Hepatitis B protein HBx binds the DLEU2 IncRNA to sustain cccDNA and host cancer-related gene transcription

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ABSTRACT

Objective The HBV HBx regulatory protein is required for transcription from the covalently closed circular DNA (cccDNA) minichromosome and affects the epigenetic control of both viral and host cellular chromatin.

Design We explored, in relevant cellular models of HBV replication, the functional consequences of HBx interaction with DLEU2, a long non-coding RNA (lncRNA) expressed in the liver and increased in human hepatocellular carcinoma (HCC), in the regulation of host target genes and the HBV cccDNA.

Results We show that HBx binds the promoter region, enhances the transcription and induces the accumulation of DLEU2 in infected hepatocytes. We found that nuclear DLEU2 directly binds HBx and the histone methyltransferase enhancer of zeste homolog 2 (EZH2), the catalytic active subunit of the polycomb repressor complex 2 (PRC2) complex. Computational modelling and biochemical evidence suggest that HBx and EZH2 share two preferential binding sites in DLEU2 intron 1. HBx and DLEU2 co-recruitment on the cccDNA displaces EZH2 from the viral chromatin to boost transcription and viral replication. DLEU2-HBx association with target host promoters relieves EZH2 repression and leads to the transcriptional activation of a subset of EZH2/PRC2 target genes in HBV-infected cells and HBV-related HCCs.

Conclusions Our results highlight the ability of HBx to bind RNA to impact on the epigenetic control of both viral cccDNA and host genes and provide a new key to understand the role of DLEU2 and EZH2 overexpression in HBV-related HCCs and HBx contribution to hepatocytes transformation.

INTRODUCTION

Despite the availability of a preventive vaccine and antiviral treatments that arrest disease progression and reduce liver cancer risk, hepatitis B still remains a major global public health problem with about 257 million persons living with chronic HBV infection. HBV accounts for over 850 000 deaths/year and is responsible for >50% of the hepatocellular carcinomas (HCCs) worldwide. Currently, only 10% of chronically infected people are diagnosed and only 1% are treated. Hepatitis B surface antigen (HBsAg) loss is viewed as an important

Significance of this study

What is already known on this subject?

- HBx is recruited to and regulates the activity of a variety of coding genes and non-coding RNA promoters.
- Long non-coding RNAs (lncRNAs) are frequently dysregulated in both HBV-related hepatocellular carcinoma (HCC) tissues and HBV-expressing/HBV-expressing cell lines.
- LncRNAs can regulate multiple cellular processes by various mechanisms including chromatin remodelling.
- A number of lncRNAs has been described to guide chromatin-modifying complexes, including enhancer of zeste homolog 2 (EZH2)/polycomb repressor complex 2 (PRC2).

What are the new findings?

- HBx binds the promoter region of the DLEU2 lncRNA, enhances DLEU2 transcription and induces the accumulation of DLEU2 RNA.
- HBx directly binds DLEU2 and functionally competes with EZH2 for partially overlapping sites on the DLEU2.
- HBx and DLEU2 modulates transcription from the HBV covalently closed circular DNA minichromosome, hence boosting HBV replication, and from host genes promoters.
- HBx cooperates with DLEU2 by activating the promoters of a subset of EZH2/PRC2 targets in HBV-replicating cells and in HBV-related HCC.

How might it impact on clinical practice in the foreseeable future?

- These observations:
  - provide a new key to understand the role of EZH2 overexpression in HBV-related HCCs and the impact of HBV and HBx in hepatocyte transformation;
  - identify the interaction between HBx and DLEU2 as a new potential target to both inhibit HBV replication and hepatocyte transformation.
goal of therapy, but it is achieved only in a minority of patients treated with pegylated interferon alpha2a and nucleos(t)ide analogues (NUCs) and life-long treatments are recommended with NUCs. HBsAg loss is not accompanied by viral eradication and most patients never clear the HBV covalently closed circular DNA (cccDNA) and bear viral sequences integrated into the host DNA. The cccDNA minichromosome is the matrix for transcription of all viral mRNAs and the 3.5 kb pregenomic RNA (pgRNA) that serves as template for viral replication. The level of HBV replication is determined by the size of the cccDNA pool (ie, total number of cccDNA molecules) and its transcriptional productivity (ie, the amount of HBV RNAs transcribed from each cccDNA). cccDNA transcription is regulated by epigenetic modifications imposed to cccDNA-bound histones by viral and cellular proteins as well as inflammatory cytokines. HBx plays a key role through two independent mechanisms that cooperate to establish and maintain a transcriptionally active cccDNA minichromosome: (a) the degradation of the Sme5/6 restriction factors mediated by the activation of the DDB1-Cul4 E3 ligase early after infection and (b) the prevention of transcriptional repressor recruitment on the cccDNA. In addition to viral chromatin, HBx is recruited to and regulates a variety of coding genes and non-coding RNA promoters.

Long non-coding RNAs (lncRNAs) are frequently dysregulated in HBV-related HCC and HBV-expressing/HBx-expressing cells. LncRNAs play a crucial role in the modulation of signalling pathways and gene expression. Viral infections may induce cellular lncRNAs with antiviral effect and viruses can use lncRNAs to regulate metabolic networks promoting viral survival. lncRNAs have been described to remodel chromatin by guiding chromatin-modifying complexes, including enhancer of zeste homolog 2 (EZH2)/polycomb repressor complex 2 (PRC2), towards their target loci, the major cellular H3K27 trimethyltransferase, catalyses addition of methyl groups at lysine 27 of histone H3 (H3K27me3). EZH2, as a subunit of the canonical PRC2, along with EED, SUZ12 and RBBP4, is primarily involved in repression of transcription. Multiple DNA-binding proteins, including JARID2 and ATRX, contribute to PRC2 complex recruitment to target genes to silence gene expression. EZH2 is overexpressed in many cancers including HCC. Small molecule EZH2 inhibitors that target its catalytic SET domain are in clinical trials. However, EZH2 catalytic activity may not recapitulate all EZH2/PRC2 functions in cancer and EZH2/PRC2 recruitment can be uncoupled from H3K27me3 deposition/spreading. EZH2 also acts as a transcriptional co-activator of oestrogen-regulated, WNT-regulated and NOTCH-regulated proliferation pathways in breast cancer.

Here we show, in relevant cellular models of HBV replication, that HBx activates the expression and directly binds the lncRNA DLEU2 to modulate transcription from the HBV cccDNA minichromosome, hence boosting HBV replication, and from host genes promoters. HBx-mediated increase in DLEU2 and HBx recruitment onto target gene regulatory sequences increases chromatin accessibility and activates a subset of EZH2/PRC2 targets in HBV-replicating cells and in HBV-related HCCs. These observations provide a new key to understand the role of DLEU2 and EZH2 overexpression in HBV-related HCCs and the impact of HBx in hepatocyte transformation.

RESULTS

DLEU2 lncRNA is a direct target of HBx upregulated in HBV infection and HBV-related HCC

Several lncRNAs have been shown to be deregulated in HBV infection and in HBV-related HCCs. Recently, using a genome-wide analysis of HBx chromatin recruitment in HBV-replicating cells, we identified 16 lncRNA promoters and 26 lncRNA intragenic regions specifically bound by HBx (online supplementary table S1). The expression of the 34 unique lncRNAs that are directly targeted by HBx (figure 1A, online supplementary table S1) and of 15 additional lncRNAs that are known to be modulated in human HCCs (figure 1B) has been evaluated in mock-infected and HBV-infected primary human hepatocytes (PHHs) using a custom Nanostring-GE panel assay. As shown in figures 1A, 9 out of the 34 HBx-targeted lncRNAs were significantly upregulated and 4 were strongly downregulated by HBV at day 7 postinfection. Notably, 8 out of 15 HBx-modulated lncRNAs were strongly upregulated by HBV infection (figure 1B). Among the lncRNAs with the highest levels of induction in HBV-infected PHHs, DLEU2, LINC00441, LINC00478 are direct targets of HBx (ie, positive in the anti-HBx chromatin immunoprecipitation (ChIP)), whereas for HULC, HEIH, H19 and MALAT1 we do not have direct evidence of HBx promoter recruitment. We focused on DLEU2, which is differentially expressed during liver maturation and overexpressed in solid human cancers, including HCCs.

DLEU2 gene extends for 142 990 bp in Ch13(q14.2) and overlaps with the miR-15a/miR-16-1 cluster, the TRIM13 gene and, partially, with the DLEU1 gene (figure 1C). The HBx peak detected by HBx chromatin immunoprecipitation sequencing (ChIP-seq) (figure 1C, black circle) is located ~6500 bp downstream the DLEU2 promoter previously described. HBx binding on the HBx peak region was confirmed in independent ChIP assays performed in HBV-infected PHHs (figure 1D, left panel) and was accompanied by an increase in polymerase II (Pol II) binding (figure 1D, right panel) and DLEU2 steady state RNA levels (figure 1E–F). HBx recruitment on the DLEU2 promoter and increased DLEU2 expression were confirmed in other HBV infection/replication systems (online supplementary figure S1a-c). Figure 1G shows baseline levels of DLEU2 quantified by ddPCR in PHHs, HepG2 and HepG2-NTCP cells as well as in HBV-related HCCs and their paired HBV-infected non-tumorous liver tissues. The increase in DLEU2 RNA containing intron 1 sequences (figure 1E–G, right panels) and the accumulation of DLEU2 in the nuclear fraction of HBV-infected PHHs (figure 1H) as well as in HBV-replicating (online supplementary figures S2d) and HBx-HA-transfected HepG2 cells (online supplementary figure S2e), all supports the notion that DLEU2 induction by HBV occurs at the transcriptional level. The increase of DLEU2 levels after exogenous HBx expression in HepG2 cells (online supplementary figure S2e) and the loss of DLEU2 induction in PHHs infected with the HBx-deficient HBV (x-) virus (figure 1H) confirm the key role of HBx in increasing DLEU2 levels. Finally, HBx recruitment on the HBx peak region has no impact on the levels of the antisense DLEU1 lncRNA (online supplementary figure S2f).

DLEU2 lncRNA physically interacts with EZH2 and HBx

LncRNAs have been shown to guide chromatin-modifying complexes towards their chromatin targets and to regulate gene expression. Multiple lncRNAs interact in vivo with the EZH2/PRC2 complex in embryonic stem cells (ESCs). In EZH2 RIP-seq performed in colon cancer cells, DLEU2 is highly enriched, together with the lncRNAs XIST, TSIX, MALAT1 and GASS. Since HBx has been reported to modulate EZH2/PRC2 host target gene transcription, we sought to further investigate whether DLEU2 interacts with EZH2 and HBx in PHHs and...
Figure 1  HBx modulates DLEU2 expression. (A) Heatmap of the expression levels in HBV-infected primary human hepatocytes (PHHs) of 34 long non-coding RNAs (lncRNAs) that are direct transcriptional targets of HBx12 analysed by Nanostring. Blue and yellow colours of 34 long non-coding RNAs are shown. (B) Expression levels of 15 hepatocellular carcinoma (HCC)-associated lncRNAs, respectively. The red and black arrows identify lncRNAs upregulated in HBV-infected PHHs (7 days). Results are expressed as copies for 5 ng/μL of total RNA. (C) HBx and polymerase II antibodies in HBV-infected PHHs (7 days). (D) HBx antibodies in HBV-infected PHHs displayed a significant enrichment of MALAT1 binding to HBx was observed (figure 2C and online supplementary figure S3a). As expected, no DLEU2 can be immunoprecipitated with anti-HBx antibodies in HBV-defective HBV (+)-infected PHHs (figure 2D). These results indicate that HBx and DLEU2 interact in the nuclei of HBV-infected cells but do not exclude that this association might be mediated by additional partners. To ascertain whether HBx and DLEU2 directly interact, we performed RNA pull-down experiments using recombinant HBx and synthetic DLEU2 species designed in intron 1 sequence. Deethylated DLEU2 60-mer oligonucleotides were able to pull down recombinant HBx in contrast to biotinylated reverse DLEU2 control oligonucleotides (figure 2E, upper panel). The specificity of the pulled down recombinant HBx band was confirmed by immunoblot (online supplementary figure S3b) and the same antibody immunoprecipitated a 17Kd HBx band that was recognised specifically by two anti-HBx antibodies in HBV-infected HepG2-NTCP cells (online supplementary figure S3c). Altogether, these results indicate that DLEU2 binds EZH2 in liver cells and, in HBV-infected cells, the viral protein HBx.

Modelling DLEU2-EZH2-HBx interaction in silico

Our experimental data do not allow to conclude whether HBx and EZH2 compete for DLEU2 binding or whether HBx, EZH2 and DLEU2 may form a tripartite complex. We modelled via structural bioinformatics tools the binary DLEU2-EZH2 and DLEU2-HBx as well as the ternary DLEU2-HBx-EZH2 protein-RNA complexes. The CatRapid sequence-based method36 and three-dimensional (3D) atomic structures generated using the HEX and HADDOCK tools17 18 were used to model the physical interactions between proteins and DLEU2. Methodological details and challenges related to atomic structure prediction are discussed in online supplementary materials.

In contrast to EZH2 for which a 3D structure is known39 the 3D experimental structures of HBx and DLEU2 remain elusive. Using a homology modelling approach, we confirmed that HBx comprises disordered regions,40 essential for the interaction with protein and nucleic acid partners,41 as well as more structured domains (online supplementary figure S4). Using RNABindRplus42 we found that the HBx residues predicted to bind RNA mainly comprise charged amino acids as arginines and lysines that are mostly located in the disordered region corresponding to the first half of the sequence (online supplementary figure S4a). DLEU2 analysis by CatRapid36 corroborated the interaction of intron 1 of DLEU2 with HBx and EZH2, whereas in line with the RIP experiments (figure 2C), our analysis does not favour a direct interaction between HBx and MALAT1.

Next, we modelled the secondary (online supplementary figure S5) and 3D structure (figure 3) of the DLEU2 intron 1 region encompassing the sequences that interact with HBx in the RNA pull-down experiments (figure 2C) and exploited the HEX and HADDOCK biomolecular docking methods37 38 43 to...
model the binary and ternary interactions of DLEU2 with EZH2 and HBx. We found that two loci on intron 1 display a high probability to be occupied by HBx (figure 3A). Interestingly, HBx preferentially binds to internal loop motifs predicted in the secondary structure of DLEU2 intron 1 (online supplementary figure S5). Using the same biomolecular docking calculations, we confirmed the well-known interaction between HBx and DDB1 (PDB entry: 3I7H44) and the docking results for HBx–EZH2 complex functions. To verify this hypothesis, we performed DLEU2 RNA pull-down experiments with different stoichiometric ratios of HBx and EZH2. As shown in figure 3D, both EZH2 (lane 3) and HBx (lanes 1–2) can individually bind directly DLEU2 and HBx binding is dose-dependent (lanes 1–2). At a higher EZH2:HBx ratio (2:1), EZH2 binds HBx and prevents its interaction with HBx (lane 4). Conversely, at higher HBx:EZH2 ratios (6:1), HBx binding to DLEU2 precludes EZH2 binding (lane 5). In the presence of equimolar amounts of EZH2 and HBx, we observe a strong cooperative effect on HBx binding (figure 3E, lanes 1 and 3; online supplementary figure S3d), whereas EZH2 binding does not change (figure 3E, lanes 2–3). Thus, EZH2 seems to favour HBx binding to DLEU2, whereas the binding of EZH2 does not appear to be influenced by HBx. These findings can be explained if EZH2 facilitates HBx binding to DLEU2 sites that are not bound when HBx is alone. Notably, when the amount of HBx increases, EZH2 binding to DLEU2 decreases (compare figure 3E, lane 4 (HBx:EZH2 ratio 2:1) with lane 3 (equimolar amounts of HBx and EZH2) or lane 2 (EZH2 alone)). The binding of HBx in figure 3E, lane 4 (58 pmol) is higher than in lane 1 (29 pmol) but lower than in lane 3 (HBx 29 pmol and EZH2 29 pmol). The lower binding of HBx to DLEU2 observed in lane 4 as compared with lane 3 is likely the result of the displacement of EZH2 and the consequent loss of its ability to facilitate HBx binding on alternative binding sites. Altogether, the in silico modelling and the results of the RNA pull-down
HBx and DHLEU2 and compete for partially overlapping sites. (A) Configurations obtained from docking of HBx (surface representation, orange) on three-dimensional (3D) structure of DHLEU2 intron 1 (green). Panels 1–2 present the two most probable loci for HBx adsorption on DHLEU2 intron 1. (B) Configurations obtained from docking of EZH2 (surface representation, mauve) on 3D structure of DHLEU2 intron 1 (green). Panels 1–2 present the two most probable loci for EZH2 adsorption on DHLEU2 intron 1. (C) Panels 1–2: two most probable configurations obtained from docking of EZH2 on the most probable HBx-DHLEU2 intron 1 complex (panel (A)—1). Panels 3–4: two most probable configurations obtained from docking of EZH2 on the second most probable HBx-DHLEU2 intron 1 complex (panel (A)—2). Panels 5–6: two most probable configurations obtained from docking of HBx on the most probable EZH2-DHLEU2 intron 1 complex (panel (B)—1). Panels 7–8: two most probable configurations obtained from docking of HBx on the second most probable EZH2-DHLEU2 intron 1 complex (panel (B)—2). (D) Immunoblot analysis of RNA pull-downs showing the interaction between DHLEU2 RNA, HBx and EZH2. HBx (0.75 µg = 44 pmol or 1.5 µg = 88 pmol) or EZH2 (1.2 µg = 14 pmol, 2 µg = 24 pmol or 7.5 µg = 88 pmol) recombinant proteins alone or in combination (EZH2:HBx ratios of 2:1 or 1:6) were added to a fixed amount of DHLEU2 RNA (100 pmol). (E) Immunoblot analysis of RNA pull-downs showing the interaction between DHLEU2 RNA (100 pmol), HBx and EZH2. Increasing concentrations of HBx (0.5 µg = 29 pmol, 1 µg = 58 pmol) were added at a fixed concentration of EZH2 (2.5 µg = 29 pmol) recombinant proteins corresponding to EZH2:HBx ratios of 1:1 and 1:2, respectively. Data from one representative experiment out of three independent experiments are shown.

experiments reveal a highly dynamic interaction between EZH2 and HBx for DHLEU2 binding that leads, depending on their relative abundance, to a functional competition between HBx and EZH2 for partially overlapping sites on DHLEU2.

HBx-DHLEU2 interaction regulates cccDNA transcription and HBV replication
HBx is required for the transcription of HBV mRNAs from the cccDNA, including the HBV pgRNA that serves as template for reverse transcription and HBV replication. Since DHLEU2 interacts with HBx and EZH2, we next sought to assess whether DHLEU2, and its interaction with HBx, contributes to cccDNA transcription. We first performed cccDNA chromatin isolation by RNA purification (ChIRP) experiments in HBV-replicating cells, using three independent antisense probe sets that specifically recover DLEU2 intronic sequences, to ascertain the binding of DHLEU2 to the cccDNA (figure 4A). Notably, in HBV HBx mt-transfected HepG2 cells DHLEU2 expression is reduced (figure 4B) and DHLEU2 binding to the cccDNA is abrogated (figure 4C). DHLEU2 depletion by specific locked nucleic acid (LNA) longRNA Gapmers (online supplementary figure S6a) resulted in a reduction of both HBV pgRNA levels (figure 4D) and total HBV DNA (data not shown) in HBV-infected PHHs, whereas cccDNA levels are not affected (figure 4E). According to these results, DLEU2 interaction with HBx and its recruitment on the viral minichromosome affect cccDNA transcription and viral replication but do not interfere with the establishment of the cccDNA pool. Similar results were obtained in both HBV-transfected HepG2 cells and HBV-infected HepG2-NTCP cells (online supplementary figure S6b). Since EZH2 is recruited onto the cccDNA in HBV-infected HepG2-NTCP cells, we sought to investigate whether the ability of DLEU2 to interact with EZH2 (figure 2A) could be relevant in the regulation of cccDNA transcription. Although in the absence of HBx, the K9 methylation transferase SETDB1 and the arginine protein methyltransferase PRMT5 seem to play a predominant role in cccDNA transcriptional repression, EZH2-mediated K27 methylation of cccDNA-bound H3 also increases and EZH2 silencing results in increased of HBsAg production. Notably, in HBV HBx mt-transfected HepG2 cells the recruitment of EZH2 onto the cccDNA is significantly increased (figure 4F). These results and the reduction of cccDNA-bound H4 histone acetylation in the presence of DLEU2-targeting Gapmers (figure 4G) implicate DLEU2 in the epigenetic control of cccDNA transcription and in HBV replication.

HBx and DHLEU2 coregulation of host genes
In view of the ability of HBx to complex with DHLEU2 and EZH2, which are both overexpressed in tumour liver tissues of patients with HBV-related HCC (figure 5A), we sought to determine whether DHLEU2 and EZH2 might regulate a shared set of genes and to evaluate the involvement of HBx in this process. To this aim, we extracted the genes whose expression is positively correlated with DHLEU2 or EZH2 in 76 HBV-related HCCs from the transcriptomic TCGA_LIHC dataset and intersected them with the genes identified as HBx direct targets by Chip-Seq. As shown in figures 5B, 261 genes were coregulated with DHLEU2 or EZH2 in 76 HBV-related HCCs from the transcriptomic TCGA_LIHC dataset and intersected them with the genes identified as HBx direct targets by Chip-Seq. As shown in figures 5B, 261 genes were coregulated with DHLEU2 or EZH2 in 76 HBV-related HCCs from the transcriptomic TCGA_LIHC dataset and intersected them with the genes identified as HBx direct targets by Chip-Seq. As shown in figures 5B, 261 genes were coregulated with DHLEU2 or EZH2 in 76 HBV-related HCCs from the transcriptomic TCGA_LIHC dataset and intersected them with the genes identified as HBx direct targets by Chip-Seq. As shown in figures 5B, 261 genes were coregulated with DHLEU2 or EZH2 in 76 HBV-related HCCs from the transcriptomic TCGA_LIHC dataset and intersected them with the genes identified as HBx direct targets by Chip-Seq.
coregulated by HBX, DLEU2 and EZH2 (figure 5B). Notably, they are all upregulated in tumour liver tissues of patients with HBV-related HCC (figure 5C) and, with the exception of TRIM13, already reported to act as tumour suppressors in breast cancer cell lines and to be downregulated in aggressive breast cancer, associated with a reduced overall survival (online supplementary figure S7).

LncRNAs can regulate the expression of both neighbouring genes in cis and distantly located genes in trans. To gain mechanistic insights on how DLEU2 and HBx cooperate in the transcriptional regulation of host genes, and on the role of EZH2 in this process, we focused on TRIM13 and CCNB2, as examples of genes coregulated by EZH2 and DLEU2 and targeted by DLEU2 in cis and in trans, respectively. TRIM13 and CCNB2 expression is increased in HBV-infected PHHs (figure 6A) and other cell-based HBV infection/replication models (online supplementary figure S8a). The recruitment of HBx on the TRIM13 and CCNB2 promoters (figure 6B) in HBV-infected PHHs is accompanied by an increase in promoter-bound Pol II (figure 6B) and H4 acetylation (online supplementary figure S8b). Next, we investigated DLEU2 involvement in the regulation of TRIM13 and CCNB2 genes. ChIRP experiments showed that DLEU2 is recruited onto the TRIM13 and CCNB2 promoter regions in HBV-negative cells (figure 6C) and, consistent with the increased DLEU2 expression in HBV-infected cells (figure 1E–F and online supplementary figure S2b), its binding is further enriched in HBV-replicating cells (figure 6C). Selective degradation of DLEU2 by Gapmers (online supplementary figure S6a) resulted in decreased TRIM13 and CCNB2 expression in mock-infected and HBV-infected PHHs (figure 6D) and HepG2-Ntcp cells (online supplementary figure S8c) as well as in wt HBV-replicating HepG2 cells (online supplementary figure S8d). Notably, TRIM13 transcription is not induced in HBx mt HBV-replicating HepG2 cells and is not affected by DLEU2-specific Gapmers (online supplementary figure S8d, left panel). In HBV-replicating HepG2 cells co-transfected with HBV monomers and DLEU2-specific Gapmers, where the degradation of DLEU2 is more efficient (online supplementary figure S6a), we also showed a sharp decrease of H4 acetylation at the TRIM13 promoter (online supplementary figure S8e). Collectively, these results indicate that DLEU2 and HBx cooperate to increase TRIM13 and CCNB2 expression. Next, we investigated whether the increased recruitment of DLEU2 on the TRIM2 and CCN2 promoters (figure 6C) and their transcriptional activation is accompanied by changes in EZH2/PRC2 occupancy. As shown in figure 6E, both EZH2 and SUZ12 bind TRIM13 and CCNB2 promoters in uninfected cells and their chromatin occupancy on both promoters remains stable or even increases in HBV-replicating HepG2-Ntcp cells (figure 6E) and is accompanied by an increase of Pol II occupancy and H4 acetylation (figure 6F). The protein levels of PRC2 complex components in uninfected and HBV-infected PHHs and HepG2-Ntcp cells are shown in online supplementary figure S9. Finally, in HBV-replicating HepG2 cells both EZH2 chromatin occupancy and the repressive mark H3me3K27 decrease at the TRIM13 promoter, whereas in the absence of HBx both EZH2 binding and H3me3K27 increase (online supplementary figure S8f).
Figure 5 DLEU2 and enhancer of zeste homolog 2 (EZH2) coregulated HBx direct target gene expression in human HBV-related hepatocellular carcinoma (HCC). (A) DLEU2 and EZH2 expression data from TCGA in non-tumour (NT) and in tumour human liver tissues (T) from 76 HBV-related patients with HCC. (B) Venn diagram showing the intersection of genes whose expression is positively correlated with DLEU2 or EZH2 in 76 HBV-related HCCs from the transcriptomic TCGA-LIHC dataset accessed via the R2 platform (https://r2.amc.nl) with the genes identified as HBx direct targets by chromatin immunoprecipitation sequencing (ChIP-Seq). (C) TRIM13, CCNB2, DNMT1, PRC1, POLE2 and ZBTB34 mRNA levels in NT and T human liver tissues from HBV-related patients with HCC (transcriptomic data from TCGA, HBV-related HCCs=76).

Altogether, these results suggest that HBx and DLEU2 cooperate to activate transcription from a subset of cellular genes, including genes that are negatively regulated by EZH2/PRC2 in non-infected cells and activated in HBV-infected cells as well as HBV-related HCCs.

CONCLUSIONS

HBx, whose primary role in the HBV life cycle is to bind the nuclear cccDNA minichromosome in order to initiate and maintain viral transcription and drive HBV replication,10 11 45 also binds a large number of target sequences on the cellular genome.12 20 HBx interacts with multiple transcription factors, coregulators and chromatin modifying complexes15 50 in order to modulate the transcription of host genes. Here, we show that HBx binds the promoter region of DLEU2, enhances DLEU2 transcription and induces the accumulation of DLEU2 RNA species in infected hepatocytes. We showed by RIP experiments that DLEU2 binds both EZH2, the catalytic subunit of the PRC2 chromatin complex, in liver cells and HBx in HBV-infected hepatocytes. These results highlight a novel capacity of HBx to bind ncRNAs and prompt us to investigate the role of these interactions in the transcriptional regulation of cccDNA and HBx host target genes. cccDNA ChIP and functional experiments with DLEU2-specific Gapmers supported the role of DLEU2 recruitment in the regulation of cccDNA transcription. HBx interaction with DLEU2 on the cccDNA may represent a novel therapeutic target to silence cccDNA transcription and foster a functional cure of HBV infection.

To gain mechanistic insights on how DLEU2 and HBx cooperate in the transcriptional regulation of host genes, and the role of the EZH2/PRC2 complex in this process, we focused on TRIM13 and CCNB2 as examples of genes targeted by DLEU2 in cis and in trans, respectively. Notably, TRIM13 and CCNB2 are part of a subset of six genes coregulated with DLEU2 or EZH2 in HBV-related patients with HCC and identified as direct HBx targets in ChIP-Seq experiments.12 The contribution of PRC2-mediated deposition of the H3K27me3 repressive chromatin mark to the epigenetic silencing during embryonic development and differentiation51 and the impact of its dysregulation in cancer52 are well established, although...
the epigenetic control of host genes and provide a new key to understand the role of HBx, and the overexpression of DLEU2 and EZH2 in HBV-related HCCs.

**EXPERIMENTAL PROCEDURES**

Materials and methods are described in the online supplementary information. Primer pairs and probes used throughout the manuscript are listed in online supplementary table 8.

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**Contributors**

DS and LC share co-first authorship. FG and ML conceived and designed the study. FG supervised the study. DS, VA, OF, AP, M-LP, MZ, SJ, LB and FG performed experiments and analysed data. LC and GC conducted computational analysis. M-LP performed bioinformatic analysis. LC, ML and FG wrote the manuscript.

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**Competing interests**

None declared.

**Patient consent for publication**

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**Data availability statement**

The transcriptomic data used to generate the Venn diagram in Figure 5B (‘genes whose expression is positively correlated with DLEU2 or EZH2’) can be accessed on the TCGA-LIHC dataset and extracted using the R2 platform (https://r2.amc.nl) with the function ‘Find correlated Genes with a Single P’. The ChiP-Seq dataset used in Figure 5B (‘genes identified as HBX direct genes’; listed in online supplementary table B) can be accessed at http://www. ebi.ac.uk/ena/data/view/PRJEB13227. All other raw data, materials and reagents are available on request from the corresponding authors (FG and ML).

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