Cyanobacterial circadian clock system through the chemistry of rhythm, structure, and evolutionary diversity

Shuji AKIYAMA[1,2]
[1] CIMoS, Institute for Molecular Science, NINS; [2] SOKENDAI

We have addressed a longstanding question in chronobiology: how is the period length of biological clocks determined and temperature-compensated? Clock genes and proteins constitute a negative-feedback loop to produce transcriptional-translational oscillation in eukaryotes. However, the transcription and translation themselves are intrinsically the fast events occurring in the order of minutes, and thus it remains unclear how and why the circadian systems made up of fast-moving bio-macromolecules can be so slow and stable [1].

To address the issue, we have used cyanobacterium *Synechococcus elongatus* PCC 7942 as the model system. The Kai oscillator reconstitutable *in vitro* by mixing three kinds of clock proteins called KaiA, KaiB, and KaiC is advantageous for studying slow but temperature-compensated 24 h dynamics through a complementary usage of X-ray crystallography [2], solution scattering [3, 4], and physicochemical techniques [5]. On the basis of our recent observations, I will discuss an emerging concept and origins of slow but temperature-compensated dynamics of the Kai oscillator.

Reference

[1] Akiyama S., *Cell Mol. Life Sci.* **69**, 2147-2160 (2012); [2] Abe J. *et al.*, *Science* **349**, 312-316 (2015); [3] Akiyama S. *et al.*, *Mol. Cell* **29**, 703-716 (2008); [4] Murayama Y. *et al.*, *EMBO J.* **30**, 68-78 (2011); [5] Mukaiyama A. *et al.*, *Sci. Rep.* **8**, 8803 (2018).