July 16-21, 2017 at UC San Diego, CA, USA

Host-parasite oscillation dynamics and evolution in a compartmentalized RNA replication system

Y. Bansho[1], T. Furubayashi[1], N. Ichihashi[1,2]
[1]Frontier Bioscience, Osaka University, [2]Information Science and Technologies, Osaka University,
* ichihashi@ist.osaka-u.ac.jp

Introduction: The ability of evolution is a prominent characteristic of living things, which produces the present-day complex and sophisticated living world. To understand how such evolutionary ability can appear from a mixture of molecules, we constructed an evolvable system from a reconstituted translation system of *Escherichia coli* and an artificial RNA genome that encodes RNA replicase[1]. In this system, the RNA genome replicate using the replicase translated from itself, and spontaneous mutations are introduced though replication error.

Result: We found that when we repeated the replication process, the RNA genome autonomously evolves according to the Darwinian principle only under a compartmentalized condition, indicating that a cell-like compartment is one of the requirements for evolution in this system. We further analyzed the evolutionary process in detail by using next-generation sequencing technology, and observed that evolution proceeds by repeating two overlapping phases: diversification and domination phases[2]. We also found that a parasitic replicator, which lost the replicase gene but retained recognition sequence for replicase, spontaneously appears in the system. The appearance of such parasitic replicators produced a Lotka-Volterra-like oscillation dynamics only when the system is compartmentalized and caused a large impact on the evolution of the RNA genome, implying that a parasitic replicator might play an important role on host evolution (Figure 1) [3]. We believe that this in vitro system can be a useful experimental model to understand a possible evolutionary scenario for a primitive life-like system to be closer to the present-day living things.

References: [1] Ichihashi et al. (2013) *Nature communications* 4:2494. [2] Ichihashi et al. (2015) *Molecular Biology and Evolution* 32:3205-3214. [3] Bansho et al (2016) *Proc Natl Acad Sci USA* 12:4045-4050

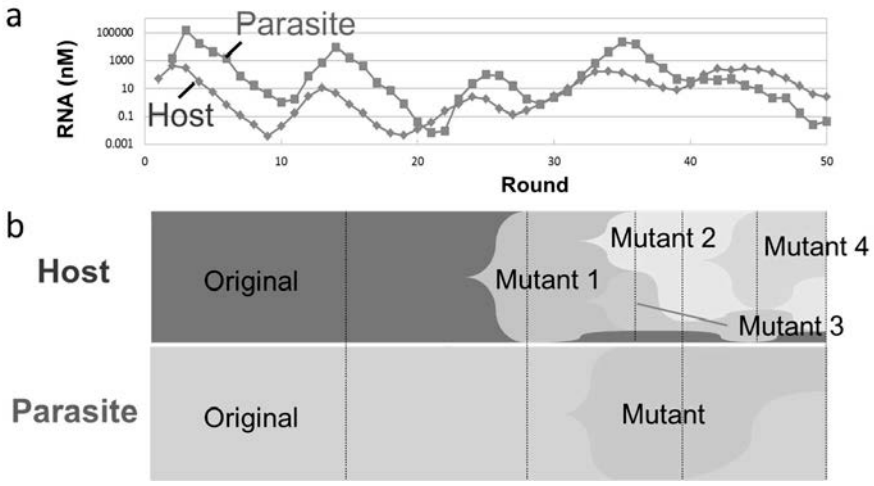

Figure 1 – a) Population dynamics of the artificial RNA genome (host) and parasitic RNA (parasite). The concentrations of both RNA oscillate when they are compartmentalized. b) Sequnece analysis of the host and parasite. Several mutants appeared and dominated the population, which explain the change in the oscillation pattern.