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**Molecular mechanism of hepatitis B virus X protein function in hepatocarcinogenesis**

GengM *et al.* HBx and HCC

Ming Geng, Xuan Xin, Li-Quan Bi, Lu-Ting Zhou, Xiao-Hong Liu

**Ming Geng, Xuan Xin, Li-Quan Bi, Lu-Ting Zhou, Xiao-Hong Liu,** Department of Pathology, General Hospital of Jinan Military Command, Jinan 250031, Shandong Province, China

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**Correspondence to: Xiao-Hong Liu, MD, PhD,** Department of Pathology, General Hospital of Jinan Military Command, Shifang Road 25, Jinan 250031, Shandong Province, China. liuxh333@126.com

**Telephone:** +86-531-51666857

**Fax:** +86-531-51666284

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**Abstract**

Many factors are considered to contribute to hepatitis B virus (HBV)-associated hepatocellular carcinoma (HCC), including products of HBV, HBV integration and mutation, and host susceptibility. HBV X protein (HBx) can interfere with several signal pathways associated with cell proliferation and  invasion, and HBx C-terminal truncation has been suggested to have an impact in the development of HCC. This review focuses on the pathological functions of HBx in HBV-induced hepatocarcinogenesis. As a transactivator, HBx can affect regulatory non-coding RNAs including microRNAs and long ncRNAs. HBx is also involved in epigenetic modification and DNA repair. HBx interacts with various signal-transduction pathways, such as the p53, Wnt, and nuclear factor-κB pathways. We conclude that HBx hastens the development of hepatoma.

**Key words:** Hepatocellular carcinoma; Hepatitis B virus; Hepatitis B virus X protein; Hepatocarcinogenesis

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**Core tip:** The mechanisms underlying hepatitis B virus (HBV)-induced malignant transformation remain ambiguous, but research has suggested that HBV X (HBx) protein has a crucial function in the pathogenesis of hepatocellular carcinoma. This review focuses on the pathological functions of HBx in HBV-induced hepatocarcinogenesis.

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**Introduction**

Hepatocellular carcinoma (HCC) is the fifth most common cancer worldwide and the third most common cause of cancer mortality[1]. Chronic hepatitis B virus (HBV) infection has been demonstrated to be a risk factor for liver carcinogenesis, accounting for 55% of cases worldwide. Notably, 80% or more of such cases are found in the eastern Pacific region and sub-Saharan Africa, which are the areas with the highest tumor incidence[2,3]. The mechanisms underlying HBV-induced malignant transformation remain ambiguous, but previous research has suggested that HBV X (HBx) protein has a crucial function in the pathogenesis of HCC[4]. In this review, we focus on the molecular mechanisms of HBx in HCC pathogenesis.

**HBx gene and HBx protein**

HBV is considered to be the smallest DNA virus and contains a 3.2-kb circular double-stranded viral DNA genome, including a long minus-strand that is complementary to viral mRNA sequences and a short plus-strand. The open reading frame (ORF) of HBx is 465 bp long from 1376 to 1837 bp and is translated into a 154-amino acid (aa) protein. The HBx gene is located upstream of gene C and close to the sticky end of the viral genome, where it also overlaps with other genes including viral polymerase, Pre C, ORF5, and ORF6. Although HBx cannot directly bind to the DNA helix, it can activate other protein factors to further bind to their or other promoters and enhancers. Thus, this allows HBx to *trans*-regulate gene transcription[5].

The plus-strand HBx viral genome contains several transcriptional regulation element sequences including gene expression basic core promoter (BCP), core upstream regulatory sequence (CURS), negative regulatory element (NRE), enhancer II (EnH II), direct repeat 1 (DR1), and direct repeat 2 (DR2). Also, the 5’ end of the HBx gene overlaps with the ORF of DNA polymerase P[6,7]. Thus, the X gene of HBV contains the longest overlapping region between structural and functional sequences in the viral genome. More importantly, because of the overlapping of the coding region and regulation elements in the X gene of HBV, any DNA mutation and/or deletion can affect functions at both the gene and transcriptional regulation levels.

**HBx and DNA repair**

Current studies indicate that DNA repair is one of the driving mechanisms of carcinogenesis. Accumulation of DNA damage causes genomic instability and eventually leads to mutations. Recent studies showed that the expression level of HBx positively correlates with that of 8-hydroxy-2 deoxyguanosine (8-OHdG), a key oxidative stress indicator that causes DNA mis-pairing. Meanwhile, a high level of HBx inhibits human DNA glycosylase alpha (hMHα) activity, which causes suppression of DNA repair machinery, long-term DNA damage, and tumorigenesis[8].

Jung *et al*[9] reported that HBx with C terminal truncation does not induce reactive oxygen species (ROS) production and has no effect on level of 8-OHdG. This indicates an important role for the HBx C terminal region in oxidative stress-induced ROS production, consequential mitochondrial DNA (mtDNA) damage, and HCC pathogenesis. Another study also reported that HBx can regulate p53 expression and further depress the DNA repair capability[10].

**HBx and methylation**

Epigenetic studies allow us to understand how DNA methyltransferases (DNMTs) involved in DNA methylation can control gene expression through chromatin structural modification, changes in regional DNA accessibility, changes in DNA stability, and shifts in DNA-protein interactions. HBx can affect the cell cycle, proliferation, invasion, apoptosis, etc. of HCC cells by regulating DNMTs involved in DNA methylation of specific genes. A recent publication demonstrated that HBx can up-regulate DNMT1 and DNMT3A through transactivation[11]. The research group of Wei proved that down-regulation of miR-101 by HBx can lead to abnormal DNA methylation by the miR-101–targeting DNMT3A and promote HCC malignancy[12]. A similar study showed that HBx up-regulates DNMT1 and DNMT3A at both the transcriptional and translational levels. These up-regulations induce p16 (INK4A) promoter methylation and thus inhibit p16 expression[13].

**HBx and non-coding RNA****s**

Non-coding RNAs (ncRNAs) compose a large group of RNAs transcribed from non-coding regions of the human genome. ncRNAs account for about 90% of the genome and can be categorized in two types: 18–200-nt small ncRNAs, including microRNAs, small interfering (siRNAs), Piwi-interacting RNAs (piRNAs), small nuclear RNAs (snRNAs), small nucleolar RNAs (snoRNAs), etc.; 200-nt to 100-kb long ncRNAs (lncRNA), including mRNA-like ncRNAs, long no-poly A tail ncRNAs, *etc.*[14,15]. Most of these RNAs have been rarely studied, and although their functions are still unclear, they have a variety of important biological functions.

MicroRNAs play a critical role in the control of gene expression and signal transduction in HCC carcinogenesis. Several *in vitro* studies demonstrated that HBx can promote early stage HCC progression by inducing high levels of miR-21 expression, which inhibits programmed cell death 4 (PDCD4) in cancer cells[16,17]. Up-regulated miR-21 and miR-222 also can directly target tumor suppressor p27 and Kipl, a key regulator of the cell cycle, to contribute to cancer progression[18]. In a previous study, Bandopadhyay *et al*[19] found that miR-21 and miR-222 are down-regulated when HepG2 cells are transfected with HBx and HBV plasmid DNA or HepG2.2.15 cells are infected with HBV. This result was confirmed in clinical plasma samples from HCC patients. Interestingly, similar down-regulated effects also were observed in transfected HepG2 cells and patients’ plasma for miR-145, whereas miR-145 was up-regulated in an infected HepG2.2.15 cell line. These results suggest that HBx can control multiple miRNAs in different manners to promote HCC progression[19]. More evidence in an animal model showed that HBx inhibits tumor suppressor p53 to control the expression of miR-148a and further to increase the expression of hematopoietic pre-B cell leukemia transcription factor-interacting protein, which results in activation of the Akt, extracellular-related kinase (ERK), and mammalian target of rapamycin (mTOR) signaling pathways to enhance tumor cell growth, invasion, and metastasis[20]. A recent study also showed that HBx can down-regulate miR-192 and thereby play an anti-apoptotic role in HCC[21].

Long noncoding RNAs (lncRNAs) play crucial roles in human cancers. It has been reported that the lncRNA highly up-regulated in liver cancer (HULC) is dramatically up-regulated in hepatocellular carcinoma (HCC)[22]. Du *et al*[23] reported that HBx can increase expression of HULC *via* the cAMP-response element binding protein (CREB) activated promoter of lncRNA HULC. Then downregulation of P18, a HULC downstream gene, can promote liver cell proliferation. Additionally, it has been proved that another lncRNA can be down-regualted by HBx (termed lncRNA-Dreh), and down-regulation of Derh can enhance HCC cell invasion and migration *in vitro*[24]. It is known that deregulation of lncRNA is one of the key factors in HCC tumor initiation and progression.

**HBx mutants and tumor imitation**

HBV infection-induced HCC usually happens within 10-30 years after the initial HBV infection. During this period, mutations of the HBV genome accumulate. Two dominant types of HBx mutations can be detected in chronic hepatitis: type I are single nucleotide mutations at multiple sites, and type II are C-terminal truncations causing higher levels of protein accumulation in the tumor region. Liver cells with these two types of mutation may have proliferative advantage in colony formation.

Past studies have shown that HBV genome integration is random, and there are no specific integration sites or rules. HBx and HBV core gene (HBc) mutations and deletions commonly occur in viral genome integration[25-28]. A polymerase chain reaction DNA amplification study of 45 tumor samples and sequencing results of 19 samples showed a high frequency of HBx mutation in HCC. Those mutations were mostly located close to the carboxyl terminus. It is believed that a strong correlation exists between HBx mutation and liver cell cancer transformation[29]. We obtained a similar result in that the hot spot of HBx mutation is highly regional. Blood tests of HBx mutations from patients in Europe and Africa show a higher incidence of mutation at 130 and 131 aa of HBx for mild hepatitis patients, and accumulation of HBx C-terminal truncation is more common in HCC peri-tumor tissues[30-34]. In contrast, a study of 153 HCC patients from Vietnam showed more 130 and 131 aa mutations in tumor tissue, and only 4 out of 48 samples had HBx C-terminal truncation accumulation[35]. A report from Hong Kong claimed that more than 54 mutations were detected in 95.2% of tissue samples and 95.3% of blood samples from 113 patients and at least one mutation in most of the samples[36]. There were 12 mutation sites in tissue samples and 9 mutation sites in blood samples, which suggest a mutation-driven HCC pathogenesis. Another study demonstrated that mutations were complicated and changeable in both HCC and peri-carcinoma liver tissue (PCLT). C-terminal truncation is more frequently found in HCC than in benign liver tissues. However, there is no single site mutation of a nucleic acid or amino acid that results in a distribution discrepancy between HCC and PCLT[37]. The reports described above indicate a regional distribution of HBx mutants, which reflects the high degree of complexity of HBV caused HCC.

The results of a comparison study between HBx C-terminal truncation and full-length HBx transfection indicate that each play different roles in cancer cell biology[38,39]. Specifically, overexpression of HBx 20-aa and 40-aa C-terminal deletion mutants can enhance cell growth, colony formation, tumor volume, and G1 to S phase cell cycle transition. In contrast, a HBx 30-aa C-terminal deletion mutant can inhibit cell proliferation. These results suggest that 125–134 aa of HBx is important for cell proliferation. More recent studies have shown that HBx spontaneous deletion mutations are usually located in the same region. Wang *et al* reported that the HBx 127 mutant contributes to tumor cell proliferation metastasis better than wild-type HBx by promoting cell growth through a positive feedback loop involving 5-lipoxygenase, fatty acid synthase, and miR-215[40,41]. This finding is consistent with a report from Fu *et al*[42] that concluded that the HBx-d382 deletion mutant (128–145 aa) enhances cell proliferation. The dual mutations K130M/V131I strengthen the capability of HBx as they up-regulate the expression and transcriptional activity of hypoxia-inducible factor 1-alpha (HIF-1α). The C-terminal truncation and deletion mutations, however, weaken the ability of HBx to up-regulate HIF-1α. Furthermore, the C-terminus was found to be essential for HBx stability and transactivation. A positive correlation was found between the HBx mutants and HIF-1α expression in clinical HCC samples[43]. In brief, it is believed that C-terminal truncation and deletion promote tumor malignancy. However, the detailed mechanism needs to be further investigated.

**HBx and the p53 signaling pathway**

Tumor suppressor gene p53 is the most commonly mutated in all types of cancers. p53 disorder plays an important role in HCC tumorigenesis. Many studies have indicated a complex transactivation between HBx and p53: HBx directly inhibit p53 activity by binding to its C-terminus[44]. In addition, overexpression of the p53 target gene murine double minute2 (MdM2) can induce degradation of HBx in HCC[45]. Xian *et al*[46] investigated the effect of wild-type and mutant HBx on p53 and found that HBx mutants, but not wild-type HBx, can inhibit p53 expression and its downstream signaling.

Recent studies suggest that overexpression of a HBx C-terminal mutant in HHT4 cells, a normal liver cell line, significantly increased the colony forming efficiency (CFE), wherease its corresponding wild-type allele CNT significantly decreased the CFE in HHT4 cells. Meanwhile, the p53-249Ser mutant interacts with HBx mutants to regulate cell proliferation and mitochondrial stability[47]. A report from another group showed that the HBx gene overlaps with the HBV core promoter region. Thus, core promoter mutations can also lead to HBx mutants and further up-regulate S-phase kinase-associated protein 2 (SKP2). SKP2 can down-regulate p53 though ubiquitination and consequentially promote tumorigenesis[48].

**HBx and the** nuclear factor**-κB signaling pathway**

Nuclear factor (NF)-κB is one of driving transcriptional factors in cancer biology and participates in cross talk with multiple pathways to control tumor initiation, development, invasion, and metastasis. Previous studies showed that HBx interacts with NF-κB to increase the expression of metastasis-associated protein 1 (MTA1). MTA1 is a major chromatin modulator that plays important roles in inflammation and tumor initiation. NF-κB cross talk with Notch signaling has also been demonstrated, and Notch 1 signaling can be blocked by HBx transfection in the normal liver cell line L02[49]. Lim *et al*[50] demonstrated that endogenous P22-FLIP, a cleavage product of c-FLIPL, can interact with HBx to activate NF-κB signaling. Further investigation showed that P22-FLIP, HBx, and NEMO, a regulatory subunit of IκB kinase (IKK), also known as IKKγ, can form a trimer complex to activate NF-κB signaling and promote tumor formation.

Lee *et al*[51] showed that NF-κB is highly associated with HBx131, HBx130, HBx5, HBx94, and HBx38 mutants, as well as HBx130-HBx131 double mutation and HBx5-HBx130-HBx131 triple mutation. These double and triple mutations increase the HCC incidence to 3.75 and 5.34 times the normal risk level, respectively. HBx5 mutants and double mutants show much higher NF-κB activity than wild-type and triple -mutation HBx. Notably, triple-mutation HBx cannot enhance NF-κB activity.

Many studies have demonstrated that HBx can promote HCC cell invasion and metastasis through NF-κB signaling. Zhang *et al*[52] reported that HBx activates NF-κB binding to the calpain small subunit 1 (Capn4) promoter and, thus, up-regulates expression of Capn4 in HCC cell. This HBx-induced Capn4 up-regulation can be significant blocked by specific siRNA knockdown of NF-κB or pyrrolidinedithiocarbamic acid (PDTC). Studies from other groups also showed that HBx increases the expression of NF-κB target genes, including vascular endothelial growth factor (VEGF), matrix metalloproteinase 2 (MMP2), MMP9, and MMP14. In addition, PDTC can inhibit HBx stimulation of NF-κB signaling, which leads to a decrease in the expression of VEGF, MMP9, and MMP14 but MMP2. PDTC also showed an anti-angiogenic effect in HepG2 tumor xenograft nude mice. These results prove that HBx promotes tumor cell invasion, angiogenesis, and metastasis by activating NF-κB signaling and up-regulating downstream target genes VEGF and MMPs[53]. HBx also can associate with peroxidase to enhance the level of ROS. This leads to greater activation of NF-κB and the formation of a positive feedback loop in cancer cells. Peroxidase-associated HBx up-regulates MMPs and down-regulates E-cadherin to enhance tumor cell invasion[54].

**HBx and the Wnt signaling pathway**

Highly preserved Wnt signaling has important functions in embryo development, and abnormal Wnt signaling can stimulate tumorigenesis. Wnt signaling molecules can be divided in two categories: (1) canonical Wnt/β-catenin signaling molecules including Wnt-1, Wnt-3a, Wnt-8a Wnt-8b, *etc.*[55]; and (2) non-canonical Wnt signaling molecules including Wnt-4, Wnt5a, Wnt-11[56], as well as Wnt/Ca2+, Wnt/planar cell polarity, and others[57,58].

Many studies have shown that HBx competitively binds to adenomatous polyposis coli to disassociate β-catenin from its degradation complex, resulting in nuclear β-catenin accumulation and activation of Wnt signaling to induce tumor transformation[59]. In addition, overexpression of HBx with Wnt-1 can activate Wnt/β-catenin signaling in Huh7 cells by stabilizing cytoplasmic β-catenin. Furthermore, stabilization of β-catenin by HBx can be achieved by inhibiting glycogen synthase kinase 3 (GSK-3) activity via the activation of Src kinase[60].

Liu *et al* found that the Wnt5a gene is regulated by HBx mutants through gene expression library screening. Further research showed that Wnt-5a may suppress tumor progression in HBV-induced HCC[61-63]. An immunohistochemical study of 114 HCC samples demonstrated that Wnt-5a as well as its receptor, receptor tyrosine kinase-like orphan receptor 2 (ROR2), were down-regulated in 80.7% (92/114) of samples. The expression of Wnt-5a is negatively correlated with β-catenin expression and positively correlated with E-cadherin expression. Thus, the expression of Wnt-5a and ROR2 is associated with patient prognosis. Huh7 HCC cells transfected with Wnt-5a have a decreased proliferation rate, and Wnt-5a siRNA knockdown can increase cell proliferation[64]. These findings suggest that HBx mutants can control tumor growth via signaling through the Wnt pathway.

**Conclusion**

HBx is the only expressed HBV viral protein in malignant HCC and has been shown to be a key molecule in HCC carcinogenesis. However, the molecular mechanism of HBx-induced HCC progression remains unclear. HBx is maintained as an important player in HCC tumorigenesis, and HBx functions in HCC through its nuclear translocation, protein–protein interactions, regulation of transcription factors, induction of chromosome instability, and nuclear localized HBx-involved signal transduction and then ultimately controls cancer cell proliferation, transformation, invasion, and metastasis. After more studies of HBx mutant and the involved molecular mechanisms, it has been found that these mutants have different biological functions and activities compared to wild-type HBx, and they may play important regulatory roles in the pathogenesis of HCC.

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