Temporal and Tight Hepatitis C Virus Gene Activation in Cultured Human Hepatoma Cells Mediated by a Cell-Permeable Cre Recombinase

Dong XIAO*, Kang XU1, Ying YUE, Zhong-Min GUO, Bing HUANG, Xin-Yan DENG, Huan TANG2, and Xi-Gu CHEN*

Center of Experimental Animals, Zhongshan University, Guangzhou 510080, China;  
1The first affiliated hospital of Sun Yat-sen University, Zhongshan University, Guangzhou 510080, China;  
2The Third Military Medical University, Chongqing 400010, China

Abstract  Conditional gene expression has greatly facilitated the examination of the functions of particular gene products. Using the Cre/lox P switching expression system, we plan to develop efficient conditional transgene activation of hepatitis C virus core protein (HCV-C) cDNA (nucleotide 342–914) in the transgenic mice to overcome “immune tolerance” formed during the embryonic period and “immune escape” against hepatitis virus antigen in our project. To use this system in vivo, the dormant transgenic construct, i.e., pApoE-SCS-EGFP-HCV-C, was generated using techniques of standard molecular biology. The liver-specific human apoE promoter was here used to target expression of genes of interest (EGFP and HCV-C) to murine liver. Prior to generating the transgenic mice, the availability of Cre/lox P system and construct functionality were successfully verified by a cell-free recombination system and via checking the expression of EGFP and HCV-C in the human hepatoma cells at the mRNA and protein levels. These results suggest that the Cre/lox P system could tightly control expression of EGFP and HCV-C in vitro, which laid a solid foundation to conditionally activate expression of target gene(s) in transgenic mice by Cre-mediated site-specific recombination.

Key words  hepatitis C virus; Cre/lox P switching expression system; cell-free and intracellular recombination systems; cell-permeable Cre recombinase; EGFP; human hepatoma cells

Hepatitis C virus (HCV) is not infectious in vivo except for primates, so the proper HCV culture system and inbred animal model are difficult to set up, which has hampered detailed analysis on viral life cycle and pathogenesis of HCV infection [1,2]. Hepatitis B virus (HBV) and HCV transgenic mouse models have been created by micro-injecting the full or selected parts of the virus genome into the fertilized eggs of inbred immunodeficient mice to provide new insights into the pathogenesis of hepatitis and hepatocellular carcinoma (HCC) [3–6]. A disadvantage of the transgenic animals produced by the consistent gene expression system is that they aren’t immunocompetent for the transgene products. Therefore, the immune system of newborn transgenic mice can’t recognize the exotic identity of viral antigens. However, in human chronic hepatitis C, hepatocyte injury is not directly caused by HCV infection, but is a consequence of the destruction of infected hepatocytes by cytotoxic lymphocytes [7]. In these HCV transgenic mice, the antigen genes express normally, but little pathological changes are observed in the liver and the serum alanine aminotransferase levels keep unchanged, indirectly suggesting that the immune system plays a rather important role in hepatitis pathogenesis [3–6].

Recently, a development in transgene technology is the control of tissue/organ-specific target gene expression at particular developmental stage, to mimic HBV or HCV infection in immunocompetent transgenic mice like that in human. Two systems successfully and frequently employed are tetracycline-inducible system (tet-off system or tet-on system) and Cre/lox P site-specific recombinase system [8–10]. The tetracycline-inducible expression system is
not very tight in controlling [8,9,11]. Chisari’s lab has pro-
duced transgenic mice expressing HBV envelope protein
or HCV core protein (HCV-C) by using the tet-off system.
The results showed that the transgene expression was
undetectable in utero or early life, but the transgene mice
were tolerant to HBV envelope protein or HCV-C immuni-
(Chisari, 2003, personal communication), which
might be caused by the leakiness. New variants of the
tetracycline-based regulatory elements that can minimize
or eliminate leaky transgene expression have been tested
successfully in vitro, but approaches that can be used to
eliminate basal transgene leak in vivo have not been well

The Cre-mediated gene in vivo and in vitro conditional
activation/inactivation have been widely employed in the
different research fields [12,13] and the general strategy
is fully demonstrated in Fig. 1(B). In conjunction with the
inducible system controlling Cre expression [8–10], the
administration of the cell-permeable Cre protein [14–16]
or Cre-expressing adenovirus vector [12], the Cre/lox
switching expression system is a true “off/on” system.
The “off/on” nature of this regulation will be very useful
to express hepatitis virus antigen genes in a temporally
restricted fashion and precisely define the immunological
reactions against antigens and pathogenesis of HCV
infection. Wakita et al. [17–19] used the Cre/lox P system
to efficiently conditionally express the core, E1 and E2
protein genes in transgenic mice, which provided useful
animal models for investigating host immune response and
pathogenesis of HCV infection.

Spatially and temporally expressing HCV-C gene in
immunocompetent transgenic mice can be mediated by
Cre/lox P system, so that the host immune response against
HCV infection and pathogenesis of HCV infection can be
fully and precisely elucidated.

In the present study, the dormant transgene vector was
generated, followed by in vitro identifying Cre/lox P
system for availability and construct for functionality.

Materials and Methods

Materials

Human hepatoma cell line BEL-7402 was from Cell
Bank, Center of Experimental Animals, Sun Yat-sen
University. Lipofectamine™ 2000, RPMI 1640 medium,
fetal bovine serum (FBS), 0.25% trypsin solution, HEPES,

![Fig. 1 Experimental design](https://academic.oup.com/abbs/article-abstract/36/10/687/94)
dimethyl sulfoxide (DMSO), culture flask and plate were supplied by Gibco BRL (Life Technologies Inc.). Other chemicals and materials were of analytical grade obtained from commercial sources.

The pLiv.7 vector [20] containing a 3.0 kb human apolipoprotein E (apoE) gene promoter for expression of the liver-specific gene was used to clone HCV-C genomic region. The plasmid pMA-HCV [21] containing complete coding sequence of HCV type 2b gene for polyprotein region. The plasmid pApoE-HCV [21] containing complete apoE gene promoter for expression of transgene construct [Fig. 1(A)] containing enhanced green fluorescent protein (EGFP) and HCV-C gene under the control of the liver-specific apoE promoter was constructed as described in Sambrook et al. [23].

pApoE-HCV-C  HCV-C cDNA (position 342–914) was amplified from pMA-HCV with primer HCV-C-FP/HCV-C-RP, and inserted into the T-vector of pMD18-T (TaKaRa) to construct pMD18-T-HCV-C. The PCR reaction was set up for 7 min at 94 °C, followed by 30 cycles of 45 s at 94 °C, 45 s at 58 °C, 1 min at 72 °C, and a final cycle of 7 min at 72 °C.

Forward primer HCV-C-FP: 5'-CGGAACCGGATATGAGC-ACAAATCCTAAACCTC-3' (MluI site underlined)
Reverse primer HCV-C-RP: 5'-ATGACTCGAGCTATGA-AGACACTGGCAGCTTAC-3' (Xhol site underlined, and stop codon double-underlined)

HCV-C fragment (573 bp) was recovered from pMD18-T-HCV-C by digestion with MluI and XhoI, and directionally subcloned into the MluI and Xhol sites in the polylinker (5'‐KpnI‐MunI‐Hpal‐MluI‐Clal‐Xhol‐3') of pLiv.7 (9.3 kb) to create pApoE-HCV-C, as verified by restriction enzyme digestion.

pApoE-EGFP-HCV-C  To generate the plasmid containing EGFP reporter gene, 742 bp EGFP gene segment was excised from pBl-EGFP (Clontech) by digestion with EcoRV and SpeI, blunt ended at the SpeI site, and subsequently subcloned into pApoE-HCV-C at the dephosphorylated Hpal site, designated pApoE-EGFP-HCV-C. The orientation of EGFP fragment inserted in the frame was identified with EcoRI.

pApoE-SCS-EGFP-HCV-C  For conditional expression of HCV-C in vitro and in vivo mediated by the Cre/loxP system, an expression vector with SCS between the promoter and the target coding sequence was generated. SCS fragment (about 1.487 kb) was amplified by PCR with primer SCS-FP/SCS-RP using pBS302 as template, and cloned into pMD18-T to give pMD18-T-SCS. PCR reactions involved 30 cycles of denaturation for 45 s at 94 °C, annealing for 45 s at 62 °C, and extension for 2 min at 72 °C.

Forward primer SCS-FP: 5'-GCACGAATTCTCAAGC-TTAGGATCCG-3' (EcoRI site underlined)
Reverse primer SCS-RP: 5'-ATTAGGTAACCAGTGA-CCTCTTGGAGG-3' (KpnI site underlined)

The KpnI-EcoRI SCS fragment released from pMD18-T-SCS was orientatively subcloned into KpnI and MunI sites of pApoE-EGFP-HCV-C to prepare pApoE-SCS-EGFP-HCV-C. This complete sequence of the dormant transgene was further verified by sequencing.

Identification of lox P sites in the vector by Cre-mediated in vitro recombination

The pApoE-SCS-EGFP-HCV-C was digested with Cre protein (Novagen) in vitro, followed by plasmid DNA transformation, restriction enzyme digestion and PCR to confirm lox P site sequence. Cre digestion on pApoE-SCS-EGFP-HCV-C was carried out according to the manufacturer’s instructions.

Intracellular confirmation for recombination system

Cell transfection  BEL-7402 cells were transiently transfected with plasmids mentioned in Fig. 4 to further test the function of pApoE-SCS-EGFP-HCV-C at cell level. The cell culture and transient transfection were performed as previously reported [24].

BEL-7402 cells were cultured in RPMI 1640 supplemented with 10% heat-inactivated FBS, 10 mM HEPES, 2 mM L-glutamine (Sigma), 100 U/ml penicillin (Sigma), and 100 mg/ml streptomycin (Sigma), refreshed 2–3 times per week and passed when being confluent. The cells were kept at 5% CO₂ in a humidified 37 °C incubator. The day before transfection, BEL-7402 cells were added into 6-well culture plate, and transiently transfected with the corresponding plasmid (Fig. 4) according to the liposome-mediated transfection method using Lipofectamine™ 2000 once cells reached 50%–80% confluency. 6–10 h after transfection, transfecting solution was replaced with the complete medium. In pApoE-SCS-EGFP-HCV-C+Cre transfecting group, the complete medium and 10 μM His₆-NLS-Cre-MTS (recombinant cell-permeable
Cre protein) [14] were together added into the corresponding well after discarding the transfecting solution. The transfection experiment was repeated three times with 1 µg, 5 µg and 10 µg of each corresponding plasmid being employed, respectively. In addition, all the plasmids used for transfection were purified using EndoFree plasmid maxi kit (Qiagen) and non-linearized.

**EGFP assay** 48–96 h after transfection, cells were screened for the EGFP expression under fluorescence microscopy (excitation 450–490 nm).

**Analysis of RNA using RT-PCR** After activation of target genes, the HCV-C RNA level in BEL-7402 cells was examined by RT-PCR. RNA was isolated using the RNeasy mini kit (Qiagen) following the manufacturer’s recommendations. Isolated RNA was fully treated with amplification grade RNase free DNase (Promega) at 37 °C for 30 min to remove any contaminating DNA, and then heated at 72 °C for 30 min to inactivate the DNase. A specific system for the amplification of HCV-C mRNA used was One-step mRNA selective RT-PCR kit (Ver. 1.1, TaRaKa). RT-PCR was carried out as recommended by the manufacturer with primer pairs HCV-C-FP/RP (PCR product size: about 573 bp). RT-PCR amplification was carried out: 30 min at 50 °C for RT, denaturation for 5 min at 85 °C; then a succession of 35 cycles as follows, 1 min at 85 °C, 1 min at 58 °C, 60 s at 72 °C; a final extension at 72 °C for 10 min. Human β-actin gene was used as an internal standard with following primers (product size being 758 bp):

- Sense primer: 5'-GATATCGCTGCGCTGGTCGT-3'  
- Antisense primer: 5'-CGGAACCGCTCGTTGCCAAT-3'

For β-actin mRNA, one-step RT-PCR was carried out: 30 min at 50 °C for RT; and then a succession of 30 cycles as follows, 85 °C for 1 min, 62 °C for 1 min, and 72 °C for 1 min. All experiments were performed in triplicate.

**Western blot analysis of HCV-C expression** After activation of target genes, HCV-C expression in BEL-7402 cells was also tested by Western blot. Cell lysates were prepared and 100 µg of crude protein was processed for Western blot analysis as Sambrook et al. [23] described. Western blot was performed with monoclonal anti-HCV-C (1:25, Bidesign International) as primary antibody and Horseradish peroxidase-conjugated goat anti-mouse IgG (1:2000, Amersham) as secondary antibody. Hybridization reaction was developed with enhanced chemiluminescence (ECL, Amersham) following the manufacturer’s instructions.

**Results**

**Construction of pApoE-SCS-EGFP-HCV-C**

**pApoE-HCV-C** HCV-C was amplified by PCR, and inserted into pMD18-T to prepare pMD18-T-HCV-C and confirmed by sequencing. After that, the 573 bp HCV-C cDNA was excised, isolated, purified, and subsequently directionally subcloned into the MluI and XhoI sites of pLiv.7 (8.3 kb) linearized with MluI and XhoI to give pApoE-HCV-C (8.873 kb), as confirmed by enzyme digestion (Fig. 2).

**pApoE-EGFP-HCV-C** The 742 bp EGFP segment was excised from pBI-EGFP with EcoRV and SpeI and blunted at SpeI site, and cloned into the dephosphorylated HpaI site of pApoE-HCV-C to obtain pApoE-EGFP-HCV-C (9.613 kb), which was verified by enzyme digestion.
(Fig. 2). The orientation of EGFP insert in the frame was identified by EcoRI digestion. The positive recombinant showed 8.742 kb and 0.826 kb bands (Fig. 2), while the inverted recombinant generated two fragments of 8 kb and 1.568 kb after EcoRI digestion (data not shown).

pApoE-SCS-EGFP-HCV-C. The 1.487 kb SCS amplified by PCR was cloned into the pMD18-T to give pMD18-T-SCS, and confirmed by sequencing. SCS fragment with KpnI-EcoRI site, released from pMD18-T-SCS, was targetedly subcloned into the KpnI and MunI sites of pApoE-EGFP-HCV-C to produce the final desired plasmid pApoE-SCS-EGFP-HCV-C (11.1 kb). The desired resulting pApoE-SCS-EGFP-HCV-C digested by KpnI showed a 11.1 kb band, while cut by HindIII produced 1.56 kb and 9.48 kb bands (Fig. 2). The 1.56 kb, 1.4 kb and 8 kb fragments were excised from the resultant pApoE-SCS-EGFP-HCV-C through double enzyme digestion of KpnI and HindIII (Fig. 2).

Consequently the genes of interest, such as SCS flanked by directly repeated lox P sequences, EGFP and HCV-C, were successively positioned downstream of apoE promoter/intron and upstream of the apoE polyadenylation sequences/liver element to prepare the desired construct pApoE-SCS-EGFP-HCV-C [Fig. 1(A)].

Confirmation of lox P site sequences in the vector

In pApoE-SCS-EGFP-HCV-C, SCS was flanked by two lox P sites (Fig. 1). The recombination event in vitro mediated by Cre between two lox P sites will lead to the excision of the lox P-flanked (“floxed”) intervening DNA sequence to create the resulting plasmid pApoE-lox P-EGFP-HCV-C. Under conditions used in this study, 1.487 kb of the intervening sequence between lox P sites was amplified efficiently by PCR using pApoE-SCS-EGFP-HCV-C as template, whereas actually Cre mediated recombination theoretically allowed amplification of an 84 bp PCR product that could not observed on the electrophoresis map (Fig. 3). That Cre could excise efficiently STOP cassette between two lox P sites from pApoE-SCS-EGFP-HCV-C was verified by enzyme digestion analysis (Fig. 3).

Cell-permeable Cre-mediated conditional expression in the cultured cell

In negative control I and II experiments [Fig. 4(A): a,b], the control cells had no background under fluorescence microscopy phase, as well as under phase contrast microscopy (data not shown). That EGFP fluorescence was observed 48 h after transfection in BEL-7402 cells transfected with pApoE-EGFP-HCV-C [Fig. 4(A): d] and pApoE-lox P-EGFP-HCV-C [Fig. 4(A): e] confirmed the construct (e.g. pApoE-EGFP-HCV-C) for functionality and that EGFP could express normally in the presence of one lox P site in the frame. In the absence of Cre, no background expression of EGFP could be detected in BEL-7402 cells transfected with pApoE-SCS-EGFP-HCV-C [Fig. 4(A): c], due to the strong transcriptional stop sequence inserted between the promoter and the coding sequences. However, when the cell-permeable Cre proteins (final conc: 10 µM) were added into the well containing BEL-7402 cells transfected with pApoE-SCS-EGFP-HCV-C [Fig. 4(A): f], indicating efficient excision of the floxed
Fig. 4 Assay for the cell-permeable Cre-mediated DNA recombination in the cell level

(A) EGFP assay under fluorescence microscopy. (B) Checking Cre-mediated activation of HCV-C expression in the mRNA level. β-actin was used as an internal. The molecular weight of HCV-C and β-actin was 573 bp and 758 bp, respectively. (C) Western blot analysis of Cre-mediated HCV-C expression in BEL-7402 cells. M1, DL2000 DNA marker; PC, cells transfected with pApoE-SCS-EGFP-HCV-C expressing HCV-C; a, untransfected cells; b, cells transfected with pLiv.7; c, cells transfected with pApoE-EGFP-HCV-C; d, cells transfected with pApoE-lox P-EGFP-HCV-C resulted from pApoE-SCS-EGFP-HCV-C cut in vitro by Cre; e, cells transfected with pApoE-SCS-EGFP-HCV-C; f, 7402 cells transfected with pApoE-SCS-EGFP-HCV-C with the addition of Cre.
stop sequence. Moreover, HCV-C activation expression further confirmed the availability of Cre/loxP system and construct functionality [Fig. 4(B,C)].

Taken together, these data demonstrate the tight and conditional regulation of EGFP and HCV-C expression mediated by the Cre/loxP switching expression system in the cell.

Discussion

Since the harmful transgene product will behave as a self-antigen inducing negative selection of reactive T cells in the thymus, immunologic response can only be studied through a system by which the transgene will be expressed in the transgenic animal only when being induced at desired time points [8–10]. The Cre-mediated conditional expression system developed recently can dissolve this problem [17–19]. The Cre/loxP conditional transgene activation system stringently controlling HCV-C transgene expression in vivo and in vitro was well elucidated in Fig. 1(B). In this system, the lox P² STOP cassette must locate between the desired promoter and target gene/reporter gene to give the dormant transgenic construct. Transgenic mice carrying the dormant transgene can mate Cre transgenic mice to generate bi-transgenic mice, in which Cre could be inducibly expressed to evict the STOP sequence to activate the dormant transgene. Transgenic mice carrying the dormant transgene can also be administered with cell-permeable Cre protein or Cre-expressing virus vectors by intravenous injection to induce Cre-mediated recombination.

A critical issue in using the lox P² STOP strategy is that after recombination the remaining lox P site must not interfere with expression of the target transgene [13]. Because lox P contains two ATG translational start codons in one orientation, but not in the other, as verified by sequencing, it is important that the lox P² STOP cassette be properly oriented (Fig. 2) so that there remains no false ATG codon that could interfere with downstream transgene expression after recombination [13,25]. Generally speaking, Cre-mediated activation system can tightly control the expression of dormant transgenes [12,13].

The tissue specific expression of the recombinationally activated dormant transgene is regulated by the promoter specificity of the target transgene and Cre transgene. In this study, Cre-mediated excision was realized by the intravenous injection of cell-permeable Cre protein or Cre-expressing virus vectors. The liver-specific apoE promoter system was employed to target the expression of the viral proteins to the physiologically relevant site of hepatocyte after activated. Actually, when the target gene(s) is/are placed downstream of the human apoE promoter, and upstream of the apoE polyadenylation sequence [Fig. 1(A)], the high expression of target gene can be ensured [20,26–28].

The non-invasive visualization is the key for GFP to be able to monitor physiological and biochemical processes in vitro, in vivo and in real time [29]. In this study, EGFP gene served as a reporter gene to conveniently monitor the in vitro function of Cre/loxP system and the apoE promoter.

In summary, we conclude that the Cre/loxP switching expression system is able to successfully and stringently control the expression of the dormant transgene EGFP and HCV-C in the cultured human hepatoma cells, which lays a solid foundation for efficient and conditional HCV-C gene activation in transgenic mice by Cre-mediated site-specific recombination.

Acknowledgements

We thank Dr. Chun-Yang FAN (Department of Pathology and Otolaryngology, University of Arkansas for Medical Sciences, USA), Dr. Akio Nomoto (Department of Microbiology, Graduate School of Medicine, The University of Tokyo, Japan), Dr. Brian Sauer (Stowers Institute for Medical Research, Kansas City, USA), Dr. H. Earl Ruley (Department of Microbiology and Immunology, Vanderbilt University School of Medicine, USA), and Dr. Tong-Gong DU (Cornell University, USA) for generously providing plasmid pLiv.7, pMA-HCV, pBS302 and pBS185, pDJHisCre, pBI-EGFP, respectively. We are also indebted to the expert technical assistance of Han JY, Hong X, Zhong LQ, Ma Y, Zhang HH, Qiu GG, Guo FF, Huang WG, Chen FY, Ni FR, Xie JY, Wang JH (Center of Experimental Animals, Zhongshan University), and other members in our lab.

References

4 Feitelson MA, Larkin JD. New animal models of hepatitis B and C. ILAR J,

Milich DR. Transgenic technology and the study of hepatitis viruses: A review of what we have learned. Can J Gastroenterol, 2000, 14(9): 781–787


Downloaded from https://academic.oup.com/abbs/article-abstract/36/10/687/94 by guest on 08 November 2018