

Characterization of Transcriptional Regulator ArgR in *Corynebacterium glutamicum*

이수연, 민지호*

전북대학교

(jihomin@chonbuk.ac.kr*)

ArgR, the master regulator to control the arginine biosynthesis, represses transcription of arg operon. Repression of the arg operon results in decrease of ornithine production, an intermediate metabolite in arginine biosynthesis in *Corynebacterium glutamicum*. In this study, we constructed pEMBTL-SY1 which is able to over produce ArgR in *C. glutamicum* and analyzed DNA-binding affinities of ArgR by ChIP assay. The expression level of ArgR in the plasmid-carrying *C. glutamicum* was increased than wild-type strain. On the other hands, it was not increased to DNA-binding affinity of ArgR on the arg operon and the level of ornithine production. In addition we investigated the DNA-binding affinity of ArgR on the arg operon and the ornithine production in the presence of five metabolites which are Glu, Orn, Cit, Arg, and Pro as feedback controlling effectors. ChIP assay revealed that the ArgR-binding affinity on the arg operon was changed by supplemented metabolites, and this result was consistent in the change of ornithine production. It means that the regulation of ornithine biosynthesis by ArgR depends on DNA-binding affinity on the arg operon regulated by feedback controlling effectors.