Global Transcriptional Analysis of Adaptive Response to Methylation Damage in *Escherichia coli*

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Escherichia coli has a specific machinery for responding to methylation damages. This adaptive response is occurred Ada-dependently when the environmental concentration of methylating agents is high.[1] In this study, the adaptive response was investigated at transcriptome level using DNA microarray, followed by real-time PCR analysis. The growth-dependent transcriptome levels were compared between the wild type and *ada* deletion mutant strains with or without treating methyl methanesulfonate (MMS). It was revealed the expression levels of some genes relating to energy metabolism and propionate metabolism were different between the strains, but there were small differences between the two when MMS was not added, indicating the roles of Ada in the high concentration of methylating agents. In addition, Ada-dependently regulated gene could be divided into the *ada*- and *alk*A-like regulated genes based on their expression profiles, suggesting the different regulatory mechanisms among them.[2] Surprisingly, some genes which were not directly related with the adaptive response showed Ada-dependent regulations and had putative Ada boxes, suggesting the additional roles of Ada as a transcription factor. [This work was supported by the Korean Systems Biology Research Grant (M10309020000-03B5002-00000) from the Ministry of Science and Technology. Further supports by LG Chem Chair Professorship and the IBM SUR program are greatly appreciated.]

References

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