



# Inflammatory bowel disease and carcinogenesis

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## Abstract

Colorectal cancer (CRC) is the third most common cancer and the fourth most common cause of cancer mortality worldwide. Colitis-associated colorectal cancer (CAC) is a subtype of CRC associated with inflammatory bowel disease (IBD). It is well known that individuals with IBD have a 2–3 times higher risk of developing CRC than those who do not, rendering CAC a major cause of death in this group. Although the etiology and pathogenesis of CAC are incompletely understood, animal models of chronic inflammation and human cohort data indicate that changes in the intestinal environment, including host response dysregulation and gut microbiota perturbations, may contribute to the development of CAC. Genomic alterations are a hallmark of CAC, with patterns that are distinct from those in sporadic CRC. The discovery of the biological changes that underlie the development of CAC is ongoing; however, current data suggest that chronic inflammation in IBD increases the risk of developing CAC. Therefore, a deeper understanding of the precise mechanisms by which inflammation triggers genetic alterations and disrupts intestinal homeostasis may provide insight into novel therapeutic strategies for the prevention of CAC.

**Keywords** Inflammation · Microbiota · IBD · CAC

## Abbreviations

APC	Adenomatous polyposis coli	H <sub>2</sub> S	Hydrogen sulfide
CD	Crohn's disease	IL-22BP	IL-22 binding protein
CAC	Colitis-associated colorectal cancer	IBD	Inflammatory bowel disease
CRC	Colorectal cancer	IEC	Intestinal epithelial cell
CSCs	Cancer stem cells	KRAS	Kirsten rat sarcoma virus
DCC	Deleted in colon cancer	Lcn2	Lipocalin-2
DSS	Dextran sulfate sodium	LGR5	Leucine-rich repeat-containing G-protein-coupled receptor 5
EMT	Epithelial–mesenchymal transition	MSI	Microsatellite instability
ETBF	Enterotoxigenic <i>Bacteroides fragilis</i>	Myd88	Myeloid differentiation factor 88
FAP	Familial adenomatous polyposis	NF-κB	Nuclear factor kappa-light-chain enhancer
FMT	Fecal microbiota transplantation	NLRP3	NOD-like receptor protein 3
GI	Gastrointestinal	NOS	Nitric oxide synthase
GSK3β	Glycogen synthase kinase-3β	pks	Polyketide synthase
HDC	Histidine decarboxylase	PRR	Pattern recognition receptor
		RNS	Reactive nitrogen species
		ROS	Reactive oxygen species
		STAT3	Signal transducer and activator of transcription 3
		Th	T helper
		TLR	Toll-like receptor
		TNF	Tumor necrosis factor
		Tregs	Regulatory T cells
		UC	Ulcerative colitis
		5-ASA	5-Aminosalicylic acid

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## 1 Introduction

Inflammatory bowel disease (IBD), including Crohn's disease (CD) and ulcerative colitis (UC), is a chronic, idiopathic, relapsing inflammatory disease of the gastrointestinal (GI) tract [1]. A subset of individuals with IBD (10–15%) develops colorectal cancer (CRC), referred to as colitis-associated CRC (CAC), which appears to carry a worse prognosis than CRC in patients with no history of IBD [2–4]. The knowledge that CAC is a major cause of death in IBD [5, 6] necessitates the development of novel therapy. The inflammation–dysplasia–carcinoma sequence of CAC is distinct from the normal–adenoma–adenocarcinoma sequence in sporadic CRC, with inflammation playing a central role in the development of CAC. A growing number of studies show that intestinal inflammation drives the initiation of cancer and conducts its development. With the recent advances in “omics” analyses and the detailed characterization of animal models of chronic GI inflammation, it is evident that intestinal inflammation can induce genetic alternation, oxidative stress-driven DNA damage, host immune response dysregulation, and gut microbiota/metabolite community disruption, which are strongly associated with CAC development [7]. In addition, clinical studies suggest that preventing the burden of inflammation may be essential to minimize the incidence and pathogenesis of CAC [8–10]. However, the development of inflammation-induced CAC follows a complicated trajectory. Many fundamental questions remain, including elucidation of disease immunopathogenesis. Hence, we will review the recent advances in the field, focusing on the mechanisms involved in the inflammation, immune responses, and gut dysbiosis in CAC.

## 2 Molecular pathogenesis of CAC and sporadic CRC

Studies using next-generation sequencing have reported several genomic alterations in patients with CAC and in patients with sporadic CRC [11, 12]. Both CAC and sporadic CRC arise in the precancerous dysplastic intestinal mucosa. However, CAC typically arises from flat dysplastic mucosa, whereas most sporadic CRC arises from polyps [13]. CAC develops in a chronically inflamed mucosa and follows the sequence of indefinite dysplasia to low-grade dysplasia to high-grade dysplasia to carcinoma. In comparison, most sporadic CRC develops from the dysplastic precursor, early adenoma, and progresses to invasive carcinoma [12–14]. Animal models show that inflammation induces both the initiation and progression of

colonic neoplasia [15, 16], suggesting that chronic inflammation leads to genomic changes that increase CAC risk. Although multiple gene mutations are common between CAC and sporadic CRC, their timing varies [12, 13, 17, 18]. For example, the loss-of-function mutation of adenomatous polyposis coli (*APC*), the tumor suppressor gene, occurs early in the progression of sporadic CRC, whereas it usually occurs in the late phase of CAC development [19]. On the other hand, it is reported that the frequency and timing of microsatellite instability (MSI) is similar in CAC and sporadic CRC; i.e., the early stage of carcinoma progression [20]. The loss-of-function mutation of *p53*, an important step in the progression of carcinoma, occurs early in CAC, whereas it is a late phenomenon in sporadic CRC [21]. The loss of heterozygosity at *p53* correlates with the malignant progression of CAC. The deletion of *p53* was detected in 85% of biopsy specimens with carcinoma, whereas it was detected in 6% without dysplasia in CAC [22]. More than 50% of UC patients who do not have cancer have *p53* mutations in the inflamed mucosa, indicating that chronic inflammation may cause these mutations [23]. DNA hypermethylation also is a critical feature of CAC. The methylation of CpG islands in several genes has been detected in chronically inflamed mucosal tissue, in the early phase of CAC development, without visible dysplasia. The hypermethylation of tumor suppressor genes, including *hMLH1*, *p16INK4a*, and *p14ARF*, has been observed in CAC patients [20, 24, 25]. Besides *APC* mutations, Kirsten rat sarcoma virus (*KRAS*) activation, the most common type of mutation reported in CRC, differs between CAC and sporadic CRC. *KRAS* mutation frequently occurs in the early stage of sporadic CRC, and in the late stage of CAC. In UC patients, the mutation of *KRAS* occurs in the advanced stages of CAC, such as high-grade dysplasia. Furthermore, *KRAS* mutations correlate with a disease duration longer than 10 years [26]. Previous studies indicate that alterations of the deleted in colorectal cancer (*DCC*) gene and the *SMAD4* gene located on chromosome 18q are increased in CAC [27–29]. Of note, alteration in chromosome 18q genes occurs earlier in CAC (i.e., the indefinite dysplasia to low-grade dysplasia pathway) compared with sporadic CRC (i.e., the late adenoma to carcinoma pathway) [12, 30]. As with *APC* mutation, the alteration of the glycogen synthase kinase-3 $\beta$  (*GSK3 $\beta$* ) gene, which is involved in multiple inflammatory signaling pathways, is also required for the stage progression of CAC, from high-grade dysplasia to carcinoma [31, 32]. Moreover, the expression patterns of genes related to cancer stem cells (CSCs), which are involved in tumor development, progression, metastasis, and drug resistance [33], differ between sporadic CRCs and CACs. Leucine-rich repeat-containing G-protein-coupled receptor 5 (*LGR5*), a crypt stem cell marker, is recognized as a CSC maker

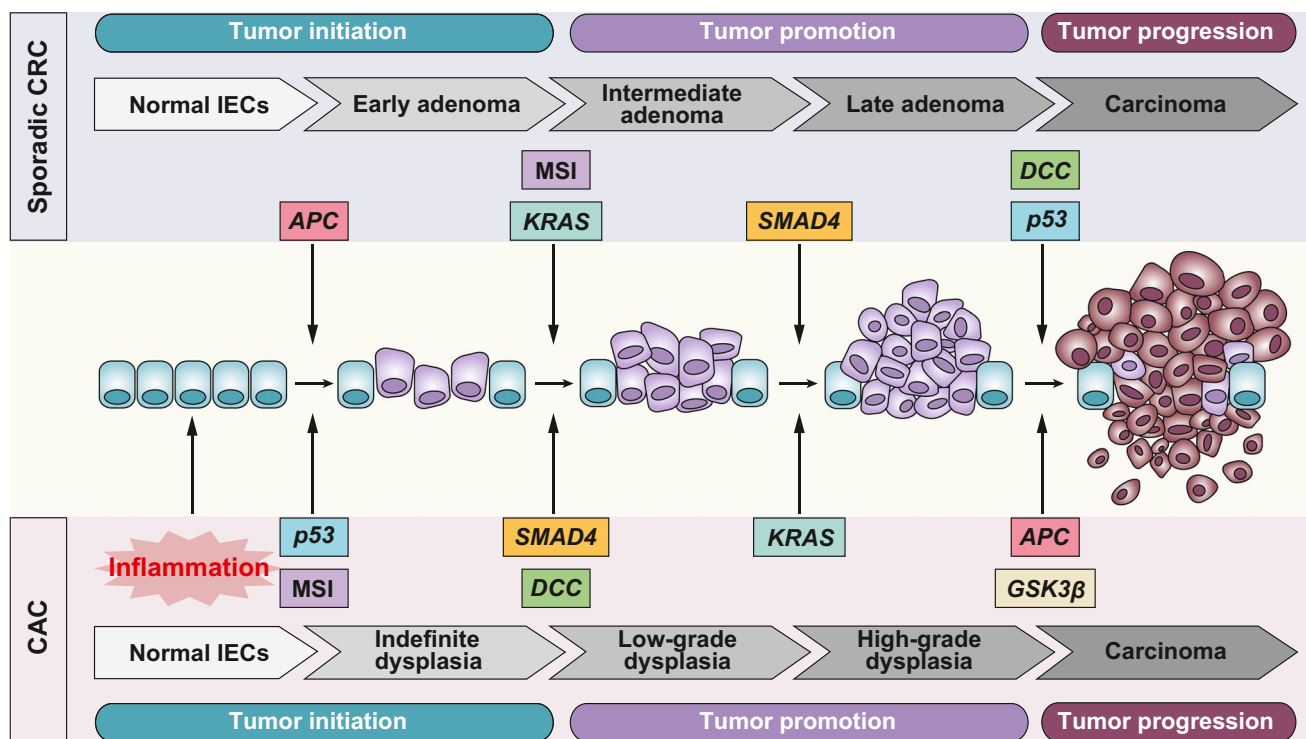
in the colon [34]. The expression of *LGR5* is reported to be less frequent in CAC than in sporadic CRC [35]. Furthermore, the expression of CD133, a cell surface marker of colon CSCs, is also lower in CAC than in sporadic CRC [36]. A further understanding of the genomic events underlying the development of CAC may lead to the development of novel therapeutic approaches for the treatment of CAC and its early detection (Fig. 1).

### 3 The role of inflammation in CAC

In contrast to sporadic CRC, the pathogenesis of CAC involves the continuous stimulation of epithelial proliferation in an inflammatory environment [37]. Mounting evidence shows that chronic inflammation is a risk factor for cancer [7, 13–15]. Chronic inflammation enhances CAC development through various mechanisms, including oxidative stress, DNA damage, abnormal immune response, and perturbation of the gut microbiota.

### 3.1 Oxidative stress

IBD has been considered an oxyradical overload disease because chronic intestinal inflammation is related to the overproduction of reactive oxygen species (ROS) and reactive nitrogen species (RNS), leading to oxidative stress. Oxidative stress, which is mainly produced by innate immune cells such as macrophages and neutrophils, promotes DNA damage in the intestinal epithelial cells (IECs), resulting in an increased tumorigenic alteration and accelerated growth of cancer cells [38, 39]. Inflammation-mediated oxidative stress is known to contribute to the pathogenesis of CAC in humans. Accordingly, elevated oxidative DNA damage induced by etheno-DNA adducts has been observed in colonic biopsy specimens from patients with CAC [40]. Furthermore, accumulated ROS and RNS are detected in the inflamed tissues of patients with active UC and CD [38, 41, 42]. ROS reacts with DNA leading to chromosomal breaks and increased chromosomal instability. Interestingly, chromosomal aberrations, represented by telomere shortening, are increased in biopsy specimens from UC patients who have progressed dysplasia or cancer compared to specimens



**Fig. 1** Tumor development in sporadic CRC and CAC. Differences in molecular pathogenesis of sporadic CRC (upper) and CAC (lower). Intestinal inflammation is a hallmark of CAC, and the inflammation–dysplasia–carcinoma sequence of CAC is distinct from the sporadic sequence of CRC—normal to adenoma to adenocarcinoma. Loss of *APC* and mutations of *KRAS* occur in the early phase of the development of sporadic CRC, whereas these mutageneses occur late in the

development of CAC. On the other hand, the mutation and loss of *p53*, *SMAD4*, and *DCC* are a late occurrence in sporadic CRC, and a characteristic early phenomenon in CAC. The occurrence and timing of MSI mutations is similar in sporadic CRC and CAC (i.e., the early stage of carcinoma progression). The mutations of *GSK3β* are required in the late stage of CAC development

from UC non-progressors or control individuals [43]. An animal study showed that mice deficient in nuclear factor erythroid 2 (NF-E2)-related factor 2 (Nrf2), a master regulator of antioxidant genes, develop enhanced CAC [44]. These findings indicate that inflammation-driven oxidative stress contributes to the development of CAC.

## 3.2 Immune-mediated pathways and signaling

### 3.2.1 STAT3 signaling

The phosphorylation activation of signal transducer and activator of transcription 3 (STAT3), a major oncogenic transcription factor in colonic epithelial cells, regulates antiapoptotic genes (e.g., Bcl-2 and Bcl-xl), cell cycle regulators (e.g., cyclin D1 and c-Myc), tissue-resistance factors (e.g., Hsp70, Reg3, and S100A9), and angiogenesis genes (e.g., bFGF and VEGF), which are all related to the tumor invasion, metastasis, and worsening progression of CAC [45–50]. STAT3 signaling is considered a specific pathway-targeted approach for CAC therapy because of the accumulating evidence of its pathogenic role in IBD and CRC [51] and the observation of activated STAT3 in patients with CAC [52]. Furthermore, *in vivo* loss-of-function and gain-of-function studies show that STAT3 regulates the impact of IL-6 and IL-11 on the initiation and development of CAC. In addition, inhibiting STAT3 in IECs results in the suppression of CAC induction and growth, demonstrating the critical oncogenic function of STAT3 in CAC [53]. Notably, STAT3 plays an essential role in CAC through crosstalk with other critical pathways and signaling related to inflammation and carcinogenesis (e.g., Wnt/ $\beta$ -catenin, NF- $\kappa$ B, PI3K/Akt/mTOR pathway, Notch pathway) [54, 55].

### 3.2.2 NF- $\kappa$ B pathway

The transcriptional factor nuclear factor kappa B (NF- $\kappa$ B) appears to be involved in cancer development. Deficiency in NF- $\kappa$ B results in increased IEC apoptosis, disturbed expression of antimicrobial peptides, and interruption of bacterial translocation to the mucosa, suggesting that NF- $\kappa$ B regulates epithelial integrity and interactions with the mucosal immune system [56]. IEC-specific inhibition of NF- $\kappa$ B in mice induces the spontaneous development of severe chronic inflammation [56]. A CAC mouse model involving azoxymethane (AOM) plus DSS treatment revealed that NF- $\kappa$ B activation in IECs is essential for the development of colonic adenomas [57, 58]. NF- $\kappa$ B also regulates the expression of various proinflammatory cytokines and chemokines, including TNF- $\alpha$  and IL-6, which contributes to the inflammatory processes of IBD [59]. Consistently, a high level of activated NF- $\kappa$ B is detected in IECs and macrophages in patients with IBD [60].

### 3.2.3 Wnt/ $\beta$ -catenin signaling

$\beta$ -catenin signaling regulates vital cellular functions, including cell proliferation, polarity, migration, genetic stability, apoptosis, and tissue homeostasis [61]. The pivotal component of Wnt signaling is the cytoplasmic protein  $\beta$ -catenin, which is critical in CAC progression [61]. The inhibition of the Wnt/ $\beta$ -catenin pathway by 5-ASA, the most common anti-inflammatory therapy for UC patients, reduces colitis and is effective for therapy for CAC [62, 63]. Wnt signaling is detected only in polypoid lesions (91.3%), not in flat lesions (0%), in colitic mice [64, 65]. Moreover, the accumulation of nuclear  $\beta$ -catenin is observed in nondysplastic lesions in half of CAC patients [66], suggesting that dysregulation of the Wnt/ $\beta$ -catenin pathway plays a vital role in CAC progression, especially in the early phase.

### 3.2.4 TNF- $\alpha$

Tumor necrosis factor (TNF)- $\alpha$  is a well-known proinflammatory cytokine that relates to a variety of cellular processes such as cell proliferation, differentiation, and cell death [67]. Considering that TNF neutralization is effective in the treatment of acute and chronic inflammatory conditions, the presence of TNF during the inflammatory response is important for the maintenance of chronic inflammation [68, 69]. TNF- $\alpha$ , which is produced by activated macrophages and T cells, acts as an initiator of carcinogenesis through DNA damage, stimulating tumor angiogenesis. It is striking that TNF- $\alpha$  activates NF- $\kappa$ B, which contributes to CAC development, as mentioned. Of note, TNF- $\alpha$  production is upregulated in UC patients, and it seems to contribute to the pathogenesis of IBD, an underlying condition for CAC development [70]. Administration of anti-TNF monoclonal antibodies has been shown to effectively treat CD and UC patients [71]. Moreover, elevated TNF expression occurs in the process of CAC carcinogenesis, and blockade of TNF- $\alpha$  signaling suppresses tumorigenicity and tumor growth in a CAC mouse model [72].

### 3.2.5 IL-1 $\beta$

IL-1 $\beta$  is a proinflammatory cytokine that is upregulated in patients with IBD and in patients with colon cancer [73]. IL-1 $\beta$ , which is produced by macrophage and neutrophils, can induce the expression of IL-6, which is another important component in mediating CAC through the activation of STAT3 signaling pathway [74]. Consistent with this notion, blocking IL-1 $\beta$  activity reduces tumorigenesis in CAC mice by disordering macrophage-dependent IL-6 secretion [74]. Furthermore, the ablation of the TIR8 gene, a negative regulator of IL-1 receptor signaling, increased intestinal

inflammation and CAC in AOM/DSS-treated mice [75]. IL-1 $\beta$  secretion in innate immune cells is regulated by the NOD-like receptor protein 3 (NLRP3) inflammasome [76]. A study demonstrated that inhibiting NLRP3 activation by small molecule andrographolide induces a decline in IL-1 $\beta$  production in vitro and in vivo, reducing the risk of CAC [77]. These findings imply that IL-1 $\beta$  may be a potential therapeutic target for CAC.

### 3.2.6 IL-6

Animal and human studies suggest that IL-6 plays a crucial role in IBD pathogenesis. It is conceivable that IL-6 can control the survival of colitogenic T cells, the differentiation of T helper 17 (Th17) cells, and the suppression of regulatory T cells (Tregs); all mechanisms that are associated with CAC progression [71, 78, 79]. The most crucial role of IL-6 is to activate STAT3 and NF- $\kappa$ B signaling, the keystone of CAC development, as mentioned. A correlation between IL-6-mediated STAT3 activation and CAC progression has been reported [80]. In the AOM/DSS-treated CAC mouse model, IL-6<sup>-/-</sup> mice have reduced tumor formation and growth compared to wild-type (WT) mice [53]. In addition, the inhibition of IL-6 signaling has been proven to ameliorate symptoms in patients with active CD [53, 81–83].

### 3.2.7 IL-17/IL-23

Accumulating evidence highlights the clinical significance of IL-17 to IBD and CAC. IL-17 family members, such as IL-17A, IL-17C, and IL-17F, are related to a proinflammatory signature, and they influence different aspects of the progression of IBD and colon cancer [84, 85]. Indeed, several studies have proven that IL-17A is a protumorigenic cytokine in various CAC mouse models, such as the APC<sup>Min</sup> model [86] and the AOM/DSS model [86, 87]. A remarkable feature of IL-17A is its ability to regulate intestinal inflammation and tumor growth, and further, IL-17A-deficient CAC mice have been shown to develop fewer tumors in the AOM/DSS CAC model [87, 88]. Also, the deletion of IL-17A reduces spontaneous small intestinal tumors in APC<sup>Min</sup> mice [89]. Similarly, epithelial IL-17C, driven by the microbiota, is associated with IEC survival and the development of colon cancer [90]. Contrary to IL-17A and IL-17C, colonic tumor development was enhanced in the absence of IL-17F in the AOM/DSS CAC model [91]. IL-23, produced by antigen-presenting cells, plays a role in tumor progression by inducing inflammation in the tumor microenvironment. IL-23 is upregulated in CAC patients and CAC model mice compared with the healthy colonic mucosa [92]. IL-23- or IL-23 receptor-deficient mice exhibit reduced secretion of proinflammatory cytokines, including IL-17A, in colon tissue, and decreased colon cancer development

[92], whereas the overexpression of IL-23 promotes colitis and colon cancer by inducing IL-17 production [93]. These findings suggest that IL-23 regulates IL-17 production during inflammation and the IL-17/IL-23 axis plays an essential role in the development of chronic inflammation and CAC.

### 3.2.8 IL-22

Given that IL-22 plays an essential role in mucosal healing, epithelial barrier, and chronic inflammation, it likely acts as a tumor-promoting cytokine in various cancers [94–96]. For example, a study of *Helicobacter hepaticus*-infected Rag2<sup>-/-</sup> CAC mice showed that IL-22-driven nitric oxide causes DNA damage in crypt epithelial cells and leads to the development of dysplasia. Furthermore, depletion of IL-22 influences the severity of *H. hepaticus*-induced inflammation and tumorigenesis [97]. Notably, the loss of IL-22 binding protein (IL-22BP), a soluble IL-22 receptor that neutralizes the abilities of IL-22, in APC<sup>Min</sup> CAC mice, which have continuous activation of IL-22 signaling, promotes colonic tumorigenesis as compared to IL-22-deficient APC<sup>Min</sup> mice and WT mice, suggesting that the IL-22 and IL-22BP pathway regulates mucosal healing and tumor development [98]. Further, it has been reported that a dysregulated IL-22–STAT3 axis is related to UC-induced carcinogenesis, and a positive correlation is observed between IL-22 expression level and CAC progression [99, 100]. Thus, IL-22 can be used as a biomarker to detect the severity of CAC.

### 3.2.9 IL-33

The functions of IL-33 in the GI tract have also received much attention in recent years. IL-33 is a member of the IL-1 cytokine family, and it acts as an epithelial alarmin. Damaged or stressed tissue and necrosis cells release IL-33 to alert the immune system [101]. Several studies have shown that the expression of IL-33 and ST2, an IL-33 receptor, is increased in IBD patients and CAC patients [102, 103]. Activation of the IL-33–ST2 axis was observed in adenomatous polyps of APC<sup>Min</sup> mice, and deactivation of this signal decreased intestinal polyp development [104]. Similarly, in the AOM/DSS model, it was shown that the IL-33–ST2 pathway is closely associated with the development of colonic tumorigenesis by the induction of epithelial leakiness and IL-6 production. In addition, AOM/DSS mice with ST2 deletion, displayed delayed CAC formation compared to AOM/DSS mice with intact ST2 [105], suggesting that IL-33 may be a potential target of CAC therapy. On the other hand, IL-33 serves a protective function in CAC. IL-33 maintains gut homeostasis by regulating IgA production in the intestine. IL-33 deficient mice are highly susceptible to AOM/DSS-induced CAC. Of note, reduced intestinal IgA production in IL-33<sup>-/-</sup> mice treated with AOM and DSS

induced gut dysbiosis characterized by an enhanced level of mucolytic and colitogenic bacteria, including *Akkermansia muciniphila* and segmented filamentous bacteria (SFB) [106]. Hence, the role and mechanism of IL-33 in CAC are important to elucidate the pathogenesis of CAC and to assess potential therapies for CAC.

## 4 The role of the gut microbiota in CAC

### 4.1 Pathobionts in CAC

Accumulating evidence suggests that the intestinal microbiota plays an essential role in maintaining intestinal homeostasis [107–109]. The gut microbiota takes on a role in beneficial functions for the host cells, including protection from pathogen colonization and shaping the immune cell network, and thus, its disruption, termed dysbiosis, is associated with the risk of intestinal inflammation and CAC [110, 111]. Interestingly, studies have reported that chronic inflammation induced by AOM/DSS treatment leads to gut dysbiosis in SPF mice. In this CAC model, bacterial diversity in the gut is significantly decreased and subsequently, the mice develop tumors in the gut. However, antibiotic exposure can reverse this phenotype. Consistently, APC<sup>Min</sup> CAC mice develop fewer tumors when housed in germ-free conditions [112]. Furthermore, gnotobiotic mice colonized with microbiota derived from CAC mice have an increased tumor burden and incidence compared to those colonized with microbiota derived from healthy mice [113]. Vancomycin administration in AOM/DSS mice reduces tumor development by the loss of neutrophils that induced DNA damage in the IECs [114]. These findings strongly suggest that inflammation-driven tumorigenesis is dependent on the gut microbiota. Another CAC mouse model, such as *H. hepaticus* infection, also proves that bacteria are required to initiate tumor development [115]. In clinical studies, it has been demonstrated that gut dysbiosis contributes to the pathogenesis of CAC. As observed in IBD patients, the composition of the mucosa-associated microbe population in CAC patients is strikingly different compared to that in the control individuals, such as a significant reduction in bacterial  $\alpha$ -diversity [110]. The mucosa-associated microbiota in CAC patients is enriched in the Enterobacteriaceae family and *Sphingomonas* genus and diminished in *Fusobacterium* and *Ruminococcus* genera compared to the microbiota in patients with sporadic cancer [110]. *Escherichia coli* is the most well-studied procarcinogenic species in the Enterobacteriaceae family. It is known that some *E. coli* strains can produce the polyketide synthase (pks)-derived genotoxin colibactin, which causes chronic DNA damage in IECs [116]. It was reported that deletion of the pks genotoxic island from colibactin-producing *E. coli* reduced CRC

in AOM–IL-10<sup>-/-</sup> and APC<sup>Min</sup>–IL-10<sup>-/-</sup> CAC mice [117, 118]. In addition to its genotoxic capacity, it was reported that mice colonized with pks<sup>+</sup> *E. coli* had increased TNF expression compared with mice colonized with commensal *E. coli*. Given that the blockade of TNF signaling decreased colitis and colonic tumor development in pks<sup>+</sup> *E. coli* colonized mice, proinflammatory cytokines induced by the colonization of pks<sup>+</sup> *E. coli* also contribute to the tumorigenesis [119]. Interestingly, administration of sodium tungstate has a significant effect on the reduced intestinal inflammation and decreased tumorigenesis in AOM/DSS and AOM-treated IL-10<sup>-/-</sup> CAC models by inhibiting the gut colonization of colibactin-producing *E. coli* [120].

*Bacteroides fragilis* is known to harbor metalloprotease enterotoxin, which induces the cleavage of E-cadherin, disrupting the intestinal barrier. The colonization of enterotoxigenic *B. fragilis* (ETBF) promotes Th17 responses, resulting in the activation of NF- $\kappa$ B–STAT3 signaling in IECs following CAC development in APC<sup>Min</sup> mice. The neutralization of Th17 cell-derived IL-17, alone or in combination with IL-23 receptor blocking, suppressed ETBF-induced colonic tumorigenesis [86, 121]. ETBF was also shown to elicit polyp development in an AOM/DSS CAC model through elevated protumorigenic inflammatory cytokine production (e.g., IFN- $\gamma$ , IL-17A, IL-6, TNF- $\alpha$ ) [122].

More recently, the formation of a bacterial biofilm has been recognized as a driving factor in the early phase of CRC development [123, 124]. Interestingly, a study using mucosal tissue samples from patients with familial adenomatous polyposis (FAP) revealed that pks<sup>+</sup> *E. coli* and ETBF dominated the bacterial population of the colonic biofilm in FAP polyps. In line with this finding, co-colonization of pks<sup>+</sup> *E. coli* and ETBF enhanced the development of CRC. In vitro experiments further suggested that mucus degradation by ETBF enhances the colonization of pks<sup>+</sup> *E. coli* in the gut, and induces epithelial damage as mentioned [125]. This indicates that bacterial biofilms and toxins promote the development of CRC.

Although *Fusobacterium nucleatum* is a major pathogen involved in chronic periodontitis, recent studies have shown that this bacterium plays a crucial role in CAC progression. For instance, in APC<sup>Min</sup> mice, colonization by *F. nucleatum* promotes the development of colonic tumors by recruiting tumor-infiltrating myeloid cells [126]. Moreover, *F. nucleatum* is known to promote epithelial–mesenchymal transition (EMT), an important process in colonic tumorigenesis [127].

*Porphyromonas gingivalis*, which often coexists with *F. nucleatum* in oral biofilms, is recognized as an oral pathobiont [128], and was recently reported to be enriched in feces and tissue samples from CRC patients compared with the samples from healthy subjects. Cohort research showed a positive correlation between *P. gingivalis* abundance in carcinoma tissue and a poor prognosis [129]. In addition, a

study of APC<sup>Min</sup> mice revealed that *P. gingivalis* facilitates protumorigenic IL-1 $\beta$  production via NLRP3 inflammatory activation in recruited tumor-infiltrating myeloid cells, resulting in the promotion of CAC formation [130]. Like *P. gingivalis*, *Streptococcus gallolyticus*, previously known as *S. bovis*, an oral pathobiont that forms an oral biofilm community, can promote cancer progression [131]. Given that *S. gallolyticus* can degrade tannic acids, inhibiting the proliferation of tumor cells such as CRC, this bacterium appears to be a tumorigenic player. Cohort analyses indicate that *S. gallolyticus* is enriched in CAC tissue compared with sporadic CRC tissue [110]. Consistent with human studies, the accumulation of *S. gallolyticus* was observed in the colonic mucosa of carcinoma tissue from AOM/DSS mice (3 cycles DSS) compared to the adenoma tissues from AOM/DSS mice (2 cycles DSS) and healthy tissues from normal mice. Colonization by *S. gallolyticus* aggravates the development of CAC in AOM/DSS mice. In this model, the recruitment of CD11b<sup>+</sup> myeloid cells was induced by *S. gallolyticus* to promote CAC progression [132].

Infection with *Helicobacter* species is endemic in many animal facilities and may influence the penetrance of CAC phenotypes. Numerous studies report the relationship between *Helicobacter* spp. and IBD pathogenesis, and the apparent association between *Helicobacter* spp. and CAC pathogenesis. In IL-10<sup>-/-</sup> mice, infection with *H. rodentium* or *H. typhlonius* causes CAC development, which can be prevented by antibiotic treatment [133]. Furthermore, it has been reported that *H. hepaticus* can cause CAC in *Rag2*<sup>-/-</sup> mice through the induction of TNF- $\alpha$  and IL-6 [115]. Another group found that infection with *H. hepaticus* in *Rag2*<sup>-/-</sup> mice led to an accumulation of nitric oxide (NO) and *H. hepaticus*-driven inflammation and carcinogenesis, which was suppressed by TNF- $\alpha$  neutralization, acting upstream of NO production [134]. In contrast, *H. pylori* infection in AOM/DSS CAC mice can attenuate the development of CAC by reducing the infiltration of tumor-associated macrophages [135].

*Akkermansia muciniphila* is a mucin-degrading bacterium that has important regulatory effects on gut homeostasis [136, 137]. *A. muciniphila* is thought to be inversely correlated with inflammation status; however, the relationship between *A. muciniphila* and CAC remains controversial. It has been reported that *A. muciniphila* abundance was decreased in IBD patients and AOM/DSS mice, and the incidence of CAC in mice colonized by *A. muciniphila* was ameliorated by reducing the infiltration of macrophages [138]. However, several studies of the effects of *A. muciniphila* in CAC have drawn opposite conclusions. The abundance of *A. muciniphila* is significantly increased in IL-33-deficient AOM/DSS CAC mice, which are highly susceptible to colitis and CAC [106]. In addition, a recent study has revealed that *A. muciniphila* acts as a promoter in CAC development.

In AOM/DSS mice, the administration of *A. muciniphila* enhanced the susceptibility of mice to CAC by enhancing the proliferation of IECs [139]. Clearly, further large-scale animal studies and human studies are needed to clarify the role of *A. muciniphila* in CAC pathogenesis.

Lipocalin-2 (Lcn2) is a host defense protein that is upregulated during inflammation. The antimicrobial peptide Lcn2 was induced in IL-10<sup>-/-</sup> colitis mice and Lcn2 deficiency aggravated IL-10<sup>-/-</sup> colitis and CAC. This study also demonstrated that Lcn2<sup>-/-</sup>IL-10<sup>-/-</sup> mice harbored increased *Alistipes* spp., and *A. finegoldii* challenge to IL-10<sup>-/-</sup> mice yielded increased susceptibility to CAC via activation of IL-6–STAT3 signaling [140]. Hydrogen sulfide (H<sub>2</sub>S) is a mediator of inflammation, homeostasis, and repair in the GI tract [141]. Although the function of endogenously and exogenously produced H<sub>2</sub>S in IBD remains controversial, it has been shown that the abundance of H<sub>2</sub>S-producing *Atopobium parvulum* positively correlates with the severity of pediatric IBD. *A. parvulum* induced colitis in IL-10<sup>-/-</sup> mice, and was mitigated by administering the H<sub>2</sub>S scavenger bis-muth [142] (Table 1).

## 4.2 Beneficial microbiota in CAC

As mentioned, gut dysbiosis may closely contribute to CAC pathogenesis. Various publications have reported that the normalization of gut dysbiosis by fecal microbiota transplantation (FMT) ameliorates the incidence and symptoms of GI disease, including *Clostridioides difficile* infection [150, 151]. Notably, revision of a perturbed gut microbiota by FMT of the gut microbiota derived from healthy control mice markedly suppressed CAC tumorigenesis in an AOM/DSS model. In addition, FMT-treated CAC mice had increased anti-inflammatory responses through suppression of NF- $\kappa$ B activation. Moreover, FMT triggered the accumulation of butyrate-producing regulatory T cells (Tregs), but not colitogenic Th17 cells in CAC mice [149]. These findings imply that FMT has potential as a therapeutic approach to CAC.

Not only the bulk population of microbiota transplantation but also transplantation of a single bacterium may be effective in cancer management. For example, a study using a CAC model revealed that *Bifidobacterium lactis*, a commensal-derived probiotic species, inhibits NF- $\kappa$ B activation in IECs and suppresses acute colitis and CAC development [143].

*B. bifidum* is also a widely used probiotic bacterium. Administration of *B. bifidum* has been shown to attenuate intestinal tumorigenesis by modulating the gut microbiome and metabolome compositions. Enrichment of Ruminococcaceae and Lachnospiraceae, two major families known as anti-inflammatory factors, was observed in *B. bifidum*-colonized AOM/DSS mice compared with

**Table 1** Role of gut microbiota in CAC

	CAC mouse model	Possible mechanism of CAC development by bacteria	Reference
<b>Pathogen in CAC</b>			
Colibactin-producing <i>E. coli</i>	AOM/DSS	DNA damage in intestinal epithelium cells	[123]
Colibactin-producing <i>E. coli</i>	AOM-IL-10 <sup>-/-</sup>	DNA damage in intestinal epithelium cells	[118]
Colibactin-producing <i>E. coli</i>	APC <sup>Min</sup> -IL-10 <sup>-/-</sup>	DNA damage in intestinal epithelium cells	[117]
<i>F. nucleatum</i>	APC <sup>Min</sup>	Recruitment of tumor-inflating myeloid cells, promoting EMT	[126, 127]
Enterotoxigenic <i>B. fragilis</i> (ETBF)	APC <sup>Min</sup>	NF-κB-STAT3 axis activation dependent on Th17 pathway	[121]
Enterotoxigenic <i>B. fragilis</i> (ETBF)	AOM/DSS	Increasing pro-tumorigenic inflammatory cytokines	[122]
<i>A. muciniphila</i>	AOM/DSS	Promoting the proliferation of IECs	[139]
<i>S. gallolyticus</i>	AOM/DSS	Recruiting CD11b <sup>+</sup> tumor-infiltrating myeloid cells	[132]
<i>P. gingivalis</i>	APC <sup>Min</sup>	Increasing IL-1b production via NLRP3 inflammasome activation	[130]
<i>H. rodentium</i>	IL-10 <sup>-/-</sup>	Unknown	[133]
<i>H. typhlonius</i>	IL-10 <sup>-/-</sup>	Unknown	[133]
<i>H. hepaticus</i>	Rag2 <sup>-/-</sup>	Increasing pro-tumorigenic inflammatory cytokines	[115]
<i>H. hepaticus</i>	Rag2 <sup>-/-</sup>	Increasing iNOS production	[134]
<i>A. finegoldii</i>	IL-10 <sup>-/-</sup>	IL-6-STAT3 axis activation	[140]
Vancomycin-sensitive bacteria	AOM/DSS	Increasing DNA damage and cell death by attracting neutrophils in IECs	[114]
<i>A. parvulum</i>	IL-10 <sup>-/-</sup>	Unknown	[142]
<b>Beneficial bacteria in CAC</b>			
<i>B. lactis</i>	AOM/DSS	NF-κB deactivation in IECs	[143]
<i>B. bifidum</i>	AOM/DSS	Regulating gut microbiota and metabolome	[144]
<i>L. bulgaricus</i>	AOM/DSS	Decreasing of pro-inflammatory cytokines	[145]
<i>L. casei</i> Shirota	DSS-BALB/c	IL-6-STAT3 axis deactivation	[146]
<i>L. reuteri</i>	AOM/DSS	Decreasing of pro-inflammatory cytokines Decreasing of CD11b <sup>+</sup> Gr-1 <sup>+</sup> immature myeloid cells	[147]
<i>L. fermentum</i> + <i>L. acidophilus</i>	APC <sup>Min</sup>	Decreasing of tumor cell proliferation Deactivation of b-catenin pathway activation	[148]
FMT	AOM/DSS	Increasing anti-inflammatory response by NF-κB deactivation	[149]

the control group. In addition, metabolome analysis demonstrated that fatty acid metabolism pathways related to CRC formation were also regulated by the administration of *B. bifidum* in CAC mice [144].

Like *Bifidobacterium* spp., *Lactobacillus* genera are broadly acknowledged to have health-promoting and immunomodulatory properties. *Lactobacillus bulgaricus* treatment reduces tumor progression and intestinal inflammation in AOM/DSS mice by regulating the inflammatory response, and reducing proinflammatory cytokines in tumors [145]. In addition, a pilot study revealed that supplementation of the *L. casei* strain Shirota in fermented milk ameliorated disease activity in patients with active UC [152]. A component of the polysaccharide peptidoglycan complex in *L. casei* Shirota inhibits IL-6–STAT3 axis activation, thereby attenuating colonic tumor development in CAC-induced BALB/c mice. Consistent with this finding, a mutant strain of the *L. casei* Shirota strain lacking the polysaccharide peptidoglycan complex had no effect on the suppression of CAC development [146]. *L. reuteri* has the unique capacity to convert histidine to histamine. Given that the lack of

histidine decarboxylase (HDC) has been shown to promote CAC by accumulating CD11b<sup>+</sup> Gr-1<sup>+</sup> immature myeloid cells, histamine appears to be a potential antitumorigenic factor [153]. Note, the administration of histamine-producing *L. reuteri* reduced tumor number and size in AOM/DSS-induced *Hdc*-deficient CAC mice, whereas the *Hdc*-deficient *L. reuteri* mutant, which cannot generate histamine, failed to suppress colitis and CAC. Furthermore, colonization of *L. reuteri* decreased the expression of inflammation- and cancer-related genes, including IL-6 and IL-22, and it reduced the infiltration of CD11b<sup>+</sup> Gr-1<sup>+</sup> immature myeloid cells in the spleen [147]. These findings indicate that the regulation of luminal histamine may be considered as one of the therapeutic approaches to intestinal inflammation and CAC. Furthermore, a combination of *L. acidophilus* and *L. fermentum* reduces intestinal tumorigenesis by decreasing cell proliferation and suppressing β-catenin signal activation in tumor cells [148, 154].

Besides the microbiota per se, the microbiota's metabolic by-products are also an important factor in CAC development. Indeed, administration of the microbial metabolites short-chain



fatty acids (SCFAs), such as acetate, butyrate, and propionate, results in the decreased expression of IL-6, IL-17A, and TNF- $\alpha$ , thereby reducing colitis and tumor incidence in the AOM/DSS-induced CAC mouse model [155] (Table 1).

### 4.3 The role of pattern recognition receptors in CAC

Innate immunity acts as a primary host response to microbial invasion. The pivotal elements of this process are pattern recognition receptors (PRRs), particularly toll-like receptors (TLRs). A study has shown that TLR2<sup>-/-</sup> mice display higher IL-6, IL-17A, and STAT3 activation following enhanced tumor development in the AOM/DSS CAC model, indicating the protective role of TLR2 in CAC [156]. The protumorigenic role of TLR4 in CAC is well established. TLR4 expression in IECs is upregulated in patients with dysplasia and CAC. In support of this human data, TLR4 deletions significantly decreased gut inflammation and tumorigenesis in AOM/DSS-induced CAC mice compared with control mice, and antibody blockade of TLR4 ameliorated the incidence of CAC [157]. Further, the constitutive activation of TLR4 signaling in IECs augmented colitis-associated tumorigenesis in a transgenic mouse model [158]. In addition, in the absence of myeloid differentiation factor 88 (MyD88), a downstream mediator of TLR4, colonic tumors failed to develop in AOM-treated IL-10<sup>-/-</sup> CAC mice by decreasing protumorigenic cytokines (e.g., IL-12 and TNF- $\alpha$ ) [159]. These findings indicate that the bidirectional roles of the bacterial recognition sensors—PRRs—are related to the CAC protection or development process. Further detailed functional analysis of TLRs in CAC biology is needed to establish novel therapeutic strategies for CAC patients.

## 5 Antitumorigenic colitis therapy

The development of CAC is thought to be multifactorial—a combination of genetic, host immunity, and microbial influences. Consequently, the control of these factors may be a strategy for the prevention of CAC.

### 5.1 5-ASA

5-Aminosalicylic acid (5-ASA), the most used medication for UC treatment, attenuates tumor development by reducing oxidative stress, inhibiting cell proliferation,  $\beta$ -catenin accumulation, and promoting apoptosis [160]. Accordingly, 5-ASA was shown to decrease tumor incidence and growth of CAC in a mouse model [161]. Consistent with the animal study, the risk of CAC in humans was decreased by 5-ASA treatment [162, 163]. However, a meta-analysis yielded an inconsistent result, suggesting that 5-ASA treatment is not

protective against CAC [164]; hence, additional studies are needed to analyze the effect of 5-ASA on the risk of CAC.

### 5.2 Anti-TNF- $\alpha$

In CAC, chronic inflammation induces TNF- $\alpha$  production, which induces DNA damage and IEC disproportion, resulting in the generation of dysplastic lesions. CAC animal studies have shown that TNF- $\alpha$  blockade decreases colitis and the risk of CAC development [165]. TNF- $\alpha$  antagonists are one of the most effective medications for the treatment of patients with IBD. Notably, a clinical study has shown that 734 IBD patients treated long-term with infliximab, a chimeric monoclonal antibody against TNF- $\alpha$ , did not develop CRC, while 8 of 666 IBD patients without exposure to infliximab developed CRC [166]. The protective effect of anti-TNF agents was also validated by another group [167]. As clinical studies of the use of anti-TNF- $\alpha$  agents for the treatment of patients with CAC are limited, we cannot draw a concrete conclusion regarding the protective effect of this medication. However, long-term treatment of infliximab may be highly protective against CAC development.

### 5.3 Thiopurines

Thiopurines are antimetabolites and immunomodulators, and their efficacy against CAC remains controversial. In a cohort study including the data from 144 IBD patients with CRC, the treatment of thiopurines did not protect against CAC. In contrast, a meta-analysis of 24 observational studies involving 76,999 patients with IBD revealed that thiopurine exposure significantly decreased the risk of high-grade dysplasia and CRC, particularly in those patients with UC [168]. Further studies are needed to explore the protective effects of thiopurines on CRC development.

### 5.4 Antioxidants

Antioxidants can also prevent cancer cells from oxidation-induced death [169]. Long-term administration of antioxidants such as *N*-acetylcysteine decreases oxidative damage in colonic tissue and protects against CAC development. In addition, the synthetic compound growth factor 9 (GF-9), a flavonoid derivative with antioxidant properties, protects against CAC by deactivating NLRP3 inflammasome via autophagy [170]. Among natural antioxidants, vitamin C attenuates oxidative DNA damage by neutralizing ROS and protecting against inflammation-associated tumorigenesis in different animal models of CAC [171]. Although epidemiological studies have shown the protective effects of antioxidants against CAC, further studies are required to validate their association with disease pathophysiology.

## 6 Conclusion and perspective

In patients with IBD, chronic inflammation is a major risk factor for CAC development. The pathogenesis of CAC is distinct from that of sporadic CRC, and the critical molecular mechanisms underlying this process have yet to be elucidated. Accumulating evidence shows that chronic inflammation enhances the elements related to CAC development by various mechanisms, including oxidative stress-driven DNA damage, abnormal immune responses, and gut dysbiosis. This suggests that inflammation plays a pivotal role in creating a favorable environment for tumor initiation and development. Remarkably, the intertwined relationship between inflammation and the microbiota is complex. As mentioned, intestinal inflammation is a critical factor that drives gut dysbiosis. On the other hand, gut dysbiosis can, in turn, induce inflammation. Therefore, it will be necessary to consider an overview of scientific findings of the interaction of gut dysbiosis and inflammation to use the gut microbiota as a target for CAC treatment. Biological knowledge of the intestinal mucosal system has advanced markedly in the past decade with powerful technologies such as improved anaerobic bacterial culture methods, next-generation bacterial sequencing, high-throughput analysis of luminal metabolites, and the widespread use of gnotobiotic mouse models. In the future, primary epithelial cells derived from CAC patients can be cultured in vitro in an organoid system to test the effects of genetic mutations in humans. The tissue organoid system can also be applied to the study of epithelial-microbial interactions in the context of tumorigenesis. In addition, single-cell RNA sequencing technologies will enable a more sophisticated understanding of the functional impact of intestinal epithelial and immune cells networks on host physiology, inflammation, and tumorigenesis.

Taken together, a better understanding of the genomic events and the intestinal environment underlying the development of CAC could have implications for the early detection of CAC and the development of new therapeutic strategies for more advanced CAC.

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## Declarations

**Conflict of interest** The authors declare no conflict of interest.

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