

### Transcriptome profiling of *Escherichia coli fadR* mutant

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The identification of regulatory circuit of global regulators is a prerequisite for construction of industrially useful strains. In this study we examined the regulatory circuit of FadR, which is one of the global regulators in *Escherichia coli*, at transcriptional level using DNA microarray experiment. In *Escherichia coli* expression of the genes of fatty acid metabolism is regulated by FadR. It negatively regulates the expression of fatty acid degradation-related genes, and positively regulates the expression of fatty acid biosynthetic genes by binding the promoter region of corresponding genes. The global effect of *fadR* knockout is identified by transcriptome profiling in the presence of glucose or oleic acid as a carbon source. In the presence of glucose, 190 genes are up-regulated (fold change ratio > 2.0) and 270 genes are down-regulated (fold change ratio < 0.5) in *fadR* knockout mutant. With oleic acid as a carbon source, 78 genes are up-regulated and 145 genes are down-regulated in *fadR* knockout mutant. With glucose, more genes are down or up-regulated than with oleic acid.

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