

MS11-P4 Exploring molecular recognition mechanisms in the multistep phosphorelay signaling in plants: crystal structure of His phosphotransmitter AHP2 and modeling of its interaction with sensor histidine kinase CKI1

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In plants, histidine phosphotransfer proteins (HPTs) transmit the signal between diverse sensor histidine kinases (HKs) and response regulators within multistep phosphorelay (MSP) pathway. The ability of HPTs to interact with the receiver domains of sensor histidine kinases with different affinities indicates the certain specificity of the interaction between two partners. In order to explore the structural determinants of the interaction specificity between AHP2 and the receiver domain of histidine kinase CKI1 (CKI1_{RD}) from model plant *Arabidopsis thaliana*, we determined the crystal structure of AHP2 by SIRAS protocol at 2.53 Å resolution. Molecular dynamics simulations for 100 ns were applied to identify the key residues responsible for the AHP2-CKI1_{RD} interaction. The AHP2-CKI1_{RD} interaction was confirmed by NMR measurements – resulting chemical shifts partially overlap with the model. AHP2-CKI1_{RD} model reveal strong protein-protein complex; the comparison of the model with recently published crystal structure of AHP1-AHK5_{RD} suggests significant differences in binding interface between both complexes, mostly in the amino acid residues mediating hydrophilic interactions. Due to the fact that the vast majority of interacting residues in AHP1 and AHP2 are represented by highly conserved residues, small structural differences of both AHPs and AHK_{RD}s seem to be sufficient for determination of specific molecular recognition as could be seen by our bioinformatical and structural comparisons.

Keywords: protein crystallography, MD simulations, NMR, Arabidopsis, signal transduction, multistep phosphorelay, molecular recognition

MS11-P5 The keratin-10 binding region of the pneumococcal serine rich repeat protein (PsrP) forms a domain-swapped dimer and intermolecular β-sheets – implications for biofilm formation of *Streptococcus pneumoniae*

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The commensal bacterial pathogen *Streptococcus pneumoniae* colonizes the upper respiratory tract of humans and can cause pneumonia, sepsis and meningitis. The role of the pneumococcal serine-rich repeat protein (PsrP) is to present the basic region (BR) domain for interaction with keratin 10 (KRT10) on the extracellular surface of host lung cells through its MSCRAMM-related globular binding region domain [1,2] as well as for biofilm formation through self-oligomerization [3]. PsrP belongs to the family of serine-rich repeat (SRR) proteins with a long, putatively glycosylated serine rich repeat domain that is covalently anchored to the cell wall and extends the functional domain out of the capsule [3,4].

Biophysical analysis of the BR domain by small-angle X-ray scattering (SAXS), analytical ultracentrifugation and X-ray crystallography reveals the formation of a domain-swapped dimer and an intermolecular β-sheet that could be relevant for the function of PsrP in biofilm formation. Furthermore, SAXS and circular dichroism experiments revealed the N-terminal BR₁₂₂₋₁₆₆ region as a non-globular and probably disordered structure. We also demonstrate that this disordered N-terminal fragment is cleaved off by the human furin protease, a known activator of other toxins and virulence factors, potentially promoting pneumococcal biofilm formation.

References

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