

Analysis of genomic response of *B. subtilis* to salt stress using time series microarray data

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The adaptation to osmotic stress is crucial for growth and survival of *Bacillus subtilis* in its natural ecosystem. The time series microarray data of *B. subtilis* in the response to osmotic stress were used to examine temporal gene expression patterns. The microarray data were composed of four time points including 5, 10, 30, 60 min after the exposure to a sudden osmotic upshift. Differentially expression genes were identified and ranked by using the software package BATS (Bayesian Analysis of Time Series). Among 4000 genes, 449 genes showed differential expression patterns. The clustering results of these differential genes suggest that functionally related genes would seem to have similar expression profiles. The information of identified genes could be helpful for the understanding of cell adaptation process to an osmotic upshift in *B. subtilis*.