

Genome-scale reconstruction and *in silico* analysis of *Ralstonia eutropha* H16

손승범, 박종명, 김태용, 이상엽\*

KAIST

(leesy@kaist.ac.kr\*)

*Ralstonia eutropha* H16 is a Gram-negative lithoautotrophic bacterium that can utilize CO<sub>2</sub> and H<sub>2</sub> as sources of carbon and energy in the absence of organic substrates. It is the best known as a promising producer of polyhydroxyalkanoates (PHAs) from various carbon substrates and is an environmentally important bacterium that can degrade aromatic compounds. To make *R. eutropha* H16 a more efficient and robust biofactory, system-wide metabolic engineering to improve its metabolic performance is essential. Thus, we present the lithoautotrophic genome-scale metabolic model of *R. eutropha* H16 based on the annotated genome with biochemical and physiological information. The stoichiometric model, RehMBEL1391, is composed of 1391 reactions and 1171 metabolites. Constraints-based flux analyses were performed to refine and validate the genome-scale metabolic model under environmental and genetic perturbations. [This work was supported by the Korean Systems Biology Research Project (20100002164) of the Ministry of Education, Science and Technology (MEST) through the National Research Foundation of Korea. Further support by the WCU Program (R32-2009-000-10142-0) through the National Research Foundation of Korea funded by the MEST is appreciated.]