Structures and Function Studies of Microbial P-loop-containing Phosphatases

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The P-loop-containing phosphatases are composed of a conserved sequence of DX(30)HCXXGXXR(T/S). It is well-known that tyrosine phosphatases (PTP), dual specificity phosphatases (DSP) and inositol polyphosphate (IPP) phosphatase are important regulators in signal transduction of cell cycle and IPP signaling molecules. Up to date, we have solved two the P-loop-containing phosphatases which are the inositol hexakisphosphate phosphatase (phytase) from *Selenomonas ruminantium* and DSP in *Sulfolobus Solfataricus*. We have solved two crystal forms of the complex structure of the phytase with an inhibitor, *myo*-inositol hexasulfate. In the "standby" and the "inhibited" crystal forms, the inhibitor is bound, respectively, in a pocket slightly away from Cys241 and at the substrate-binding site where the to-be-hydrolyzed phosphate group is held close to the –SH group of Cys241.

P-loop-containing phosphatase from *S. Solfataricus* was also solved. Comparison of the structures of *S. Solfataricus* and other phosphatases have revealed a extensive substrate binding surface which implying the possibility of low specificity. Overall, these investigations help us to evaluate the evolution of tyrosine phosphatase in microbial and the role it plays in the signal transduction among Achaea.

Keywords: dual specificity phosphatase, phytase, myo-inositol polyphosphates