

Fiscal Year 2015, Tokyo Institute of Technology ASPIRE League Research Grant

Selected Research Project for Type 1 in FY2015

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	Position	Associate Professor
Co-researchers	HKUST	Qian Pei-Yuan, Chair Professor Division of Life Science
	KAIST	Byung-Kwan Cho, Assistant Professor Department of Biological Science
	NTU	Kevin Pethe, Associate Professor Lee Kong Chian School of Medicine & School of Biological Sciences
	Tsinghua	Ting Zhu, Investigator, Associate Professor School of Life Sciences
Subject of the research project		Discovery of valuable genes by massive sequencing and time lapse analysis of environmental RNAs.
Summary of the research project		<p>Development of a new method, named Time Lapse Analysis of Massive RNA Sequences (TILAMS), to isolate valuable genes from environmental DNA/RNA samples</p> <p>The utilization of enzyme proteins has become important for the pharmaceutical and chemical industries. When identifying new genetic coding for industrially valuable enzyme proteins, the “metagenomics” approach is frequently employed. Using the metagenomics approach, DNAs/RNAs are extracted from environmental microbial populations without isolating individual microbes, and DNA/RNA libraries are constructed. Then, genes of interest are screened from the libraries by hybridization experiments based on sequence homology or by evaluating enzyme activities of proteins. However, such screening methods</p>

are labor-intensive and time-consuming, so easier screening methods are demanded. In view of this situation, we hereby propose a new screening method named TILAMS.

In TILAMS, two microbial populations are prepared; one sample is treated with a target substrate and the other is untreated. RNAs are extracted from both samples over time, and RNA sequences are read massively using the next generation sequencer. Then, RNA species that are increased after addition of the substrate are found *in silico*. False positive RNAs are eliminated through bioinformatics analyses, identifying candidate enzyme proteins that act on the substrate. Since TILAMS can screen vast amounts of genes without using microbial cells, it is expected that the bottleneck in metagenomics research will be eliminated. The Nagoya Protocol, which restricts access to genetic resources over countries, was signed in 2010, so it is important to facilitate rapid access to such resources.