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Streptomyces strain improvement using interspecies DNA Microarray System

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The bacterial genus *Streptomyces* has long been appreciated for its ability to produce various kinds of medically important secondary metabolites such as antibiotic actinorhodin (ACT) in *S. coelicolor* and anti-tumor doxorubicin (DXR) in *S. peucetius*. Although traditional random mutation has been one of the most widely-practiced strategies for *Streptomyces* strain improvement, genome sequencing, targeted-gene disruption, and omics-guided reverse engineering approaches were successfully used to identify, analyze, and modify specific biosynthetic and regulatory genes involved in most of the secondary metabolites in *Streptomyces* species. Here, I present an example of rational polyketide pathway redesign strategies through *Streptomyces* genome engineering. Recursive comparative transcriptome analyses using *S. coelicolor* microarrays, followed by sequential targeted-gene disruptions of independently-functioning regulatory as well as precursor flux-controlling systems could be synergistically optimized for ACT and DXR productions in *Streptomyces* species.

Biography

Prof. Eung-Soo Kim, microbiologist and molecular biotechnologist, graduated from microbiology department, University of Minnesota, USA in 1994. He worked as a post-doctoral fellow at genetics department in Stanford University, USA during 1995-1997. Since 2001, he became the professor of biological engineering department at Inha University in Korea. He is currently an editorial board member of Society for Industrial Microbiology, USA, and an editor of Journal of Microbiology and Biotechnology. His current research focus is actinomycetes systems-&-synthetic biotechnology, omics-driven strain improvement, and novel drug-lead development.