

A clinical perspective on the role of chronic inflammation in gastrointestinal cancer

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Abstract: Chronic inflammation has been identified as an important risk factor for the development of malignancy, and knowledge about its molecular and cellular mechanisms is increasing. Several chronic inflammatory diseases of the gastrointestinal tract are important as risk factors for malignancy and have been studied in detail. In this review, we summarize important molecular mechanisms in chronic inflammation and highlight established and potential links between chronic inflammation and gastrointestinal cancer. In addition, we present the role of chronic inflammation in numerous tumors within the gastrointestinal tract as well as the relevant pathways or epidemiologic observations linking the pathogenesis of these tumors to inflammation.

Keywords: inflammation, immune response, carcinogenesis, gastrointestinal cancer, risk factor

Different entities of gastrointestinal cancer

Despite advances in cancer therapy, including targeted therapies, many malignancies are still associated with high mortality. Several cancers with a particularly poor prognosis, such as pancreatic ductal adenocarcinoma (PDAC) or gastric carcinoma, are located within the gastrointestinal (GI) tract. According to the GLOBOCAN database, neoplastic disorders of the GI tract account for more than 37% of cancer-related deaths worldwide, and the incidence of some GI malignancies, such as esophageal adenocarcinoma (EAC), has even been increasing over the last decade.^{1,2}

GI cancers are a very heterogeneous group, as they can derive from various cell types. There are lymphoproliferative disorders like mucosa-associated lymphoid tissue (MALT) lymphoma and neuroendocrine tumors, predominantly located in the small intestine and pancreas. In addition to hepatocellular carcinoma (HCC), cholangiocarcinomas also occur in the liver, and stromal neoplasias such as GI stromal tumors (GIST) and squamous cell carcinomas can be found in the stomach and esophagus. However, most GI cancers are adenocarcinomas.

As a barrier to the environment on the one hand, and as the main organ system for digestion and absorption on the other, the GI tract is exposed to many substances, microorganisms, and irritants. Some of these, such as alcohol, *Helicobacter pylori*, and arsenic are well established risk factors for GI cancers.^{3–5} The common link between most of these carcinogens is chronic inflammation (Table 1).

Virchow⁶ first described an infiltration of leukocytes in cancer in 1881. In the meantime, inflammation is considered to be one of the hallmarks of carcinogenesis and has become a main focus of research.

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Processes of chronic inflammation

The immune system acts as a defense against bacterial, viral, or parasitic infections. It is also responsible for identification, destruction, and phagocytosis of damaged, apoptotic, or neoplastic cells. Local activation of the immune system results in inflammation. The presentation of antigens from pathogens, mechanical or chemical cell irritation, necrotic cells, or autoimmune processes can induce an immune response and inflammation.

In general, the immune system can be distinguished into an innate and an adaptive immune system. Natural killer cells, mast cells, monocytes, macrophages, dendritic cells, and granulocytes usually evoke the first immune reaction and initiate inflammation. They activate specialized T- and B-lymphocytes as part of the adaptive immune system that play an important role in the regulation of inflammation and in the pathogen-specific immune response. However, the latest research has revealed a group of innate lymphoid cells that resemble T-helper (T_H) cells in function, and are presumably involved in the initiation of the immune response and inflammation.^{7,8}

Accordingly, acute inflammation is characterized by activation and infiltration of innate immune cells. After interaction with pathogens or through attraction by chemokines, such as transforming growth factor (TGF)- β or platelet-derived growth factor (PDGF) from damaged epithelial cells, neutrophils, macrophages, and mast cells secrete proinflammatory cytokines as well as more chemokines. This signaling results in invasion and activation of additional immune cells. Infiltrating granulocytes produce cytotoxic oxygen and nitrogen radicals to fight pathogens.

Interleukin (IL)-1 from mononuclear phagocytes induces an autocrine activation. Together with tumor necrosis factor (TNF), it enhances the presentation of adhesion molecules and stimulates macrophages to segregate metalloproteinases (MMPs) and collagenases, leading to connective tissue damage. In addition TNF, histamine, and prostaglandins synergistically increase endothelial permeability, which facilitates leukocyte infiltration.

TNF also induces fibroblast growth and differentiation as well as apoptosis of affected epithelial cells, but it also stimulates IL-1 and IL-6 release. It can act as a pro-angiogenic at the site of inflammation, but can also act as an anti-angiogenic at high concentrations.⁹

After phagocytosis of damaged cells or pathogens, the adaptive immune response is mediated by antigen-presenting cells (APCs) such as dendritic cells. An infiltration with T- and B-lymphocytes is typical for sites of chronic

inflammation. According to their IL secretion, T_H cells are divided into T_H1 , T_H2 , and T_H17 cells.^{10,11} T_H1 cells produce interferon (IFN)- γ , TNF- α , and IL-12 and thus control cellular immunity. T_H2 cells produce IL-4, IL-5, and IL-13, mediating B-cell-associated humoral immunity, and T_H17 cells produce IL-17, IL-6, and IL-23, regulating chronic inflammation via regulatory T-cells (T_{reg}).¹²

The extent of cytokine release by innate, T_H , and T_{reg} cells and the cytokine composition is crucial for the degree and duration of inflammation.¹³

The role of inflammation in cancer development and maintenance

Genetic instability and cell death resistance

In more than 15% of cancer patients worldwide, the cancer is believed to be caused by infection. Persistent infections, like some other causes, can be a reason for chronic inflammation.^{14,15} At sites of acute and chronic inflammation, cells are exposed to oxidative cell stress as well as to aggressive oxygen and nitrogen radicals from mononuclear phagocytes and leukocytes. Release of reactive oxygen and nitrogen species is enhanced by proinflammatory cytokines such as TNF, IL-1 β , and IFN- α . Particularly in proliferating cells, these radicals can cause DNA damage by nitration and strand breakage.¹⁶ Thus, chronic inflammation creates an environment of genomic instability.

Cells can accumulate several mutations as DNA control and repair mechanisms are suppressed in inflammatory tissue. Nitric oxide itself can inhibit DNA mismatch repair (MMR) directly at the protein level and also by induction of hypermethylation.^{17,18} In this fashion, it inactivates the promoter of the MMR protein hMLH1.¹⁹ Another mechanism to alter MMR activity is the induction of hypoxia-inducible factor (HIF)-1 α by TNF, IL-1 β , and prostaglandin E2. Furthermore, HIF-1 α removes c-MYC from the promoter of the MMR genes *MSH2* and *MSH6*.^{20,21}

Besides downregulation of MMR activity, it has been shown that DNA damage-induced apoptosis via the p53 pathway is impaired in chronic inflammation. TNF- α and the T_H2 cytokines IL-4 and IL-13, for example, can lead to mutations in the *TP53* gene by amplification of activation-induced cytidine deaminase expression.²² Furthermore, migration inhibitory factor (MIF) from macrophages can repress p53 function.²³ The dimension of genomic instability together with impaired MMR and cell cycle control in chronic inflammation is emphasized by a high frequency

of p53 mutations in chronic inflammatory diseases such as rheumatoid arthritis.²⁴

In addition to p53, inflammation alters a wide range of other cell-cycle control mechanisms. TNF induces fibroblast proliferation (compare page 2), and IL-1 advances the growth of gastric carcinoma.²⁵ Proliferation is stimulated by the activation of toll-like receptor (TLR)-4 by bacteria. This results in increased prostaglandin E2 production by induction of cyclooxygenase (COX)-2 and activation of epidermal growth factor receptor (EGFR) signaling.²⁶

Another mechanism leading to activation of signal transducer and activator of transcription (STAT)-3 is the secretion of IL-6 from cells of the innate immune system and IL-22 from T_H17 cells. Apart from various other genes, STAT3 is involved in the transcriptional regulation of cyclin B, cyclin D1, and cyclin D2, which play important roles in cell-cycle control and proliferation.²⁷ Similarly, upregulation of the expression of *BCL2* and *BCL2-like1* genes by STAT3 results in prolonged cell survival by avoiding apoptosis.^{28,29}

In summary, inflammation leads to DNA damage by oxygen and nitrogen radicals, especially in cells that are prone because of diminished capacity for DNA repair, apoptosis, and/or cell-cycle control.

Persistent proliferation and perpetual tumorigenic signaling in chronic inflammation

Persistence of this mutagenic environment in chronic inflammation enables cells to accumulate several mutations that are required for neoplastic transformation. For example, *Kras* and *p53* gene mutations are very common in patients with GI malignancies. Tumor suppressor p53 is often designated as ‘guardian of the genome’ as it prompts cell-cycle arrest and apoptosis in defective cells via Mdm2, p21, mammalian target of rapamycin (mTOR), and PUMA signaling. In contrast, *Kras* is an oncogene, which is activated in many different tumors. It belongs to the Ras family of guanosine triphosphates (GTPases) and is involved in many cellular processes, such as cell proliferation, differentiation, apoptosis, and senescence. Phosphatidylinositol 3-kinase (PI-3-K), Raf, Rac, Rho, and TGF- β belong to its key downstream effector pathway.^{30–32}

IL-6/STAT3 signaling can maintain a mutagenic state. Upregulation of sphingosine-1-phosphate (S1P) activates nuclear factor (NF)- κ B, which in turn induces IL-6 transcription.³³ NF- κ B can also be activated by TNF and IL-1.³⁴ A self-augmenting loop maintaining chronic inflammation is described after the activation of the proto-oncogene

SRC. SRC activation as the triggering event initiates NF- κ B/STAT3-mediated cell growth and malignant transformation. Concurrently, NF- κ B rapidly reduces let7-microRNA via Lin28 activation, which acts as a direct inhibitor of IL-6. High IL-6 concentrations in return activate NF- κ B signaling and by these means start a positive feedback loop and link signaling in chronic inflammation to malignant transformation.³⁵ NF- κ B directly, but also via WNT- β -catenin activation, has been shown to provoke dedifferentiation, proliferation, and resistance to cell death in many tumors.^{36,37} NF- κ B as the signal pathway relating carcinogenesis to inflammation was first described by Greten et al³⁸ in colorectal cancer (CRC). In fact, there is evidence for a role of NF- κ B in the carcinogenesis of various GI tumors. NF- κ B can be activated by TNF and is involved in the transcriptional regulation of many cellular functions. Amongst these are a plethora of tumorigenic functions such as proliferation, invasion, and suppression of apoptosis. Beyond that, NF- κ B influences the inflammatory response by controlling the secretion of cytokines such as TNF- α and IL-1.³⁹

Angiogenesis, invasion, and migration

Genomic instability and evasion of cell death are considered to be key steps in carcinogenesis and metastasis formation. But inflammatory cytokines are involved in several of these processes.⁴⁰ For example, TNF, IL-1, and IL-6 from neutrophils, mast cells, and macrophages increase transcription of vascular endothelial growth factor (VEGF) – an important stimulating factor for angiogenesis.^{41,42} Another example is the pro-angiogenic effect of IL-8. IL-8 can also be induced by TNF and IL-1.^{43,44}

In accordance with Hanahan and Weinberg’s *Hallmarks of Cancer*,⁴⁰ infiltration and migration are crucial features of malignant cells. Altered endothelial permeability by TNF and degradation of extracellular matrix by MMP and cathepsins not only fosters leukocyte infiltration during inflammation, but also paves the way for invasive growth, migration, and intravasation of tumor cells.^{45,46} Inhibition of IL-1 in a metastatic mouse model actually revealed a distinct decrease in the rate of metastasis.⁴⁷ To detach epithelial cells and enable these cells to migrate, an epithelial mesenchymal transition (EMT) is assumed to be decisive. STAT3 transcriptional regulation also includes transcription of E-cadherin, which is characteristic for epithelial cells and transcription of MMP. TNF, IL-1, and IL-6-associated NF- κ B and STAT3 activation leads to downregulation of E-cadherin and increased MMP transcription, constituting a mesenchymal cell phenotype. A switch from E-cadherin to N-cadherin is typical of EMT. As

the switch from E- to N-cadherin depends on the transcription factor Snail, Snail is an important regulator of EMT.^{48,49} In CRC, active NF- κ B has been shown to inhibit Snail ubiquitination and degradation downstream, thereby highlighting the significance of inflammatory cytokine signaling for metastasis.^{50–52} Through Wnt and Ras signaling, TGF- β can also induce EMT.⁵³

Through these mechanisms, chronic inflammation is a decisive player in early carcinogenesis. It generates a mutagenic environment and may enable susceptible cells with inherited or spontaneously altered genes to accumulate enough mutations for malignant transformation. This is supported by studies that show that treatment with nonsteroidal anti-inflammatory drugs (NSAIDs) consistently decreases the risk of cancer, most likely by direct inhibition of the NF- κ B/STAT3 signaling pathway. NF- κ B/STAT3 signaling increases expression of COX-2 and in turn is activated itself by COX-2. COX-2 is significantly overexpressed in malignancies, and NSAIDs also increase cell death in existing tumors.^{27,54–58} The anti-neoplastic activity of NSAIDs seems to be mediated by several effectors. NSAIDs without COX inhibitory activity, for example, have similar anti-tumorigenic efficacy. Among others, induction of apoptosis as well as suppression of cyclic guanosine monophosphate (cGMP)- and β -catenin-dependent transcription were identified as alternative NSAID properties. This leads to the assumption that inflammatory cytokines have an influence on tumor progression.^{59,60}

Inflammation in tumor progression

Tumor interactions with the immune system have recently been the focus of extensive research, and a comprehensive description would be beyond the scope of this article. However, as tumors induce a peritumoral chronic state of inflammation, major aspects of tumor-immune cell interactions will be illustrated in this article. To maintain carcinogenic signaling from immune cells, tumors actively attract macrophages and T-cells by chemokines such as IL-4 and TGF- β , bridging the gap to Virchow's description of leukocyte infiltration of tumors. Cytokines, MMPs, and cathepsins from the so-called tumor-associated macrophages (TAMs) are pivotal for further growth, angiogenesis, and invasion. In addition, macrophage-derived EGF forms a paracrine signaling loop, with tumor-derived colony-stimulating factor (CSF)-1 driving neoplastic invasion.^{61,62} These experimental findings have been confirmed by demonstrating an association of macrophage infiltration with a poor prognosis in human cancer patients.⁶³ As necrotic tissue fosters macrophage

invasion, tumors might even benefit from limited intratumoral necrosis.⁶² In contrast, the immune system poses a threat to malignant cells and it is essential for tumors to escape a cytotoxic immune response. Gabrilovich et al.⁶⁴ discovered tumor-derived VEGF-A, which has the potential to suppress dendritic cell antigen presentation. APC function is also directly impaired by TGF- β and IL-10 secretion of tumor cells.^{62,65} Another mechanism to avoid natural killer cells is to attract myeloid-derived suppressor cells (MDSCs). Amongst others, the release of chemokines such as CC-chemokine ligands (CCL)-2, -5, and -12, prostaglandins, and granulocyte colony-stimulating factor (G-CSF) can evoke MDSC accumulation in tumor tissue. As a consequence, MDSCs suppress T-cell function by production of IL-10 and TGF- β .^{42,62,66,67} Only the immune-suppressive function of T_{reg} cells is maintained by TGF- β , and elevated levels of MDSC and T_{reg} correlate with tumor burden.⁶⁸

In conclusion, inflammatory signaling can both support and suppress the growth of established tumors. By partial immune suppression with concomitant selective activation of myeloid cells, tumors influence the inflammatory response to their favor.

Specific role of chronic inflammation in gastrointestinal cancer

Esophagus

Barrett's esophagus and esophageal adenocarcinoma

Gastroesophageal reflux disease (GERD), smoking, body mass index, and a low fruit consumption are well established risk factors for EAC and account for the majority of cases. Although the interaction of several of these risk factors is crucial for the development of this cancer, GERD appears to be the most important individual risk factor.⁶⁹ The reflux of gastric acid causes mucosal damage of the distal esophagus, leading to chronic esophagitis. In some patients, metaplasia from a squamous to a columnar epithelium occurs as a consequence of chronic inflammation during mucosal regeneration – the so-called Barrett's mucosa. Whether Barrett's mucosa is caused by a translocation or migration of gastric cells, by bone marrow stem cells, or by true metaplasia of esophageal cells is controversial. However, proinflammatory cytokines such as IL-6, IL-8, and IL-1 β appear to be involved in the development of Barrett's mucosa.^{70–73} Consistently, inhibition of COX-2 inhibits proliferation of Barrett's mucosal cells.⁷⁴ As a result, the incidence of EAC is 30 times higher in people with Barrett's esophagus than in the general population.⁷⁴ Nevertheless, the annual risk

Table I Gastrointestinal tumors that have been associated with chronic inflammation

Organ	Malignancy	Association with chronic inflammation
Esophagus	Adenocarcinoma	GERD
	Squamous cell carcinoma	Irritation and inflammation by hot beverages and fungi
Stomach	Gastric adenocarcinoma	<i>H. pylori</i> infection, autoimmune and chronic gastritis
	MALT lymphoma	<i>H. pylori</i> infection, HCV, <i>Campylobacter jejuni</i> (small intestine)
Colorectal	Colorectal cancer	Ulcerative colitis, Crohn's disease, pancolitis, Colonization/ infection with specific pathogens
Pancreas	Pancreatic ductal adenocarcinoma	Chronic pancreatitis, <i>H. pylori</i> infection, periodontal disease
Liver	HCC	HBV, cirrhosis (due to alcohol, NAFLD, PBC, HCV)
Biliary system	Gall bladder carcinoma	Chronic gallbladder cystitis
	Cholangiocarcinoma	PSC, recurrent cholangitis, liver cirrhosis

Abbreviations: GERD, gastroesophageal reflux disease; *H. pylori*, *Helicobacter pylori*; HBV, hepatitis B virus; HCC, hepatocellular carcinoma; HCV, hepatitis C virus; MALT, mucosa-associated lymphoid tissue; NAFLD, nonalcoholic fatty liver disease; PBC, primary biliary cirrhosis; PSC, primary sclerosing cholangitis.

of patients with Barrett's mucosa for developing EAC is 0.12%–0.4% and is relatively low overall.^{75,76}

Squamous cell carcinoma

Besides the major risk factors of alcohol, smoking, and genetic polymorphisms, a carcinogenesis-promoting role of chronic inflammation in squamous cell carcinoma is assumed. Hot beverages and fungal invasion are suspected to cause chronic irritation and inflammation of the squamous cell mucosa. The influence of human papilloma virus is still under debate, but its pathogenetic influence on carcinogenesis might be by way of genomic integration rather than inflammation.^{77–79}

Stomach

Carcinomas other than adenocarcinomas are very rare in the stomach. Gastric adenocarcinomas are classified into an intestinal and a diffuse type. A total of 80% of gastric cancer cases are associated with *H. pylori* infections, and *H. pylori*-associated gastric cancer is one of the best elucidated relationships between chronic inflammation and cancer overall. While being protected by antioxidants itself, *H. pylori* can expose host cells to oxidative stress, impair MMR, and alter DNA methylation.^{80,81} In response to *H. pylori*, the gastric mucosa releases the inflammatory cytokine IL-8, an

overexpression of which correlates with a poor prognosis.⁸² Virulence factor cytotoxin-associated gene A (cagA)-positive *H. pylori* strains were identified as particularly carcinogenic. After delivering cagA into gastric epithelial cells, *H. pylori* can initiate signaling that activates growth factor receptors that increase proliferation, invasion, and angiogenesis and also inhibit apoptosis.⁸³ Additionally, chronic inflammation caused by infection with *H. pylori* contributes to neoplastic transformation by establishing a positive feedback loop via STAT3-dependent COX-2 induction, which in turn influences STAT3 regulation via IL-6.⁸⁴

However, gastric carcinogenesis is considered a multistep process, and other inflammatory risk factors have been identified that either act independently of *H. pylori* infections or further enhance their effects. For example, chronic gastritis caused by bile reflux can cause intestinal metaplasia as a neoplastic precursor lesion. Also, T-cell-mediated autoimmune gastritis fosters the development of intestinal-type gastric cancer.^{85,86}

All of these risk factors lead to a state of chronic inflammation. Activation of signaling mediators that are typical of chronic inflammation such as TNF, IL-6, and prostaglandin E2 has been identified as a promoter of gastric tumorigenesis. For example, TNF- α fosters carcinogenesis by upregulating nicotinamide adenine dinucleotide phosphate (NADPH) oxidase organizer 1 (Nox1) and Gna14, resulting in dedifferentiation of gastric epithelial cells.^{87–89} Furthermore, tumor suppressor microRNA miR-7, which inhibits proliferation in vitro, is downregulated in gastric tumors in an inflammation-dependent manner.⁹⁰

Colorectal cancer

Inflammatory bowel disease (IBD) has long been identified as risk factor for CRC. As CRC in IBD arises from flat dysplastic tissue or dysplasia-associated lesions or masses, carcinogenesis seems to differ from the well described adenoma–carcinoma sequence. Concomitantly, IBD-associated CRC has a worse prognosis. The risk of CRC in patients with colonic manifestation of Crohn's disease and in patients with ulcerative colitis is similar. Recent population-based studies have shown an overall standardized incidence ratio of CRC in patients with IBD of 1.7, with a significantly lower age of CRC manifestation (7–12 years earlier). However, this ratio is lower than those reported for years before 2000, which might be a result of aging cohorts.^{91,92} The risk of malignancy correlates with the duration of IBD (10 years after IBD diagnosis: increase of approximately 1% per year). Several clinical symptoms of IBD, such as anatomic extent of

disease, disease activity, and primary sclerosing cholangitis (PSC) characterize patients with a comparatively higher risk for malignancy.^{93,94} Inflammation-driven carcinogenesis in patients with CRC is based on the above-illustrated conditions in chronic inflammation, with oxidative stress and impaired MMR combined with proliferation, invasion, and angiogenesis promoting signaling. In contrast with sporadic CRC, p53 mutations occur rather early in disease development, and APC mutations rather late.⁹⁵ Downregulation of tumor-suppressor genes by hypermethylation was often found at sites of chronic inflammation, and recently the role of intestinal pathogens in carcinogenesis has attracted increasing attention. The DNA repair gene *MUTYH* is a homologue to the *Escherichia coli* gene *mutY*, and colonization by exclusively intracellular *E. coli* was detected at tumor sites.^{95,96} Pathogen antigen binding to TLRs, such as TLR9, can initiate inflammation and could provide a link between pathogens such as *E. coli* and neoplastic transformation.⁹⁷ As T_{reg} concentration in CRC correlates with morbidity, activation of T_{regs} in IBD might also contribute to cancer initiation and progression.⁹⁸

Pancreas

Chronic pancreatitis is a well established risk factor for the development of PDAC, and the risk correlates with the duration of chronic pancreatitis. As mutations found in hereditary pancreatitis differ from those found in tumors, this epidemiologic observation has to be based on enhanced carcinogenesis due to inflammation.^{99,100} In fact, chemokine receptor 2 (CXCR2) ligands such as IL-6 and IL-8 have been identified as autocrine promoters of tumor growth in pancreatic cancer.¹⁰¹ Another inflammatory chemokine, the so-called macrophage pro-inflammatory chemokine-3a (MIP-3a/CCL20), is overexpressed in pancreatic cancer cells and TAMs. It stimulates growth and migration of neoplastic cells and activates further macrophages.¹⁰² Furthermore, patients with homozygous allele 2 of IL-1 β , which is associated with higher IL-1 β concentrations in pancreatic cancer, had a significantly shorter survival, which once again points to the importance of crosstalk of pancreatic cancer and immune cells.¹⁰³ TGF- β signaling is enhanced in chronic inflammation and plays a prominent role in its regulation (compare pages 2 and 4). Concomitantly, inhibition of TGF- β signaling in pancreatic cancer resulted in increased survival.¹⁰⁴ In 90% of pancreatic cancers, Kras-activating mutations are responsible for continuous proliferative and anti-apoptotic signaling. Interestingly, activation of NF- κ B signaling in chronic pancreatitis can ultimately lead to Kras activation and

neoplastic transformation. Also, permanently mutated Kras has been detected in chronic pancreatitis.^{105–108} Only recently has a pivotal role of the IL-6/STAT3 pathway in pancreatic cancer been described. Oncogenic Ras (Kras^{G12D}) induces the secretion of IL-6 from different cell types, and genetic inactivation of IL-6 impedes Ras-driven tumorigenesis.¹⁰⁹ The activation of mutant Kras (Kras^{G12D}) in pancreatic ductal epithelial cells reprograms the tumor microenvironment and is associated with a robust inflammatory response characterized by release of inflammatory cytokines, such as granulocyte macrophage (GM)-CSF. Kras^{G12D}-dependent GM-CSF production promotes infiltration of myeloid cells into the surrounding stroma.^{110,111} TAMs secrete IL-6 that directly activates the Janus kinases (JAKs), thus influencing pancreatic intraepithelial neoplasia (PanIN) progression and pancreatic cancer development.^{112,113} The activated JAK in turn phosphorylates several downstream targets, including cytoplasmic STAT3, which after dimerization rapidly translocates into the nucleus and promotes PanIN progression through transcriptional regulation of anti-apoptotic and pro-proliferative genes. Pancreatic epithelial STAT3 deletion and inactivation of IL-6 trans-signaling impairs PanIN formation and inhibits PDAC development.¹¹³ These studies, together with numerous other observations, suggest that Kras serves as a link between chronic inflammation and carcinogenesis. In combination with other risk factors, *H. pylori* infection and periodontal disease also appear to contribute to carcinogenesis in the pancreas.¹¹⁴

Hepatobiliary

Hepatocellular carcinoma

In recent decades, incidence of HCC has been increasing in the USA, and a growing number of hepatitis C virus (HCV) and hepatitis B virus (HBV) infections have been identified as the underlying cause. Other risk factors for HCC have not increased in incidence during this time.¹¹⁵ HBV is a DNA-integrating virus. Accordingly, activation or suppression of oncogenes and tumor suppressor genes by random integration of viral DNA is suspected to be the key effect in HBV-associated carcinogenesis. However, HBV infection-induced inflammation with activation of NF- κ B signaling and DNA damage by oxidative stress appear to be important pathogenetic mechanisms.¹¹⁶ In contrast, no specific virally induced oncogenes have been identified in HCV infection. Carcinogenesis in patients with HCV (an RNA virus) infection is considered to be an inflammation-mediated process (eg, TGF- β signaling) with a high cell turnover, fibrosis, and cirrhosis. This hypothesis is supported by the

fact that HCV-related HCC correlates with the degree of inflammation, whereas HCC can emerge in HBV-infected patients even without evidence of cirrhosis.^{117–119} This hypothesis was further supported by the finding that antiviral therapy was beneficial in select patients with HBV/HCV-related HCC.¹²⁰

However, as these lesions develop secondary to hepatic cirrhosis in most patients with HCC, this is considered to be the major risk factor. While hepatocytes are more susceptible to mutagenesis because of the high cell turnover during regeneration, recurrent necrosis of liver cells induces chronic inflammation. This process leads to hepatic fibrosis, which ultimately culminates in cirrhosis.^{121–123} Hepatocellular necrosis can be caused by toxins such as alcohol, other environmental factors such as diet, or by chronic inflammation itself. Accordingly, non-alcoholic fatty liver disease and primary biliary cirrhosis have also been identified as risk factors of HCC that are based on chronic inflammation.^{124–126}

During inflammation, macrophages (ie, Kupffer cells) activate fibroblasts and stellate cells by release of TNF and PDGF. Activated fibroblasts produce numerous cytokines, including EGF, hepatocyte growth factor, fibroblast growth factor, IL-6, and MMP-9. This combined signaling causes fibroblastic differentiation of stellate cells, which plays a central role in the pathogenesis of fibrosis. After initiation of the tumor, infiltrating T_{reg} cells that are attracted by Kupffer cells and TAMs modify the immune response and stimulate angiogenesis. Taken together, accumulation of mutations during inflammation-driven fibrosis or cirrhosis is a prerequisite for HCC development.^{127,128}

Cholangiocarcinoma

The risk factor that accounts for the most cases of cholangiocarcinoma worldwide is infection with parasites such as *Opisthorchis viverrini*, *Clonorchis sinensis*, or *Ascaris lumbricoides*. These parasites are endemic in several Asian regions, cause chronic inflammation of the biliary tree, and expose the biliary epithelium to reactive oxygen and nitrogen species.^{129,130}

In Western nations, almost one-third of the patients with cholangiocarcinoma suffer from PSC and, on average, develop the malignancy at a significantly lower age.¹³¹ Interestingly, the duration of PSC does not correlate with the incidence of cholangiocarcinoma. DNA damage and proliferative and mutagenic signaling in chronic inflammation of PSC are considered key steps in the development of cholangiocarcinoma.¹³²

Similar to HCC, chronic infection with HBV or HCV, hepatic cirrhosis, and non-alcoholic fatty liver disease also increase the risk of cholangiocarcinoma.^{133,134}

Recurrent bacterial infections due to cholestasis by biliary stones, congenital abnormalities such as fibropolycystic liver disease, or due to choledocho-enteric anastomoses are also associated with a higher incidence of cholangiocarcinoma. Chronic infections of the biliary tree are presumably not solitary triggers of carcinogenesis and can provide the necessary second hit for malignant transformation in genetically predisposed patients.¹³⁵

Several causative signaling pathways linking inflammation to carcinogenesis in biliary disease have been identified. Human immune response to parasitic biliary infections is mediated by metastasis-associated protein 1 (MTA1) with its adjunctive cytokeratins K-18 and 19. Besides regulating T_{H1} and T_{H2} immune responses, MTA1 has a central role in carcinogenesis and is overexpressed in malignant cells.¹³⁶ Auto- and paracrine stimulation of proliferation mediated by IL-6, IL-8, TGF- β , and TNF- α can be found in cholangiocytes. This stimulation is mediated by IL-6-related activation of p38 mitogen-activated protein kinase and overexpression of the anti-apoptotic myeloid cell leukemia (Mcl)-1.^{137–139}

A similar correlation of recurrent cholecystitis and chronic inflammation of the bile ducts with malignancy is evident for the gallbladder.¹⁴⁰

Mucosa-associated lymphoid tissue lymphoma

MALT lymphoma is an extra-nodal B-cell non-Hodgkin lymphoma that can manifest itself in epithelial tissues throughout the body. Typical GI organs of manifestation are the stomach and the small intestine. Although several chromosomal translocations have been identified in MALT lymphomas, recent research provides augmenting evidence for an inflammatory genesis. Chronic inflammation by infections with *Campylobacter jejuni*, HCV, or, predominantly, *H. pylori* precede many cases of MALT lymphoma and an association of extra-intestinal MALT and autoimmune disease has been described.^{141–143} The release of a proliferation-inducing ligand (APRIL), which belongs to the TNF family, by macrophages as response to infection is a potential link between inflammation and neoplastic transformation. APRIL is important for B-cell maturation and survival. Also, NF- κ B is frequently activated in MALT lymphoma. This signaling pathway can be induced in inflammation or might be permanently mutated by oxygen radicals during chronic inflammation.^{141,144} *H. pylori* virulence factor *cagA* is found in approximately 90%

of patients with gastric MALT lymphoma. Also, eradication of *H. pylori* leads to regression of GI MALT lymphomas in about 90% of the cases, and *H. pylori* eradication is the standard therapy for patients affected.^{145,146}

Clinical perspective

There is accumulating evidence for the involvement of chronic inflammation in the carcinogenesis of most GI malignancies, and the underlying cellular and molecular processes are increasingly understood. Chronic inflammation as a potent player in tumor initiation and progression has extended our concept of the multivariate process of neoplastic transformation (Figure 1). This knowledge has already been implemented in clinical routine. For example, in patients with Barrett's esophagus, *H. pylori* is eradicated to prevent esophageal or gastric cancer. In patients with MALT lymphoma, eradication of *H. pylori* is used to induce remission in these patients. In many inflammatory diseases such as IBD, anti-inflammatory drugs are the mainstay of therapy. However, while mucosal healing in IBD patients results in a decreasing rate of dysplasia, a similar effect could not be proven for single agents such as 5-aminosalicylates or thiopurines.^{147,148} In contrast, many studies showed a chemoprophylactic property of NSAIDs in other inflammation-associated malignancies, such as gastric carcinoma and CRC. Nevertheless, unselective COX inhibitors carry a notable

risk of GI bleeding, and selective COX-2 inhibitors also carry a risk of cardiovascular complications that outweigh the anti-neoplastic benefits.¹⁴⁹ Thus, the identification of COX-independent anti-neoplastic activity of NSAIDs and the development of NSAIDs that are more selective might offer future treatment options for defined patient populations that carry a high risk of cancer, such as patients with a history of familial adenomatous polyposis.

Nowadays, immune-suppressive drugs not only restrict chronic inflammation but are also associated with an increased risk of developing malignancies. More specific agents that interfere with selected immune functions might actually be equally effective as an anti-inflammatory and as an anti-neoplastic medication. Inhibition of IL-6 signaling via IL-6 receptor antibodies (Tocilizumab®; Hoffmann-La Roche AG, Basel, Swiss) represents an effective treatment for patients with rheumatoid arthritis, but also showed promising results in a mouse model of Crohn's disease.¹⁵⁰

However, similar to TNF, with its pro- and anti-angiogenic effects, many mediators of the immune response have a dual role in carcinogenesis; further research is required for clarification.

Also complicating is the fact that many cytokines and signaling pathways have multiple functions throughout the human body. For example, Tocilizumab-induced inhibition of IL-6 – a decisive cytokine linking inflammation and

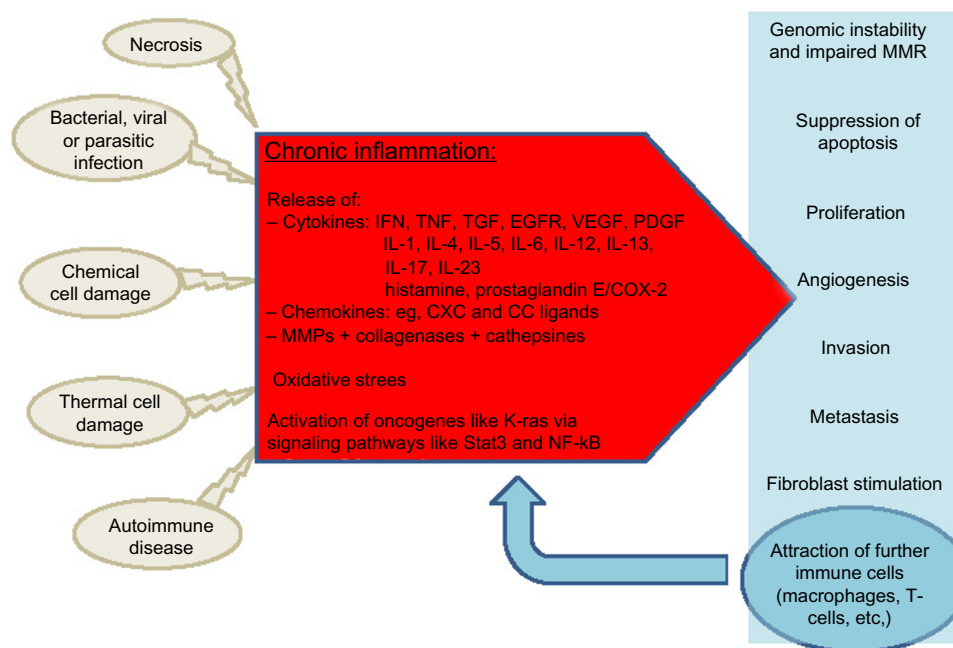


Figure 1 Chronic inflammation in carcinogenesis.

Abbreviations: COX, cyclooxygenase; EGFR, epidermal growth factor receptor; IFN, interferon; IL, interleukin; MMR, DNA mismatch repair; NF, nuclear factor; PDGF, platelet-derived growth factor; Stat, signal transducers and activators of transcription; TGF, transforming growth factor; TNF, tumor necrosis factor; VEGF, vascular endothelial growth factor; MMP, metalloproteinase.

carcinogenesis – is associated with severe side effects such as gastric perforation.¹⁵¹

More importantly, it is crucial to obtain further insight into the molecular pathways that drive carcinogenesis in inflammation. Identification of such signaling pathways is therefore of utmost importance. For example, blocking the soluble IL-6 receptor that is predominantly activated during stress situations such as chronic inflammation and cancer might evolve into a future treatment option.¹⁵² Another potentially interesting target is the JAK2/STAT3 pathway. In fact, several studies are currently underway that address the pharmacological inhibition of the IL-6-dependent JAK2/STAT3 pathway in patients with various solid GI tumors.

Furthermore, there is already evidence of NK cells being capable of restoring the antigen-presenting function of dendritic cells and MDSC.⁶⁸ Detailed understanding of the tumor-immune system interaction would provide the possibility to redirect the immune response against neoplastic cells. Such immune-modulatory drugs could be beneficial for cancer prevention as well as for limiting cancer progression or improving response to existing therapies.

Conclusion

Chronic inflammation is a major risk factor for the development of GI malignancies. As ‘wounds that do not heal’, tumors benefit from inflammatory signaling while escaping damage through the immune system by modifying the immune response in their favor. Further insight into the function of the mediators and the regulation of the immune response could help to identify more specific future treatment targets. In our opinion, understanding of the tumor microenvironment and tumor-immune system interactions will be crucial, as these aspects have not yet been implemented in therapeutic regimens. Altering a tumor-susceptible micro environment, or even avoiding formation of the so-called metastatic niche, might reduce metastasis. In addition, re-establishing an immune response against neoplastic cells might improve the efficacy of existing therapies. This estimation is supported by the finding that assessment of the immunologic tumor environment allows better conclusions regarding prognosis and response to therapy than the traditional anatomic International Union Against Cancer ‘Tumor/Node/Metastasis’ (UICC-TNM) classification system for tumor staging.¹⁵³ As assay availability and protocols vary among laboratories, an international task force has proposed the ‘Immunoscore’ as a standardized prognostic tool.¹⁵⁴ The ongoing clinical evaluation of this score will reveal its relevance for clinical practice.

Disclosure

The authors do not have any conflicts of interest to disclose.

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