MS7-P12 Structural analysis of response regulator spr1814 from *Streptococcus pneumoniae* in the absence and presence of the phosphoryl analog beryllofluoride

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Organisms that live in a changing environment sense and respond to a wide variety of stimuli through a complex network of signalling systems. Of these, two-component systems (TCSs) are the common pathways by which bacteria sense and respond to their environments. Typical bacterial TCSs consists of a membrane-bound histidine kinase (HK) and a cytosolic cognate response regulator (RR) protein. In the simplest form, a HK catalyzes its own auto-phosphorylation of conserved histidine residue and the phosphoryl group is relayed to the conserved aspartic acid residue of RR. Phosphorylated RRs in turn undergo a conformational change that induces the appropriate cellular response. In general, phosphorylated RRs function as transcription factors triggering the expression of target genes. According to the structure of the DNA-binding domain, spr1814, the RR that is studied here, belongs to the NarL/FixJ subfamily, which is characterized by a helix-turn-helix (HTH) DNA-binding domain, and accounts for approximately 19 % of all response regulators. Until now, there have only been four full-length structures of NarL/FixJ subfamily identified. Despite of a similar overall structure in terms of their receiver and effector domains, different contacts between domains have been observed. The most extensive interdomain interactions were found to occur in NarL, DosR and VraR in very distinct manners, but few contacts were observed in StyR. Although they have different domain arrangements, the NarL/FixJ subfamily RRs have been suggested to release the blockage of the effector domain from the receiver domain upon phosphorylation. Here, we determined the crystal structure of full-length spr1814 in the presence and absence of a phosphate analog beryllium fluoride . This allows us to describe the conformational changes of spr1814 upon phosphorylation. The phosphorylation of conserved aspartic acid residue of N-terminal receiver domain triggers a structural perturbation at the α4-β5-α5 interface, leading to the domain reorganization of spr1814, and this is achieved by a rotational change in the C-terminal DNA-binding domain.

Keywords: Response regulator, a phosphate analog beryllium fluoride

MS7-P13 Structural and mechanistic insights into a *Bacteroides vulgatus* retaining *N*-acetyl-β-galactosaminidase that uses neighbouring group participation

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Bacteroides vulgatus is a member of the human microbiota whose abundance is increased in patients with Crohn's disease. We show that a *B. vulgatus* glycoside hydrolase from the carbohydrate active enzyme family GH123, *Bv*GH123, is an *N*-acetyl-β-galactosaminidase that acts with retention of stereochemistry, and through a 3-D structure in complex with Gal-thiazoline, provide evidence in support of a neighbouring group participation mechanism.

Keywords: glycoside hydrolase, crystal structure, neighbouring group participation