Use of metabolic pathway analysis for the improved succinic acid production

_____,　　　　,　　　　　*

(leesy@kaist.ac.kr*)

Mannheimia succiniciproducens has been known to produce a large amount of succinic acid. For improved production of succinic acid, we designed a small scale model of *M. succiniciproducens* that consists of central metabolic reactions including biomass equation. Among the thousands of EMs, we used a efficient strategy, pathway clustering analysis, by clustering optimal EMs that have the higher succinic acid production without loss of growth rates to identify metabolism. Pathway clustering analysis could show linear relationships with biomass or succinic acid. In this proof-of-concept study, the metabolism of *M. succiniciproducens* was designed to enhance succinate production by overexpressing *zwf* gene and *mdh* gene in LPK7 strain. [This work was supported by the Technology Development Program to Solve Climate Changes on Systems Metabolic Engineering for Biorefineries from the Ministry of Science, ICT and Future Planning (MSIP) through the National Research Foundation (NRF) of Korea (NRF-2012M1A2A2026556).]