

Improved succinic acid production based on proteomic and physiological analysis of  
*Mannheimia succiniciproducens*

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A genetically engineered succinic acid overproducing mutant, *M. succiniciproducens* LPK7, was also developed based on full genome sequence. In this study, 2-DE and tandem mass spectrometry were used to analyze proteome of the mutant cells at the exponential and stationary phases. These results were compared with those of the wild type strain (MBEL55E) to elucidate the global physiological and metabolic changes responsible for succinic acid overproduction. Several features including expression level changes of pyruvate metabolism associated enzymes, NAD(P)H-dependent enzymes, and ATP-dependent enzymes were described in detail. Based on these proteome analyses, we finally improved the succinic acid production. [This work was supported by the Korea Science and Engineering Foundation (KOSEF) grant funded by the Korea government (MOST) (2005-01294). Further supports by the LG Chem Chair Professorship, IBM SUR program, Microsoft, and by the KOSEF through the Center for Ultramicrochemical Process Systems are appreciated.].