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ORAL ABSTRACT PRESENTATIONS

SESSION TITLE: STRUCTURE OF VIRUSES AND CHAPERONINS

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Abstract OR-6: Baseplate Structure of Bacteriophage Phi812 and Mechanism of Cell Wall Binding and Penetration

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Background: Antibiotic-resistant strains of *Staphylococcus aureus* cause human infections that are difficult to treat and can lead to death. Bacteriophage (phage) phi812K1/420 from the family Myoviridae infects 95% of clinical isolates of *S. aureus* and therefore is a promising candidate for a phage therapy agent. As the native phage particle approaches its host cell, phage receptor-binding proteins make a contact with the host cell wall. This interaction triggers a cascade of structural changes in the baseplate resulting in phage tail contraction and genome ejection. Mechanistic description of the baseplate re-organization, however, remains unknown.
Methods: Using cryo-electron microscopy (cryo-EM), we studied the baseplate of the phage phi812K1/420. Also, selected proteins involved in the host cell wall binding and penetration were produced in recombinant form and their structures were solved using X-ray crystallography and cryo-EM single-particle reconstruction.
Results: We reconstructed the phage baseplate in native and contracted states. The reconstruction of the native baseplate reaches a resolution of 4 Å, which enables us to discern individual protein structures. Solved protein structures will be fitted into the reconstruction of the contracted baseplate.
Conclusion: Our results provide the first structural characterization of contractile phage infecting a Gram-positive bacterium. Comparison of the two distinct baseplate states will allow us to describe the molecular mechanism of the initial stage of phage infection in detail.

Key Words: *Staphylococcus aureus* • bacteriophage • cryo-EM

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