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### **Virulence factors of *Helicobacter pylori***

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#### **Abstract**

One of the most common cancers in both genders, gastric cancer is currently the fourth leading cause of cancer-related deaths globally. The interplay of hereditary and environmental variables, including *Helicobacter pylori* (*H. pylori*) infection, is linked to the etiology of stomach cancer. Due to a number of evasive mechanisms brought on by the virulence factors that the bacteria express, the invasion, survival, colonization, and stimulation of further inflammation within the gastric mucosa are all conceivable. To improve eradication efforts and stop the potential induction of carcinogenesis, it is essential to understand the pathogenicity mechanisms of *H. pylori*. This review focuses on the most recent research on the relevance between *H. pylori* virulence factors, subsequent carcinogenesis, and stomach premalignant lesions.

**Keywords:** *Helicobacter pylori*, Virulence factors, Mucosa-associated lymphoid tissue lymphoma (MALT)

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#### **Introduction**

The gram-negative, microaerophilic, spiral-shaped, flagellated bacterium *Helicobacter pylori* (*H. pylori*) may indeed change its form from spiral to coccoid, which is thought to be important for bacterial survival in the human gastric microenvironment [1]. While *H. pylori*'s coccoid form gives the bacterium the capacity to colonize the mucus layer of the gastric epithelium, further increasing its invasiveness, the spiral shape promotes the bacteria's successful motility.

Moreover, *H. pylori* has the capacity to create biofilms that reduce its sensitivity to a number of medications, which increases the risk of antibiotic resistance mutations and complicates efforts to eradicate the bacteria [2].

Since 1994, both the World Health Organization (WHO) and the International Agency for Research on Cancer have designated *H. pylori* as a class I carcinogen linked to the development of gastric cancer (GC) [1,2].

### **Pathogenesis**

*Helicobacter pylori's* pathogenicity had linked to a number of processes, but the host signaling pathway changes, the indirect inflammatory responses they cause in the gastric mucosa, and the direct epigenetic effects they have on the gastric epithelial cells are crucial [3]. Most of all people on earth have *H. pylori* in their stomach mucosa, and it actively manipulates host tissues to create an immunosuppressive environment that sustains chronic infection [4].

Earlier studies showed that *H. pylori* infection is adversely correlated with systemic inflammatory illnesses such asthma, lupus, inflammatory bowel disease, and eosinophilic esophagitis in the human population and in animal models [5]. Many gastrointestinal conditions, including severe gastritis, peptic ulcer disease, and gastric mucosa-associated lymphoid tissue lymphoma (MALT), can be brought on by *H. pylori*. The World Health Organization's International Agency for Research on Cancer (WHO/IARC) has classified it as a Category I carcinogen [6].

### **Virulence factors**

Many effector proteins and toxins produced by *H. pylori* cause harm to the host's tissues. Chemokines that are released during an infection cause innate immunity to be triggered [7].

1. Vac A: the 88-kDa protein known as vacuolating cytotoxin type A (VacA) is made up of the p33 and p55 protein subunits. Vacuoles are formed by VacA in the epithelial cell of the host [8]. Because since vacA is varied, gastric cancer risk is increased by polymorphism at a particular gene location. The s region (signal region), which is at the end of the 5' region, the m region (middle region), and the intermediate region can be used to categorize the regions of vacA. (i region). Alleles from the s and m regions fall into the s1, s2, m1, and m2 categories [9]. The beginning of apoptosis is one of the important roles of VacA [10].

2. *cagA*: The *cagA* gene, which is found at the 30 end of *cagPAI*, produces the 128-kDa CagA protein [11]. CagA-positive *H. pylori* more dangerous than CagA-negative *H. pylori* [12]. There are two different varieties of CagA: Western and East Asian. CagA is built on an EPIYA (glutamineproline-isoleucine-tyrosine-alanine) repeating amino acid sequence at its 30 ends. When the T4SS injects this protein motif into cells, it gets phosphorylated.

Whereas the East Asian EPIYA has an A-B-D sequence, the Western EPIYA motif has an A-B-C pattern where EPIYA-C can be repeated more than once [13].

3. Urease is the most frequently expressed protein by *H. pylori* and is one of the most important virulence factors involved in bacterial metabolism and colonization within the gastric mucosa. Both the intracellular compartment and the surface of *H. pylori* bacteria contain urease; hence, internal and external urease can be separated based on their location [14]. As urease is essential for bacterial colonization of the gastric mucosa, urease-negative mutants are unable to do so at physiological pH levels to the same extent as urease-positive *H. pylori* strains [15].
4. Flagellum: *H. pylori* flagellum is an essential component for permitting the chemotaxis and movement of bacteria. The precise number of flagella is related to the movement speed of *H. pylori* and may vary across species [16].
5. Catalase: one of the most highly expressed proteins in *H. pylori* strains isolated from the stomach mucosa, catalase levels are thought to range between 4 and 5% of the total protein composition of *H. pylori* [17]. Compared to catalase from other species, *H. pylori* catalase is more resistant to inhibition by cyanide or aminotriazole [18].
6. One of the *H. pylori* enzymes, superoxidase dismutase (SOD), shields the bacteria from reactive oxygen species (ROS), permitting the preservation of the appropriate homeostasis. SOD is exclusively found on the cell surface, unlike catalase. SOD speeds up the conversion of superoxide to oxygen, avoiding the production of too many harmful superoxide free radicals [19].

7. Lewis Antigens: majority of *H. pylori* strains exhibit at least one kind of Lewis (Le) antigen, which are fucosylated glycolipids that are a part of the *H. pylori* O-specific chain of the lipopolysaccharide (LPS). Le antigens are expressed on gastric epithelial cells, making Le antigen expression on bacterial cell surfaces one of the most efficient ways for *H. pylori* colonization of the stomach mucosa and provoking host immunological responses [20].
8. Phospholipases: *H. pylori* phospholipases destroy the mucus layer, the physiological activities of the gastric epithelial cells are gradually lost. In addition to causing mucosal injury, phospholipases encourage persistent inflammation, which may further contribute to the development of peptic ulcers. As a result, the stomach microenvironment can support more bacterial colonization and survival [21].
9. Outer Inflammatory Protein A Outer inflammatory protein A (OipA), a member of the OMPs family and a virulence factor for *H. pylori*, is encoded by the hopH gene, It may have an impact on the clinical outcome of infected individuals since it is closely related to the adherence, colonization, onset, and development of gastrointestinal illnesses caused by bacteria [22].
10. Duodenal Ulcer Promoting Gene (DupA) is the *H. pylori* virulence factor, and its pathogenicity is linked to both the risk of gastritis and the development of duodenal ulcers. Nevertheless, DupA expression is adversely correlated with the risk of GC [23].
11. *Helicobacter pylori* neutrophil-activating protein (HP-NAP): a key component of *H. pylori*'s pathogenicity, which contributes to both human inflammation and bacterial defense. To promote their pro-oxidant and pro-inflammatory actions, neutrophils, monocytes, and mast cells are among the innate immune cells that HP-NAP activates. Moreover, this protein stimulates T-helper type 1 (Th1) and cytotoxic T lymphocyte (CTL) activity, providing evidence that HP-NAP might cause stomach inflammation by triggering adaptive immunological responses [24].

## Treatment

In the lack of a reliable vaccination, treating chronic *H. pylori* infection has become the primary method for controlling the bacteria's population spread, curing gastric lesions in infected individuals, and preventing the development of stomach cancer in the future [25].

Primary antibiotic resistance in *H. pylori* has emerged quickly because to the lack of effective treatment options, widespread use of certain antibiotics in the general population (such as clarithromycin for respiratory infections), and the species' outstanding capacity for adaptability [26].

The development of alternative treatment methods includes the use of probiotics and prebiotics as adjuvants in the treatment of *H. pylori*, antimicrobial peptides as antibiotic substitutes, ingestible photodynamic therapy devices, micro- and nanoparticles used as drug delivery systems, vaccines, natural products, and phage therapy [27].

## Conclusions

Gastric cancer has a complicated and multifaceted etiology that includes genetic and epigenetic variations, host-related factors, and environmental variables. The most significant risk factor in the pathogenesis of this neoplasia is *H. pylori* infection, which has been proven to call upon several known pathways (and possibly more that have yet to be found) to cause the start and progression of gastric cancer. And therefore, preventative techniques must be established in order to identify high-risk individuals and provide a customized therapy before the onset of precancerous lesions, in addition to efforts to discover and verify novel biomarkers and changes in people's lifestyle and dietary habits.

## Ethical Approval

The study was approved by the Ethical Committee. It was conducted in accordance with the ethical standards of the Helsinki Declaration of 1975, as revised in 2008.

## Conflicts of Interest

The authors declare that he has no competing interests.

## Funding

None

## Study registration

Not required.

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