

The Role of Gene Expression Regulation in Yeast Cell Cycle Pathway

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1 Introduction

We have constructed a cell cycle regulatory pathway of the yeast *Saccharomyces cerevisiae* as a knowledge base of molecular interactions (KEGG[1]/BRITE) and graphical networks (KEGG/PATHWAY). It has been reported that about 800 genes are cell cycle-regulated in yeast according to the microarray experiment [2], but it is not clear what fraction of the cell cycle regulatory pathway is controlled at the level of gene expressions. Generally speaking, the cell cycle regulatory pathway consists of complex molecular interaction networks including phosphorylation/dephosphorylation, molecular bindings, and proteolysis, besides gene expression control. To determine the role of gene expression regulation, we have mapped the microarray gene expression data onto our KEGG cell cycle regulatory pathway.

2 Method and Results

The KEGG cell cycle pathway map currently consists of 100 genes. In the article of Spellman's, they mentioned that there were 104 cell cycle regulated genes determined by traditional methods (known regulated gene : KRG) but they could not identify 9 genes of them as cell cycle regulated by their microarray analysis due to possible noises in their data. By using a threshold which separates 9 genes from 104 genes in their expression data, we could divide 100 genes on our KEGG cell cycle pathway map into 62 identifiable genes and 38 non-identifiable genes based on the changes in Spellman's microarray gene expression data only. Among them, 27 out of 62 genes were also identified as KRGs and 4 out of 38 genes were also identified as non-KRGs (Table 1).

Table 1: Number of known cell cycle regulated genes on the KEGG pathway.

	KRGs	KEGG	KRGs on KEGG
identified	95	62	27/62
not identified	9	38	4/38

3 Discussions

3.1 Cyclin Dependent Kinase

Cdc28 is the only cyclin dependent kinase (CDK) in yeast and its activity is regulated by cyclins (Cln1-3, Clb1-6) depending on the cell cycle phases. So, if cyclins are transcriptionally regulated, the CDC28 gene does not need to be regulated by gene expression. Consistently, CDC28 gene expression could not be identified by Spellman's gene expression data (Fig. 1).

