

# Epigenetic alterations associated with cholangiocarcinoma (Review)

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**Abstract.** Cholangiocarcinoma (CCA) is a highly lethal malignant tumor arising from the biliary tract epithelium. Chronic inflammatory conditions, including primary sclerosing cholangitis, liver fluke infestation, and hepatolithiasis, are considered risk factors, but the cause is still unknown in most cases. Recent advances in molecular pathogenesis have highlighted the importance of epigenetic alterations, including promoter hypermethylation and histone deacetylation, in the process of cholangiocarcinogenesis. More recently, research interest has been focusing on microRNA (mir), a major subtype of non-coding RNA. Mir is highly conserved among species and regulates the expression of specific target genes by binding to the 3'-untranslated regions of messenger RNA. The number of studies on a possible link between mir and various cancers is growing. This review provides a comprehensive overview of the genes currently known to be hypermethylated in CCA and their putative roles in cholangiocarcinogenesis. The epigenetic role of mir in the pathogenesis of CCA is also discussed.

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## 1. Introduction

Cholangiocarcinoma (CCA) is a devastating neoplasm originating from cholangiocytes, the epithelial cells that line the biliary apparatus (1). It accounts for only 10-15% of

hepatobiliary neoplasm (2,3). Two-thirds of CCAs involve the extrahepatic bile duct, whereas the remaining one-third affects the intrahepatic biliary tree (1,4). The disease is notoriously difficult to diagnose and is usually fatal because of its typically late clinical presentation and the lack of effective therapeutic modalities (1,4). Most patients have unresectable disease at presentation, and the overall survival rate, including resected patients, is poor, with less than 5% of patients surviving 5 years (5). Although CCA is a relatively rare tumor, interest in this disease is rising as the incidence and mortality rates are increasing worldwide (2,3). CCA is associated with chronic inflammatory conditions of the biliary system, including hepatolithiasis, liver fluke infestation, choledochal cysts, and primary sclerosing cholangitis (PSC) (1,4). However, for most CCA cases, the cause is unknown, and affected individuals have no history of exposure to, or association with, such risk factors (1,4).

At present, little is known about the molecular mechanisms in CCA. As for many other tumors, the development of CCA must be understood as a multistep process, with the accumulation of genetic and epigenetic alterations in regulatory genes, leading to the activation of oncogenes and the inactivation or loss of tumor suppressor genes (TSGs) (6). This review discusses the epigenetic inactivation of different TSGs in CCA. The limited data regarding microRNA (mir) regulation of cholangiocarcinogenesis are also summarized.

## 2. Genetic alterations in CCA

The milieu of chronic biliary inflammation, along with cholestasis, leads to the production of cytokines and reactive oxygen species, and this causes protracted cellular stress and irreversible DNA damage (1,2). As a result, cholangiocytes attain cellular phenotypes that result in malignant transformation (1). The proposed pathways that participate in cholangiocarcinogenesis include: self-sufficiency and proliferation; apoptosis resistance; escape from senescence; and tumor invasiveness and metastasis (1). Molecular mechanisms responsible for bile duct carcinogenesis likely include the interaction of genetic variants and somatic cell alterations (1,4,6). The genetic changes in CCA include: mutations of K-ras, p53, p16<sup>INK4a</sup>, and Smad4; loss of heterozygosity (LOH) of APC; and allelic losses on 3p13-p21 and 8q22 (7-11). Among the genetic abnormalities that have been demonstrated in CCA, p53 mutations and activating K-ras mutations are the most frequent (6). Nevertheless, the

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reported rates of genetic alterations in CCA vary widely among studies (4,6). These variations are presumably due to differences in the subsites of cancers, racial and geographical variations in the study populations, and the use of different assay techniques (4).

### 3. Epigenetic alterations in CCA

**Histone modifications.** Histones are basic proteins that complex with genomic DNA to form nucleosomes, the basic units of the compacted structure of chromatin. Histones are modified post-translationally by acetylation, methylation and phosphorylation. Histone acetylation appears to be the major regulator of histone function. Histones are acetylated on lysine residues at their amino termini by histone acetyltransferases (HATs), and acetylated histones are deacetylated by histone deacetylases (HDACs). The HDAC-mediated removal of acetyl groups from lysine residues in the amino termini of histones leads to chromatin condensation and transcriptional inactivation of the involved DNA (12,13). This transcriptional inactivation can contribute to suppression of TSG expression and enhanced tumorigenesis (14). In fact, HDAC inhibitors enhance the acetylation state of histones, leading to chromatin decondensation and increased gene expression (15,16). HDAC inhibitors can, therefore, reverse the aberrant epigenetic state associated with cancer, and they have been shown to act in synergy with DNA methylation inhibitors to inhibit tumor growth (15,16). Nevertheless, there is only nominal information on the etiologic roles of histone modifications in cholangiocarcinogenesis.

**DNA methylation.** DNA methylation refers to the addition of a methyl group to one of the four bases that constitute the coding sequence of DNA (17,18). DNA methylation plays a key role in chromatin structure, suppression of the activity of endogenous parasitic sequences, and stable suppression of gene expression (epigenetic silencing), a process normally reserved for special situations, such as the inactive X-chromosome and imprinted genes (19,20). DNA methylation occurs via the covalent addition of a methyl group to the 5-position of the cytosine ring within the context of a cytosine nucleotide followed by a guanine nucleotide (CpG dinucleotide or CpG site) (18). It has been estimated that almost half of the human gene promoter regions contain CpG-rich regions, called CpG islands (21,22). Promoter hypermethylation of CpG islands results in downregulation or silencing of gene transcription (Fig. 1); thus, the aberrant promoter hypermethylation of TSGs is an alternative mechanism of gene inactivation that contributes to the carcinogenesis of human neoplasms, including CCA (4,6,22).

**Genes hypermethylated in CCA.** Genes hypermethylated in the promoter CpG islands in CCA are summarized in Table I. Through epigenetic silencing, TSGs are involved in important molecular pathways of cholangiocarcinogenesis, e.g., cell-cycle regulation, apoptosis, DNA repair and cell adhesion (23), and are herein briefly reviewed.

p16<sup>INK4A</sup>, also called cyclin-dependent kinase inhibitor 2A, is a TSG located at human chromosome 9p21 that inhibits interaction with cyclin D1 (24). This TSG is frequently

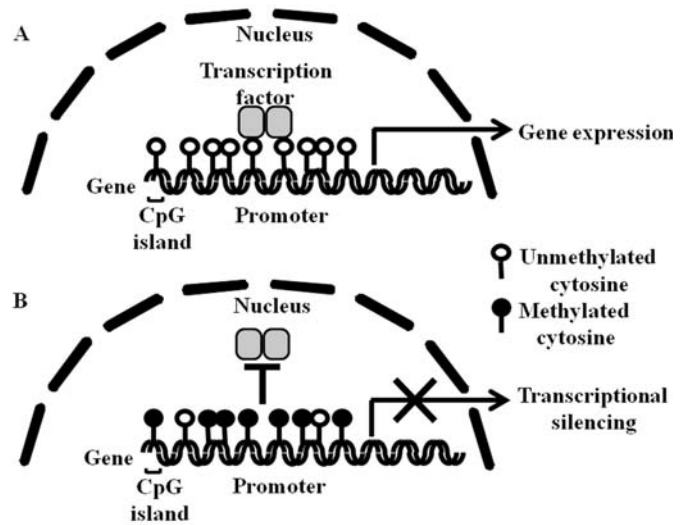


Figure 1. (A) When CpG sites in the gene promoter are unmethylated, the gene is transcribed to messenger RNA in most normal steady cells. (B) However, CpG island hypermethylation of the gene promoter inhibits transcription factor-DNA interactions, leading to inhibition of gene expression.

inactivated in a variety of tumors by deletion, mutations and promoter hypermethylation (6). In CCA, CpG island methylation appears to be the main cause of p16<sup>INK4a</sup> inactivation despite variable methylation frequencies (25-32). This promoter region hypermethylation has been shown to be associated with a poor clinical outcome. The DNA methylation frequencies of other genes related to cell cycle regulation, including p14<sup>ARF28,32</sup>, p15<sup>INK4b28</sup>, p73<sup>28</sup>, and ras association domain family 1A (RASSF1A) (26,28,33,34), and their chromosomal locations are shown in Table I.

Death-associated protein kinase (DAPK) gene is located at chromosome 9q34.1, and its product is a proapoptotic mediator of interferon- $\gamma$ -induced programmed cell death (4,35). The DNA methylation frequencies ranged from 3 to 32% in CCA (26,28,30). This promoter hypermethylation is likely to be associated with poorly differentiated CCA and with a poor prognosis (26,28). The DNA methylation frequencies of other genes related to apoptosis, including target of methylation-mediated silencing/apoptosis speck like protein containing a caspase recruit domain (TMS1/ASC) (36), semaphorin 3B (SEMA3B) (37), 14-3-3 (25), Runt-related transcription factor 3 (RUNX3) (26), and checkpoint with forkhead and ring finger domains (CHFR) (26), and their chromosomal locations are shown in Table I.

Human mutL homologue 1 (hMLH1) is a DNA mismatch repair gene located at 3p21.3 (38). Genetic and epigenetic alterations of hMLH1 have been reported in various cancers (38,39). In CCA, DNA methylation frequencies of the hMLH1 gene promoter varied from 0 to 46% (26,28,30,40,41). Limpaiboon *et al* found an association between this promoter hypermethylation and poorly differentiated CCA with vascular invasion (41). O<sup>6</sup>-methylguanine-DNA methyltransferase (MGMT) gene is located at chromosome 10q26. This gene is responsible for repairing alkylation DNA damage (42). Koga *et al* found a high methylation frequency of 49% in MGMT gene (30), whereas Yang *et al* reported a 33% methylation frequency of MGMT gene in CCA (28).

Table I. Promoter hypermethylation frequencies in various genes in cholangiocarcinoma.

Gene	Location	Function	Incidence (%)	Refs.
p14 <sup>ARF</sup>	9p21	Cell cycle regulation	25-38	(28,32)
p15 <sup>INK4b</sup>	9p21	Cell cycle regulation	50	(28)
p16 <sup>INK4a</sup>	9p21	Cell cycle regulation	18-83	(25,26,27,28,29,30,31,32)
p73	1p36.3	Cell cycle regulation	36-49	(28)
RASSF1A	3p21.3	Cell cycle regulation	27-69	(26,28,33,34)
DAPK	9q34.1	Apoptosis	3-32	(26,28,30)
TMS1/ASC	16p11.2	Apoptosis	5	(36)
SEMA3B	3p21.3	Apoptosis	100	(37)
14X3X3	1p36.11	Apoptosis	60	(25)
RUNX3	1p36	Apoptosis	57	(26)
CHFR	12q24.33	Apoptosis	16	(26)
hMLH1	3p21.3	DNA repair	8-46	(26,28,30,40,41)
MGMT	10q26	DNA repair	33-49	(28,30)
RARb2	3p24.2	Cell growth and differentiation	14	(28)
APC	5q21	Cell adhesion	27-46	(25,28)
E-cadherin	16q22.1	Cell adhesion	22-43	(25,26,28,30)
TIMP3	22q12.1	Cell adhesion	9	(25,28)
THBS1	15q15	Cell adhesion	11	(25,37)
GSTP1	11q13	Drug/xenobiotic metabolism	14	(28)
FHIT	3q14.2	Purine metabolism	42	(33)
SOCS3	17q25.3	Cytokine signaling	88	(45)
MINT1	22q11	Unknown	41	(25)
MINT12	22q11	Unknown	51	(25)
MINT25	22q11	Unknown	15	(25)
MINT31	22q11	Unknown	1	(25)
MINT32	22q11	Unknown	35	(25)
BLU	3p21.3	Unknown	20	(37)

This promoter hypermethylation can be associated with an increased frequency of GC to AT transitions in oncogenes and TSGs and with a poor prognosis (30).

Epithelial (E) cadherin gene is located at chromosome 16q22.1. The encoded protein is a calcium-dependent cell adhesion molecule (43). Genetic and epigenetic alterations in this gene lead to loss of function, permitting progression of cancer by increasing proliferation, invasion and metastasis (4,43). DNA methylation frequencies of this gene in CCA range from 22 to 43% (25,26,28,30). Adenomatous polyposis coli (APC) gene is located at 5q21-q22. APC is a TSG that controls cell division, cell-cell interactions, and cell migration and invasion (4). APC gene hypermethylation ranges from 27 to 46% in CCA (25,28). This gene hypermethylation is associated with a worse clinical outcome in CCA patients (25). The DNA methylation frequencies of other genes related to cell adhesion, including tissue inhibitor of metalloproteinase (TIMP3) (25,28) and thrombospondin 1 (THBS1) (25,37), and their chromosomal locations are shown in Table I.

The DNA methylation frequencies of retinoic acid receptor- $\beta$  2 (RAR $\beta$ 2; function, cell growth and differentiation) (28), glutathione S-transferase  $\pi$  1 (GSTP1; function, drug/xenobiotic metabolism) (28), fragile histone triad (FHIT;

function, purine metabolism) (33), Blunt protein (BLU; function, unknown) (37), methylated in tumor (MINT) 1, 12, 25, 31, 32 (function, unknown) (25), and their chromosomal locations are shown in Table I.

Suppressor of the cytokine signaling 3 (SOCS3) gene is at chromosome 17q25.3. The expression of this gene is induced by various cytokines, including interleukin-6 (IL-6), IL-10, and IFN- $\gamma$  (44). SOCS3 can bind to and inhibit the activity of janus kinases (JAKs), turning off signal transducers and activators of transcription 3 (STAT3) signaling in response to IL-6 (Fig. 2) (44). Sustained overexpression of IL-6 has an integral role in CCA biology (45). Indeed, we demonstrated that IL-6-mediated STAT3 signaling is sustained in human CCA cells (46). More recently, we have shown that IL-6-mediated sustained STAT3 activation in human CCA is likely due to SOCS3 epigenetic silencing via hypermethylation of CpG islands within its promoter region (47), contributing to sustained IL-6/JAKs/STAT3 signaling in CCA cells. Thus, the loss of this negative regulator of IL-6 in CCA may contribute to cholangiocarcinogenesis.

Again, the downstream consequences of aberrant IL-6 expression may be further hypermethylation of the promoter regions of target genes in CCA (48). IL-6 has been shown to

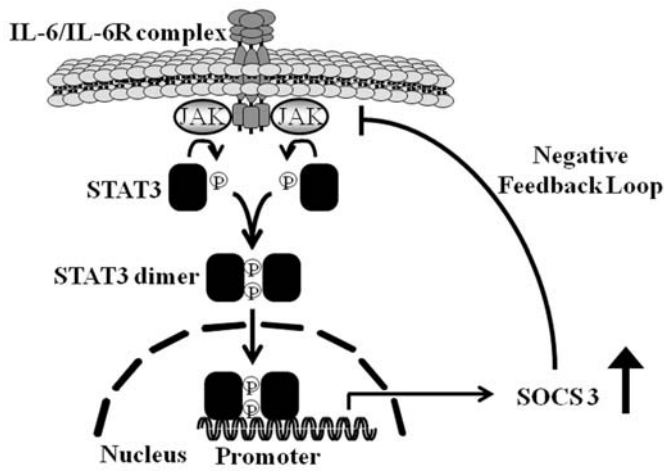


Figure 2. Interleukin 6 (IL-6) binds to its cognate receptor (IL-6R), leading to activation of janus kinases (JAKs). Following phosphorylation (activation) of signal transducers and activators of transcription 3 (STAT3) by JAKs, it dimerizes and translocates into the nucleus, where the STAT3 dimer binds to the promoter region of suppressor of the cytokine signaling 3 (SOCS3) gene. SOCS3 can bind to and inhibit the activity of janus kinases (JAKs), turning off STAT3 signaling in response to IL-6.

regulate the enzyme activity of DNA methyltransferase responsible for DNA hypermethylation (49). For instance, the promoter methylation of epidermal growth factor receptor (EGFR) gene was decreased, and, consequently, EGFR gene and protein expressions were increased by IL-6 (48), suggesting epigenetic regulation of EGFR by the inflated IL-6 expression seen in CCA.

**Mir and CCA.** Mir is encoded in the genome of many species from plants to animals and is transcribed by RNA polymerase II as long precursor transcripts, which are known as primary mir (pri-mir) (50). Mature mir is generated from pri-mir by sequential processing steps. The pri-mir is initially recognized by the microprocessor complex in the nucleus, whose core component is Drosha. The microprocessor complex excises the stem-loop hairpin structure that contains the mir, a 60-80 nucleotide intermediate termed precursor mir (pre-mir). The pre-mir is recognized by exportin 5, which transports it to the cytoplasm (51,52). Pre-mir is exported to the cytoplasm by exportin 5. Further cytoplasmic processing by Dicer performs a second cleavage to generate the double-stranded 18-24 nucleotide-long mir duplex (53,54). One of these two strands is incorporated into RNA-induced silencing complex, RISC (55). Only one strand of the mir duplex remains stably associated with RISC. This strand becomes the mature mir. The mature mir guides the RISC complex to the target mRNA, which is then cleaved or translationally silenced. Thus, mature mir regulates the expression of specific target genes by binding to the 3'-untranslated regions of messenger RNA (56). The biogenesis of mir and the targeted regulatory processes for gene expression are shown in Fig. 3. It has been well established that multicellular eukaryotes utilize mir to regulate biological processes such as embryonic development, proliferation, differentiation and cell death (56). Recent studies have shown that mir may provide new insight in cancer research (57,58). Many mir genes are located in

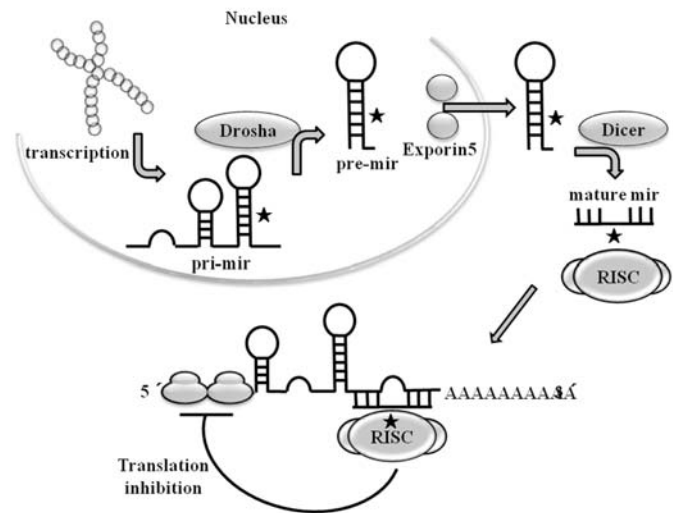


Figure 3. MicroRNA (mir) is encoded in the genome and is transcribed by RNA polymerase II as long precursor transcripts, which are known as primary miRNA (pri-mir). The pri-mir is initially recognized by the microprocessor complex in the nucleus, whose core component is Drosha. The microprocessor complex excises the stem-loop hairpin structure that contains the pri-mir, a 60-80 nucleotide intermediate termed precursor mir (pre-mir). The pre-mir is recognized by exportin 5, which transports it to the cytoplasm. Further cytoplasmic processing by Dicer performs a second cleavage to generate a double-stranded 18-24 nucleotide-long mir duplex. One of these two strands is incorporated into RNA-induced silencing complex, RISC. Only one strand of the mir duplex remains stably associated with RISC. This strand becomes the mature mir. The mature mir guides the RISC complex to the target mRNA, which is then cleaved or translationally silenced.

fragile sites and cancer-associated genomic regions, and studies have suggested that mir expression profiling can be correlated with disease pathogenesis and prognosis, which may ultimately be useful in cancer treatment (56,59).

To date, the data concerning mir regulation of cholangiocarcinogenesis is sparse. Meng *et al* showed that mir-141 was overexpressed in human CCA cells (60). Inhibiting mir-141 effectively increased the expression of CLOCK, which regulates circadian rhythms and can act as a tumor suppressor in CCA. They also found overexpression of mir-200b and its target, the protein tyrosine phosphatase non-receptor type 12, the dysregulation of which may contribute to tumor cell survival and carcinogenesis. Similarly, the expression of mir-21 was overexpressed in CCA, which blocks tumor suppressor gene PTEN (phosphatase and tensin homolog deleted on chromosome 10) expression (61).

Again, enforced IL-6 overexpression in human CCA cell lines significantly increased let-7a expression (62). Let-7a is likely to contribute to survival effects attributable to the inflated IL-6. A putative target of let-7a is the neurofibromatosis 2 (NF2) gene (62), which is a negative regulator of STAT3 (63). Thus, overexpression of IL-6 in CCA and subsequent up-regulation of let-7a decrease NF2 expression, thereby removing the negative regulation of STAT3, which may be linked to constitutive activation of STAT3, the pivotal transcription factor implicated in a number of cancers, including CCA.

Conversely, other mir species have been identified as being downregulated in CCA cells compared to non-malignant



cholangiocytes. In terms of carcinogenesis, these types of mir are considered as TSG. Mir-29b expression was suppressed in a CCA cell line, and enforced miR-29b expression effectively reduced the target molecule, myeloid cell leukemia 1, an anti-apoptotic protein of the Bcl-2 family (64), possibly leading to apoptotic resistance of CCA. Interestingly, mir-370, whose expression was substantially reduced in CCA cells, was shown to be under epigenetic regulation by DNA hypermethylation (65).

*Other epigenetic mechanisms and CCA.* More recently, Sasaki *et al* revealed that p16<sup>INK4a</sup> promoter hypermethylation was related to aberrant expression of enhancer of zeste *Drosophila* homologue 2 (EZH2), a component of the polycomb family of gene-silencing proteins, in cholangiocarcinogenesis in hepatolithiasis (66). There is a mechanism in which modifications of histones mark a gene for hypermethylation by the binding of methyltransferase enhancers such as EZH2 to histones (67).

#### 4. Conclusions

DNA methylation and histone modifications are the hallmarks of epigenetic gene regulation. Mir is a recently discovered category of non-coding RNAs with important regulatory functions. Aberrancies in both the epigenetic and the miRNA regulation of genes have been documented in CCA. A deeper understanding of the association of epigenetic mechanisms with CCA could lead to new therapeutic avenues.

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