



Bile acids as endogenous etiologic agents in gastrointestinal cancer

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Abstract

Bile acids are implicated as etiologic agents in cancer of the gastrointestinal (GI) tract, including cancer of the esophagus, stomach, small intestine, liver, biliary tract, pancreas and colon/rectum. Deleterious effects of bile acid exposure, likely related to carcinogenesis, include: induction of reactive oxygen and reactive nitrogen species; induction of DNA damage; stimulation of mutation; induction of apoptosis in the short term, and selection for apoptosis resistance in the long term. These deleterious effects have, so far, been reported most consistently in relation to esophageal and colorectal cancer, but also to some extent in relation to cancer of other organs. In addition, evidence is reviewed for an association of increased bile acid exposure with cancer risk in human populations, in specific human genetic conditions, and in animal experiments. A model for the role of bile acids in GI carcinogenesis is presented from a Darwinian perspective that offers an

explanation for how the observed effects of bile acids on cells contribute to cancer development.

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INTRODUCTION

Although it was proposed that bile acids are carcinogens as early as 1939 and 1940, there was little evidence at that early time that bile acids act as carcinogens in the gastrointestinal (GI) tract (reviewed in^[1]). Since then, however, evidence has accumulated that exposure of cells of the GI tract to repeated high physiologic levels of bile acids is an important risk factor for GI cancer. Here we review the substantial evidence, much of it obtained in the last few years, for a role of bile acids in cancers of the esophagus, stomach, small intestine, liver, biliary tract, pancreas and colon/rectum. High exposure to bile acids may occur in a number of settings, but, most importantly, is prevalent among individuals who have a high dietary fat intake^[2]. A rapid effect on cells of high bile acid exposure is the generation of reactive oxygen species (ROS) and reactive nitrogen species (RNS). Increased production of ROS/RNS, can lead to increased DNA damage and then increased mutation. The production of ROS/RNS following bile acid exposure likely occurs through multiple pathways involving disruptions of the cell membrane and mitochondria^[1]. For each organ of the GI tract, we

review evidence, where available, on deleterious effects of bile acids, including the induction of ROS/RNS, induction of DNA damage, mutation and apoptosis, and the development of reduced apoptosis capability upon chronic exposure. Reduced ability to undergo apoptosis is important because apoptosis is a beneficial process that rids the body of cells with unrepaired DNA damage that can cause mutation. Reduced apoptosis capability has been linked to increased mutagenesis^[3-5]. We also review epidemiologic evidence and results of animal experiments indicating that long-term exposure to elevated levels of bile acids increases GI cancer risk.

The annual world-wide number of deaths due to cancer is about 7.6 million, and among these about 2.8 million (36%) are due to cancers of the GI tract^[6]. A recent prospective study was carried out on red and processed meat in relation to cancer incidence in a cohort of approximately half a million men and women^[7]. Individuals in the highest quintile of red meat intake, compared with those in the lowest, had a statistically significant elevated risk of esophageal, colorectal and liver cancer. Also, for processed meat, the risk of colorectal cancer was elevated. Both types of meat are sources of saturated fat and iron, which have independently been associated with carcinogenesis. In addition, processed meats contain nitrates and nitrites, precursors of N-nitroso mutagenic compounds.

ESOPHAGUS

The estimated yearly number of deaths world-wide from esophageal cancer is 300 034 for men and 142 228 for women^[6], making it the sixth leading cause of cancer deaths among men and women combined. There are two principal histologic types of esophageal cancer, adenocarcinoma and squamous cell carcinoma. In the United States, the incidence of adenocarcinoma has increased four-fold between 1973 and 2002, whereas squamous cell carcinoma has declined 30% over the same period, making adenocarcinoma the predominant form of esophageal cancer^[8]. Barrett's metaplasia of the esophagus is an important predisposing condition for the development of esophageal adenocarcinoma^[9]. Barrett's esophagus (BE) is a metaplastic lesion of the distal esophagus, characterized by the replacement of the normal squamous epithelium by columnar intestinal epithelium containing goblet cells. BE is associated with increased duodeno-gastro-esophageal reflux^[10,11], which causes increased exposure of the esophagus to bile acids from the duodenum and acidity (gastric acidity) from the stomach. Individuals with esophageal adenocarcinoma experience even greater exposure to bile than persons with uncomplicated BE^[12]. Expression of bile acid transporter proteins is increased in BE tissues, suggesting that the development of BE metaplasia may be an adaptation to protect cells from bile acids^[13]. Thus progression to BE and to adenocarcinoma may be strongly influenced by bile acid exposure. As discussed next, evidence indicates that short-term exposure of esophageal cells to bile acids induces oxidative stress, DNA damage, mutation and apoptosis; and among surviving cells selects over the long-run for resistance to apoptosis and ultimately cancer.

Five studies have shown that bile acids cause increased production of ROS in esophageal cells, including those from BE metaplasia. A cocktail of five bile acids designed to mimic the bile acids present in gastroesophageal reflux was used to test whether reflux induces ROS^[14]. The five bile acids were glycocholic acid (GCA), taurocholic acid (TCA), glycodeoxycholic acid (GDCA), glycochenodeoxycholic acid (GCDCA) and deoxycholic acid (DCA). This cocktail induced ROS in biopsies from human BE metaplastic tissue. The bile acid cocktail also induced ROS in cultured SV40-transformed squamous esophageal epithelial cells (HET1-A). DCA induced ROS in cultured human esophageal adenocarcinoma cells (OE33) and squamous cell carcinoma cells (KYSE-30)^[15]. GCDCA in acidic media induced ROS in cultured esophageal squamous cell lines derived from patients with gastroesophageal reflux disease (GERD) with BE, or without BE^[16]. When mice were fed a zinc deficient diet containing a DCA supplement, ROS production was increased and BE-like lesions developed^[17].

Six studies showed that bile acids induce DNA damage in esophageal cells (Table 1), and five of these reported evidence for oxidative DNA damage.

The findings that bile acids induce DNA damage suggest that bile acids may also increase the frequency of mutation, since replication of a damaged DNA template strand often results in a replication error and thus a mutation.

Esophagoduodenostomies were performed on Big Blue F1 *lacI* transgenic rats to surgically increase duodeno-gastro-esophageal reflux^[21]. The frequency of *lacI* mutant cells proved to be significantly higher in the esophageal mucosa of the surgically altered rats than in the unaltered control rats, indicating that components of refluxate, such as bile acids, increase mutation. Forty-six percent of the mutant cells were altered at CpG dinucleotide sites, and the majority of these mutations (61%) were C to T or G to A transitions. This pattern of mutation is similar to that in human esophageal adenocarcinoma, suggesting that reflux is not only mutagenic, but also carcinogenic. Consistent with these findings, it was found that DCA treatment of cultured esophageal cells cause an increase in the frequency of GC to AT mutations in the *p53* gene^[15]. In addition, increased duodeno-gastro-esophageal reflux was observed to increase mutagenesis using a surgical model in Big Blue mice (rather than rats)^[22].

Bile acids induce apoptosis in esophageal cells, perhaps through the mediation of damaging ROS. DCA induced apoptosis in esophageal biopsies from normal human squamous epithelium^[23]. Also, five different bile acids [GCDCA, GDCA, TCA, taurochenodeoxycholic acid (TCDC) and taurodeoxycholic acid (TDCA)] individually, and also in a mixture, induced apoptosis of cultured human normal esophageal mucosal epithelial cells^[24].

Although a short-term effect of high bile acid exposure is induction of apoptosis, a longer-term effect of repeated high exposure to apoptosis-inducing agents, such as bile acids, appears to be selection for apoptosis resistant cells. When tissue samples from patients with normal esophagus, esophagitis, BE lesions and

Table 1 Bile acids induce DNA damage in cells of the esophagus

Cells/tissues	Bile acids that induce DNA damage	Assay for damage	Ref.
Cultured SV40-transformed, squamous esophageal epithelial cells (HET1-A) and Barrett's associated adenocarcinoma cells (FLO-1)	DCA; also cocktail containing GCA, TCA, TCDCA	Comet assay ¹ for strand breaks	[18]
Cultured SV40-transformed, squamous esophageal epithelial cells (HET1-A)	DCA	Comet assay for strand breaks; evidence for oxidative mechanism involving nitric oxide	[19]
Cultured human adenocarcinoma cells (OE33)	DCA	Micronuclei assay; induction of micronuclei by DCA, reduced by antioxidants	[15,20]
Biopsies from human Barrett's esophageal metaplastic tissue	Cocktail containing DCA, GCA, TCA, GDCA, GCDCA	8-OHdG, an oxidized form of the DNA base guanine; assayed by IHC	[14]
Mouse model of esophagitis and Barrett's esophagus	DCA (as dietary supplement; also zinc deficiency)	8-OHdG assayed by IHC	[17]

¹Comet assay, also known as the single cell gel electrophoresis assay; 8-OHdG: 8-hydroxydeoxyguanosine; IHC: Immunohistochemical assay.

adenocarcinomas were studied for apoptosis capability, it was found that apoptosis is inhibited early in the dysplasia-carcinoma sequence of BE by over-expression of the anti-apoptotic protein, Bcl-2^[25], presumably as a result of chronic gastroesophageal reflux containing bile acids. BE cells have high levels of the anti-apoptotic proteins IL-6, Bcl-xL and Mcl-1^[26]. Studies of tissues obtained from patient biopsies, indicated that BE cells are resistant to apoptosis induction by DCA compared to esophageal squamous epithelium and normal colon epithelium^[23]. Reduced apoptosis competence may arise by mutation in genes encoding proteins necessary for apoptosis. Since cells resistant to apoptosis have a growth advantage in the presence of agents that ordinarily induce apoptosis, such as bile acids, these cells will tend to proliferate to form a field of apoptosis resistant cells^[27]. Within such a defective field, repeated encounters with bile acids in reflux would cause further DNA damage. Such DNA damage, leading to further mutation, may give rise to malignancy.

Considerable evidence indicates an association of bile acid exposure with esophageal cancer. In rats, reflux of duodenal or gastro-duodenal contents, that include bile acids, induced esophageal carcinoma in the absence of exogenous carcinogen^[28]. Rat surgical models with increased duodenal reflux into the esophagus, but without added carcinogen, caused esophagitis, BE-like lesions and adenocarcinomas^[29-32]. Persons with BE were found to have increased duodeno-esophageal reflux and increased exposure to bile acids in their refluxate, suggesting that the BE premalignant lesion is linked to bile acid exposure^[10,11]. In a rat duodenal-contents reflux model, a high animal-fat intake changed the bile acid composition of bile juice and increased the development of BE and esophageal adenocarcinoma^[33].

In summary, evidence indicates that, in esophageal cells and tissues, bile acids have the short-term effect of inducing oxidative stress, oxidative DNA damage, mutation and apoptosis. Over a longer period, bile acids are implicated in the development of apoptosis resistance and eventually the development of adenocarcinoma.

STOMACH

The estimated yearly number of deaths world-wide from gastric cancer is 511 549 for men and 288 681 for women^[7],

making it the second leading cause of cancer deaths among men and women combined. Infection by the bacterium *Helicobacter pylori* is the major etiologic risk factor in gastric carcinogenesis. However, gastroesophageal reflux appears to have an important role in the development of gastric cardia adenocarcinoma^[34,35] which may have an etiology similar to that of esophageal adenocarcinoma^[34].

Exposure of cultured gastric carcinoma cells (St23123) to TCDCA increased production of ROS^[36]. DCA induced apoptosis in cultured human gastric epithelial cells^[37]. In rats, TCA increased stomach tumorigenesis induced by the carcinogen N-methyl-N'-nitro-N-nitrosoguanidine^[38]. Carcinoma in the gastric stump (generated in rats by surgical gastrectomy) was increased by dietary fat intake and increased bile acid output^[39]. Gastric adenocarcinomas were found to develop in a rat surgical model of duodenal reflux^[40]. Gastroesophageal reflux in humans is implicated in adenocarcinoma of the gastric cardia^[34,35,41]. Thus, elevated bile acid exposure is associated with increased ROS, induction of apoptosis and increased development of cancer of the gastric cardia.

SMALL INTESTINE

Small intestinal cancer is relatively infrequent compared to other cancers of the GI tract. In the United States, only 0.2% of all cancer deaths are due to cancer of the small intestine. Elevated risk of carcinoid tumor of the small intestine is associated with saturated fat intake^[42], consistent with an etiologic role of bile acids. Fifty-three percent of adenocarcinomas of the small intestine arise in the duodenum, although the length of the duodenum is only 4% of the entire length of the small intestine. In addition, 57% of these duodenal cancers arise in the 6-7 cm segment that includes the outlet (Ampulla of Vater) of the common bile duct where bile (including bile acids) and pancreatic secretions empty into the small intestine^[43]. Most adenomas and carcinomas of the small intestine and extrahepatic bile ducts arise in the region of the Papilla of Vater (which includes the Ampulla of Vater)^[44]. Patients who have undergone a cholecystectomy are at increased risk of cancer of the small intestine, a risk that declines with increasing distance from the common bile duct^[45]. These findings indicate that exposure to high levels of bile might be the

Table 2 Bile acids induce apoptosis in liver cells

Cells/tissues	Bile acid(s) that induced apoptosis	Ref.
Isolated rat hepatocytes	GDCA	[64,65]
	GCDCA	[55,66]
	GCDCA, GCA	[57]
	GCDCA	[67]
Isolated rat and mouse hepatocytes	DCA	[68]
Liver tissue sections from rats fed DCA, and cultured human hepatocellular carcinoma cells (HuH-7)	DCA	[58]
Cultured rat hepatocytes (McNtcp.24 cells)	GCDCA	[69,70]
Cultured human hepatocellular carcinoma cells (HuH-7)	GCDCA	[71]
Rat hepatocytes and human hepatoma carcinoma cells (HuH-7)	Taurolithocholate-3-sulfate	[59]

underlying cause of carcinomas of the small intestine.

Individuals with familial adenomatous polyposis (FAP) have an increased risk of developing adenomas and cancer of the small and large intestine. In the small intestine, these lesions arise mostly near the outlet of the common bile duct, where their distribution parallels bile acid exposure^[46,47]. In a mouse model of FAP (*Apc^{min/+}*), higher dietary fat intake was associated with an increase in small intestinal tumors^[48]. Administration of CDCA in this FAP mouse model increased duodenal tumors, suggesting that unconjugated bile acids contribute to periampullary tumor formation in the setting of an *Apc^{min/+}* genotype^[49].

The farnesoid X receptor (FXR) is a member of the nuclear receptor superfamily, and bile acids are endogenous ligands of FXR. FXR is necessary for maintaining bile acid homeostasis, and activation of FXR induces the expression of ileal bile acid binding protein (IBAB) and ileal bile acid transporters. In *Apc^{min/+}* mice, FXR deficiency led to an increase in the size of small intestine adenocarcinomas^[50]. Taken together, these results indicate that bile acids play a central role in cancer of the small intestine.

LIVER

The estimated yearly number of deaths world-wide from liver cancer is 474215 for men and 205656 for women^[6], making it the third leading cause of cancer deaths among men and women combined. The majority of liver cancers world-wide arise as a result of chronic infection by hepatitis B or C virus, or from exposure to aflatoxin B1, a carcinogenic food contaminant. Excessive alcohol consumption is another risk factor. However, the risk of hepatocellular carcinoma is elevated in individuals with late stage primary biliary cirrhosis, a possible autoimmune disease^[51]. Liver cancer can also arise in children with a defect in the bile acid export pump^[52]. Thus bile acids are implicated in at least some cases of liver cancer.

Several studies have shown that bile acids induce ROS in cells of the liver. TCDCA induced ROS in isolated rat hepatocytes^[53,54]. ROS were also induced in rat hepatocytes by GCDCA^[55-57] and by DCA^[58]. Taurolithocholate-3-sulfate induced ROS both in rat hepatocytes and a human hepatoma cell line (Huh7)^[59].

Treatment of human hepatoma cells (HepG2) with DCA activated the *gadd153 promoter*^[60]. This promoter is activated by DNA damage, suggesting that DCA induces

DNA damage in hepatoma cells.

DCA is a promoter of preneoplastic lesions (hyperplastic nodules) in hepatocellular carcinogenesis^[61,62]. Evidence has also been presented that DCA, given as a dietary supplement in rats, possess initiating activity for hepatocarcinogenesis^[63]. At least 12 studies have shown that bile acids induce apoptosis in liver cells. These are listed in Table 2. Apoptosis induced in liver cells by hydrophobic bile acids is likely caused by oxidative stress^[59].

Four studies indicated that bile acid-induced apoptosis in liver cells is mediated by ROS. A lazaroid antioxidant (U83836E) inhibited induction of apoptosis in isolated rat hepatocytes^[55]. The antioxidants α -tocopherol, ebselen or idebenone (a coenzyme Q analogue) inhibited apoptosis of isolated rat hepatocytes by GCDCA and GCA^[57]. Also in isolated rat hepatocytes, the antioxidants β -carotene and α -tocopherol inhibited GCDCA induced apoptosis^[67]. LCA and CDCA activated the antioxidant responsive element Nrf2 in human hepatoma-derived cells (HepG2), mouse hepatoma-derived cells (Hepa1c1c7) and primary human hepatocytes^[72]. Nrf2 activation inhibits apoptosis, and the target genes of activated Nrf2 include the genes that encode the rate-limiting enzyme in glutathione biosynthesis and thioredoxin reductase 1. The general finding that induction of apoptosis in liver cells by bile acids can be reduced by anti-oxidants implies that this induction is mediated by ROS.

The bile salt export pump conveys bile acids from the hepatocyte cytoplasm into bile canaliculi. Mutations in the *ABCB11* gene cause a deficiency in the bile salt export pump, leading to intrahepatic accumulation of toxic bile salts. Children with such mutations have an increased incidence of hepatocellular carcinoma^[52,73]. Mice lacking the farnesoid X receptor, which controls the synthesis and export of bile acids, have increased hepatic bile acids. These mice have a high incidence of liver tumors^[74,75]. Such findings led to the suggestion that in cholestatic liver disease, chronic exposure to bile acids may play an important role in hepatocellular carcinogenesis^[51].

BILIARY TRACT

Cholangiocarcinoma (CC) is an adenocarcinoma that arises from the bile duct epithelium. The CCs that occur within the liver are referred to as intrahepatic CCs. Those that occur at the confluence of the left and right hepatic duct are termed hilar CCs. The CCs that arise between the hepatic hilum and the duodenal papilla (or

Ampulla of Vater) are called extra hepatic CCs^[76].

The gallbladder and bile duct are exposed to high concentrations of bile acids. The bile acids excreted from the liver into the gall bladder are at a concentration of approximately 100 mmol/L^[77]. The lifetime risk for developing cholangiocarcinoma in patients with primary sclerosing cholangitis is estimated at 7%–13%^[78], and it was suggested that chronic exposure to bile acids may play an important role in cholangiocellular carcinogenesis^[51]. Two children with progressive familial intrahepatic cholestasis and cholangiocarcinoma were found to have an absence of bile salt export pump expression and mutations in the *ABCB11* gene^[79]. Loss of a functional bile salt export pump may cause cholangiocarcinoma through intracellular accumulation of bile acids. Incubation of immortalized mouse cholangiocytes with GCDC resulted in the generation of ROS and an increase the percentage of cells with oxidative DNA damage (8-OHdG), suggesting that the a long-term effect of excessive exposure of the biliary tract to GCDC may be carcinogenesis^[80].

PANCREAS

The estimated yearly number of deaths world-wide from pancreatic cancer is 137 206 for men and 122 185 for women^[6], making it the eighth leading cause of cancer deaths among men and women combined. Most adenocarcinomas of the pancreas occur in the head of the gland, which is in close proximity to bile^[81]. In a hamster surgical model, bile reflux into the pancreatic duct was shown to induce development of intraductal papillary carcinomas of the pancreas^[82], suggesting that bile acid may be an etiologic agent in pancreatic cancer. Consistent with this idea, epidemiological studies found a positive correlation between ingestion of a western style high fat diet and the incidence of pancreatic cancer^[83–85]. Treatment of human pancreatic cancer cell lines with bile acids (CDCA, DCA or TCDCa) induced cyclooxygenase-2 (COX-2) expression^[81]. Since COX-2 is overexpressed in human pancreatic adenocarcinomas, these results also suggest a possible role for bile acids in pancreatic carcinogenesis.

COLON AND RECTUM

The estimated yearly number of deaths world-wide from cancer of the colon and rectum is 318 798 for men and 284 169 for women^[6], making it the fourth leading cause of cancer deaths among men and women combined. Although both inherited mutations, environmental factors (e.g. smoking) and dietary factors are involved in colorectal cancer development, sporadic colorectal cancer appears to be caused predominantly by dietary factors.

The association of risk of colorectal cancer and consumption of red meat and processed meat was assessed in a meta-analysis of 15 prospective studies on red meat and 14 studies on processed meat^[86]. The results showed consistent associations between high consumption of red and of processed meat and risk of colorectal cancer. In another recent study, a dose-dependent positive

Table 3 Bile acids induce ROS/RNS in colon cells

Cells/tissues	Bile acid(s) that induced ROS/RNS	Ref.
Human colon surgical resections	DCA (RNS)	[110]
Cultured human adenocarcinoma cells (CACO-2)	DCA, LCA (ROS)	[111]
Cultured human adenocarcinoma cells (HT-29)	DCA, LCA (ROS)	[112]
	DCA (ROS)	[36,113]
	DCA (RNS)	[114]
Cultured human adenocarcinoma cells (HCT116)	DCA (ROS)	[109,115,116]
	DCA (RNS)	[117]
Rat colonic mucosa	DCA (ROS)	[118]
Mouse colonic mucosa	DCA (ROS, RNS)	[119]

association between saturated fat intake and localized colorectal cancer was found in women, but not in men^[87]. In earlier work, a positive association between dietary fat consumption and cancer incidence was reported^[88–93]. Dietary total fat intake and saturated fat intake, but not polyunsaturated fat intake, are positively associated with colon cancer incidence^[94]. In cancer prone *Apc*^{min/+} mice, a high fat diet results in a significant increase in tumors^[48]. A Western-style diet, containing elevated lipids and decreased calcium and vitamin D, induced colonic tumors in normal CB7Bl/6 mice^[95–97]. Taken together, these studies implicate dietary fat (primarily from red and processed meat) in the etiology of human colorectal cancer.

Dietary intake of high-fat and high-beef foods results in a significantly higher excretion of fecal secondary bile acids, mainly DCA and LCA^[98]. Presumably the increase in DCA and LCA reflects increased production of bile acids in order to emulsify the increased level of dietary fat. Epidemiologic studies have also found that fecal bile acid concentrations are increased in populations with a high incidence of colorectal cancer^[99–106]. The most significant bile acids with respect to human colorectal cancer appear to be the secondary bile acids, DCA and LCA^[99].

Although repeated exposure of the colorectal epithelium to high physiological concentrations of bile acids appears to be the major etiologic factor in colorectal carcinogenesis, other factors may also be significant. Intake of dietary heme iron is associated with increased risk of colorectal cancer^[107], suggesting that iron catalyzed formation of ROS may play a role. The risk of colorectal cancer is also increased by smoking^[108]. Bile acids and nicotine from smoking can interact synergistically in colon cells to increase oxidative stress and DNA damage^[109].

Twelve studies have reported that bile acids induce production of ROS or RNS in colon cells (Table 3).

Fourteen studies showed that bile acids induce DNA damage in colon cells (Table 4), of which a component is likely oxidative DNA damage. Defective repair of oxidative DNA damage is linked to increased risk of colon cancer. The base excision repair pathway deals with oxidative damages in DNA caused by ROS. 8-OHdG is a major oxidative damage in DNA that can mispair with adenine causing G:C to T:A transversion mutations, unless the mispair is corrected. MUTYH is a mammalian DNA glycosylase that initiates base excision repair by excising adenine opposite 8-OHdG. Genetic

Table 4 Bile acids induce DNA damage in colon cells

Cells/tissues	Bile acid(s)	Assay for DNA damage	Ref.
Isolated mouse colon crypt cells	LCA	Nucleoid sedimentation for strand breaks	[122]
Isolated human and rat colon cells LCA	LCA	Comet assay for strand breaks	[123]
Isolated rat colon cells	DCA	Immunostaining for poly (ADP-ribose) an indicator of DNA damage	[124]
Freshly isolated normal human colonocytes	DCA, CDCA	Comet assay for strand breaks	[125]
Cultured human adenocarcinoma cells (HT-29)	DCA, CDCA	Comet assay for strand breaks and modified comet assay for oxidative DNA damage	[112,126]
Cultured human adenocarcinoma cells (HT-29)	DCA, LCA	Comet assay for strand breaks	[111]
Cultured human adenocarcinoma cells (CACO-2)	DCA, LCA	Comet assay for oxidative DNA damage	[127]
Cultured human colon adenocarcinoma cells (HCT-116 & HCT-15)	DCA	Comet assay for strand breaks	[128]
Cultured human colon adenocarcinoma cells (HCT-116 & HT-29)	DCA	Comet assay for strand breaks	[129]
Cultured human colon adenocarcinoma cells (HCT-116)	DCA	Induction of the DNA repair protein BRCA-1	[130]
		Induction of DNA damage inducible gene GADD153	[116]
		Comet assay	[131]
Cultured human colon adenocarcinoma cells (HCT-116 and HCT-15)	DCA	Induction of DNA damage inducible genes GADD34, GADD45, GADD153	[119]
Colon samples from mouse dietary colitis model	DCA	Oxidative DNA damage: 8-OHdG assayed by immunohistochemistry	

Table 5 Bile acids induce apoptosis in colon cells

Cells/tissues	Bile acid(s) that induced apoptosis	Ref.
Biopsies from normal human colonic mucosa	DCA	[135-139]
Colon adenoma cell lines (AA/C1 and RG/C2), and carcinoma cell line (PC/JW/F1)	DCA	[140]
Cultured human adenocarcinoma cells (HT-29 and CaCo-2)	DCA	[141,142]
Cultured human adenocarcinoma cells (HCT-116)	DCA, CDCA	[130,143-146]
	DCA	[116,147-149]
Cultured human adenocarcinoma cells (HT-29)	DCA	[114]
Cultured human adenocarcinoma cells (HT-29 and HCT-116)	DCA	[150]
	DCA	[128]
	DCA, LCA, CDCA	[151]
Cultured human adenocarcinoma cells (HT-29) and human fetal colonic mucosal cells (FHC)	DCA, LCA, CA, CDCA	[152]
Cultured human adenocarcinoma cells (HT-29, SW480, SW620)	DCA, CDCA	[153,154]
Cultured human adenocarcinoma cells [HCT-116 (p53 ⁻) and HCT-15 (p53 ⁺)]	DCA	[127]
Cultured human adenocarcinoma cells (HCT-116SA apoptosis-sensitive and HCT-116RB, HCT-116RC and HCT-116RD apoptosis resistant)	DCA	[155]
Human colonic mucosal samples from surgical resections	DCA	[156]

defects in MUTYH cause multiple polyps^[120] and greatly increased risk of colorectal cancer^[121] in humans.

The numerous studies showing that bile acids induce DNA damage in colon cells suggest that bile acids may also induce mutation and genomic instability. In a model system for inducing tumors in the rat using the carcinogen azoxymethane, DCA not only increased the incidence of colon tumors, but also increased the incidence of tumors with *K-ras* point mutations^[132], suggesting that DCA may induce *K-ras* mutations. Hydrophobic bile acids cause aneuploidy and micronuclei formation, indicators of genomic instability, in a variety of cell types including colon epithelial cells^[133]. Persistent exposure of cultured colon epithelial cells to DCA results in alterations in expression of chromosomal maintenance/mitosis-related genes that might give rise to the observed genomic instability^[133].

The 27 studies listed in Table 5 indicate that hydrophobic bile acids induce apoptosis in colon cells. Exposure of colon epithelial cells to DCA causes induction of growth arrest and DNA damage-inducible genes *GADD34*, *GADD45* and *GADD153*, probably in

response to the DNA damage caused by DCA^[131]. DCA induced expression of *GADD153* is essential for DCA induction of apoptosis^[130]. These findings suggest that induction of DNA damage by DCA results in apoptosis. Induction of apoptosis by DCA may protect against the survival of cells with damaged template DNA that upon replication might undergo mutation leading to cancer^[134].

Repeated long-term exposure of colonic epithelial cells to high physiologic concentrations of bile acids appears to select for cells that are resistant to induction of apoptosis by bile acids. Such apoptosis-resistant cells might arise and clonally expand through the processes of mutation (or epimutation) and natural selection. Several studies of colon cancer patients have shown that epithelial cells in areas of the colonic mucosa that do not contain the cancer itself have increased resistance to induction of apoptosis by DCA^[115,135,137-139]. The expression of anti-apoptotic protein Bcl-xL is elevated in the colorectal mucosa adjacent to colorectal adenocarcinomas^[157]. These findings suggest that tumors may often arise in a field of apoptosis-resistant epithelial cells. A variant of ileal bile acid binding protein (IBABP), termed IBABP-L,

is upregulated in colorectal cancer and is necessary for survival of HCT116 colon cancer cells in the presence of physiologic levels of hydrophobic bile acid^[158]. This finding suggests that IBABP-L is a key factor in the development of resistance to bile acids in colon cancer cells. Furthermore, repeated long-term exposure of HCT-116 human colonic epithelial cells in culture to sublethal concentrations of DCA selects for cells that have further increased resistance to DCA-induced apoptosis^[159]. These observations suggest a link between development of resistance to bile acid-induced apoptosis and colon cancer.

In summary, evidence indicates that, in colonic epithelial cells and tissues, bile acids have the short-term effect of inducing oxidative stress that causes DNA damage leading to mutation and apoptosis. Over a longer period, repeated exposure to high levels of bile acid may select for the development of apoptosis resistant fields of cells and eventually to the development of adenocarcinoma.

DNA DAMAGE COUPLED WITH RESISTANCE TO CELL DEATH DRIVES TUMORIGENESIS

We have emphasized, above, the role of bile acids in inducing ROS/RNS and DNA damage in cells of the GI tract. These stresses, if excessive, can overwhelm cellular defenses resulting in cell death^[139,160-163]. However, we have also shown that bile acids can activate two major cell survival pathways, NF- κ B^[115,124] and autophagy^[164] (Figure 1). Both of the pathways are known to be activated by ROS^[165,166]. Results from our laboratory indicate that the activation of both pathways by DCA can be attenuated by the use of antioxidants^[113,115,124,164]. We have also shown that the NF- κ B and autophagy pathways contribute to the stable apoptosis resistance that characterizes cell lines persistently exposed to DCA^[159,164]. The sensitization to DOC-induced cell death after interfering with these pathways was documented using antisense oligonucleotides against the p65 subunit of NF- κ B^[159] and pharmacologically through the use of 3-methyladenine^[164], an inhibitor of autophagy.

The induction of persistent DNA damage in apoptosis-resistant cells is a dangerous situation that can lead to further mutation and ultimately cancer (Figure 1). An increase in Bcl-2 (an anti-apoptotic protein), for example, may also downregulate Ku DNA binding activity, thereby further amplifying genomic instability through interference with the non-homologous end-joining pathway of DNA repair^[167]. The cross-talk between anti-apoptotic proteins and DNA repair proteins is a current area of investigation.

NUCLEAR BILE ACID RECEPTORS FXR, VDR AND PXR/SXR

Recently, it has become apparent that nuclear bile acid receptors FXR, VDR and PXR/SXR play an

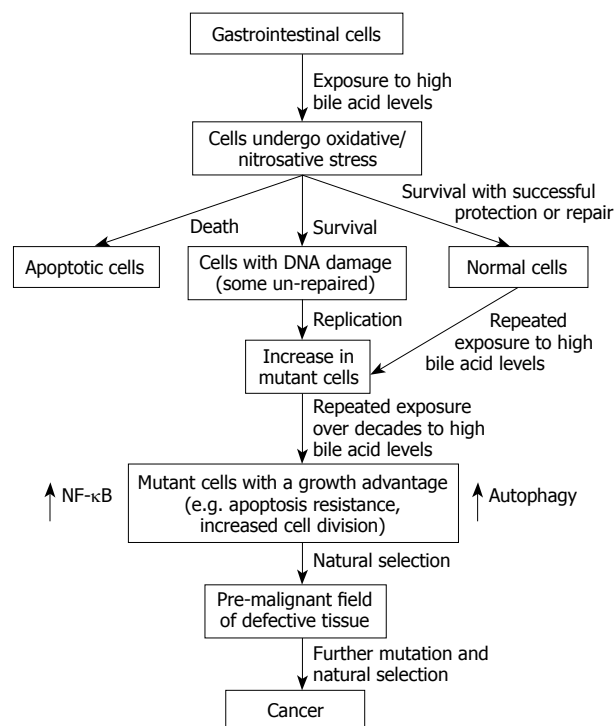


Figure 1 The role of bile acids in the sequence of events leading to gastrointestinal cancer.

important role in protecting against carcinogenic effects of bile acids. FXR, a member of the nuclear receptor superfamily, responds to bile acids as physiological ligands^[168-170]. FXR has a key role in activating pathways that maintain bile acid homeostasis^[50]. FXR protects against intestinal tumorigenesis, possibly by a mechanism involving induction of apoptosis^[50,171].

The vitamin D receptor (VDR) functions as a receptor for the secondary bile acid lithocholic acid, and has a key role in activating a pathway that detoxifies lithocholic acid^[172]. Similarly, the human xenobiotic receptor SXR (steroid xenobiotic receptor) and its rodent homolog PXR (pregnane X receptor) are bile acid receptors that, when activated, induce a response that detoxifies bile acids^[173,174]. PXR promotes bile acid detoxification by activating bile acid metabolizing enzymes and transporters. In both human colon cancer cells and normal mouse colon epithelium PXR/SXR protects against bile acid induced apoptosis^[149].

CONCLUSION

In Figure 1, we suggest a possible general pathway for bile acid induced carcinogenesis based on evidence reviewed above. An immediate effect on cells of the GI tract to exposure to a high physiologic level of bile acids is the induction of ROS/RNS. This can lead to DNA damage and apoptosis in some cells. Among surviving cells, some may remain normal by successfully employing protective and repair mechanisms. Other surviving cells, however, may retain unrepaired DNA damage. When such cells undergo DNA replication using a damaged strand as template, mutations will likely arise. Over years of frequently repeated exposure to high

levels of bile acids many mutations will occur, and some of these mutations may provide a growth advantage to the cell in which they occur. The growth advantage may involve apoptosis resistance, and increased and/or aberrant proliferation. Such cells will tend to expand clonally at the expense of neighboring cells to form a field of defective cells. Further repeated exposure to high levels of bile acids will lead to additional mutations. Should some of these mutations arise within a defective field and also provide additional growth advantages, a secondary field will spread within the first field by natural selection. Repetition of this "mutation-and-selection" process over many years, perhaps decades, will lead to a pre-malignant field and eventually to cancer.

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