Elucidation of Metabolic Pathway under the Influence of Gene Regulatory Network

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1 Introduction

Recently, the reconstruction and analysis of genome-scale genetic and metabolic regulatory networks has become an area of active research. It requires the integration of existing knowledge as a first step towards systems biology. But few genome-scale models of organisms focus on the regulatory networks and none of them integrates all known levels of regulation. We focus on the networks that underlie three key cellular processes: transcriptional regulation, transcription and translation, and metabolism (Fig. 1). In the present study, we have developed elucidation system of metabolic pathway influenced by the gene regulatory network. Using this system, we examine which metabolic reactions are affected by the deleted genes in the minimum genome Batilis subtilis :MGB874.

2 Method

In this work we reconstructed the genetic and metabolic regulatory networks associated to metabolism of Bacillus subtilis (transcriptional regulations and modulation of enzymatic activities collected from KEGG, DBTBS, and many other published literatures). The transcriptional regulatory network includes the interactions between transcription factors and their target genes that lead to activation or repression of
transcription. In this study, regulation relations do not include upstream environmental and intracellular signal transductions that regulate transcription factor activity or any additional regulatory mechanisms but include only direct transcriptional regulations. Next, the relations from gene to reactions were determined via enzymes or enzyme modules which are products of genes. We collected the related information from KEGG as well as from other published literatures (manually curated).

3 Results and Discussion

We construct the integrated map from regulation to transcription and translation to metabolic reactions and examined it thoroughly. Table1 shows this summary of the integrated map.

![Table 1](image)

The minimum genome *Batilis subtilis*:MGB874 can survive with lowest number of genes. Using the information that which genes are deleted in *Batilis subtilis*:MGB874, we investigated which reactions are affected in the integrated map. Figure2 shows the part of the integrated map affected by the deleted genes.

![Figure 2](image)

Total 76 genes corresponding to enzymes and 12 regulation factor genes associated to the integrated map are deleted (marked by red color in Fig 2) in *Batilis subtilis*:MGB874 compared to wild type *Batilis subtilis*. And total 145 reactions are affected by gene deletions. As future work, we will estimate the effect to growth and changes of metabolic networks due to gene deletions and expression data and so on.

References