

Proteomic Investigation of *Mannheimia* and its Use for Developing Metabolic Engineering Strategies

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Proteome of succinic acid overproducing mutant, *M. succiniciproducens* LPK7, at the exponential and stationary phases was compared with those of the wild type strain (*M. succiniciproducens* MBEL55E) to elucidate the global physiological and metabolic changes responsible for succinic acid overproduction. Through the statistical analysis, ATP associated enzymes, glycolytic enzymes, NADH-dependent enzymes, and pyruvate metabolizing enzymes were changed significantly in expression level. Two distinctively and exclusively expressed proteins associated with NADH were further characterized by gene deletion experiment. These results clearly suggest that further comparative proteome profiling under various genetic and/or environmental perturbations will reveal more new insights into the physiology and metabolic characteristics [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.].