Genome-Wide Mapping of Binding Sites Reveals Multiple Biological Functions of the Transcription Factor Cst6p in Saccharomyces cerevisiae

In the model eukaryote Saccharomyces cerevisiae, the transcription factor Cst6p has been reported to play important roles in several biological processes. However, the genome-wide targets of Cst6p and its physiological functions remain unknown. Here, we mapped the genome-wide binding sites of Cst6p at high resolution. Cst6p binds to the promoter regions of 59 genes with various biological functions when cells are grown on ethanol but hardly binds to the promoter at any gene when cells are grown on glucose. The retarded growth of the CST6 deletion mutant on ethanol is attributed to the markedly decreased expression of NCE103, encoding a carbonic anhydrase, which is a direct target of Cst6p. The target genes of Cst6p have a large overlap with those of stress-responsive transcription factors, such as Sko1p and Skn7p. In addition, a CST6 deletion mutant growing on ethanol shows hypersensitivity to oxidative stress and ethanol stress, assigning Cst6p as a new member of the stress-responsive transcriptional regulatory network. These results show that mapping of genome-wide binding sites can provide new insights into the function of transcription factors and highlight the highly connected and condition-dependent nature of the transcriptional regulatory network in S. cerevisiae.

Transcription factors regulate the activity of various biological processes through binding to specific DNA sequences. Therefore, the determination of binding positions is important for the understanding of the regulatory effects of transcription factors. In the model eukaryote Saccharomyces cerevisiae, the transcription factor Cst6p has been reported to regulate several biological processes, while its genome-wide targets remain unknown. Here, we mapped the genome-wide binding sites of Cst6p at high resolution. We show that the binding of Cst6p to its target promoters is condition dependent and explain the mechanism for the retarded growth of the CST6 deletion mutant on ethanol. Furthermore, we demonstrate that Cst6p is a new member of a stress-responsive transcriptional regulatory network. These results provide deeper understanding of the function of the dynamic transcriptional regulatory network in S. cerevisiae.

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