

Reconstruction of Coenzyme B<sub>12</sub> Production Pathway in an Engineered *Escherichia coli*이지훈, 노명현, 임현규, 박성훈<sup>1</sup>, 정규열<sup>†</sup>포항공과대학교; <sup>1</sup>부산대학교(gyjung@postech.ac.kr<sup>†</sup>)

Coenzyme B<sub>12</sub> is one of the largest and the most structurally complicated chemical in nature. Because it plays essential role in various metabolic functions and in many enzymatic reactions as a cofactor, its economic production are highly meaningful. Due to its complex structure, chemical synthesis is virtually impossible. Instead, B<sub>12</sub> can be obtained from native producers such as *Pseudomonas denitrificans* and *Klebsiella pneumoniae*. However, a lack of genetic engineering tool for these microorganisms limits us to further develop B<sub>12</sub> high producer. Rather than engineering native producers, reconstruction of B<sub>12</sub> pathway in genetically well-known microorganisms such as an *Escherichia coli* could be more conceivable to achieve high production. In this study, we applied multiple synthetic biology based approaches in *E. coli*. Initially, the genes for B<sub>12</sub> biosynthesis in *P. denitrificans* were introduced; the genes were expressed under a strong promoter and optimized 5' untranslated regions (5'-UTR) for maximum expression. Then, an amplification of precursor pool and developing an efficient screening device allowed further strain improvement for increased B<sub>12</sub> production.