

POINT OF VIEW

***Helicobacter pylori* infection and gastric mucosal epithelial cell apoptosis**

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ABBREVIATIONS

NF- κ B: nuclear factor κ B; TNF- α : tumor necrosis factor α ; DD: death domain; FADD: Fas-associated death domain; FasL: Fas receptor ligand; TNFR: TNF receptor; TRADD: TNFR-associated death domain; TRAF: TNFR-associated factor; COX: cyclooxygenase; PG: prostaglandin; iNOS: inducible nitric oxide synthase; NO: nitric oxide; *MDR-1*: multiple drug resistance gene; IL: interleukin; EGF: epithelial growth factor; IGF: insulin-like growth factor; HGF: hepatocyte growth factor; PI-3 kinase: phosphoinositol-3 kinase, RIP: receptor interacting protein, SOD: superoxide dismutase, MTP: mitochondrial transition pore, Apaf-1: apoptotic protease activation factor, MHC: major histocompatibility complex, TGF- α : transforming growth factor α , ROS: reactive oxygen species, MAPK: mitogen-activated protein kinase, NSAID: non-steroidal anti-inflammatory drug.

INTRODUCTION

Apoptosis was first described by its morphological characteristics, including cell shrinkage, plasma membrane disruption, chromatin condensation, and nuclear DNA cleavage into discrete fragments (1-3). It is a genet-

ically-managed cell death program that may be interrupted by mutations. In fact, mutations in apoptotic routes contribute to a number of human diseases ranging from neurodegenerative disorders to tumors (4).

Other types of cell death

While apoptosis is a programmed cell death, not all programmed deaths are apoptotic. Other programmed responses contribute to clear potential cancer cells. The sequence is an irreversible cell cycle arrest program with distinct characteristics that appears to be interrupted in some tumors. Selected stimuli may induce phenotypes suggesting senescence, including mitogenic oncogene activation or ionizing radiation (5-8). For instance, an excessive shortening of terminal DNA sequences or telomeres, which may naturally occur in any replication cycle, would result in chromosomal instability, thus activating a cell cycle arrest to prevent potential mutations (9) and then leading to a common program for cell death.

In contrast to apoptosis, where cells play an active role in their own destruction, in necrosis cells undergo lysis by cytokines produced by inflammatory cells. When nuclear remnants from cells having undergone necrosis are studied by electrophoresis, a diffuse pattern may be seen, since DNA fragments are in a continuous spectrum. However, nuclear remnants from cells having undergone apoptosis exhibit an alternating band pattern—in the shape of ladder rungs—known as the ladder pattern that is an unmistakable sign that the death process studied was apoptotic in nature.

H. pylori and apoptosis

On the other hand, gastric mucosal infection by *Helicobacter pylori* may affect the normal balance between

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gastric epithelial proliferation and death from apoptosis, thus deregulating the normal cell cycle and initially leading to gastritis. The latter may become gastric atrophy, and then subsequently metaplasia, dysplasia and gastric cancer (10). The outcome of this process correlates with a severe reduction of the apoptotic rate in early stages (gastritis and atrophy), and with a disproportionate proliferative response in the host in more advanced stages (metaplasia and dysplasia), which may ultimately end in a malignant condition. Therefore, a definition of predictive values for genetic and biochemical markers just prior to *H. pylori* eradication and the long-term follow-up of patients with gastric paraneoplastic lesions may help establish preventive therapeutic options.

Objective

The aim of this paper is to review the major events involved in apoptosis, their causes at both the molecular and cellular level, and their pathologic consequences, focusing on *H. pylori*-induced apoptosis in gastric mucosal epithelial cells as well as on bacterial strains.

GENES INVOLVED IN APOPTOSIS

The clonation and characterization of oncogene *bcl-2* established the importance of apoptosis in tumor development (11). *Bcl-2* promotes cell survival by blocking programmed cell death (12-14). In transgenic mice, *Bcl-2* overexpression promotes lymphoproliferation and accelerates *c-Myc*-induced lymphomagenesis (13,15). Together with *Bcl-2*, *Bcl-X_L* is a potent suppressor of cell death overexpressed in a number of tumor types (16). Immune reactivity rates for *Bcl-2* in normal glands, metaplasia, adenoma, and adenocarcinoma have been seen to be 0, 77, 38, and 11%, respectively, which suggests *Bcl-2* overexpression in premalignant lesions and *Bcl-2* repression following malignant conversion, this being responsible for early events in the cancer sequence (17).

Otherwise, *p53* was the first tumor suppressor gene ever described in association with apoptosis. Most human tumors exhibit mutations in the *p53* gene, thus increasing chromosome viability and instability (18). The disruption of several protein *p53* effectors (e.g. *bax*, *apaf-1*, and *casp-9*) may promote oncogenic transformation and tumor development (19-21). Mutated protein *p53* has been seen to activate promoters for the following genes: *Multi Drug Resistance Gene-1 (MDR-1)*, *c-myc*, *interleukin-6 (IL-6)*, *epithelial growth factor (EGF)*, and *insuline-like growth factor-II (IGF-II)*, all of them associated with increased cell proliferation. In addition, several prior and subsequent components of the *p53* pathway (e.g. *Mdm-2*, *ARF*, *Bax*) are also commonly mutated in human tumors (18).

Wild protein *p53* is also directly or indirectly involved in the regulation of genes associated with growth factors,

in the regulation of cytoskeleton-forming proteins, in the regulation of genes involved in cell adhesion, in cell cycle arrest, in the repression of cell metabolism genes, and in the maintenance of chromosome integrity following DNA damage (22). Studies in *p53*-defective mice have demonstrated that endogenous protein *p53* may play a role in apoptosis. It was also seen that *p53* was necessary for radiation-induced cell death in the thymus, but not for glucocorticoid-induced cell death (23,24). Thus, the role of protein *p53* in apoptosis is indirectly linked to DNA damage, and is dependant upon the stimulus (radiation) and tissue (thymocytes). Stimuli capable of *p53* activation to promote apoptosis include hypoxia and mitogenic oncogenes. Should mutations occur in some of the genes associated with cancer, they may suppress apoptosis. For example, a malfunction in the *Fas/CD95* pathway, which controls the number of cells in the immune system by clearing them through apoptosis, may lead to lymphoproliferative disorders and even cancer (25).

Another critical pathway implies signaling through phosphoinositol-3 (PI-3) kinase, which is activated by *Ras* and repressed by *PTEN*, a tumor suppressor. *Ras* activation and *PTEN* loss are both usual in human tumors (26).

A variety of signals may trigger apoptosis. Extracellular triggers include growth factor depletion, hypoxia, radiation, and lost cell-matrix interaction. Intracellular mechanisms include DNA damage from defective cell cycle checkpoints, endogenous toxins, telomerase (enzyme in charge of telomere replication) malfunction, and inappropriate proliferation signaling because of oncogenic mutations (27). In some cases an apoptotic signal counteracts an antiapoptotic signal. For instance, *IGF-I* promotes cell survival through the PI-3 kinase pathway, and *IGF-I* or other growth factor depletion may trigger a "depletional death" (28). In contrast, other stimuli imply true proapoptotic factors—for example, some forms of cell stress may activate protein *p53*, which promotes apoptosis through molecules such as *Bax*, a proapoptotic protein belonging in the *Bcl-2* class (20,21,29).

APOPTOSIS MECHANISMS

Better known apoptosis pathways are those starting at "death receptors" such as *Fas/CD95* or *TNFR1* and 2. The binding of *TNF- α* to *TNFR1* results in a recruitment of *TRADD* (*TNFR* death domain) messenger molecules through interactions between proteins known as intracellular "death domains" (DD). If *TRADD* recruits a receptor interacting protein (RIP) and *TNFR*-associated factor 2 (*TRAF2*), the activation of nuclear factor κ B (*NF- κ B*) ensues, which suppresses apoptosis as induced by *TNF- α* (30). In contrast, the recruitment of *FADD* (*Fas*-associated death domain) by *Fas* or by *TNFR1* (in the latter case also through *TRADD*) results in apoptosis through the activation of the protease *caspase 8*, thus initiating a pro-

tease cascade leading to apoptosis (31). Caspases are cysteine proteases that are expressed as inactive proenzymes; these associate with effectors allowing their activation, and their action is to selectively cleave proteins by an aspartate residue (32,33).

Some cytokines or DNA damage are signals for cell death through mitochondria. This pathway is a target for a number of oncogenic mutations affecting the function of members in the Bcl-2 family. These may modulate mitochondrial function through transition pores (MTP), whose TNF-induced aperture leads to a sharp increase in mitochondrial membrane Ca^{2+} permeability, which releases cytochrome c (34). Cytosolic cytochrome c may interact with apoptotic protease activation factor (Apaf-1) and procaspase 9 to initiate a protease cascade leading to apoptosis (35-37).

Selected messenger molecules alter the frequency of apoptosis induction by proapoptotic signals. For instance, cytokines such as IL-6 may suppress p53-induced apoptosis (38).

On the other hand, the PI-3 kinase pathway is involved in cell survival via extracellular cytokine receptors, which activate a kinase cascade involving PI-3 kinase and leading to the phosphorylation and inactivation of proapoptotic molecules such as Bad (another member in the Bcl-2 family) and caspase 9 (39,40). In contrast, PTEN, which acts as a lipid phosphatase, inactivates triphosphoinositols, thus repressing this pathway (41,42). In all, the previously reviewed mechanisms indicate, as summarized in figure 1, that apoptosis is a phenomenon resulting from an integration of several pro- and anti-apoptotic signals that either increase or decrease the expression of specific genes.

A LINK BETWEEN *H. PYLORI*, APOPTOSIS, AND CELL PROLIFERATION

H. pylori is the main cause of chronic gastritis and peptic ulcer, and has been categorized as a type-I carcinogen based on seroepidemiologic evidence (43-46). *H. pylori* colonizes the gastric mucosa by adhering to the epithelial tissue without ever penetrating epithelial cells (47-49). *H. pylori* has been seen to induce apoptosis in patients with gastroduodenal ulcer and gastritis (50-55). Some authors have seen greater than five-fold increases in the number of apoptotic cells in patients with duodenal ulcer versus those observed following *H. pylori* eradication (56). *In vitro* studies have shown that apoptosis is induced in tumor cell lines incubated with *H. pylori* (57), as is a cell cycle arrest between phases G1 and S (58).

Both apoptosis and cell proliferation are increased in precancer lesions (atrophy, metaplasia, dysplasia) in the presence of *H. pylori* infection (59). A dysregulation of genes controlling apoptosis and hence homeostasis between apoptosis and cell proliferation may ultimately lead to tumor development (60).

The gastric mucosal degeneration process is initiated by inflammation, and results in a destruction (atrophy) of gastric glands, their replacement by an intestinal-like epithelium (intestinal metaplasia), and progression to dysplasia (the earliest manifestation of a neoplasm that may be seen under a microscope) (61).

If the *H. pylori*-infected mucosa is invaded by an inflammatory cell infiltrate, glands become separated and compressed, and may falsely resemble atrophy (61). Of course, when glands are destroyed and then substituted for by another tissue (metaplastic epithelium or fibroblasts plus cell matrix), and they actually disappear (true atrophy), pathophysiological consequences are similar, and acid production decreases thus resulting in hypochlorhydria. Only atrophy characterized by intestinal metaplasia and fibrosis, and hence by a true loss of glands has been associated with the development of gastric cancer; cases of apparent atrophy may even show gland regeneration and a functional recovery of acid production (61).

Other authors reported that in premalignant lesions or gastric carcinoma increased cell proliferation is no longer associated with *H. pylori* from a certain point in time on, since eradication induces no reversal (51,62), which suggests a potential association with a dysregulated cell growth due to genetic changes during intestinal metaplasia, including an activation of proto-oncogenes such as *k-ras*, expression and release of gastrin and other cell growth factors, and suppression of suppressor genes such as *p53* (63,64). These mitogenic peptides, including the epithelial growth factor (EGF), hepatocyte growth factor (HGF, responsible for both epithelial and non-epithelial tumors), and transforming growth factor α (TGF- α), are synthesized in the gastric mucosa, especially following *H. pylori*-induced damage, interact with surface receptors on epithelial cells, and induce the expression of oncogenes *c-myc*, *c-jun* and *c-fos*, which stimulate cell growth (65). A mutated *k-ras* causes an overexpression of mutated *p53* protein followed by a phosphorylation and activation of MAP-kinases, thus enhancing tumor growth.

Gastrin, which is mainly synthesized by G cells at the gastric mucosa, is another factor involved in *H. pylori*-related carcinogenesis. Upon secretion to the gastric lumen in response to these bacteria, this hormone may stimulate *H. pylori* growth and G cells to release further gastrin, thus blocking the expression of gene *p21* (66) –regulated by *p53* and involved in cell cycle arrest and apoptosis– and overexpressing the mutated *p53* protein (62). *H. pylori* eradication before surgery in patients with gastric cancer is followed by a sharp drop in plasma gastrin, luminal gastrin, and cancer tissue gastrin levels (67).

The Fas/Fas-ligand system is involved in apoptosis as induced by *H. pylori* in epithelial cells and lamina propria cells (57,68-70). In a study the expression of FasL mRNA was higher in T-cells of infected patients versus healthy subjects, which suggests that local T-cells may induce apoptosis through Fas/FasL (71). In addition, the

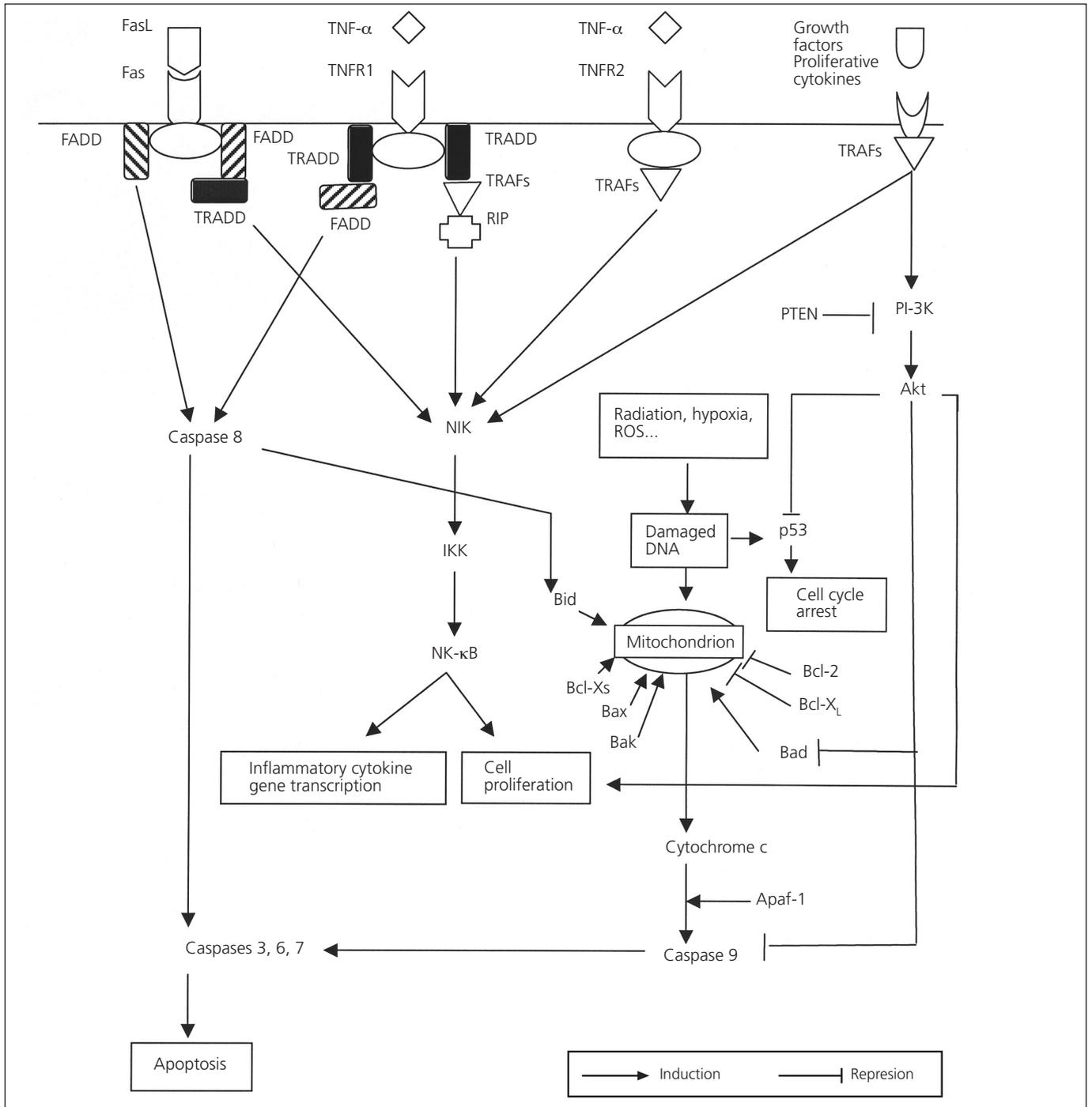


Fig. 1.- Apoptosis-related transduction routes as mediated by TNFR, Fas, or mitochondria. Receptor-mediated death and mitochondria-mediated routes are two major apoptotic routes. Receptor activation results in the recruitment of adaptor proteins. The recruitment of the Fas-associated death domain (FADD) by Fas or the tumor necrosis factor receptor (TNFR) via the TNFR-associated death domain (TRADD) activates caspase 8. Another apoptotic route begins in mitochondria. Cytochrome c is released into the cytosol and activates caspase 9. The activation of caspase 8 or caspase 9 results in the activation of the caspase cascade. The nuclear factor κ B (NF- κ B) route is also initiated via TRADD and TNFR-associated factors (TRAFs). NIK: NF- κ B-inducing kinase; IKK: I κ B kinase- α and I κ B kinase- β ; ROS: reactive oxygen species.

Las rutas de transducción de la apoptosis mediadas por TNFR, Fas, o la mitocondria. La muerte mediada por receptores y las rutas mediadas por las mitocondrias son las dos principales rutas apoptóticas. La activación de los receptores resulta en el reclutamiento de proteínas adaptadoras. El reclutamiento del Fas associated death domain (FADD) por Fas o por el receptor del Factor de Necrosis Tumoral (TNFR) a través del TNFR associated death domain (TRADD) activan la caspasa-8. Otra ruta apoptótica comienza se inicia en la mitocondria. El citocromo-c es liberado al citosol y activa a la caspasa-9. La activación de la caspasa-8 o de la caspasa-9 conduce a la activación de la cascada de caspasas. La ruta del factor nuclear κ B (NF- κ B) también se inicia a través de TRADD y de los factores asociados a TNFR (TRAF). NIK: kinasa inductora de NF- κ B; IKK: I κ B kinasa- α e I κ B kinasa- β ; ROS: especies reactivas de oxígeno.

expression of FasL mRNA is also increased in gastric epithelial cells during *H. pylori* infection, which suggests that apoptosis may also be induced by epithelial cells themselves in addition to T-cell FasL, thus bringing about their own death and that of neighboring epithelial cells (69). An interaction of *H. pylori* with the main histocompatibility complex II (MHC II) as an apoptosis induction receptor in gastric epithelial cells has also been seen (72).

Oxidative damage by *H. pylori* and apoptosis

Oxygen radicals (superoxide ion and hydrogen peroxide) derived from *H. pylori*-activated neutrophils are factors that may damage the gastric mucosa (73-78). A positive association between reactive oxygen species (ROS) production and *H. pylori*-related infection and histologic damage has been described (79). Cell protection against ROS results from the activation of ROS-sequestering enzymes, including superoxide dismutase (SOD), catalase, and glutathione peroxidase.

Some authors, using the AGS epithelial cell line, found that when exposed to ROS in the absence of *H. pylori*, cell survival was reduced by 84%. On the other hand, if such cells were exposed to ROS after incubation with *H. pylori*, survival was reduced to 73 and 39% for *cagA*⁺ and *cagA*⁻ strains, respectively. SOD activity was also measured, and was seen to be higher in cells incubated with *cagA*⁺ strains versus *cagA*⁻ strains, but only the expression of the cytokine-induced Mn-SOD was increased, with a modest increase in the constitutive CuZn-SOD. Similarly, higher levels of catalase and glutathione peroxidase activity have been reported for *cagA*⁺ strains. This increased activity of enzymes suppressing potential DNA-damaging agents following exposure to *cagA*⁺ strains is probably a cause of increased cell survival following exposure to ROS (80).

Using 8-hydroxyguanine as an oxidative damage marker in the DNA of gastric mucosal cells, *H. pylori*-positive patients would exhibit a higher presence of hydroxylated guanine in their DNA versus subjects with no *H. pylori* infection (81). This indicates that the damage induced in DNA by *H. pylori* infection in early gastritis may bring about its transformation into gastric cancer (80).

On the other hand, chloramine (NH₂Cl) is a toxic oxidizing agent produced within the gastric mucosa by *H. pylori* invasion. In neutrophils, the enzyme myeloperoxidase catalyzes chloride oxidation by H₂O₂ into HClO. The latter reacts with the NH₄⁺ resulting from *H. pylori* metabolism and becomes NH₂Cl (82), which is highly toxic due to its lipophilic and low molecular weight characteristics—it may easily cross the cell plasma membrane. *In vitro* studies have shown that apoptotic rates and chromatin condensation levels increase significantly more following treatment of gastric cells with NH₂Cl versus NH₄⁺ or HClO (83).

MTP and caspase 3 activation has been witnessed in cells exposed to NH₂Cl; these release cytochrome c (84), which forms a complex with Apaf-1 and procaspase 9, activates the latter, and initiates the caspase cascade—including caspases 3, 6 and 7—thus giving rise to the apoptotic process. In addition to NH₂Cl, other molecules produced by *H. pylori*, including cytotoxin VacA (85) or lipopolysaccharide, may induce apoptosis (86).

Cytokines released in response to *H. pylori* infection and its related inflammatory response

The host's *H. pylori*-stimulated inflammatory/immune response leads to a release of cytokines by Th1 cells, including TNF- α , interferon γ (INF- γ) or IL-2, which enhance apoptosis (57,69,72). This response is mediated by the Fas system (87), results in caspase 3 and 8 activation following DNA fragmentation, and increases MHC II expression and binding to *H. pylori* (88). In contrast, cytokines produced by Th2 cells, including IL-10, prevent apoptosis (89).

Regulation of the IL-8 gene

IL-8 is a lymphocyte- and neutrophil-activating chemotactic cytokine secreted by gastrointestinal epithelial cells in response to bacterial infection (90) that establishes a chemotactic gradient towards the epithelium surface.

The human IL-8 gene has several binding sites within its promoter—one for NF- κ B and two nearby loci for the binding of proteins c-Fos and c-Jun, which together make up transcription factor AP-1. NF- κ B is a cytoplasmic transcription factor, the activation and regulation thereof being closely regulated by a protein family designated I κ B—to be found non-covalently bound to NF- κ B—that prevents its translocation to the nucleus. Through signaling molecules such as TNF- α there is a pathway leading to I κ B α and I κ B β phosphorylation, and I κ B α proteosomal degradation; this releases NF- κ B, which migrates to the nucleus where it regulates the expression of a number of genes, including those involved in inflammation and cell survival (91). Two inducible kinases, I κ B kinase- α and I κ B kinase- β (IKK- α and IKK- β), phosphorylate I κ B α in response to proinflammatory cytokines (92), which are in turn phosphorylated and activated by the NF- κ B-inducing kinase (NIK), itself activated through proteins associated with TNF- α and IL-1 receptors (93), TRAF2 and TRAF6, respectively. Since NF- κ B stimulation requires no protein synthesis, it allows effective action on target genes, including IL-8 (91).

NF- κ B activation is followed by an increased expression of mRNA and IL-8 protein (94,95). The ability of *H. pylori* to activate NF- κ B *in vitro* has been corroborated *in vivo*, since activated NF- κ B is present in epithelial cells

from infected patients (95). Mitogen-activated protein kinases (MAPK) are mediators in the *H. pylori*-dependant activation of NF- κ B and IL-8 expression. Signal transduction takes place down a cascade of MAPK kinase phosphorylations: extracellular signal-regulated kinase 1 and 2 (ERK1/2), p38, and c-Jun aminoterminal kinase (JNK). Since MAPKs activate both NF- κ B and AP-1, and the *IL-8* gene has binding domains for both, NF- κ B activation has been researched and seen to be inadequate for IL-8 expression, with the implication of AP-1 being required (96).

ERK activation by a MAPK kinase (MEKK1) leads to Elk-1 phosphorylation, which together with JNK allows *c-fos* and *c-jun* transcription, their products making up AP-1. MEKK1 and NIK may each seemingly activate I κ B by phosphorylation, thus releasing NF- κ B (92,93).

Relationship between *H. pylori* genotype and pathogenicity

H. pylori cagA⁺ strains induce high levels of inflammation and more severe gastritis when compared to *cagA*⁻ strains, in addition to a higher risk of gastric cancer or peptic ulcer, and greater cell proliferation (56,91,97). *CagA*⁺ strains have been seen to notably increase IL-8 expression, hence inducing a more profound inflammatory response versus *cagA*⁻ strains (91). The exposure of cell cultures to *cagA*⁺ strains has been seen to result in an initial increase – followed by a decrease– of p53 and p21 protein expression, whereas *cagA*⁻ strains stimulate a continuous increase (98). In addition, the expression of Bcl-2 is increased in cells exposed to *cagA*⁺ strains, and diminished in *cagA*⁻ strains (98). Therefore, apoptosis seems to initially increase and subsequently decrease in *cagA*⁺ strains, with a persistent increase in cell proliferation. In this regard *cagA*⁻ strains have been suggested to induce mainly apoptosis, whereas proliferation would correlate to *cagA*⁺ strains (56).

However, other authors disagree with such observations, and state that both strains induce apoptosis with no differences between them (58,99,100). Some authors have investigated *H. pylori cagA*⁺-induced apoptosis in cell cultures, and found an increased expression of Bax, a pro-apoptotic protein in the Bcl-2 family, and a suppressed expression of anti-apoptotic Bcl-2's (101).

On the other hand, *H. pylori* has been seen to possess a type IV secretion system, which may translocate a bacterial factor within epithelial cells that activates NF- κ B and/or MAP-kinases, this resulting in IL-8 induction (91). A phosphorylation of protein CagA has been demonstrated in epithelial cells following contact with *H. pylori* (79,102,103). Recent data indicate that phosphorylated CagA induces changes in the cytoskeleton, including a polymerization of actin filaments (91,104).

However, *cagA* disruption does not affect NF- κ B, MAP-kinase or IL-8 activation (94,105,106), thus sug-

gesting the presence of a different factor injected into the host cell.

Changes in the expression of enzymes related to inflammation as caused by *H. pylori* infection

Cyclooxygenases (COX) catalyze the conversion of arachidonic acid into prostanoids such as prostaglandin E₂ (PGE₂), which protect the gastric mucosa against apoptosis, thus increasing cell proliferation (107,108). Two isoenzymes exist: COX-1 and COX-2, the first one being constitutive and the second one inducible in case of lesion (107-110).

Non-steroidal anti-inflammatory drugs (NSAIDs) are amongst the most widely used drugs worldwide. Classic or nonspecific NSAIDs inhibit both COX isoforms, and their benefits are to a greater or lesser extent associated with lesions induced in the gastrointestinal tract (111).

On the other hand, the relationship between NSAIDs and *H. pylori* infection has not been elucidated, and a synergic association, antagonic association, or absolute independence on the gastroduodenal mucosa have all been postulated (112).

Gastrointestinal tract cells, including macrophages, neutrophils, myofibroblasts and endothelial cells, have been shown to express COX-2 in inflammation (107,113-115). Specifically, *H. pylori*-related gastritis has been seen to induce its expression depending upon bacterial strain (113,115-123), which may partly explain its distinct pathogenic potential (123,124). Infection by *H. pylori cagA*⁺ strains has been seen to overexpress COX-2 in patients with gastric cancer (123). In addition, some studies have demonstrated that organism eradication is associated with a decrease in COX-2 gastric expression (116,121,125).

Another molecule –nitric oxide (NO)– has been seen to play a role in the protection of the gastric mucosa by increasing blood flow and inhibiting leukocyte adhesion to the endothelium (126). The normal gastric mucosa contains no inducible NO synthase (iNOS) enzyme, but its expression increases in patients with *H. pylori*-related gastritis (116).

Both iNOS and COX-2 are induced by cytokines such as IL-1 β , TNF- β or INF- γ , phorbol esters and growth factors in general, as well as bacterial polysaccharides (127-129). The induction of IL-1 β by bacterial products has been seen to stimulate PG synthesis in a number of tissues (130), while increased PGs have also been witnessed in subjects with no clinical signs of infection (131). Cells treated with IL-1 β have been shown to exhibit a decline and subsequent recovery of the NF- κ B inhibitor protein I κ B α , which suggests that treatment with IL-1 β activates NF- κ B (132).

On the other hand, the effect of mutated p53 on COX-2 expression and PGE₂ production has been investigated

using *in vitro* experiments, and cells with wild-type p53 were found to produce 90% less PGE₂ than cells with mutated p53, and to completely suppress COX-2 expression (133). Wild-type p53 also blocks the induction of COX-2 promoter activity by phorbol esters (133).

It is important to note that NO is mutagenic (134,135), and its metabolites, including nitrosamines, are involved in gastric carcinogenesis (136). COX-2 products have also been shown to be both mutagenic (137) y carcinogenic (138,139). Several binding sites for transcription factors have been identified within the COX-2 gene promoter, including two for NF-κB that regulate COX-2 transcription (132).

The extent of expression for both genes has been seen to be higher in tissues from patients with gastritis and concomitant *H. pylori* infection than in tissues of patients with gastritis and no *H. pylori* infection, whereas the level of constitutive cyclooxygenase COX-1 was approximately identical in all tissues (116). Consistent with the fact that *H. pylori* colonization is greater in the antrum *versus* the gastric body (140, 141), the extent of expression of both iNOS and COX-2 has been seen to also be considerably higher in the antrum. However, it should be noted that a recent study showed inflammation levels that were not significantly higher in the antrum *versus* the gastric body, which suggests a direct effect of *H. pylori* on the induction of expression for both genes (116).

CONCLUSIONS

In summary, a number of conclusions may be drawn, which are discussed below:

—Apoptosis is a process of programmed cell death under genetic control that may be altered by a number of factors, including oxidative stress, ionizing radiation, hypoxia, etc.; these may ultimately lead to mutations in oncogenes regulating the apoptosis/cell proliferation process, which may throw gastric homeostasis out of balance and lead to the development of tumors.

—Another factor that may alter the balance between apoptosis and proliferation, specifically at the gastric mucosa, is *H. pylori* infection. The outcome may be a dramatically increased apoptosis rate, which may lead to gastritis or ulcer, or result in increased cell proliferation and reduced apoptosis, which may potentially progress to metaplasia, dysplasia, and eventually adenocarcinoma.

—To conclude, the relationship between *H. pylori* strain genotype and the organism's pathogenic potential remains unclear, albeit a number of papers report an association of *cagA*⁺ strains with reduced apoptosis and the development of neoplastic processes on the one hand, and an association of *cagA*⁻ strains with a higher-than-normal apoptotic rate on the other hand. In contrast, other authors draw opposite conclusions when failing to demonstrate differences in apoptotic rates between *H. pylori cagA*⁺ and *cagA*⁻ strains, or to show that *cagA*⁺ strains

indeed give rise to higher apoptotic rates, this being the reason why this association remains a highly controversial topic.

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