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**Effect of Gene Inactivation of *arcA* and/or *fnr* in *Escherichia coli*
on Anaerobic Metabolic Pathway**

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E. coli has two distinct global transcriptional regulators, ArcBA and FNR proteins, encoded by *arcBA* and *fnr* gene, respectively. The two component sensor-regulatory system, ArcBA system regulates the expression of genes encoding enzymes involved both aerobic and anaerobic catabolic pathways. The FNR plays a major role in control of the transcription of anaerobically regulated genes. Here, Using knockout mutant strains of *arcA* and/or *fnr* of *E. coli* MG1655, metabolites were analyzed to investigate the effects of each gene inactivation, comparing with that of wild type under anaerobic conditions with glucose as a carbon source. The profile of metabolites was examined in log and stationary phase. Altered distribution of carbon recovery products was examined in each mutant, meaning each genetic perturbation affected the central metabolic network and impacted the carbon flow through the metabolic branch to adapt to given conditions. Also, we investigated the effects of Arc and FNR systems on expression of genes involving the metabolic system. Transcriptional level of the 15 genes involved in central anaerobic pathway and other key redox regular mechanisms were investigated by quantitative RT-PCR analysis. In all the mutants, changed pattern of gene expression was observed by the inactivation of *arcA* and/or *fnr*, meaning rearrangement of global regulation of both gene and protein level for maintenance of proper cellular redox balance in each strain.