Transcript and Protein Level Analysis of Cross-regulation in Phosphate Starvation Response in Escherichia coli

Yeonjae Kang¹, Jong Hwan Beak¹, Sang Yup Lee^{1,2}

¹Department of Chemical and Biomolecular Engineering,
Bioprocess Engineering Research Center, KAIST

² Department of BioSystems and Bioinformatics Research Center, KAIST

TEL: +82-42-869-5970, FAX: +82-42-869-8800

Abstract

Phosphorus is the essential cellular element as major building blocks of various biomolecules, and its metabolism is closely related with diverse metabolic pathways including central carbon metabolism. *Escherichia coli* has a PhoR-PhoB two-component regulatory system to detect and respond to environmental phosphate concentration. Additionally, this system is connected to other regulatory systems and cross-regulated with them. In this study, the multiple controls of pho regulon and cross-regulation were investigated at transcript and protein levels using DNA microarray followed by real-time PCR analysis and fluorescence resonance energy transfer (FRET) analysis. From this study, the interactions among PhoB, PhoR, PhoU, and CreC could be revealed in phosphate limiting condition in *E. coli*, and this is valuable to understand the cellular physiology relating to the cross-regulation of phosphate starvation response.

Acknowledgments: This work was supported by the Korean Systems Biology Research Grant (M10309020000-03B5002-00000) from the Ministry of Science and Technology. Further supports by the BK21 program and LG Chemicals Chair Professorship are greatly appreciated.

References

- 1. Vaknin, A. and Berg, H.C., Single-cell FRET imaging of phosphatatase activity in the E. coli chemotaxis system (2004), PNAS, 101: 17072-17077.
- 2. Eguchi, Y.K., and Utsumi, R., Anovel mechanism for connecting bacterial two-component signal-transducetion systems (2005), TRENDS in Biochemical Sciences, 30: 70-72.