

Aspects of molecular level pathogenesis and strategies for vaccine design/immunization with *Helicobacter pylori* as a case study

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Abstract

Bacterial pathogens utilize a wide variety of molecules called virulence factors to cause infections. Because these molecules are critical for disease, and because these virulence factors are on the bacterial surface, or secreted out of the pathogen, they make attractive targets for potential vaccine candidates. Our review aims to give a broad outline of the several virulence factors, which can be future vaccine candidates with specific emphasis on *Helicobacter pylori*. *Helicobacter pylori* has acquired great importance during the last two decades, after being recognized as an important pathogen that infects a great portion of the human population. This microorganism is recognized as the main causal agent of chronic gastritis and duodenal ulcers and is associated with the subsequent development of gastric carcinoma. At present it is well established that urease, vacuolating cytotoxin VacA, and the pathogenicity island (*cag* PAI) gene products are the main virulence factors of this organism. Thus, individuals infected with strains that express these virulence factors probably develop a severe local inflammation that may induce the development of peptic ulcer and gastric cancer. The way the infection spreads throughout the world suggests the possibility that there are multiple pathways of transmission. Due to the importance that *H. pylori* has acquired as a human pathogen, laboratories worldwide are attempting to develop a vaccine that confers long-term immunological protection against infection by this microorganism. The overall aim is to give an insight into the pathogenesis of this species and its implications on the initiatives of vaccine design.

Keywords: Microbial pathogenesis, *Helicobacter pylori*, multifocal disease, virulence factors, conserved pathogen targets, Bioinformatics approach, vaccine development.