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Poster #98: Exploring flagellotropic phage adsorption by cryoEM

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Bacteriophages of the class Caudoviricetes infect bacterial hosts through deployment of specialized tail machinery capable of adsorption and penetration of host bacterial cell walls. The mechanism of adsorption and penetration has been studied extensively using model Enterobacteriaceae phages such as T4, T7, P22, P1 and . These model phages adsorb initially to the bacterial cell wall, binding to LPS or a protein-based surface receptor. While highly informative, these studies largely neglect flagellotropic bacteriophages. Flagellotropic bacteriophages adsorb initially to bacterial flagella, followed by translocation and re-adsorption to the host cell wall. To date, much remains unknown regarding these flagellotropic processes. We decided to investigate this process using a known flagellotropic bacteriophage.

We used cryogenic electron microscopy (cryo-EM) single particle analysis to determine the flagella binding complex (FBC) produced by our target phage. Due to the unique structure of the complex, we were able to reconstruct the complex to near-atomic resolution (2.9-3.5 Å), identifying component proteins. The FBC is very large, composed of more than 150 protein chains that form a pseudo-symmetric structure weighing ~3.8 MDa. We were also able to resolve interactions between parts of the apparatus and the flagellum itself. Together with previous observations, these results allowed us to develop a testable hypothesis for the mechanism of phage–flagellum adsorption. The model accounts for previous observations regarding adsorption kinetics, including the requirement for active flagellar rotation during adsorption. These findings provide new insights into a remarkably complex flagellum binding complex, representing a significant advance in our understanding of flagellotropic phage infection.

Reference #1

Reference #2

Reference #3

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