



## From *Helicobacter pylori* infection to gastric cancer: Current evidence on the immune response

Vinícius Lima de Souza Gonçalves, Maria Luísa Cordeiro Santos, Marcel Silva Luz, Hanna Santos Marques, Breno Bittencourt de Brito, Filipe Antônio França da Silva, Cláudio Lima Souza, Márcio Vasconcelos Oliveira, Fabrício Freire de Melo

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Vinícius Lima de Souza Gonçalves, Hanna Santos Marques, Universidade Estadual do Sudoeste da Bahia, Campus Vitória da Conquista, Vitória da Conquista 45083-900, Bahia, Brazil

Maria Luísa Cordeiro Santos, Marcel Silva Luz, Breno Bittencourt de Brito, Filipe Antônio França da Silva, Cláudio Lima Souza, Márcio Vasconcelos Oliveira, Fabrício Freire de Melo, Universidade Federal da Bahia, Instituto Multidisciplinar em Saúde, Vitória da Conquista 45029-094, Bahia, Brazil

**Corresponding author:** Fabrício Freire de Melo, PhD, Professor, Universidade Federal da Bahia, Instituto Multidisciplinar em Saúde, Rua Hormindo Barros, 58, Quadra 17, Lote 58, Vitória da Conquista 45029-094, Bahia, Brazil. [freiremelo@yahoo.com.br](mailto:freiremelo@yahoo.com.br)

### Abstract

Gastric cancer (GC) is the result of a multifactorial process whose main components are infection by *Helicobacter pylori* (*H. pylori*), bacterial virulence factors, host immune response and environmental factors. The development of the neoplastic microenvironment also depends on genetic and epigenetic changes in oncogenes and tumor suppressor genes, which results in deregulation of cell signaling pathways and apoptosis process. This review summarizes the main aspects of the pathogenesis of GC and the immune response involved in chronic inflammation generated by *H. pylori*.

**Key Words:** Gastric cancer; *Helicobacter pylori*; Chronic inflammation; Host immune response

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**Core Tip:** Understanding the factors related to the host, infection by *Helicobacter pylori* and the mechanisms of tumor evasion are fundamental to understand the development of gastric cancer (GC). However, in the face of a complex immune environment, there are still many questions to be answered. Thus, we highlight in this work the main aspects related to GC, from infection and gastric microenvironment to immune response.

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## INTRODUCTION

*Helicobacter pylori* (*H. pylori*) infection is acquired mainly in early childhood and if not treated properly can remain for life. Because of this, the infection is highly present around the world and has been linked to a wide spectrum of gastrointestinal diseases[1]. The prevalence of the bacteria varies according to geographic regions, age of the patient, socioeconomic status, education, living environment and profession. In developing countries, such as those in Latin America, they can have a prevalence of up to 80% of infected adults[2]. Recent work by Elzouki *et al*[3] evaluated 114 patients with gastric cancer (GC) and indicated that the infection rate per *H. pylori* was 63.2%. Through its virulence factors, it damages the gastric mucosa and the hormonal release, changing the stomach environment, often asymptotically[4].

Thus, after a chronic inflammatory process, the host may develop GC in the long term, with adenocarcinoma as the most common type. GC is a worldwide public health problem since approximately one million new people are diagnosed each year with this pathology. Among the types of neoplasms, gastric adenocarcinoma is the fifth most common and is the third cause of cancer-related death worldwide. Although there is a strong association between *H. pylori* infection and gastric neoplasms, only 1%-3% of those infected end up developing GC[5]. Also in this sense, in 1994, the World Health Organization identified *H. pylori* as a group 1 carcinogen, which means a certain relationship to carcinogenesis, confirming the role of this bacterium in the process of GC development.

The mechanisms involved in this process are complex and not well known, but it is known that the tumor evasion mechanism of the immune response has a fundamental role in this process[5]. The development of this neoplastic microenvironment results from genetic and epigenetic changes in oncogenes and tumor suppressor genes, which results in deregulation of cell signaling pathways and the process of apoptosis[6]. It is known that the prognosis of patients with GC is not good, with an average 5-year survival rate of less than 20%[7]. The prognosis of patients with GC can also vary according to their classification, which can be based from anatomical location to recent molecular discoveries.

This work aims to provide an updated review on the main characteristics that lead to the development of gastric neoplasms from gastric infection by *H. pylori* in order to provide solid data that help in the knowledge about GC.

## VIRULENCE FACTORS OF *H. PYLORI*

*H. pylori* has a lot of virulence factors that favor its maintenance in the hostile gastric environment. The recognition of these factors can even determine how serious the infection with the bacteria can be. Here, the main factors will be listed.

### Flagella

Of primary importance for the pathogenic action of *H. pylori*, the flagella play a crucial role in colonization by this pathogen[8]. About four to eight flagella make up the *H. pylori* flagellar group, and each of these unitary flagella is made up of three structures: the basal body, the hook and the filament [9]. Such composition allows this bacterium not only the motility through gastrointestinal fluids, known as "swimming" but also in solid or semi-solid media, known as "spreading" and "swarming" movements, which are crucial for entry into gastrointestinal epithelial cells[8].

### Chemotaxis

In addition, still in the mobility and fixation of this bacterium in the gastric environment, the chemotaxis process guarantees the interaction with molecules such as mucins, sodium bicarbonate, urea and sodium chloride, facilitating the effectiveness of the infection[10,11]. Another factor of paramount importance in the role of chemotaxis occurs in the process of continuity of infection, causing it to become chronic. In this sense, the chemotaxis ability allows *H. pylori* to circumvent the host's immune responses, achieving chronic infection[12].

### Adhesion molecules

Various adhesion molecules are described as important for the colonization process by *H. pylori*, in addition to helping to protect this pathogen against mucin activity and contributing to access to important nutrients, such as nickel, which are essential for effective infection[13]. An important adherence factor that has been described in the literature is BabA, responsible for the connection with Lewis H-1 type antigens. In addition to this adhesion function, this molecule also appears to be related to the type of clinical manifestation presented by the host in the face of infection[14-16].

Another molecule of importance for the adhesion of this pathogen to gastric tissue is the outer inflammatory protein, which is also linked to the production of interleukin (IL)-8, mucosal damage and duodenal ulcer[17]. In addition, studies also argue that there is a possible relationship between outer inflammatory protein expression and greater chances of developing GC[18]. Still on the adhesion molecules of this pathogen, 33 proteins form the *H. pylori* outer membrane proteins (Hop)[19,20]. Even though most of them still do not have their activity well described or understood, some of them already have their role in the pathogenicity of *H. pylori* highlighted, such as BabA (HopS), SabA (HopP), HopQ and HopZ. BabA is related to the specific link to the b and H-1 Lewis antigens from the surface of the gastric epithelial cells, and SabA is associated with binding to Le<sup>x</sup> and the adherence of the bacterium to laminin[21-23]. Meanwhile, the HopQ and HopZ proteins are relatively consolidated as to their importance for pathogen adherence, and the former also appears to be related to gene A associated with cytotoxins (*CagA*) gene expression[24].

### Pathogenicity

Several molecules are listed as important for the pathogenesis of *H. pylori*. Among them, the role of urease stands out, which is activated even before the bacterium adheres to the gastric tissue, making an adequate acclimation of the pH of the gastric environment, regulating it to protect this bacterium[25]. In addition, urease is related to the production process of ammonia derived from urea, due to the urea channels that allow the entry of this substance in the pathogen and the intrabacterial action of this enzyme[26]. Furthermore, in addition to its role in colonization, urease seems to be important for regulating the immune response, controlling a macrophage-pathogen interaction, modulating the pH of the phagosome and ensuring the survival of *H. pylori*[27].

One of the proteins most expressed by *H. pylori* is the catalase that converts hydrogen peroxide into water and molecular oxygen[28]. Of paramount importance for the protection of the pathogen against the host's immune responses, prevention of death mediated by the complement system and avoidance against the action of phagocytes, catalase seems to be related to the clinic of gastric tumors and cancers [29,30]. Apparently, this process occurs through chronic inflammation, prevention of apoptosis and induction of mutagenesis (processes related to the action of this enzyme)[31].

*H. pylori* strains can be classified as *CagA* positive or *CagA* negative. Apparently, *CagA* is the main virulence factor of this pathogen, and its greatest expression seems to be directly related to more aggressive clinical manifestations, such as acute gastritis, gastric ulcer and GC[32-35]. This process is related to its ability to affect cellular motility, proliferation and apoptosis, affecting the entire conformation of gastric tissue and predisposing inflammatory pathways that facilitate these clinical presentations[35]. Still on the *CagA* gene, different forms of phosphorylation that occur (EPIYA A, B, C or D) are related to different results, with types C and D (Western and Eastern strains) more related to the outcome of GC[36].

Vacuolating cytotoxin A is an essential cytotoxin for the pathogenesis of *H. pylori*, promoting autophagic processes during the acute phase of infection, in addition to promoting the appearance of impaired autophagosomes and unbalancing cell proliferation and death during a chronic phase of infection[30]. Present in all strains of this pathogen, vacuolating cytotoxin A can be encoded by different genopatterns, being the strains s1 and m1 more related to higher levels of inflammation and consequently less indolent clinical presentations, such as gastric atrophy and carcinoma[37-40].

Another determinant factor in the pathogenesis of *H. pylori* is the *cag*-pathogenicity island, which is composed of approximately 32 genes[41]. The *cag*-pathogenicity island is responsible for the encoding of a type 4 secretion system that helps modulate the cellular metabolism of the host cell, translocate virulence factors such as *CagA* to the gastric epithelial cells and upregulate proinflammatory cytokine secretion[42,43]. Also, strains that present *cag*-pathogenicity island are more related to peptic ulcer and GC[44,45]. Moreover, the interaction of *CagA* with the SH2 containing protein tyrosine phosphatase-2 is extremely relevant. The *CagA*/SH2 containing protein tyrosine phosphatase-2 link happens through a tyrosine phosphorylation-dependent process, which promotes activation of the SH2 containing protein tyrosine phosphatase-2/extracellular signal-regulated kinase/mitogen-activated protein kinase pathway and consequently causes cytoskeleton alterations known as the "hummingbird" phenotype[46, 47]. These changes interfere in cellular growth and motility, which may predispose the host to genetic mutations and further GC[48]. In addition, *H. pylori* lipopolysaccharides also play an important role in the pathogenesis of this bacterium. The lipopolysaccharides are capable of binding laminin and as a consequence promote a gastric leakiness and further cellular apoptosis[49]. Furthermore, *H. pylori* lipopolysaccharides might be related to the development of GC, given that it upregulates toll-like receptor 4 and enhances cell proliferation, both *via* activation of the mitogen-activated protein kinase

kinase 1/2-extracellular signal-regulated kinase 1/2-mitogen-activated protein kinase pathway[50].

Still in the virulence factors of *H. pylori*, several others can be mentioned, such as heat shock proteins, superoxide dismutase and degrading enzymes (proteases and phospholipases), being listed in this article.

## HOST IMMUNE RESPONSE TO INFECTION

*H. pylori* induces a significant immune response in the gastric environment of infected individuals. The onset of the inflammatory processes related to the infection occurs with the promotion of innate immunity mechanisms, involving the triggering of pattern recognition receptors of gastric epithelial cells by bacterial components such as lipopolysaccharide, NapA and nucleic acids[51]. The aforementioned recognition of foreign antigens by immune system receptors leads to the activation of intracellular signaling pathways that culminate in the release of proinflammatory cytokines, which promote the activation and recruitment of CD4+ and CD8+ T cells to the gastric environment[52]. Subsequently, a chronic inflammation against *H. pylori* infection is established, being characterized by a polarization of T helper (Th) 1/Th17 responses, which is followed by the action of regulatory T (Treg) cells responsible for controlling the inflammatory process.

The inflammatory pattern varies between groups of patients and seems to be strongly influenced by age[53]. Figure 1 summarizes the main changes in the immune response to infection by *H. pylori* according to age. In general, a predominance of the Th1 response is commonly observed in adults, along with high levels of interferon  $\gamma$  (IFN- $\gamma$ ), tumor necrosis factor  $\alpha$ , IL-1 $\beta$  and IL-8[54-56], which is mostly responsible for the recruitment of neutrophils and further setup of an inflammatory environment[57]. However, when it comes to children, this pattern of cytokine release and consequent responses are not presented in the same way as adults. In a previous investigation with *H. pylori*-positive adults and children evaluating Treg and Th17 responses in the gastric mucosa, our group observed that children have higher expression of Treg-related cytokines such as IL-10 and transforming growth factor beta 1 (TGF- $\beta$ 1) than adults. On the other hand, adults had a prominent expression of cytokines associated with Th17 responses (IL-1 $\beta$ , IL-17A and IL-23) compared to children. Moreover, that study found that the expression of FoxP3+ Treg cells in the gastric mucosa was significantly higher in infants than in adults, and more intense infiltration of mononuclear and polymorphonuclear cells was observed in the latter group[58]. In another investigation evaluating the levels of cytokines associated with innate and Th1 responses in the gastric mucosa of infected individuals, we demonstrated that children express significantly higher concentrations of tumor necrosis factor  $\alpha$  and IL-1 $\alpha$  than adults, whereas the contrary was observed with regard to the expression of IL-2, IL-12p70 and IFN- $\gamma$ . In addition, a progressive reduction in the levels of IFN- $\gamma$  and IL-12p70 was observed with aging among adults, including elderly individuals, whereas a similar process was observed with the expression of IL-1, IL-2, IL-12p70 and IFN- $\gamma$  in children[59].

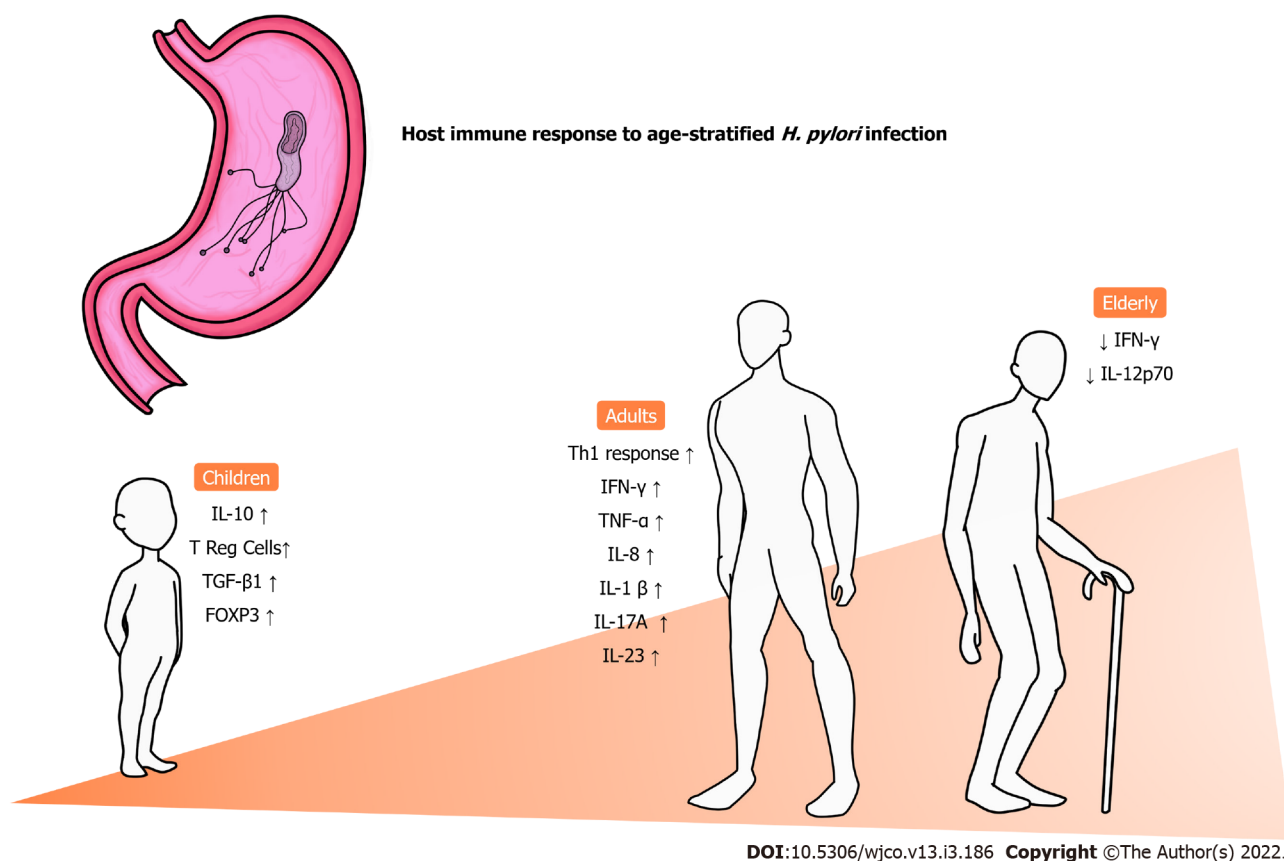
*H. pylori*-induced Th1 responses have been associated with the development of corpus gastritis, which can result in gastric atrophy and intestinal metaplasia, important in precancerous lesions[60]. Moreover, Treg cells have been associated with various relevant protumor mechanisms in the setting of GC. Enhanced tumor infiltration of FoxP3+ Treg cells have been positively correlated with poor outcomes among patients with gastric adenocarcinoma[61].

Although the aforementioned immune profiles play important roles in the GC onset and progression, growing evidence have emphasized the remarkable protumoral activities associated with Th17 cells. High levels of IL-17 in the tumor environment have been related to increased concentrations of vascular endothelial growth factor and enhanced tumor vascularization. In addition, cytokines promote IL-6 production in tumor cells, and it is a protein that induces vascular endothelial growth factor release as well but also stimulates STAT3, which suppresses apoptosis and prolongs the survival of malignant cells[62]. In a recent study enrolling patients with *H. pylori*-related diseases, our group demonstrated that GC patients lack IL-27 production both in the gastric environment and peripheral blood[63]. This cytokine is an important inhibitor of Th17 responses by impairing the expression of ROR $\gamma$ T, the main IL-17A transcription factor[64].

## GC CLASSIFICATION

The classification of GC can be useful for determining a more effective diagnosis as well as a more targeted treatment and better prognosis for cancer patients. The classification system can use anatomical location, degree of invasion, lymphatic involvement, histological type and molecular subtypes[65,66]. Among several classification options, there are older ones that have fallen out of use or continue to be used today (such as Lauren's), and there are recent updates from renowned institutions such as the World Health Organization.





**Figure 1** Host immune response to age-stratified *Helicobacter pylori* infection. *H. pylori*: *Helicobacter pylori*; IL: Interleukin; TNF-α: Tumor necrosis factor α; IFN-γ: Interferon γ; T Reg Cells: Regulatory T cells.

The anatomical classification can be divided into: (1) Cardial; and (2) Distal. The location of tumors of origin at the gastroesophageal junction, whether esophageal or gastric, may not be identified until the tumor has already reached an expressive size. The literature has shown that the tumor originating in the cardia usually presents a more aggressive behavior in relation to the distal ones, frequently invading the gastric walls[67]. In addition, the occurrence of tumors in the distal region has decreased to the detriment of those in the proximal region[68].

Classification according to the degree of invasion can be done in early or advanced cancer. The early type, limited to the mucosa and submucosa, has a lower degree of development and injury and has a 5-year survival rate of 85% to 90%, while patients with the advanced type have a 5% to 20% survival rate. Furthermore, the advanced type can be evaluated by the Borrmann classification: polypoid (type 1), ulcerated with defined edges (type 2), ulcerated with ill-defined edges (type 3) and plastic linitis, characterized by diffuse infiltrate without evidence of ulceration (type 4)[69].

Lauren's Histological Classification, widely used since its publication in 1965, has been useful in the discussion of GC. This classification divides gastric adenocarcinoma into two histomorphologic types, intestinal (well, moderately or poorly differentiated) and diffuse (undifferentiated, with or without signet ring cells). The intestinal type is more common in males and older patients, with a better prognosis. It is characterized by tumor cells that unite and organize into glandular formations, just as it occurs in intestinal adenocarcinomas. In addition, the intestinal type usually develops in an environment of atrophic gastritis and presents greater expression of the e-cadherin adhesion molecule [70]. The diffuse type, more prevalent in young individuals and more easily identified in early stages, is characterized by tumor cells that invade neighboring tissues, with little cohesion, loss of e-cadherin expression, without gland formation and with marked fibrosis. In addition, this type presents endocrine markers more frequently and has a higher production of basic fibroblast growth factor[71-73].

Among the most recent classifications, in 2019 the World Health Organization updated the classification of tumors of the digestive system, including GC. In this new approach, histogenesis and the degree of differentiation were not considered, but it recognizes several types of malignant epithelial tumors (tubular, papillary, poorly cohesive signet ring phenotype, another type of poorly cohesive, mucinous, mixed cell) as well as rare variants[74].

The National Institute of Health Cancer Genome Atlas project helped to redefine the molecular classification of GC into four subtypes: (1) GC with Epstein-Barr virus infection; (2) Microsatellite unstable tumors; (3) Genetically stable tumors; and (4) Chromosomally unstable GCs[75,76]. The first constitutes about 9% of GCs and is more common in males, has lesions in the bottom and gastric body with a lower

mortality rate and has hypermethylated DNA[77]. The second type represents 22% of GC cases and has a high mutation rate (with high frequency in the KRAS pathway), generally related to an epigenetic event[75,78]. The third type is usually aneuploid and diagnosed early, representing about 20% of GC cases, in addition to having a predominance of diffuse histology and located in the distal region of the stomach[75]. The latter type represents 50% of CG and has histology of the intestinal type, and its frequency is high in cancers of the esophagogastric junction. Chromosomal instability is the result of DNA aneuploidy and mutations in various proto-oncogenes and tumor suppressor genes[75,79].

## PATHOGENESIS

### **Precancerous lesions**

**Atrophic gastritis:** In atrophic gastritis (AG), there is an inflammatory process that promotes gland loss and decreased secretory function, modifying the gastric environment, which may be associated with a state of achlorhydria or hypochlorhydria[80]. A recent study showed that the relative risk for GC was 1.7 in moderate AG and 4.9 in severe AG compared to none or mild AG (control)[81]. However, it seems to be possible to identify the evolution of this risk early. In the study by Miki *et al*[82], it was reported that the progression of AG is closely linked with progressive reductions in the levels of pepsinogen I and II. Therefore, measuring these levels can be an opportunity to assess the progression of gastritis [82]. Another way to assess the risk of progression is through the location and extent of atrophy. A staging system based on the degree of atrophy and the topography of atrophy, called Operative Link for Gastritis Assessment was created for this purpose. In this system, stages 3 and 4 are strongly associated with GC development[83].

**Gastric intestinal metaplasia:** This lesion is characterized by the replacement of the gastric epithelium by two types of intestinal epithelium. This replacement is generally considered a condition that predisposes to malignancy and an increased risk for GC, especially type III (incomplete)[84,85]. Although the presence of this lesion is considered by many authors as a mild form of dysplasia[86], it is still controversial whether gastric intestinal metaplasia is really a precancerous lesion. After all, several studies have shown that gastric intestinal metaplasia is not always seen in patients who progress to GC [87]. However, further studies are needed to define this question.

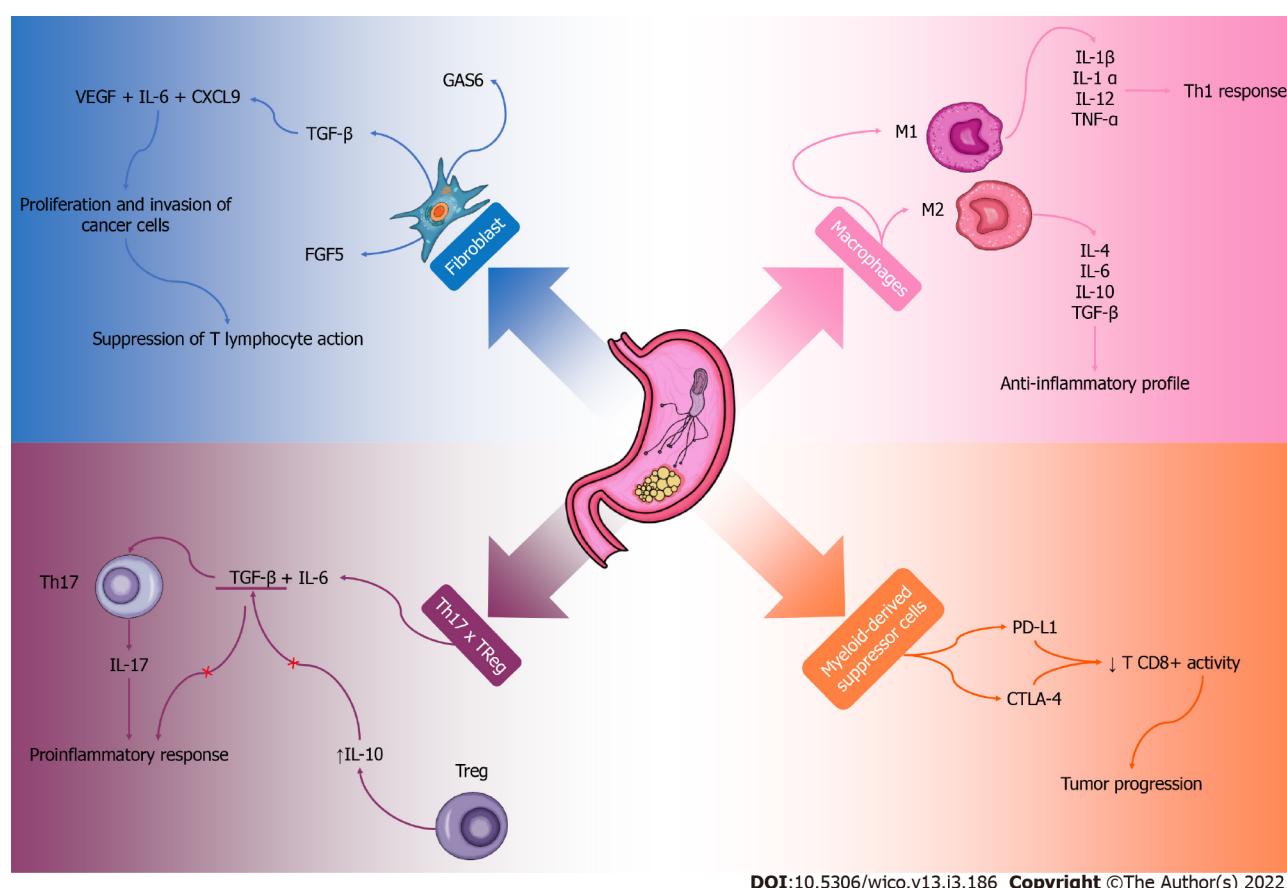
Along with this questioning, it remains uncertain whether the eradication of *H. pylori* promotes the improvement of these precancerous lesions, as there are recent works that have not found any change [88]. However, most studies that assess patients for more than 5 years after the eradication of the bacteria, demonstrate improvements in these lesions. Some possible reasons for these discrepancies are ethnic variations, disease stage, follow-up period, medications used and resistance to the drugs used[89, 90].

## GC MICROENVIRONMENT

The GC microenvironment has a complex local immune response, and factors that promote the growth and expansion of cancer cells can be observed. Although the microenvironment is still poorly elucidated, some components have already been recognized. Inflammatory cells, fibroblasts and macrophages associated with cancer, endothelial cells and other infiltrating immune components play an important role in this process[91,92] (Figure 2).

### **Cancer-associated fibroblasts**

Cancer-associated fibroblasts are involved in the synthesis and remodeling of the extracellular matrix and are directly related to angiogenesis, mechanical factors of the tumor and metastatic modulation[93]. The secretome of these cells produce TGF- $\beta$ , FGF5 and specific growth arrest protein 6 that contribute to the proliferation and invasion of cancer cells[94]. In addition, the presence of vascular endothelial growth factor, IL-6 and chemokine ligand (CXCL9) can be observed, which together with TGF- $\beta$  reduce the immune response of T lymphocytes[95]. Cancer-associated fibroblasts contribute to increase the stiffness of tumor tissue, compress blood vessels generating a hypoxemic process and contribute to a more aggressive cancer, providing immune evasion and less effective therapeutic response[96,97]. Interestingly, a study using mice found that these cells contribute to the progression of GC, but their functions are not fully understood[98]. This whole process contributes to an immunosuppression in the tumor microenvironment and creates an ideal environment for the development and progression of tumor cells in the affected tissue and possibly other tissues. These cells are probably important in the process of malignant or benign evolution of GC and should be better explored so that their knowledge is directed to therapeutic contexts.



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**Figure 2 Summary scheme on the microenvironment of gastric cancer.** TGF- $\beta$ : Transforming growth factor beta; FGF5: Fibroblast growth factor 5; GAS6: Specific growth arrest protein 6; VEGF: Vascular endothelial growth factor; CXCL9: Chemokine ligand; PD-L1: Programmed death ligand 1; CTLA-4: Cytotoxic T-lymphocyte-associated protein 4; IL: Interleukin; Th: T helper cell; TNF: Tumor necrosis factor; Treg: Regulatory T cell.

### Tumor-associated macrophages

Tumor-associated macrophages are also abundant components of the immune system that play an important role in the microenvironment of GC[99,100]. They can be M1 type and produce proinflammatory cytokines such as IL-1 $\beta$ , IL-1 $\alpha$ , IL-12, tumor necrosis factor  $\alpha$ , IL-12 and CXCL9, which polarize and recruit components of a Th1 response profile[93,101]. This process culminates in the inhibition of tumor growth[102]. In contrast, type M2 stimulates a Th2 profile secreting cytokines such as IL-4, IL-6, IL-10, IL-13, IL-33, TGF- $\beta$  and IL-10, which have an anti-inflammatory profile and important tumor activity[103]. They act on tumor progression, metastasis and angiogenesis, which are important factors for the tumor formation microenvironment[104]. The polarization of M1/M2 macrophages is conducted according to the inflammatory profile of the tumor microenvironment or therapeutic intervention. More studies would be interesting in order to observe possible therapies in order to reverse the polarization of M2 macrophages in M1 so that with a more proinflammatory profile, the immune system is stimulated, and the fight against the tumor is more effective.

### Myeloid-derived suppressor cells

Myeloid-derived suppressor cells are part of the cell population involved in immune responses and are observed in the tumor microenvironment. They suppress the cytotoxic function of CD8+T cell activity and antitumor, as they have a high expression of programmed death ligand 1 and cytotoxic T-lymphocyte-associated protein 4[93,105]. An interesting study in mice observed that the expression of IL-1 $\beta$  is associated with a greater recruitment of these suppressor cells in the tumor microenvironment [106]. Baumann *et al*[107] observed that the neutralization of the activities of these cells, concomitant with the inhibition of the checkpoint, obtained a greater efficacy in cancer therapy.

### Relationship between Th17 /Treg

Regarding the expression of cytokines in the microenvironment of GC, there is an important increase in Th17 and Treg cells causing an imbalance in the relationship between these cytokines. This phenomenon is observed gradually with the progression of cancer[108]. The increase in Th17 cells, stimulated by TGF- $\beta$  and IL-6, promote tumor progression due to increased expression of IL-17 and consequently greater local inflammation[109]. However, Treg cells provide an immunosuppressed environment,

stimulating a high production of IL-10 and inhibiting the production of TGF- $\beta$ . Thus, these Treg cells stimulate the progression of the GC, decreasing the host's immune surveillance in the tumor microenvironment[110]. Apparently, the balance of the Th17 and Treg relationship in the gastrointestinal tract reflects the integrity of the mucosal immune response and plays an important role in the mechanisms of tumor progression and metastasis.

Most studies are *in vitro* and murine models. Despite few studies on human models with GC, it is important to highlight the role of immunosuppression in the tumor microenvironment, which is essential for the development of cancer and for possible metastases. The immune response in the tumor microenvironment has a direct link to the host's general immune response to cancer. These responses are dependent on factors such as genetics, polymorphisms, chronic diseases and the use of drug therapies. In addition, the lack of studies in different stages of human life is a problem since the immunological profile is different throughout life. More studies on the microenvironment of GC are needed, so it would be possible to better understand the mechanism of the immune response and possibly find even more effective therapies in the treatment of this cancer.

## TUMOR EVASION MECHANISMS TO THE IMMUNE RESPONSE OF THE HOST

During the initial development of tumors, including GC, their cells use several mechanisms to resist innate immune response and prevail in the organism, and when the tumor achieves more advanced stages it evades from the action of T effector cells[111]. Of note, the tumor microenvironment is a protagonist in that context[112]. The immunosuppression promoted by the programmed cell death protein 1 is strongly related to the immune evasion and worse outcomes in GC[113]. In that context, the podoplanin is an immune checkpoint molecule that has been associated with the immune response evasion in various malignancies[114].

Liu *et al*[115] reported in their study that high levels of podoplanin-expressing cells infiltrating gastric tumors were associated with an increased recruitment of protumoral macrophages and T effector cell dysfunction. Moreover, the infiltrating podoplanin cells contributed to the reduction of INF- $\gamma$ , granzyme B and perforin-1 levels as well as with an increased expression of programmed cell death protein 1, T cell immunoglobulin and immunoglobulin and mucin-domain containing-3. These findings suggest that the expression of those cells is a tumor evasion mechanism by gastric tumor cells[115].

Another study observed that the macrophage-derived chemokine CXCL8 plays a crucial role in tumor progression in GC patients by mediating immune response evasion and metastasis. CXCL8 acts by reducing the infiltration of Ki67 CD8+ T cells and inhibiting them through the expression of programmed death ligand 1 in macrophages[116]. Interestingly, a study evaluated a GC-derived extracellular compound and concluded that it presents immunosuppressive activities through selective inhibition of CD161CD3 natural killer cells, proliferative stimulus and reduction of the intracellular levels of INF- $\gamma$ , granzyme B and perforin[117]. Complementarily, Zhang *et al*[118] investigated the importance of IL-10-related tumor-associated macrophages in the GC immune response evasion and observed that a tumor microenvironment with high levels of IL-10 tumor-associated macrophages was characterized by the infiltration of Treg cells and dysfunction of CD8+ T cells.

Shi *et al*[119] demonstrated in a study that the density of Foxp3+ Treg cells and A2aR/CD8+ T cells were highly expressed in the tumor microenvironment and were able to avoid immune responses against GC. The mechanism used by the FoxP3+ Treg cells was the cell apoptosis induction through the ATP decomposition into adenosine as well as the inhibition of CD8+ T cells through the A2aR pathway, leading to an immunosuppressive effect[119]. Notably, a study showed that IL-10-producing regulatory B cells have the potential to avoid the immune surveillance in patients with GC and predict poorer outcomes since the population of CD19CD24+hiCD27 B cells included cells that are able to suppress CD4+ T cells and the production of INF- $\gamma$  by autologous CD4+ T cells[120].

Another protein, the costimulatory molecule B7-H4, is a member of the B7 inhibitors family expressed in tumor-related monocytes and macrophages. It is considered an important component of GC immune system evasion, being that it is correlated to invasion depth and to the presence of venous and lymphatic invasion as well as to the expression of HLA-DR[121]. Interestingly, circulating tumor cells undergo an epithelial-mesenchymal transition that allows them to survive in several metastatic environments. In this sense, an assay demonstrated that patients with GC had subtypes of epithelial-mesenchymal transition markers able to regulate ULBP1 (a major member of the natural killer group 2 member D ligand family) in the circulating tumor cells, which aid in immune response evasion[122].

Considering that the tumor purity consists of the proportion of cancer cells in the tumor and is intimately related to the tumor microenvironment characteristics, it is important to emphasize that the low tumor purity implies an unfavorable prognosis, accentuated infiltration of Treg, M1 and M2 macrophages, high expression of immune checkpoints and recruitment of immunosuppressor molecules [123]. A computational study used the interface mimicry technology in order to predict host-pathogen interactions in the context of *H. pylori* infection and their repercussions in GC. This study found that the *H. pylori* infection interferes with the apoptosis of host cells through proteins such as HP0231, which is able to impair the CASP6 homodimerization, a crucial step for apoptotic signaling.



The aforementioned interaction might explain the *H. pylori*-induced resistance to death of host cells, a well-known characteristic associated with carcinogenesis[124]. The studies mentioned here highlight the importance of understanding the mechanisms that lead to the immune system evasion of GC in order to better understand the pathophysiology of the disease as well as to improve prognosis assessments and therapeutic tools for affected individuals. Finally, it is evident that the *H. pylori* virulence factors are closely related to the gastric carcinogenesis by means of adaptative mechanisms that not only contribute to the infection persistence but also unleash premalignant changes in the gastric microenvironment. These variations progress and perpetuate along with tumor development, aiding in its evasion from the immune response.

## FUTURE PERSPECTIVES

Faced with such complex pathways to be understood, future work needs to detail the immune response to bacterial infection, especially to help with early intervention in patients who may develop CG. This may enhance the discovery of new pharmacological therapies that interfere with precancerous lesions and even in advanced stages of cancer. In addition, they should also help in the discovery of new, non-conventional, non-invasive, highly specific biomarkers capable of providing early detection of GC.

## CONCLUSION

Infection by *H. pylori*, its relationship with the host's immune system and oncogenesis as well as the tumor evasion mechanisms is crucial for the understanding of the mechanisms involved in the appearance and progression of GC. In view of the chronic inflammation process, a variety of factors can affect the patient's prognosis, especially according to the individual's age. The gastric microenvironment has not been well established, and some fundamental components for the progression of GC have been recognized to be related to the host's immune response.

## FOOTNOTES

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**Country/Territory of origin:** Brazil

**ORCID number:** Vinicius Lima de Souza Gonçalves 0000-0002-6445-9318; Maria Luísa Cordeiro Santos 0000-0001-7078-9789; Marcel Silva Luz 0000-0003-1650-5807; Hanna Santos Marques 0000-0001-5741-1570; Breno Bittencourt de Brito 0000-0002-1831-7909; Filipe Antônio França da Silva 0000-0002-0550-1109; Cláudio Lima Souza 0000-0002-8094-8357; Márcio Vasconcelos Oliveira 0000-0002-8959-0478; Fabrício Freire de Melo 0000-0002-5680-2753.

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