Transcriptome and fluxome analysis of a metabolically engineered *E.coli* L-threonine production strain

이광호[1,2], 박진환[1], 김태용[1], 이상엽[1,*]
[1]한국과학기술원 생명화학공학과; [2](주)CJ 바이오연구소
(leesy@kaist.ac.kr*)

Rationally designed L-threonine production strain was derived from *Escherichia coli* to elucidate crucial constraints which is affecting the biosynthesis of L-threonine. The L-threonine production strain(LKH9) was constructed by releasing regulatory mechanisms such as feedback inhibition and attenuation. The LKH9 carries a deletion of *lysA* gene, *metA* gene, and *tdh* gene while a point mutation was introduced in *ilvA* gene to decrease the activity of a corresponding gene. Furthermore, the *thrABC* operon was amplified by using pKK223-3 plasmid. With the DO-regulated fed-batch fermentation, this rationally designed strain produces 22g/l of L-threonine. Transcriptome analysis was performed to investigate the global gene expression changes in a fed-batch cultivation. Metabolic flux analysis demonstrated that the carbon flux towards L-threonine biosynthesis was successfully increased. Our strategy not only successfully developed L-threonine production strain by rationally designed strain development, but revealed new constraints requiring high productivity. (This work was supported by Korean Systems Biology Research Grant, M10309020000-03B5002-00000 from the MOST.)