Inference of gene regulation network of B. subtilis under osmotic stress using state space model

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Bacillus subtilis is exposed to changing osmolarity, necessitating adaptive stress responses. Transcriptomic approach can provide a picture of the dynamic changes occurring in salt-stressed B. subtilis culutures. Thus, we analyzed the time series microarray data consisting of four time points including 5, 10, 30, 60 min after the exposure to a sudden osmotic upshift with a software TRANS-MNET based on state space model, that is a statistical dynamic model suitable for analyzing short time and/or replicated time series gene expression profiles. Among 449 genes showing differential expression patterns, the top-ranked 100 genes in the significance level were selected for the estimation of gene regulation networks. The genes within the same module showed similar expression patterns. The estimated gene network might be useful for the understanding of gene regulation structure in stress response of B. subtilis.