MS03-2-1 SorC protein family: the structural insight into their DNA recognition #MS03-2-1

M. Nováková¹, J. Škerlová¹, J. Brynda¹, I. Sieglová¹, M. Fábry², P. Řezáčová²

¹Institute of Organic Chemistry and Biochemistry, CAS - Prague (Czech Republic), ²Institute of Organic Chemistry and Biochemistry, CAS; Institute of Molecular Genetics, CAS - Czech Republic - Prague (Czech Republic)

Abstract

SorC family is a family of bacterial transcription regulators involved in the control of carbohydrate metabolism and quorum-sensing (1,2). SorC protomers consist of a DNA-binding domain (DBD) and an effector-binding domain (EBD). Several SorC structures have been determined so far (3-6), however, there has been no structural information of their complex with the cognate DNA.

We performed X-ray crystallographic studies of two functionally characterized SorC family members from Bacillus subtilis: bsDeoR and bsCggR. Each selected protein represents one of the subgroups that are recognized within the family. To gain insight into the protein/DNA atomic interactions, we determined 2.3 and 2.1 Å resolution crystal structures of bsDeoR and bsCggR DBDs in complex with DNA duplexes representing halves of the operator sequences. However, the molecular packing in the crystal allowed us to make assumptions on recognition of the full operator sequence.

Besides the interest of basic research, our work has potential even for a biotechnological industry, where, recently, transcriptional repressors started to be used as molecular sensors of the metabolic flux of microorganisms.

References

1. Fillinger, S., Boschi-Muller, S., Azza, S., Dervyn, E., Branlant, G. and Aymerich, S. (2000) Two glyceraldehyde-3-phosphate dehydrogenases with opposite physiological roles in a nonphotosynthetic bacterium. J Biol Chem, 275, 14031-14037.

2. Taga, M.E., Semmelhack, J.L. and Bassler, B.L. (2001) The LuxS-dependent autoinducer AI-2 controls the expression of an ABC transporter that functions in AI-2 uptake in Salmonella typhimurium. Mol Microbiol, 42, 777-793.

3. Řezáčová, P., Kožíšek, M., Moy, S.F., Sieglová, I., Joachimiak, A., Machius, M. and Otwinowski, Z. (2008) Crystal structures of the effector-binding domain of repressor Central glycolytic gene Regulator from Bacillus subtilis reveal ligand-induced structural changes upon binding of several glycolytic intermediates. Mol Microbiol, 69, 895-910.

4. Škerlová, J., Fábry, M., Hubálek, M., Otwinowski, Z. and Řezáčová, P. (2014) Structure of the effector-binding domain of deoxyribonucleoside regulator DeoR from Bacillus subtilis. FEBS J, 281, 4280-4292.

5. de Sanctis, D., McVey, C.E., Enguita, F.J. and Carrondo, M.A. (2009) Crystal structure of the full-length sorbitol operon regulator SorC from Klebsiella pneumoniae: structural evidence for a novel transcriptional regulation mechanism. J Mol Biol, 387, 759-770.

6. Ha, J.H., Eo, Y., Grishaev, A., Guo, M., Smith, J.A., Sintim, H.O., Kim, E.H., Cheong, H.K., Bentley, W.E. and Ryu, K.S. (2013) Crystal structures of the LsrR proteins complexed with phospho-Al-2 and two signal-interrupting analogues reveal distinct mechanisms for ligand recognition. J Am Chem Soc, 135, 15526-15535.