In silico Drug Targeting of *Vibrio vulnificus* CMCP6

김태용, 김현욱, 정관준[1], 김수영[1], 이준행[1], 이상엽*
한국과학기술원 생명화학공학과 대사공학 연구실;
[1]전남대학교 의과대학 임상백신연구개발 사업단
(leesy@kaist.ac.kr*)

Vibrio vulnificus is a halophilic and highly human-pathogenic bacterium, showing very high mortality rate when infected. In order to facilitate the drug development process for this, we undertook *in silico* analysis to identify specific drug targets in the genome-scale metabolism of *V. vulnificus*. With a newly sequenced and annotated genome of *V. vulnificus*, we first reconstructed its genome-scale metabolic network using the KEGG database. Subsequently, we employed constraints-based flux analysis using MetaFluxNet and GAMS to identify essentiality of the genes comprising the metabolic network. Enzymatic reactions whose deletions result in the failure of biomass formation were primarily considered as drug targets. This set of candidates was then compared with the human genome sequence using BLAST to exclude candidates that might cause side-effects in the human body. [This work was supported by the Korean Systems Biology Research Project (M10309020000-03B5002-00000) of the Ministry of Science and Technology. Further supports by the LG Chem Chair Professorship, Microsoft, and IBM SUR program are appreciated.]