Screening RNA-binding peptides using restricted set of amino acids

*Shota Nishikawa[1], Hidenori Watanabe[2], Naohiro Terasaka[3], Takayuki Katoh[3], Kosuke Fujishima[2]

1. School of Life Science and Technology, Tokyo Institute of Technology, 2. Earth Life Science Institute, Tokyo Institute of Technology, 3. Department of Chemistry, Graduate school of Science, The University of Tokyo

RNA stores the genetic information and catalyzes various chemical reactions. RNA with catalytic activities are called ribozymes, e.g. ribosome, whose function probably emerged in the context of a complex chemical environment. Especially, the functional cooperation between RNA and polypeptides appears to be quite important for the occurrence of ribozymes. Ribosome is consisted of RNA and polypeptides. Therefore, the interactions between RNA and polypeptides are considered to be essential in maintaining the structural stability and the function of ribosome (Lupas, A.N. & Alva, 2017).
In order to screen for RNA-binding peptides, we have recently established mRNA display technology (Reyes et al., in prep). mRNA display is a high-throughput technique to synthesize mRNA-peptide conjugate and identify peptide aptamers against proteins or RNA by using *in vitro* translation system. mRNA display allows for the preparation of peptide libraries with far greater complexity than is possible with other *in vitro* display methods, like phage display and ribosome display.
In this study, we screened for RNA-binding peptides from the libraries using restricted set of amino acids, which can serve as a model of the initial RNA-peptide complex. We investigated the peptide sequences by using mRNA display technology. So far, we designed DNA libraries against each RNA polymers (polyA, polyG, polyC, polyU (12mer)), and we succeeded in synthesizing the mRNA-peptide library for the polyC RNA by using *in vitro* translation system (PURE system). Now, we are performing an iterative selection against the RNA target (PolyC). In poster session, I would like to discuss the progress and problems of the method.

Keywords: Synthetic biology, Cell-free system, Screening

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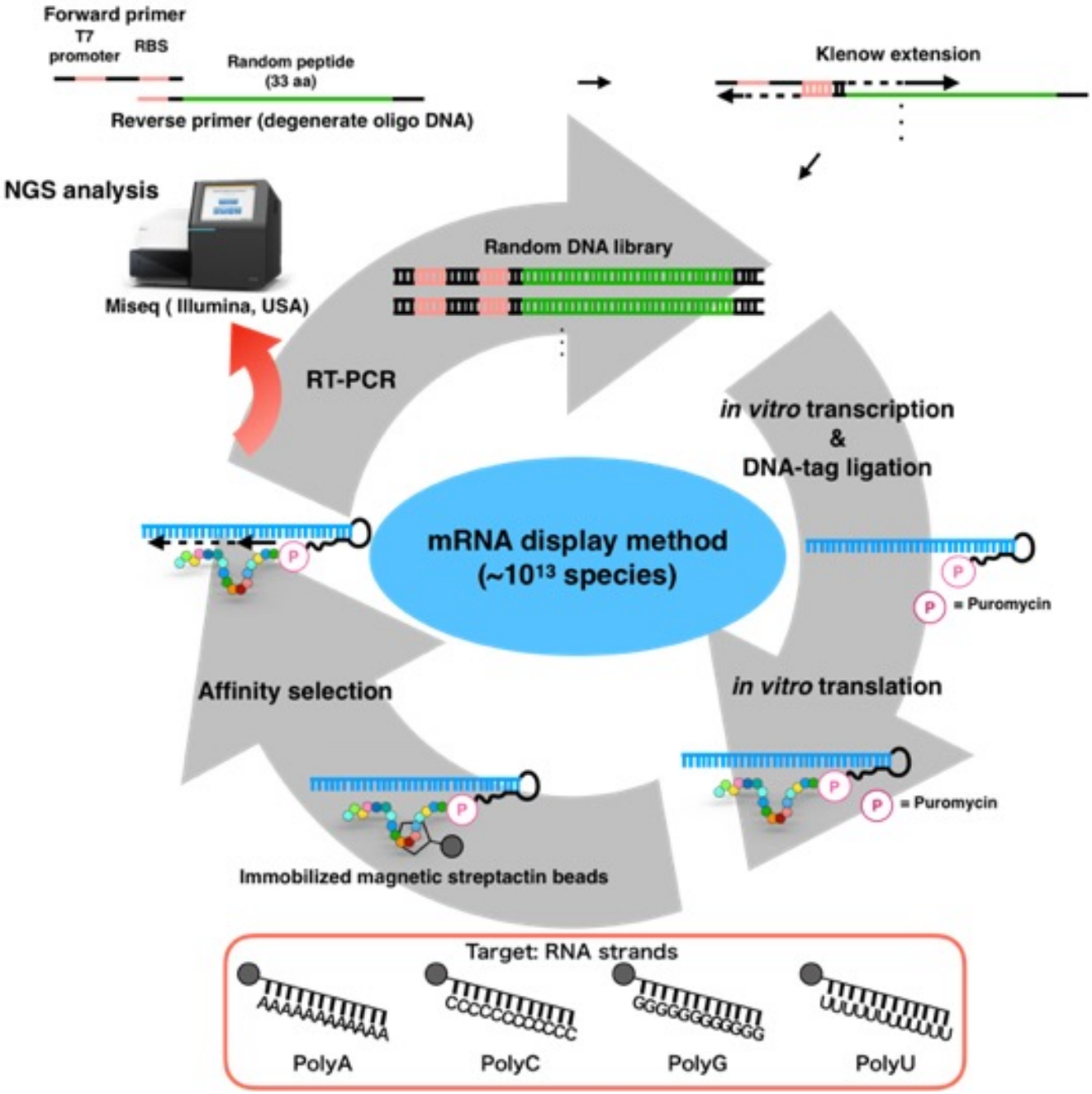

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