Desigh of 5'-UTRS for Precise Gene Expression in *Escherichia Coli*

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A large number of natural and unnatural products from microorganisms have attracted huge attention in the various industries including pharmaceutical and chemical industries. However, functional improvement of microorganisms meeting with commercial need is limited by the biological constraints developed during natural evolutionary process. "Metabolic Engineering" aims the purposeful redesign of the biological systems and requires the accurate information of the cellular metabolic networks and proper tools for the reconstruction of the biological systems. The goal of "Synthetic Biology" is to synthesize whole biological system or its subsystem intentionally and designing parts such as the regulatory elements and functional gene should be necessarily predictable. Although numerous regulatory elements can be applied for the modulation of gene expression, it is difficult to detect the proper variants required for balanced expression of multiple genes. In this study, we obtained 5'-UTR variants for precise gene expression in *Escherichia coli* using randomized 5'-UTRs, followed by superfolder GFP as a reporting system. Secondary structures of 5'-UTRs were strongly correlated with the expression level of superfolder GFP.