr.* **44**, 1294–1296 (2011).