

Structural biology of Helicobacter pylori infection.



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Helicobacter pylori is one of the most successful bacterial pathogens, infecting the stomach of about half of the world population and causing peptic ulcer or gastric cancer. Our laboratory is interested in two main aspects of *H. pylori* infection: i) the structural basis of host-cell interaction and ii) the molecular mechanisms of DNA replication initiation. To study these systems we have developed different strategies based on protein purification, Biochemistry and hybrid methods in Structural Biology (MALS, X-ray crystallography, SAXS and Electron Microscopy).

Not all *H. pylori* strains are detrimental to human. The most severe strains produce a sophisticated molecular syringe named cag type IV secretion system (cagT4SS) that attaches host cell integrin $\alpha 5\beta 1$ to deliver the oncoprotein CagA (1). The structure of the machinery and the way it delivers the toxin are still a mystery. The basis for the function of the cagT4SS relies on a complicated and dynamic set of interactions between bacterial proteins (including CagA) and $\alpha 5\beta 1$ integrin. We have solved the structure of a large CagA fragment and identified its integrin-binding domain (2). I will summarize here the current knowledge and also present unpublished results on this interaction.

Our group has also studied the structural biology of replication initiation proteins from *H. pylori*. If the hallmarks of DNA replication are conserved in *H. pylori*, this bacterium has features that deviate from the "model" systems. I will present recent discoveries on *H. pylori* DNA replication initiation (3, 4) machinery including unpublished structural work and show that this bacteria might represent a original model for DNA replication study that complement pioneer work on *E. coli* and *B. subtilis*.

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