Molecular Biology of Gallbladder Cancer: Potential Clinical Implications

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Abstract

Gallbladder cancer (GBC) is a common malignancy of the biliary tract and involves the changes in multiple oncogenes and multiple genetic genes. Since over the past decade there has been an advance in the knowledge of the genetic basis of cancer, mainly as a result of the rapid progression of molecular technology; however, conventional therapeutic approaches have not had much impact on the course of this aggressive neoplasm. Knowledge of the molecular biology of GBC is rapidly growing. Genetic alterations in GBC include adenosine triphosphate-binding cassette transporter ABCG8, membrane-bound enzyme ADAM-17 of multi-functional gene family, and other genes including p53, COX2, XPC, and RASSF1A. The advances in molecular biology have potential implications for the detection of this disease, using Synuclein-gamma, Syndecan-1, glycoprotein 72 (TAG-72), tumor endothelial marker 8 protein (TEM8) and TNF-alpha. The use of these molecular diagnostic methods is of clinical importance for the gene replacement therapy, genetic prodrug activation therapy, and antisense immunology technology for the treatment of malignancy. The author reviewed recent publications on PubMed, and summarized molecular biology of GBC, with an emphasis on features of potential clinical implications for diagnosis and management.

Keywords: Adenosine triphosphate-binding cassette transporter, Gallbladder cancer, Syndecan, Synuclein-gamma, TEM8, TNF, XPC

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Introduction

Gallbladder cancer (GBC) shows a marked geographical variation in its incidence, with the highest figures being seen in India and Chile, and relatively low levels in many Western countries. Risk factors for its development including the presence of gallstones, infection, and anomalous pancreatobiliary ductal junction are well documented, and a number of genetic alterations have also been identified in the pre-invasive and invasive stages of GBC. Some of these genetic changes are associated with particular risk factors, and some changes are associated with differences in prognosis. GBC involves the changes in multiple oncogenes and genetic

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genes.^[1] The article summarized more recent publications on PubMed, specially in the molecular biology of GBC, with an emphasis on clinical implications.

Difference between early and advanced stages

It has been shown that genetic expressions vary in early and advanced GBC.^[2] GBC usually arises against the background of gallstone disease, which may be causatively related to supersaturation of cholesterol in bile. The excretion of cholesterol from the liver is regulated by adenosine triphosphate-binding cassette transporter ABCG8. A common genetic polymorphism D19H of ABCG8 and Apolipoprotein B (APOB) associated with gallstone disease may be related to the genetic predisposition of GBC. The ABCG8 DH genotype frequency and APOB was significantly higher in GBC patients. The risk was more pronounced in GBC patients with gallstones, and in patients with an early onset of the disease. Therefore, the DH genotype and the H allele of the ABCG8 D19H polymorphism are associated with GBC susceptibility. The GBC patients with gallstone disease harboring the ABCG8 variant allele and APOB^[3] are at a higher risk.^[4]

ADAM-17, known as tumor necrosis factor-alpha converting enzyme, is involved in the progression of GBC. It has been shown that expression of ADAM-17 is significantly increased in tumors with high histological grade and pT stage compared with low histological grade and pT stage tumors. Patients with high expression of ADAM-17 had a significantly shorter overall survival compared with those with low expression.^[5,6] Moreover, annexinA3 is found to play an important role in the initiation and progression of GBC.^[7] These are of importance for the potential molecular targets for diagnosis and treatment of GBC.

Bas excision repair

Base excision repair (BER) corrects DNA damage caused by oxidative stress and chronic inflammation, putative risk factors for cancer. To understand the relationship between genetic variation in BER genes and risk of biliary tract cancer and biliary stones, it was examined nonsynonymous polymorphisms in three key BER genes-X-ray repair cross-complementing group 1 (XRCC1) (R194W, rs1799782; R280H, rs25489 and R399Q, rs25487), apurinic/apyrimidinic endonuclease (APEX1) (D148E, rs3136820), and 8-oxoguanine DNA glycosylase (OGG1) (S326C, rs1052133). Compared with subjects carrying the XRCC1 194RR genotype, those with the WW genotype had a 1.9-fold risk of bile duct cancer and compared with subjects carrying the XRCC1 280RR genotype, those with the XRCC1 280H allele had a 50% reduced risk of bile duct cancer. It was also found an inverse association between the APEX1 148E allele and gallbladder stones, but no association for the OGG1 polymorphism.^[8]

Deregulation of apoptosis is involved in the mechanisms of cancer development. Bax-interacting factor-1 (Bif-1) interacts with both Bax and Bak that are crucial for the intrinsic apoptosis signaling. Functionally, loss of Bif-1 expression has been proven to enhance tumorigenesis, possibly by inhibiting apoptosis mediated by Bif-1.^[9]

Cadherin

E-cadherin/beta-catenin

Changes of the E-cadherin/beta-catenin complex during cell-cell interactions result in loss of cell adhesion, and may account for the ability of cancer cells to metastasize. The beta-catenin membranous expression decreased between cholecystitis and malignant tissue, as well as between normal epithelium and carcinoma. The E-cadherin membranous expression was reduced in normal gallbladder epithelia compared with carcinoma. Cytoplasmatic E-cadherin was significantly different from normal gallbladders to carcinomas and between normal tissue and inflammation. Therefore, significant differences of E-cadherin and beta-catenin were detected between normal, inflamed, and cancerous tissues. These changes of the protein expressions and the associated loss of adhesive mechanisms might lead to a cancerous pathway in GBC.^[10] Loss of E-cadherin expression was high in GBC, while majority of the chronic cholecystitis (CC) and xanthogranulomatous cholecystitis (XGC) cases retained positive E-cadherin expression.^[11] Moreover, the expression of E-cadherin or beta-catenin frequently diminishes as the tumor progresses, and abnormalities of E-cadherin and beta-catenin expression were associated with decreased apoptosis in GBCs. E-cadherin expression might be a useful prognostic marker in the tumor.^[12]

T-cahderin

T-cadherin is believed to act against carcinogenesis in various tissues; however, the tumor-suppressor mechanism of T-cadherin remains largely unclear. Restoration of T-cadherin decreased the expression of Akt3 and phosphorylated Akt molecules. T-cadherin may inhibit tumor progression through multiple pathways.^[13] Zeb1 represses T-cadherin expression and increases the invasive activity of GBC.^[14]

Cancer stem cells

CSCs/tumor-initiating cells have been defined as a subset of tumor cells responsible for initiating and sustaining tumor development. Emerging evidence strongly supports the existence of CSCs in various solid tumors, but they have not yet been identified in human GBC. However, human GBC cell line GBC-SD cells were cultured in a serum-free culture medium with different concentrations of the chemotherapeutic drug cisplatin for generating sphere clones. It demonstrated that sphere clones of GBC with stem cell-like characteristics can be obtained using suspension cultures of GBC-SD cells in serum-free culture medium containing cisplatin.^[15] Alternatively, CSCs in primary GBC and in the cell line GBC-SD using the cell surface markers CD44 and CD133 were identified. These cells showed stem cell properties, including self-renewal, differentiation potential, and high tumorigenicity. In vitro culture experiments revealed that CD44+CD133+ GBC cells possessed a higher spheroid-colony forming ability in serum-free media than other subpopulations. These suggest that the CD44+CD133+ population exhibited CSC-like characteristics, and may provide a novel approach to the diagnosis and treatment of GBC.^[16]

Cluster differentiation and natural killer cells

The patient with malignant tumor always shows immunologic function drawback and ingravescent with tumor development, especially in the aspect of cell-mediated immunity. One study was undertaken to define the relationship between the immune function of local cells and cancer development by investigating the distribution of natural killer (NK) cells and T-lymphocyte subsets in peripheral blood, the cancer tissue and the tissue surrounding gallbladder carcinoma. This study indicated that the numbers of CD4+ and CD8+ T-cells and NK cells in GBC tissues were significantly higher than those in the surrounding tissue and gallbladder with gallstone. However, the ratio of CD4+/CD8+ was lower in the cancer tissue than that in the surrounding tissue and tissue from gallbladders with gallstones. The distribution of CD4+ and CD8+ T-cells and NK cells in mucous membrane of cholecystitis gallbladder and that in the tissue surrounding GBC were significantly different. Disproportionate and imbalanced distribution of NK cells and subsets of T-lymphocytes occurs in the mucous membrane proper of GBC and surrounding tissue. Although GBC tissue has higher expressions of CD4+, CD8+ and NK cells, the immune function is low or in an inhibited state. In GBC immunization therapy, local cellular immunological function should be enhanced and the protective barrier improved.^[17]

CD24, a small cell surface protein, has emerged as a novel oncogene and prognostic factor for poor outcomes in many human cancers. CD24 is an important marker of malignancy and poor prognosis in gallbladder carcinoma. Its detection combined with cancerous staging may increase the ability of investigators to predict the prognosis of patients with gallbladder carcinoma. Furthermore, the CD24 antigen represents an attractive target for specific therapies with monoclonal antibodies in patients with CD24-overexpressing gallbladder carcinoma, so the detection of CD24 may help clinicians select patients likely to benefit from novel molecular therapies.^[18]

CD133+ tumor cells are shown to be responsible for the initiation, propagation, and recurrence of tumors. Purified CD133+ gallbladder carcinoma cells are highly resistant to conventional chemotherapy. However, As2O3 effectively induces CD133+ gallbladder carcinoma cells apoptosis. Furthermore, the ectopic expression of CD133 attenuated the apoptotic effect of As2O3on cells through activation of AKT signaling pathways.^[19]

CD147

Pathologic findings demonstrated that the intensity of CD147 and MMP-2 staining in cancerous tissues was associated significantly with histological types, distant metastasis, and Nevin stages of gallbladder carcinomas. Using a proportional hazard model, the survival rate of the patients with CD147+/MMP-2+ expression was the lowest, and including information on CD147 and MMP-2 staining patterns within cancerous tissues along with clinical cancer staging may improve the accuracy of predicting patients' prognosis. The detection of these two markers combined with cancerous staging may increase

the ability of investigators to predict the prognosis of patients with gallbladder carcinomas. $^{\cite{[20]}}$

The caudal-type homeodomain transcriptional factor *CDX2*, a member of the caudal-related homeobox gene family, plays a crucial role in the regulation of cell proliferation and differentiation in the gut. CDX2 expression was an independent prognostic predictor in gallbladder adenocarcinoma. CDX2 and Hep might function as important biological markers in the development and prognosis of gallbladder adenocarcinoma.^[21-23]

c-erB-2

The inactivation of the tumor suppressor gene and activation of the proto-oncogene are the key steps in the development of the human cancer. The p53 and c-erbB-2 are the best examples. p53 and c-erbB-2 may have independent role in carcinogenesis of gall bladder cancer. c-erbB-2 over expression in adenoma and younger age group indicates its role as an early event in carcinogenesis of gallbladder.^[24]

c-FLIP

Cellular Fas-associated death domain-like interleukin-1 converting enzyme inhibitory protein (c-FLIP), an antiapoptotic protein, was over-expressed in the most of gallbladder carcinoma tissues. Thus, a potent strategy for the treatment of gallbladder carcinoma by targeting the c-FLIP was presented.^[25]

Chloride intracellular channel 1

Advanced GBC has an extremely poor prognosis because of metastasis. Identification of metastasis-related biomarkers is essential to improve patient survival. The over expression of Chloride intracellular channel 1 (CLIC1) promoted cell motility and invasion of GBC-SD18L *in vitro*, while RNA interference of CLIC1 remarkably decreased cell motility and invasive potency of GBC-SD18H *in vitro*, indicating that CLIC1 might play an important role in metastasis of gallbladder carcinoma.^[26]

Differences between gallbladder and bile duct cancers

Biliary tract cancers carry dismal prognoses. It is commonly understood that chromosomal aberrations in cancer cells have prognostic and therapeutic implications. The bacterial artificial chromosome (BAC) array comparative genomic hybridization (CGH) can facilitate detail analysis with high resolution and sensitivity. Both GBC and BDC cell lines have DNA copy number abnormalities of gains and/or losses on every chromosome, which is possible to determine the genetic differences between gallbladder and bile duct cancer cell lines.^[27]

Epidermal growth factor and receptor

EGF and transforming growth factor beta1 (TGFbeta1) play important roles in tumor biology. Single nucleotide polymorphisms in EGF and TGFB1 genes alter the expression of these growth factors and influence the tumorigenesis process.^[28] Increased EGF receptor expression has been noted in various cancers, and has become a useful target for therapeutic interventions. In GBC high expression of epidermal growth factor receptor (EGFR) is an independent predictor of survival.^[29,30] EGFR pathway is suitable therapeutic targets for biliary tract carcinomas. The combination of gemcitabine with drugs targeting these pathways gives encouraging results and further clinical studies could be warranted.^[31] Because EGF and HER-2/neu antagonists have been successfully used in adenocarcinomas from other sites, their use in cholangiocarcinoma can be potentially beneficial. Over expression of EGF correlated significantly with copy number of EGF. HER2/neu expression is uncommon in these tumors.^[32]

A recent study showed that tumor samples harboring EGFR mutation had phosphorylation of one or both downstream transducers analyzed. This suggests that patients with cholangio-carcinoma or gallbladder carcinoma exhibit somatic mutations of EGFR in the tyrosine kinase domain that can elicit cell signals sustaining survival and proliferation. These tumors might be further evaluated for their susceptibility to small-molecule inhibitor treatment.^[33]

Inflammation genes

Long-standing gallstones are generally present in 65-80% patients of GBC. It has also been suggested that inflammation caused by gallstones may be involved in the development of GBC. Interleukin-1 receptor antagonist (IL-1RN) and interleukin-1 beta (IL-1B) are proinflammatory cytokine genes at the interleukin-1 locus, and polymorphisms of these genes have been associated with various inflammatory diseases. Variants in genes that influence inflammatory responses may predispose to gallstones and biliary tract cancer.^[34]

mda-7/IL-24 has tumor-suppressor activity in a broad spectrum of human cancer cells. It was used a human gallbladder carcinoma cell line (GBC-SD) to explore the effect of adenovirus-mediated IL-24 (Ad-IL24) gene therapy on GBC-SD cells. It was show that adenovirus (AdV)-mediated IL-24 overexpression exerted potent antitumor activity via stimulating mitochondrial apoptotic pathway in GBC-SD, and that mda-7/IL-24 has the potential to serve as a tool for targeted gene therapy in the treatment of GBC.^[35] Moreover, the haplotype 1/C of IL-1RN and IL-1B was found to confer a significantly enhanced risk of GBC in cancer patients with gallstones, while higher risk resulting from 2/C haplotype was of borderline significance. Individuals with 1/C and 2/C haplotypes of IL-1RN VNTR and -5111L-1B C \rightarrow T polymorphisms were more susceptible to develop GBC with gallstones than in healthy controls.^[36]

Premalignant lesions

The sequence of molecular changes leading to neoplastic transformation in the gallbladder remains elusive. A study aiming to characterize the spectrum of nuclear p16 protein product immunohistochemical expression in tissue taken from resected gallbladders, comprising histologically normal gallbladder epithelia, dyplastic epithelia, reactive atypia, and gallbladder adenocarcinoma indicated that nuclear p16 expression is absent in normal gallbladder epithelium, and is a frequent event in high-grade dysplasia of the gallbladder and gallbladder adenocarcinoma.^[37]

The relationship between cell cycle regulatory proteins and clinicopathologic features was immunohistochemically investigated in order to identify the biomarkers related to the outcome of patients with biliary tract cancer (BTC). Absence of p21 expression independently predicted poor outcome in all cases. Determination of p21 expression in surgically resected specimens may provide prognostic information in addition to conventional pathologic findings for patients with BTC, especially those who have biologically less aggressive phenotypes.^[38] The expression of p21 between advanced stages was 90% and early stages was 54%.

The p27 expression was markedly decreased in GBC cases, and there were no significant correlation between p27KIP1 expression and all clinicopathological parameters including gender, grades, stages, and invasion, whereas the expression of p21 was 75% and there was a significant correlation between p21 and the clinicopathological parameters including gender, stages, and invasion.^[39] Aberrations of p27(Kip1)-interacting cell cycle regulators are common in gallbladder carcinomas. Skp2 overexpression is highly representative of biological aggressiveness, suggesting that it is a promising novel target for therapeutic intervention in aggressive cases.^[40]

Understanding the molecular events in gallbladder carcinogenesis may provide a novel targeted therapeutic approach. Alterations in the tumor suppressor gene, p53, are commonly observed in most human cancers.^[41] Mutations in p53 gene are found in a majority of human malignancies and usually occur in the exons 5, 6, 7, and 8. Mutated p53 protein is more stable and gets accumulated in the cells that induce the host to develop anti-p53 antibodies in sera of cancer patients. Patients with GBC have antibodies to p53 protein. The commonest identifiable alteration in the p53 gene is a frameshift mutation at codon 271.^[42]

The microsatelital instability has been found in a small subset of preneoplastic and neoplastic lesions. The existence of methylation in the promoter gene areas has been related to the cellular proliferation, invasion and metastasis, and also in cases of chronic cholecystitis, therefore, this epigenetic phenomenon represents a crucial early event in GB carcinogenesis.^[43] The p53 gene is the most frequently mutated tumor suppressor in human cancers, and the aberrant p53 expression may play a role in the occurrence of GBC.^[44.46]

Mucin core proteins are known to be present in various organs, and are specifically expressed with carcinogenesis and closely associated with the prognoses of various malignant tumors. Mucin expression was independent of various tumor growth factors and clearly reflected the prognosis of GBC. Because the relative malignancy of GBC could be evaluated by examining the level of glycoprotein expression in tumor tissue, mucin could be a more important marker than p53 for predicting prognosis in gallbladder carcinoma using surgically resected tissue specimens.^[47]

Molecular marker

Molecular markers for cancers are not only useful for cancer detection and prognostic prediction, but may also serve as potential therapeutic targets. The molecular markers for prognostic prediction in GBC, using by the immunohistochemical expression, mainly include 15 proteins, namely p53, p27, p16, RB, Smad4, PTEN, FHIT, GSTP1, MGMT, E-cadherin, nm23, CD44, TIMP3, S100A4, and promyelocytic leukemia (PML). In particular, PML and p53 showed considerable potential as independent prognostic markers. Patients with normal PML and p53 expression displayed favorable outcomes, compared with those showing abnormal expression of either or both proteins. PML and p53 are potential candidates for development as clinically applicable molecular prognostic markers of GBC, and may be effective therapeutic targets for the disease in the future.^[48] These proteins may be useful as markers to identify premalignant lesions that are likely to progress into malignant adenocarcinoma, especially p53, Rad50, and cyclin-E proteins.[49]

GBCs are shown to frequently exhibit TP53 as well as K-ras gene mutations,^[50] these findings indicate that TP53 abnormalities are early and frequent events in the pathogenesis of GBC.^[51]

Conclusion

Many other molecular markers, proteins and factors, including PIK3CA,^[52], methylation,^[53,54] protein gene

product 9.5,^[55] proteomics,^[56] Raf-1,^[57] RASSF1A,^[58] Reg IV,^[59] Rsf-1,^[60] Survivin,^[61] Syndecan-1,^[62] Synuclein-gamma,^[63]TAG-72,^[64]Telomeres,^[65]Telomerase activity (hTERT),^[66] TEM8,^[67] Thrombospondin,^[68] Thymidine phosphorylase,^[69] Angiogenesis,^[70] TNF-alpha,^[71] TLRs,^[72] Topoisomerase,^[73] Vasculogenic mimicry,^[74] VEGFs,^[75-77] and XPC^[78] are involved in the development or progress of GBC. Some of these directly exert an effect on clinical outcome, while some link with development or of GBC. The rapid development of molecular biology in GBC, especially in genetic diagnosis and treatment, still leave a room for scientific researchers and clinicians to seek for a much better future.

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