

Combined Transcriptome and Proteome Profiling of *Escherichia coli fadR* Mutant

Jin Hwan Park¹, Jeong Wook Lee¹, Byung Hun Kim¹, Jong Hyun Choi¹, and Sang Yup Lee^{1,2}

¹Department of Chemical & Biomolecular Engineering and BioProcess Engineering Research Center,

²Department of BioSystems and Bioinformatics Research Center, Korea Advanced Institute of Science and Technology

TEL: +82-42-869-3930, FAX: +82-42-869-8800

Currently, system level approaches using many different omics methods such as transcriptomics, proteomics, fluxomics and metabolomics are available to improve host strains by identifying the physiological effect of global regulators. In this study we examined the regulatory circuit of FadR, which is one of the global regulators in *Escherichia coli*, at both transcriptional and translational level. In *E. coli* expression of the genes of fatty acid metabolism is regulated by FadR. It negatively regulates the expression of fatty acid degradative genes, and positively regulates the expression of fatty acid biosynthetic genes. In this study, the carbon source-responsive global effect of *fadR* knockout was identified by transcriptome and proteome profiling in the presence of glucose or oleic acid as a carbon source. Growth-associated regulation of FadR was also identified by clustering genes according to cell concentration. Genes for cell structure and transport, and energy metabolism showed the similar regulation pattern in the presence of glucose and oleic acid. Interesting result from the proteome data is that AceA (isocitrate lyase) was not increased at all at translational level in contrast with the transcriptome result that showed much higher expression level in *fadR* knockout mutant. We can conclude that the different regulatory mechanism exists at translational level.

[This work was supported by the Korean Systems Biology Research Grant (M10309020000-03B5002-00000) from the MOST. Further supports by the BK21 program, LG Chemicals Chair Professorship and IBM SUR program are appreciated.]

References

1. John, E. Cronan, Jr., *Escherichia coli* FadR positively regulates transcription of the *fabB* fatty acid biosynthetic gene (2001), *J. Bacteriol.* Vol. 183, 5982-5990.
2. Concetta, C. DiRusso., Characterization of the fatty acid-responsive transcription factor FadR (1997), *J. Biol. Chem.* Vol. 272, 30645-30650.