Genome-scale Reconstruction of the Metabolic Network in *Zymomonas mobilis* ZM4 for Ethanol and Succinic acid Overproduction

<u>김진년</u>, 이경윤, 박종명, 김태용, 윤홍석, 이상엽* 카이스트 (jinjin2112@kaist.ac.kr*)

Zymomonas mobilis ZM4 is famous Gram-negative bacterium that can efficiently produce ethanol from glucose, fructose, and sucrose by utilizing the Entner-Doudoroff pathway. The genome-scale metabolic model of *Z. mobilis* is reconstructed based on its annotated genes, literature, physiological and biochemical information to analyze the metabolic characteristics of this bacterium. The features of *Z. mobilis* were examined using constraints-based flux analysis. First, the physiological changes of *Z. mobilis* as it shifts from anaerobic to aerobic environments were investigated. Then the intensities of flux-sum, which is the cluster of either all ingoing or outgoing fluxes through a metabolite, and the maximum in silico yields of ethanol for *Z. mobilis* and Escherichia coli were compared and analyzed. [This work was supported by the Korean Systems Biology Research Project (20100002164) of the Ministry of Education, Science and Technology (MEST). Further support by the World Class University Program (R32-2008-000-10142-0) through the National Research Foundation of Korea funded by the MEST is appreciated.]