Can peptide-RNA coevolution provide unique opportunities for evolutionary innovation? K. Fujishima[1,2], D. Greenberg[3], Y. Kuruma[1], R. Mizuuchi[4], L. J. Rothschild[5] and M. A. Ditzler[5] [1]Earth-Life Science Institute (ELSI), Tokyo Institute of Technology, Ookayama, Meguro-ku, Tokyo, 152-8550 Japan. fuji@elsi.jp, [2]Universities Space Research Association (USRA), NASA Ames Research Center, Moffett Field, CA 94035-1000, USA [3]Brown University, Providence, RI 02912, USA [4]Graduate School of Information Science and Technology, Osaka University, Yamadaoka, Suita, 565-0871, Japan, [5]NASA Ames Research Center, Moffett Field, CA 94035-1000, USA.

Introduction: The two fundamental features of life are the "Energy harvest from the environment" and "Evolvability". In modern biology, energy harvest is achieved by chemical reaction, chemiosmosis and electron transfer, a reaction dominated by polypeptides, while evolvability of the biological system is maintained through information exchange between the nucleotide polymers (DNA/RNA). In the current biological system, functional RNA-protein complexes (RNPs) represent the most conserved molecular assemblies in cells, including ribosome that carry out information conversion from nucleotide to amino acid polymer.

In order to answer questions regarding the emergence and historical trajectories of the co-evolution of RNA and proteins leading to RNPs, we have established an *in vitro* system using a synthetic DNA library that combines a random 60 mer non-coding RNA region and a random 42 aa peptide-coding region. By performing the mRNA-display method in an *in vitro* translation system [1] and screening for a well characterized function (ATP-binding) as a measurement of fitness during the *in vitro* evolution [2], we were able to generate 10^{11} random RNPs and completed the first round screening for the potential ATP-binding RNA/peptide/RNP candidates providing the initial diversity upon which co-evolution can act. We are currently evolving the candidate molecules through three different paths (RNA only, peptide only, and RNP) in order to compare the round by round sequence trajectories through high throughput sequencing. Our goal is to validate whether two essential biopolymers can co-evolve through interaction to reach higher fitness faster than a single type polymer.

References:

[1] Nagumo Y. et al. (2016). *J Biochem*. 159:519–526. [2] Sassanfar M, Szostak JW. (1993) *Nature* 364:550–553.