Fiscal Year 2016, Tokyo Institute of Technology ASPIRE League Research Grant

Selected Research Project for Type 1 in FY2016

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Subject of the research project		Discovery of valuable genes by massive sequencing and time lapse analysis of environmental RNAs
Summary of the research project		In order for society to break away from its dependence on fossil oil, microbiologists believe that producing valuable compounds from biomass feedstocks using microorganisms is effective. However, even in the case where the target valuable compounds are proved or estimated to be producible in microorganisms, it frequently happens that the appropriate metabolic pathway is unknown. Accordingly, such compounds are not produced in practical amounts. Therefore, in this grant application, we would like to solve technical problems present when identifying unknown metabolic pathways. We can suggest three reasons why the metabolic pathway remains unrevealed. First, if one microorganism is known to have the metabolic pathway of interest,

Summary of the research project	identifying enzyme genes which are responsible for the metabolic pathway is not so easy. Second, even if the metabolic pathway of interest is revealed to exist in a microorganism hidden in the environment, many microorganisms are not able to be isolated and cultured in the laboratory. Generally, 95% or more of the microorganisms on the earth are in the "viable but not culturable (VBNC)" state. Third, the metabolic pathway of interest may be present separately across multiple microorganisms. When these three problems are solved, the number of compounds that can be produced in a microorganism will increase dramatically. In order to solve the three problems, the use of a technique called "metagenome" is considered. In the metagenomic technique, 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, in the course of screening, no definitive generic method has been established, thus remaining a serious technical bottleneck. Therefore, in the study conducted via this grant application, we propose a new screening method that depends on massive RNA sequencing and an index of expression induction by the precursor compounds.