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Cancer in Inflammatory Bowel Disease: lessons from animal models

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Abstract

Purpose of the review—Human colitis-associated cancers (CAC) represent a heterogeneous group of conditions in which multiple oncogenic pathways are involved. In this manuscript we reviewed the latest studies using genetic, chemically induced, bacterial and innate immunity induced experimental models of colitis-associated cancer.

Recent findings—Using the azoxymethane-dextran sodium sulfate model wound healing pathways seems to be required in the development of CAC. There is also an emerging understanding that commensal and/or pathogenic bacteria can promote tumorigenesis, through T cell mediated inflammation. Using specific transgenic mice (villin-CD98, T cell SMAD7, villin-TLR4) or specific knock-out mice, investigators have identified that derangements in epithelial or innate and adaptive immune pathways can result in CAC. Subtle perturbations in epithelial repair—both too little or too exuberant, can render mice susceptible to tumorigenesis.

Summary—With the aid of animal models, we have witnessed a rapid expansion of our knowledge of the molecular and immunologic mechanisms underlying inflammatory cancers. Though animal models have contributed a discrete amount of information to our understanding of tumorigenesis in the setting of intestinal inflammation it is clear that no single animal model will be able to adequately recapitulate the pathogenesis of complex CRCs, but each model gets us one step closer to comprehending the nature of CAC.

Keywords

mouse; AOM; DSS; colitis cancer; APC

Introduction

CACs are malignancies occurring in the setting of chronic inflammatory disorders of the colon. In humans, CAC is most commonly encountered in inflammatory bowel diseases (IBD), both ulcerative colitis (UC) and Crohn's disease. CAC may occur in as many as 18.4% of IBD patients over the course of 30 years¹. Clinical inquiry has revealed a number of factors associated with the development of CAC in humans, including duration of IBD, extent of colonic involvement, severity of inflammation, and family history of colon cancer^{2–6}.

Despite an understanding of the clinical features associated with CAC, the molecular mechanisms underlying carcinogenesis in the setting of chronic colitis are unclear. What we

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do know regarding CAC in humans is gleaned from histopathologic observation and molecular studies. Chromosomal instability (CIN) is an early and frequent abnormality among patients with CAC, often associated with malfunction of tumor suppressor genes, shortening of telomeres, and aneuploidy⁷⁻¹⁰. Another form of genomic instability, microsatellite instability (MSI) is also frequently observed in the setting of CAC^{11, 12}. Although observed early in sporadic (or non-inflammatory) colon cancers, mutations in the adenomatous polyposis coli (APC) gene are infrequent in dysplastic mucosa or neoplasias in the setting of colitis¹³. Yet, activated β -catenin is a frequent finding in colitis-associated dysplasia, and recent work has highlighted the role of Wnt/ β -catenin signaling in maintenance of colon cancer stem cells¹³⁻¹⁷.

Knowledge of the unique pathways of carcinogenesis underlying CAC in humans is currently inadequate. In order to clarify these pathways, a variety of animal models have been developed. This review will detail progress in rodent models of CAC.

Chemically induced colitis-associated neoplasia

Azoxymethane (AOM)- Dextran Sodium Sulfate (DSS) model

In laboratory rodents, colorectal cancer (CRC) is commonly induced with AOM, a potent carcinogen. Via alkylating species, DNA adducts form covalent bonds between the reactive carcinogen and the genomic DNA, resulting in mutations during DNA repair and promotion of tumor development. Chronic inflammation can also trigger neoplasia. Long-term administration or repeated cycles of DSS, a chemical that causes epithelial injury, can induce chronic colitis and subsequent dysplasia in rodents¹⁸⁻²⁰. Currently the most used model of inflammatory CRC is the combination of AOM with DSS because tumor formation is enhanced compared to DSS alone²¹⁻²⁵. As in human CAC, the degree of inflammation correlates with dysplasia in the AOM-DSS model and is associated with the nuclear translocation of β -catenin²⁶. Up-regulation of mucosal Cox-2 and PGE₂ production are reported in the AOM-DSS model of colitis²⁷⁻²⁹. This model has been predominantly employed in mice, and its tumorigenic potential is strain dependent, as some genetic backgrounds such as A/J, BALB/c or Swiss Webster mice are more sensitive to AOM than other strains like C57Bl/6J mice³⁰⁻³².

More recent studies have attempted to further explain the pathogenic steps involved in the tumorigenic process of the rodent AOM-DSS model. Mice deficient in myeloid translocation gene related-1 (MTGR1), which display impaired wound healing, are resistant to CAC after AOM-DSS treatment despite having an active inflammatory infiltrate; this tumor resistance is due to increased intra-tumoral apoptosis³³. This finding suggests that wound healing pathways are required in the development of CAC, and that wound healing and cancer exist on a continuum.

Other carcinogens

A variety of carcinogenic compounds have been used to experimentally reproduce the inflammatory events contributing to carcinogenesis. In classic studies, CAC was modeled in rats using carrageenan, a polysaccharide derived from red seaweed that has toxic effects, causing colonic ulceration and inducing tumorigenesis³⁴⁻³⁶. Other carcinogenic chemicals such as 1,2-dimethylhydrazine (DMH)³⁷, the precursor to AOM, or dietary iron³⁸, in combination with DSS, have been also used to chemically induce CAC. Additionally, 2-amino-1-methyl-6-phenylimidazol [4,5-b] pyridine (PhIP), a heterocyclic aromatic amine formed when cooking meat at a high temperature, has also been translated into experimental CRC. Rats fed with PhIP had a 50% incidence of colonic tumors³⁹. Moreover, PhIP combined with a high fat diet or AOM enhances tumorigenesis⁴⁰. A recent study suggested that glucagon-like peptide-2 (GLP-2), an intestinal growth factor secreted by

enteroendocrine cells, might be a colon cancer promoter in rats treated with PhIP combined with a high fat diet ⁴¹.

Genetic models of colitis and cancer

Genetic models of cancer in IBD have been developed to mimic known mechanisms underlying colitis and CACs in humans. These models have focused on mimicking immune dysregulation, inflammation, and epithelial barrier dysfunction as seen in human disease. Major advances have been made in this field with respect to genetic manipulation of APC gene ^{42, 43}, p53 ^{44, 45}, and IL-10 ⁴⁶, among others ^{47–49}. Recent work in this field has built upon these findings, modifying conventional models or creating novel rodent paradigms. Table 1 provides an overview of the latest advances.

The development of mice deficient in APC gene was among the first successful applications of genetic modeling of intestinal cancers in rodents ^{50–52}. The superimposition of AOM or DSS to this model mimics CAC and results in more intestinal tumors ⁴³. Commensal microorganisms can also drive the development of colonic inflammation and colonic tumors in mice. For example, enterotoxigenic *Bacteroides fragilis*-mediated colitis in Min (*Apc^{+/-}*) mice results in the formation of colonic tumors via the inflammatory T_H17-dependent pathway ⁵³. IL-17A-secreting T cells were investigated by Chae et al. who looked at tumorigenesis, pro-inflammatory cytokines and immune abnormalities in APC^{Min/+} and IL-17A^{-/-} × APC^{Min/+} mice. IL17-A ablation showed decreases in intestinal tumorigenesis and lower levels of IL-6, IL-23 and IL-1β, implicating these mediators in inflammatory cancers ⁵⁴.

Many inflammatory colon cancers in humans also harbor genomic changes in the form of MSI that result from epigenetic deficiency in regulatory mismatch repair (MMR) proteins. These neoplasias can be flat in appearance, occur more often in the proximal colon, and histologically have mucin associated with a “Crohn’s-like” reaction. The deletion of the subunit protein Gα2 in mice causes growth retardation, diffuse spontaneous colitis resembling UC and non-polyposis right-sided, multifocal colorectal cancers arising from flat dysplastic lesions with many histologic features analogous to human dysplasia. At a young age, Gα2 knockout (KO) mice have normal colonic epithelium with a normal expression of MMR. In the setting of inflammation, however, older mice lose expression of the MMR proteins PMS2 and MLH1 in the inflamed colon tissue, cancer stroma and epithelium ⁵⁵. While epigenetic silencing by methylation of the MLH1 promoter is the abnormality identified in the majority of sporadic CRCs in humans ^{50, 51, 56}, this was not seen in the Gα2 KO mice. Hypoxia causes suppression of MLH1 and PMS2 protein levels in colonic crypts by suppressing histone H3 acetylation at the proximal MLH1 promoter, leading to silencing of MLH1 and MSI ⁵⁷.

To investigate the systemic effects of local immune dysregulation, mice with Gα2 KO and IL-10 deficiency have been created. IL-10 is produced by regulatory T cells (Tregs). Mice deficient in both Gα2 and IL-10 develop colitis at baseline; once treated with DSS, these mice acquire single and double-strand breaks in DNA of peripheral leukocytes; these systemic findings in response to local inflammation are thought to be related to the formation of systemic reactive oxygen and nitrogen species (RONS) ⁵⁸. Mice deficient in Nrf2 – a transcription factor involved in regulating oxidative stress - are more susceptible to chemically induced colitis with DSS compared to wild type mice and show higher rates of inflammation-associated neoplasia. These mice lose detoxifying enzymes and generate RONS ^{59–61}. These data suggest that colonic inflammation drives oxidative stress not only in the colon but also systemically, and that perturbations in the ability to modify production of RONS are linked to development of neoplasia.

Manipulation of IL-10 KO mice as a model for human IBD-colitis has helped to explain the role of the nucleotide-editing enzyme, activation-induced cytidine deaminase (AID), in inflammatory colon cancers. This enzyme induces somatic mutations in tumor-related genes, including p53⁶². AID expression increases in inflammation compared to non-inflamed wild type mice. Mutations in p53 were more frequent in the IL-10^{-/-} AID^{+/+} model compared to the IL-10^{-/-} AID^{-/-}, suggesting a role of AID in promoting mutations in the mouse model of CAC⁶³.

Transgenic mice have also been generated to study the role of immune dysregulation in CAC. In mice over-expressing Smad7 in T cells, a suppressor of TGF- β signaling, colitis increases in severity, but mice develop fewer colon tumors⁶⁴. Increased expression of IFN- γ and increased accumulation of cytotoxic CD8+ and natural killer T cells were observed in these tumors and surrounding inflamed colonic tissue. Interestingly, in IFN γ ^{-/-}xSmad7 transgenic mice, tumor incidence was restored to the same levels observed in WILD TYPE; thus, IFN- γ appears to play a major role in CAC.

Knock-out mice have also been generated to interrogate the role of wound healing in inflammation-related colon cancer development. Nod-like receptor pyrin domain-containing protein 6 (NLRP6) is primarily expressed by colonic myofibroblasts and plays a key role in mucosal wound healing. Following AOM-DSS administration, *Nlrp6*^{-/-} mice had accelerated tumor growth and higher tumor burden than wild type mice, suggesting a role of NLRP6 in inflammation and carcinogenesis through an effect on myofibroblasts that help in epithelial repair⁶⁵.

The role of epithelial barrier dysfunction in CAC has also been explored with rodent models. CD98, a type II transmembrane glycoprotein adhesion molecule, transgenic mice have increased epithelial barrier dysfunction compared to wild type mice⁶⁶. CD98 transgenic mice show more severe DSS colitis characterized by increased expression of the pro-inflammatory cytokines IL-1 β and TNF- α . In the CD98 transgenic mice, AOM-DSS-induced colitis generates a larger quantity and size of tumors compared to wild type mice. TIR8 – a single immunoglobulin IL-1R-related molecule - inhibits signaling from the IL-1R/TLR complex and has inhibitory activity on inflammation. Mice deficient in TIR8 showed increased susceptibility to CAC when AOM was combined with DSS but not AOM alone, showing that inflammation was a prerequisite for carcinogenesis in this model⁶⁷. TIR8^{-/-} mice display increased colon epithelial permeability compared with TIR8^{+/+} mice. In the TIR8^{-/-} mice, many pro-inflammatory mediators (e.g. IL-1 β , IL-6, and TGF β) are increased while IFN- γ is decreased⁶⁴.

Microbial models of CAC

The mammalian GI tract hosts a variety of commensal and symbiotic microorganisms that play an important role in intestinal homeostasis, maintenance, and function. Both the innate and adaptive immune systems of the host contribute to this homeostasis through the development of tolerance to commensal organisms while activating defense mechanisms against potential pathogens^{68, 69}. It is theorized that the loss of this balanced interplay between the host and the microbiota contributes to the development of CAC. Changes in the intestinal flora of CAC patients have been reported. These studies based on 16S rRNA and high throughput sequencing reveal composition and diversity differences between the microbiota of CAC patients and that of healthy subjects; these differences have also been noted between chemical and genetic based murine models of CAC⁷⁰⁻⁷³. However, these comprehensive analyses of gut microbiota could not reveal whether this dysbiosis is the cause of CAC or an outcome of the mucosal abnormality.

Other studies based on gnotobiotic animals in conjunction with chemical and genetic models of CAC demonstrated that bacteria play a crucial role in the pathophysiology of CAC by promoting intestinal inflammation. Infection with enteric pathogens such as *Helicobacter* species and *Streptococcus bovis* have been clinically associated with CAC. Commensal bacteria are increasingly being used not only for understanding the mechanistic details of CAC but also to augment the AOM-induced response in animal models⁷⁴⁻⁷⁶. Both enterotoxigenic *Bacteroides fragilis* and *Citrobacter rodentium* promote colon tumor formation in APC^{min/+} mice whereas the non-toxicogenic strain of *B. fragilis* does not cause any tumor formation^{77, 78}. The majority of the chemical and genetic models of CAC including IL-2^{-/-}, IL10^{-/-}, Gpx1^{-/-}, Tcrβ^{-/-} p53^{-/-} mice under germ free conditions do not develop any tumors⁷⁹⁻⁸¹.

Certain bacterial species can also have a differential effect on the development of CAC, resulting in differing quantities, types and location of tumors. For example, germ-free IL-10^{-/-} mice given either *E. faecalis* or *E. coli* yielded different clinical abnormalities, while more severe, earlier disease onset occurred when the mice were administered both bacteria simultaneously⁸². However, germ-free IL10^{-/-} and IL10^{-/-} mono-associated with other bacterial species including *Lactobacillus* and *Lactococcus* did not show any signs of CAC⁸³. Gnotobiotic studies of TRUC mice (Tbet^{-/-} × Rag2^{-/-}) dually associated with *Klebsiella pneumonia* and *Proteus mirabilis* did not induce colitis either; however, the addition of commensal organisms did result in colitis, indicating the necessity of both commensal and pathogenic organisms in inducing colitis⁸⁴.

Adoptive transfer models of CAC have also been studied. Adoptive transfer of Tregs from wild type mice into *H. hepaticus*-infected Rag^{-/-} and APC^{min/+} mice significantly reduced *H. hepaticus* induced CAC in these mice; this protective effect was more significant when Tregs were obtained from wild type mice that were previously infected with *H. hepaticus*^{85, 86}. Based on these results, Erdman et al proposed a hypothesis whereby infections help in maintaining the anti-inflammatory phenotype of Tregs and reduce susceptibility to carcinogenesis⁸⁷.

In addition to identify pathogens or virulence factors that promote CRC, some investigators have tried to identify bacteria that protect against CAC. *Bifidobacterium lactis* protects against acute colitis and CAC in AOM-DSS treated mice and has been proposed as a possible therapy for CAC prevention⁸⁸. The majority of the studies performed to date focus on the involvement of intestinal microbiota in CAC progression but clearly indicate that there is no single microbe or mechanism that can explain the underlying cause of CAC in humans.

Innate immune models of CAC

Another approach to model CAC in experimental animals is to target molecules involved in the innate immune response, which is the first stage of the intestinal inflammatory process. The innate immune receptors, including toll-like receptors (TLRs) and nucleotide-binding oligomerization domain receptors (NODs) have been used to study inflammation and cancer. Our group has developed a transgenic mouse that over-expresses TLR4 in the intestinal epithelium. These mice develop significantly more tumors than wild type mice after AOM-DSS treatment⁸⁹. Moreover, we demonstrated that the majority of human patients with dysplasia and CAC over-express TLR4 in the intestinal epithelium. However, lacking TLR4 expression is also detrimental, as TLR4 deficient mice have worse colitis after DSS than wild type counterparts, but intriguingly are protected from AOM-DSS-induced CAC^{89, 90}. Not all TLRs behave the same however, and Lowe et al. found that mice

deficient in TLR2 are prone to AOM-DSS tumorigenesis, showing a higher expression of inflammatory mediators such as IL-6, IL-17A, and STAT3⁹¹.

In the normal intestinal epithelium, TLRs are expressed in low levels. Inhibitors, like toll-interacting protein (TOLLIP) or single immunoglobulin IL-1-related receptor (SIGIRR), regulate TLR activity. Xiao et al reported that SIGIRR knockout mice are more susceptible to inflammation and CAC after AOM-DSS treatment. When SIGIRR was restored in the intestinal epithelium, CAC severity was decreased⁹². The myeloid differentiation primary response protein 88 (MyD88), an adaptor protein for TLR signaling pathways, also protects against AOM-DSS induced tumorigenesis. MyD88-deficient mice show impaired epithelial repair with decreased IL-18 signaling leading to increased inflammation and susceptibility to develop neoplastic lesions⁹³.

Conclusion

With the aid of animal models, we have witnessed a rapid expansion of our knowledge of the molecular and immunologic mechanisms underlying inflammatory cancers. Each of the models described above has contributed a discrete amount of information to our understanding of tumorigenesis in the setting of intestinal inflammation, and new genomic, immunologic, and gnotobiotic technologies offer promising possibilities. Yet, human inflammatory colorectal cancer is a heterogeneous disease with each tumor undergoing distinct molecular changes that accumulate over time. At present, it is clear that no single animal model will be able to adequately recapitulate the pathogenesis of complex CRCs, but each model gets us one step closer to comprehending the nature of CAC.

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Key points

- Human colitis-associated cancers (CAC) are heterogeneous and can be induced by multiple oncogenic pathways. Thus, animal models are used in research to model this disease.
- The most frequently used CAC model induced by chemicals is the AOM-DSS model.
- Some genetic models such as APC^{Min/+} and Gic2 knockout mice show a significant increase of intestinal tumors when they are under an inflammatory insult.
- Certain pathogenic bacteria can also promote tumorigenesis.
- Having a deficiency or over-expressing some innate immune key molecules also can promote the development of CAC.

Table 1

Overview of Genetic Models for Colitis-Associated Cancer.

Models of CAC	Result	Reference
NLRP6 ^{-/-}	increased AOM-DSS tumors	50
CD98 epithelial overexpression	increases AOM-DSS tumors; conditional epithelial KO protects	51
APC mutation +/- DSS or AOM or Bacteriodes fragilis infection	increases colonic tumors	52,53
Gia2 ^{-/-} spontaneous tumors	decreased MMR expression	54, 55
Nrf2 ^{-/-}	increased AOM-DSS tumors	56, 57
Villin-TLR4 (overexpressing TLR4)	increased AOM-DSS tumors	58
MyD88 ^{-/-} or TLR2 ^{-/-}	increased AOM-DSS tumors	59, 60
Single immunoglobulin IL-1-related receptor (SIGIRR) ^{-/-}	increased AOM-DSS tumors	61
TIR8 ^{-/-}	increased AOM-DSS tumors	62
Smad7 T cell overexpression	protects against AOM-DSS tumors	63
Activation-induced cytidine deaminase (AID) ^{-/-}	protects from IL-10 ^{-/-} CAC	64, 65
TRUC mice (Tbet ^{-/-} ×Rag2 ^{-/-}) + <i>Klebsiella pneumonia</i> and <i>Proteus mirabilis</i>		66

Abbreviations: Nucleotide-binding oligomerization domain Leucine rich Repeat and Pyrin domain containing (NLRP), azoxymethane (AOM), dextran sodium sulfate (DSS), adenomatous polyposis coli (APC), mismatch repair (MMR), toll-like receptor 4 (TLR4), colitis-associated cancer (CAC).