

Proteomic Analysis of Protein Expression Profiles in Response to Environmental Perturbation in *Candida magnoliae* producing erythritol

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Erythritol is a low caloric and non-cariogenic sweetener produced industrially by *Candida magnoliae*. Proteomic analysis of *C. magnoliae* with two dimensional electrophoresis, mass spectrometry and database searching was tried to construct a proteome map and investigate the response to osmotic stress at a protein level. High osmotic condition at 300g/L influenced physiological properties of *C. magnoliae* and biosynthesis of erythritol. Among protein spots dominantly present at 29~96 kDa and pI 3~10, 22 proteins were identified to be involved in glycolysis, stress response and other essential metabolisms. Six proteins showed 3-times higher or less expression level in each osmotic condition. Heat shock protein Hsp60, mitochondrial RNA polymerase Rpo41 and ribonucleoside diphosphate reductase Rnr1 were down-regulated in high osmotic conditions. Bro1 interacting with components of PKC1-MAP kinase pathway and involving in the multivesicular bodies (MVB) pathway, catabolic enzyme Eno1 and a hypothetical protein were up-regulated in the same conditions.