Cell Culture Systems for Hepatitis C Virus

Eike Steinmann and Thomas Pietschmann

Abstract Due to the obligatory intracellular lifestyle of viruses, cell culture systems for efficient viral propagation are crucial to obtain a detailed understanding of the virus–host cell interaction. For hepatitis C virus (HCV) the development of permissive and authentic culture models continues to be a challenging task. The first efforts to culture HCV had limited success and range back to before the virus was molecularly cloned in 1989. Since then several major breakthroughs have gradually overcome limitations in culturing the virus and sequentially permitted analysis of viral RNA replication, cell entry, and ultimately the complete replication cycle in cultured cells in 2005. Until today, basic and applied HCV research greatly benefit from these tremendous efforts which spurred multiple complementary cell-based model systems for distinct steps of the HCV replication cycle. When used in combination they now permit deep insights into the fascinating biology of HCV and its interplay with the host cell. In fact, drug development has been much facilitated and our understanding of the molecular determinants of HCV replication has grown in parallel to these advances. Building on this groundwork and further refining our cellular models to better mimic the architecture, polarization and differentiation of natural hepatocytes should reveal novel unique aspects of HCV replication. Ultimately, models to culture primary HCV isolates across all genotypes may teach us important new lessons about viral functional adaptations that have evolved in exchange with its human host and that may explain the variable natural course of hepatitis C.

Abbreviations

BMEC	Brain microvascular endothelial cells
CNS	Central nervous system
Con1	Consensus genome 1
DAA	Direct acting antiviral

E. Steinmann · T. Pietschmann (✉)
Division of Experimental Virology, TWINCORE, Centre for Experimental and Clinical Infection Research; a joint venture between the Medical School Hannover (MHH) and the Helmholtz Centre for Infection Research (HZI), Hannover, Germany
e-mail: pietschmann.thomas@mh-hannover.de

R. Bartenschlager (ed.), *Hepatitis C Virus: From Molecular Virology to Antiviral Therapy*, Current Topics in Microbiology and Immunology 369,
DOI: 10.1007/978-3-642-27340-7_2,

DC-SIGN	Dendritic cell-specific intracellular adhesion molecule-3-grabbing non-integrin
EGFR	Epidermal growth factor receptor
EMCV	Encephalomyocarditis virus
EphA2	Ephrin receptor A2
GFP	Green fluorescent protein
HCV	Hepatitis C virus
HCV_{TCP}	Hepatitis C virus trans-complemented particles
HBV	Hepatitis B virus
HIV	Human immunodeficiency virus
iPSC	Induced pluripotent stem cells
IRES	Internal ribosomal entry site
JFH1	Japanese fulminant hepatitis
LDL-R	Low-density lipoprotein receptor
MEF	Mouse embryonic fibroblasts
MPCC	Micropattern co-cultures
mL	Milliliter
MLV	Murine leukemia virus
NPC1L1	Niemann-Pick C1-like cholesterol adsorption receptor
PBMC	Peripheral blood mononuclear cells
PHH	Primary human hepatocytes
REM	Replication enhancing mutations
RIG-I	Retinoic acid-inducible gene I
SEAP	Secreted embryonic alkaline phosphatase
siRNA	small interfering RNAs
$TCID_{50}$	Tissue culture infectious dose 50
VSV	Vesicular stomatitis virus

Contents

1 Introduction

When HCV, the causative agent of hepatitis C, was first cloned in 1989 many attempts to culture the elusive infectious agent in vitro had already failed. These efforts were a prelude to the hurdles ahead to push the doors open for model systems fully permissive to cell culture replication of HCV. Some of these early limitations, like for instance the inefficient replication of primary HCV isolates, prevail until today. However, during the past decades several breakthrough developments have much improved our repertoire to study this virus in vitro. In fact, our increasing knowledge of molecular replication mechanisms may help to overcome the remaining roadblocks that prevent us from analyzing the complex interplay of HCV with its host cells in a yet further refined fashion.

The development of HCV-permissive cell culture models was a step-wise process. The establishment of subgenomic replicons that autonomously amplify in cultured human hepatoma cells was a first major breakthrough. Another important achievement was the generation of infectious retroviral pseudotypes displaying functional HCV glycoproteins for the study of HCV entry. Finally, the identification of a novel HCV isolate, termed JFH1, paved the way for the production of infectious virions to investigate all steps of the viral life cycle. Recently, remarkable advances were also made with regard to measuring HCV infection and replication in primary cell cultures. In this chapter, we will highlight essential components of HCV cell culture models and provide an overview of viral adaptation to replication in cell culture. In addition, we attempt to provide a perspective on future developments that may help to unravel new features of the HCV host cell interaction.

Historically, three key achievements build the foundation of the most widely used HCV tissue culture systems. Besides these models described below in greater detail, during the past years a variety of additional cell-based systems to monitor HCV cell entry and receptor interactions have been reported. The interested reader is referred to a recent review for a detailed description of these systems (Vieyres and Pietschmann 2012). Details on the HCV entry pathway are reviewed in the chapter "Hepatitis C Virus Entry" by Zeisel et al., this volume.

2 HCV Replicon System

During the 1990s, numerous attempts were made to initiate robust HCV infection and replication in cultured cells after inoculation with patient sera or transfection with cloned viral RNA. Although in the past long-term productive HCV replication was reported, these experimental systems suffered from low replication efficiency (Bartenschlager and Lohmann 2000). Highly sensitive, but also error-prone techniques, like RT-PCR were necessary to document HCV replication and only small amounts of viral proteins or infectious virus were produced precluding molecular dissection of HCV replication mechanisms. In fact, until today replication of the vast majority of cloned HCV genomes is poor in cultured cells (see also below Sect. 4).

Encouraged by reports that subgenomic RNA molecules of other plus strand RNA viruses readily replicate in transfected cells (Khromykh and Westaway 1997; Mittelholzer et al. 1997), similar approaches were attempted for HCV. By trimming the HCV genome to those components essential for RNA replication (see chapter "Hepatitis C Virus RNA Replication" by Lohmann, this volume), so-called replicons were created (Lohmann et al. 1999). Due to deletion of viral structural genes (core, envelope 1 and 2), p7 and NS2 these RNA molecules were much smaller than the authentic viral genome. This provided the freedom to insert a heterologous dominant selectable marker (e.g., neomycin phosphotransferase, neo) without exceeding the natural length of the HCV genome. The prototype replicon was a bicistronic RNA of genotype 1b (Con1 isolate) encoding a neomycin resistance gene under the control of the HCV internal ribosomal entry site (IRES), followed by a second IRES from encephalomyocarditis virus (EMCV) that controlled expression of the genes for NS3-NS5B. Upon transfection of synthetic RNAs derived from such a construct into the human hepatoma cell line Huh-7 and G418 selection, cell lines containing high amounts of self-replicating HCV RNAs could be obtained (Lohmann et al. 1999). Based on quantification by Northern hybridization, an average copy number of 1,000–5,000 positive-strand RNA molecules per cell was determined. Minus-strand RNA was present in about tenfold lower amounts in comparison with plus-strand RNA and HCV protein expression was readily detected by metabolic radiolabeling and immunoprecipitation (Lohmann et al. 1999). Replicon cell clones continuously passaged under selective pressure maintain the viral RNA for many years. After the introduction of the replicon system in 1999 this cell culture system has been widely applied in HCV research. During the following years an increasing number of replicon constructs with varying reporter genes including luciferases and fluorescent proteins were developed to tailor the system to the needs of the researcher and to facilitate exploration of the mechanisms of HCV RNA replication. A detailed summary of replicon constructs currently in use was compiled by Bartenschlager et al. (2006). While initially replicons were developed for the genotype 1b (GT1b) consensus genome Con1 (Lohmann et al. 1999), meanwhile replicons are available for GT1a, various GT1b isolates, GT2a and GT4a strains (Table 1), thus increasing the versatility of this important model tremendously.

2.1 Replication Enhancing Mutations

The HCV RNA-dependent RNA polymerase NS5B lacks a proof-reading activity and as observed for many other viruses HCV replicates with a high mutation rate (see chapter "Hepatitis C Virus RNA Replication" by Lohmann, this volume). Initially, genotype 1b replicons showed a low G418 transduction efficiency despite high level of RNA replication within the surviving cell clones. It turned out that the reason for this was twofold. First, during the selection procedure replicons acquired so-called replication enhancing mutations (REMs) permitting more efficient RNA replication in transfected Huh-7 cells. Second, the selection process

Table 1 Molecular HCV clones

Strain	Genotype	Replicon		HCVcc	
		Wild type	Adapted	Wild type	Chimeric/adapted
H77	1a	–	Blight et al. (2003), Grobler et al. (2003), Tscherne et al. (2006)	–	Pietschmann et al. (2006), McMullan et al. (2007)
H77C	1a	–	Yi et al. (2004)	–	Russell et al. (2009), Yi et al. (2007), Scheel et al. (2008), Yi et al. (2006)
HCV-1	1a	–	Lanford et al. (2006)	–	–
Con1	1b	Lohmann et al. (1999)	Blight et al. 2000), Guo et al. (2001), Krieger et al. (2001), Lohman et al. (2003)	Pietschmann et al. (2009)	Gottwein et al. (2009), Kaul et al. (2007), Pietschmann et al. (2006)
HCV-N	1b	Guo et al. (2001), Ikeda et al. (2002), Yi et al. (2002)	–	–	–
HCV-BK	1b	–	Grobler et al. (2003)	–	–
HC-J4	1b	–	Maekawa et al. (2004)	–	–
O	1b	–	Abe et al. (2007), Ikeda et al. (2005), Kato et al. (2003a)	–	
AH1	1b	–	Mori et al. (2008)	–	–
NC1	1b	–	Date et al. (2012)	–	Date et al. (2012)
BHCV1	1b	–	–	–	Koutsoudakis et al. (2011)
JFH1	2a	Kato et al. (2003b)	–	Wakita et al. (2005), Zhong et al. (2005)	Delgrange et al. (2007), Kang et al. (2009), Kaul et al. (2007), Russell et al. (2008), Zhong et al. (2006)

(continued)

Table 1 (continued)

Strain	Genotype	Replicon		HCVcc	
		Wild type	Adapted	Wild type	Chimeric/adapted
J6/JFHI, Jc1	2a	–	–	Lindenbach et al. (2005), Pietschmann et al. (2006)	Bungyoku et al. (2009)
HC-J8	2b	–	–	–	Gottwein et al. (2007)
S52	3a	–	–	–	Gottwein et al. (2007), Gottwein et al. (2009)
452	3a	–	–	–	Kaul et al. (2007), Pietschmann et al. (2006)
ED43	4a	Peng et al. (2012)	Peng et al. (2012)	–	Scheel et al. (2008)
SA13	5a	–	–	–	Gottwein et al. (2007), Jensen et al. (2008)
HK6a	6a	–	–	–	Gottwein et al. (2007)
QC69	7a	–	–	–	Gottwein et al. (2007)

enriched for those few host cells in the total population of transfected cells that were more permissive to HCV replication than "standard" Huh-7 cells. Evidence for this second mechanism was elegantly provided by transfection of replicons into individual Huh-7 clones that had been obtained after transfection and selection with selectable replicons and subsequent purging of the replicon by inhibitor or IFN-treatment (Blight et al. 2002; Friebe et al. 2005). In fact, the most widely used host cells for HCV research—Huh-7.5, Huh-7.5.1, and Huh7-Lunet—were all obtained by this strategy (Blight et al. 2002; Friebe et al. 2005; Zhong et al. 2005).

While for most of these highly permissive cells it remains elusive why they are so amenable for HCV replication, viral adaptation permitting increased replication has been linked to distinct mutations within individual non-structural proteins. These mutations have originally been designated 'cell culture adaptive mutations', but should be renamed as 'replication enhancing mutations' (REMs) in order to discriminate them from cell culture adaptive mutations that increase virus titers without affecting replication (Pietschmann et al. 2009). Sequence analysis of replicons within selected cell clones identified numerous conserved changes within the coding region of the viral non-structural proteins. Introduction of these mutations back into the parental genome and transfection of in vitro transcribed RNA revealed an enhancement of RNA replication to various degrees as determined by the number of G418-resistant colonies (Blight et al. 2000; Guo et al. 2001; Lohmann et al. 2001; Ikeda et al. 2002; Kishine et al. 2002; Grobler et al. 2003; Gu et al. 2003; Kato et al. 2003a; Lohmann et al. 2003).

REMs were mainly located in the N-terminus of NS3, at two distinct amino acids in NS4B and in the central domain of NS5A. Several of the most potent REMs in NS5A change phosphorylation sites within the protein suggesting that replication efficiency may be regulated via phosphorylation. Interestingly, Evans et al. (2004) observed an interaction between HCV NS5A and human vesicle-associated membrane protein-associated protein A (hVAP-A) which is modulated by NS5A phosphorylation. Their findings support a model where NS5A hyperphosphorylation disrupts the interaction with h-VAP-A which negatively regulates viral RNA replication (Evans et al. 2004). With the generation of replicons from other HCV isolates it could be shown that Con1 adaptive mutations also enhanced replication efficiency of other genotype 1b strains, including HCV-O (Kato et al. 2003a; Ikeda et al. 2005; Abe et al. 2007), HCV-BK (Grobler et al. 2003), J4 (Maekawa et al. 2004) and AH1 (Mori et al. 2008). In case of the HCV N-isolate adaptive mutations were not required for efficient replication due to a unique four amino acid insertion naturally present in NS5A (Guo et al. 2001; Ikeda et al. 2002; Yi et al. 2002).

The establishment of genotype 1a replicons turned out to be more difficult as even the introduction of genotype 1b-specific mutations did not result in high levels of RNA replication (Blight et al. 2000; Guo et al. 2001; Lanford et al. 2003; Yi and Lemon 2004; Liang et al. 2005). However, with passage of genotype 1a replicon RNA in highly permissive cell lines REMs could be identified in NS3, NS4B, or NS5A (Blight et al. 2003; Grobler et al. 2003; Yi and Lemon 2004; Lanford et al. 2006). Generation of non-genotype 1 replicons have not been described so far except for a genotype 4a (Peng et al. 2012) and genotype 2a isolate that replicates with high efficiency without the requirement of adaptive mutations (Kato

et al. 2003b). The latter genome was cloned from a Japanese patient suffering a fulminant course of hepatitis and thus designated "Japanese fulminant hepatitis 1" (JFH1). This genome has become the basis of the most widely used HCV cell culture system which will be described in more detail below (see Sect. 4).

With the identifications of REMs further improvements of the original replicon system could be developed. These include alternative drug resistance genes (Frese et al. 2002; Evans et al. 2004; Appel et al. 2005; Liang et al. 2005), monocistronic replicons (Blight et al. 2003), and transient replication assays that are based on the detection of reporter genes like luciferase, ß-lactamase, green fluorescent protein (GFP), and secreted alkaline phosphatase (Krieger et al. 2001; Yi et al. 2002; Lohmann et al. 2003; Murray et al. 2003; Ikeda et al. 2005). The exact mode of action of cell culture REMs is still not fully understood. Generally, these mutations have not been observed in natural HCV isolates suggesting that the stimulatory effect on HCV RNA replication in vitro does not increase viral fitness in vivo. In fact, at least for Con1 evidence has been provided that REMs interfere with production of infection virus and viral spread in vitro and in vivo (Bukh et al. 2002; Pietschmann et al. 2009) and see also below Sect. 4.

3 Retroviral Pseudoparticles

In the absence of an efficient cell culture system encompassing the entire life cycle of the virus, surrogate models were developed that were useful to study the role of HCV glycoproteins in virus entry (see chapter "Hepatitis C Virus Entry" by Zeisel et al., this volume). The most successful among the models to investigate early steps of HCV infection was the establishment of retroviral pseudotypes bearing unmodified HCV glycoproteins (HCVpp) (Bartosch et al. 2003; Hsu et al. 2003). This system is based on the co-transfection of 293T cells with expression vectors encoding HCV E1 and E2, the gag-pol proteins of either murine leukemia virus (MLV) or human immunodeficiency virus (HIV) and a retroviral genome encoding a reporter gene. Entry of these particles leads to the delivery of the retroviral capsid into the cytoplasm of the target cell following reverse transcription and integration of the viral genome into the host cell genome. The reporter gene is expressed by the integrated provirus to detect productive entry events in a rapid manner. Importantly, attachment and receptor interaction of these retroviral pseudotypes is governed by the functional HCV E1-E2 protein complex incorporated into the envelope of these particles. Therefore, HCVpp's can be neutralized with antibodies targeting the viral glycoproteins E1, E2, and with sera of infected patients (Hsu et al. 2003; Cai et al. 2005). The incorporation of patient-derived glycoproteins has also been described for HCVpp and can be used to study cross-neutralizing antibodies (Bartosch et al. 2003; Owsianka et al. 2005; Tarr et al. 2007). Moreover, utilization of HCVpp is an elegant way of analyzing HCV cell entry independent of the other parts of the viral life cycle. Consequently, this system offers the freedom to investigate cell entry into cells that are not permissive to HCV RNA replication. Various viral entry attachment factors and receptors have been identified or verified using this system

including glycosaminoglycans, low-density lipoprotein receptor (LDL-R), dendritic cell-specific intercellular adhesion molecule-3-grabbing non-integrin (DC-SIGN), claudin-1, claudin-6, claudin-9, occludin, and recently also epidermal growth factor receptor (EGFR), ephrin receptor A2 (EphA2), and the Niemann-Pick C1-like cholesterol adsorption receptor (NPC1L1) [for review see (Ploss and Evans 2012)]. A limitation of the HCVpp system is that these particles are produced in a non-liver cell line (293T) and that they assemble in post-Golgi compartments and/or the plasma membrane as retroviruses do. Therefore, the close association of HCV particles with lipoproteins cannot be reproduced which may affect studies including antibody neutralization assays and entry studies with lipid receptors LDL-R, SR-BI, and NPC1L1. However, this "limitation" offers the exciting opportunity to learn about the relevance of these host-derived modifications of HCV particles by directly comparing cell entry properties of HCVpp with natural HCV particles.

In summary, although not covered with lipoproteins, HCVpps can be used to study viral entry events of HCV independent of RNA replication and assembly and have been a valuable tool to identify cellular entry molecules.

3.1 Other Models to Study Individual Steps of HCV Cell Entry

In addition to HCVpp, additional model systems have been developed to study HCV entry. These include the most widely used cell culture model systems HCVcc and HCV_{TCP} that are covered in separate sections. For the identification of cellular receptors C-terminally truncated secreted forms or cell surface expressed versions of the glycoprotein E2 have been described (Flint et al. 1999; Flint et al. 2000). One of the first tools used to study HCV cell entry and to discover receptors involved in this pathway was a soluble and truncated form of the E2 glycoprotein ($sE2_{661}$), in which the last 85 amino acids, encompassing the hydrophobic transmembrane domain, are deleted (Spaete et al. 1992; Michalak et al. 1997). It is not clear to which degree this truncated form reflects the proper folding of E2 in the context of the E1/E2 complexes within the HCV envelope (see also chapter "Hepatitis C Virus Proteins: From Structure to Function" Moradpour and Penin, this volume). However, the discovery of CD81 and SR-BI as part of the HCV receptor complex was achieved using $sE2_{661}$ (Pileri et al. 1998; Scarselli et al. 2002). Current approaches to solve the structure of the E2 glycoprotein are based on differently truncated forms of the E2 protein (Krey et al. 2010; McCaffrey et al. 2011). Further surrogate models to study glycoprotein and receptor interaction as well as early entry events include E1-E2 liposomes (Lambot et al. 2002), virus-like particles generated in insect cells (Baumert et al. 1998; Triyatni et al. 2002; Wellnitz et al. 2002), and vesicular stomatitis virus (VSV) pseudotyped with chimeric glycoproteins consisting of the ectodomains of HCV E1 and E2 fused to the transmembrane domain of the VSV-G glycoprotein (Lagging et al. 1998; Matsuura et al. 2001; Buonocore et al. 2002). More recently, a soluble form of E2 was reported that blocks HCVcc entry and is produced in mammalian or insect cells (Whidby et al. 2009).

Virus binding to the cellular surface can be measured by quantification of cell-bound RNA copy numbers (Vieyres et al. 2009; Calland et al. 2012) or by radioactive labeling of HCV virions (Ciesek et al. 2011a). After cell binding, receptor interactions and conformational changes in the glycoproteins the virus is taken up by endocytosis (Ploss and Evans 2012). Molecular inhibitors like small interfering RNAs (siRNAs) and dominant-negative constructs have been applied in addition to the use of chemical inhibitors in specifically blocking distinct stages of endocytosis (Sieczkarski and Whittaker 2002). With respect to HCV, trafficking, acidification, and clathrin-mediated endocytosis has been studied with different inhibitors (Blanchard et al. 2006; Meertens et al. 2006; Tscherne et al. 2006). Recently, Coller et al. (2009) developed infectious fluorescent particles to visualize the association of HCV virions with the endocytosis machinery. They labeled particles with membrane-permeable lipophilic dyes, called DiD (1,1′dioctadecyl-3,3,3′,3′tetramethyl-indodicarbo-cyanine 4-chlorobenzenesulfonate salt) and DiI (1,1′-dioctadecyl-3,3,3′3′-tetramethylindocarbocyanine perchlorate), that can be used to study HCV cell interactions in the HCV entry process (Coller et al. 2009). Uptake of HCV particles can also be analyzed by protease treatment. Internalized viral particles are resistant to proteolysis, whereas viruses remaining on the cell surface are inactivated (Meertens et al. 2006; Aizaki et al. 2008; Schwarz et al. 2009; Vieyres et al. 2009).

As structural information about the HCV glycoproteins is lacking, the fusion process is not fully understood at a molecular level. Several different fusion assays have been designed that rely on cell-to-cell fusion or fusion between HCVpp/HCVcc and liposomes or target cells. The ‘cell-to-cell’ fusion assay is based on 293T cells that ectopically express the HCV glycoproteins and that encode a T7-polymerase-dependent GFP gene. These cells are co-cultured with Huh-7 cells expressing the T7-polymerase and successful fusion results in multinucleated cells expressing the GFP reporter gene (Kobayashi et al. 2006). Modifications of this system for example with luciferase as reporter gene have been developed (Evans et al. 2007; Lavillette et al. 2007). Productive fusion in vitro can be also monitored with fluorescent probes that are incorporated into either the virus particles or liposomes and upon fusion membrane mixing results in fluorescence dequenching and emission (Lavillette et al. 2006; Haid et al. 2009). Recently, another fluorescence-based fusion assay was developed in which HCVcc viruses were labeled with the hydrophobic DiD fluorophore that inserts into the membrane at self-quenching doses. After fusion of viral and target membranes the DiD fluorophores diffuse away causing dequenching which can be monitored in real time (Sainz et al. 2012).

It has been reported that HCV can also be transmitted via cell-to-cell spread. This mode of transmission may be particularly relevant in vivo in the context of infected liver tissue. It was reported that infection via cell-to-cell spread was refractory to neutralization by E2 monoclonal antibodies and that it may occur in a CD81-independent manner (Timpe et al. 2008; Witteveldt et al. 2009). Cell-to-cell spread of HCV can be studied by co-culturing HCV-positive donor cells with target cells that can be monitored by fluorescent markers. Cell-free spread can be blocked by the presence of neutralizing antibodies or an agarose overlay (Timpe et al. 2008; Witteveldt et al. 2009;

Brimacombe et al. 2011). A recently described cell-based reporter system that is based on NS3/4A-mediated cleavage of a fluorescent substrate can also be applied to investigate this route of transmission at a single cell level (Jones et al. 2010). Combination of this system with an agarose overlay facilitates this assay setup (Ciesek et al. 2011a; Ciesek et al. 2011b). Instead of using two distinct cell populations, quantification of the number of infected cells per infection focus under an agarose overlay similarly allows to study cell-to-cell spread (Baldick et al. 2010; Calland et al. 2012).

4 Cell Culture Infectious HCV Genomes and Host Cells

Initial attempts of transfecting genomic in vitro transcripts of HCV derived from cloned viral genomes into human liver cells were unsuccessful, due to non-functional sequences or mutations introduced by RT-PCR. To circumvent these problems, consensus genomes were constructed which were based on a master sequence that is representative of the dominant nucleotide sequences at each position of the genome. The consensus sequence was established by sequencing of multiple clones of a single isolate which then guided construction a consensus genome based on this sequence information. The first constructs generated by this procedure were derived from a patient designated "H77" who had been infected with a genotype 1a virus (Kolykhalov et al. 1997; Yanagi et al. 1997). Importantly, intrahepatic inoculation of these consensus RNA genomes into chimpanzees initiated a productive infection of the animals (for detailed description of HCV animal models see chapter "Animal Models for Hepatitis C" by Billerbeck et al., this volume). This evidence provided formal proof that indeed these H77 consensus genomes are functional and infectious in vivo (Kolykhalov et al. 1997; Yanagi et al. 1997). However, despite the availability of these and a few other consensus genomes with proven infectivity in vivo, attempts to initiate robust replication and production of infectious progeny with these genomes were initially not fruitful (Fig. 1).

After the successful construction of autonomously replicating selectable subgenomic Con1-derived replicons, we added the viral structural genes and thus created selectable full-length genomes expressing the complete HCV open reading frame of this isolate. Adaptive mutations initially identified with the subgenomic replicons were added to increase RNA replication and virus protein expression. While these selectable genomes as well as authentic genomes with only the adaptive mutations but no selectable marker replicated relatively efficiently, neither stable cell lines harboring selectable full-length replicons of Con1, nor the transiently replicating Con1 full-length RNAs gave rise to infectious HCV progeny (Pietschmann et al. 2002). Likewise full-length RNA of the HCV N strain (GT1b) did not support the production of infectious particles (Ikeda et al. 2002). It was suggested that either the host cells lack factors important for particle formation or that REMs interfere with the production of infectious particles. In line with the second hypothesis, replication-promoting mutations selected for tissue culture experiments are rarely found in HCV sequences from human or chimpanzee (Grobler et al. 2003; Sarrazin et al. 2005).

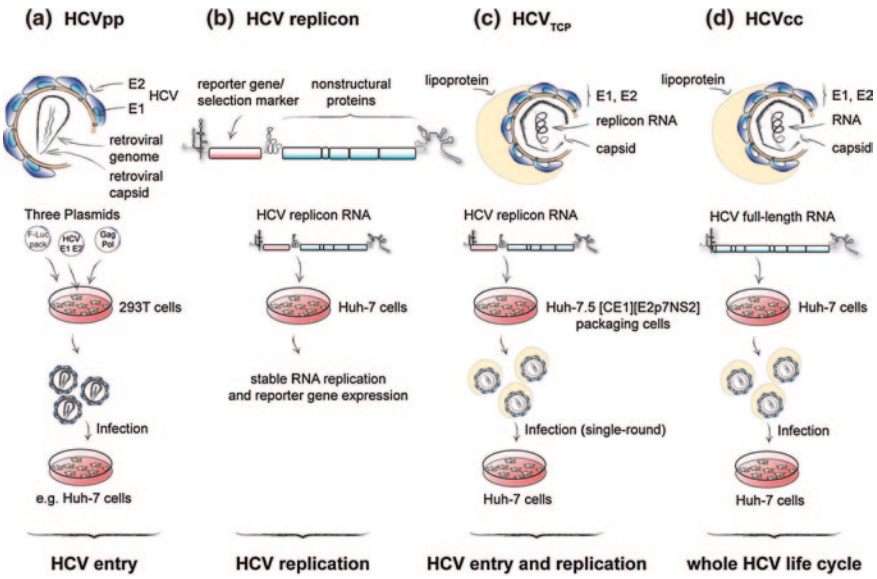


Fig. 1 Key HCV cell culture systems to investigate different steps of the viral replication cycle. **a** For dissection of the entry process HCV pseudoparticles (HCVpp) can be utilized. HCVpp are produced by transfection of 293T cells with three plasmids encoding for (1) retroviral gag and pol genes, (2) a retroviral vector harboring a reporter gene, and (3) the HCV glycoproteins E1, E2. These retroviral particles contain a vector that encodes the reporter gene and display the HCV glycoproteins in their envelope and thus, enter cells in an HCV-dependent manner. **b** HCV RNA replication can be quantified using subgenomic replicons. Those self-replicating HCV RNAs are based on a selectable marker or reporter gene replacing the coding region from core to NS2 upstream of a second IRES from EMCV that allows translation of the non-structural proteins NS3 to NS5B. After transfection, the viral RNA is directly translated and replication can be monitored for example by reporter gene expression. **c** HCV trans-complemented particles (HCV_{TCP}) are authentic viral particles that contain a replicon RNA instead of the full-length genome. They are produced by transfection of replicon RNA into so-called packaging cell lines that stably express the lacking structural proteins and thus, provide them in *trans*. Infection of naïve cells with HCV_{TCP} results in a single round infection with only viral entry and RNA replication taking place since the structural proteins necessary for virus production are missing. **d** Production of cell culture-derived HCV particles (HCVcc) are based on the genotype 2a isolate JFH1 and derivatives thereof. Full-length viral genomes are transfected into permissive human hepatocytes which leads to translation and RNA replication giving rise to the production of viral particles that are able to infect new target cells, thereby completing the whole viral life cycle of HCV

Pietschmann et al. (2009) recently reported that those very same REMs which were used to increase the replication capacity of Con1 genomes actually interfered with production of infectious virus. In fact most of the Con1-replication enhancing changes within the viral non-structural proteins stimulated replication at the expense of production of infectious particles. This observation was a first hint suggesting that the non-structural proteins contribute to production of infectious HCV, an observation which was much refined and extended using the infectious JFH1 system (Jones et al. 2007; Steinmann et al. 2007; Yi et al. 2007; Appel et al. 2008; Ma et al. 2008;

Jones et al. 2009; Phan et al. 2009). Besides this, the observation that REMs can interfere with virus production in Con1 genomes provided a simple explanation why the adapted Con1 genomes unlike the wild type were noninfectious in Chimpanzee or reverted back to the wild-type sequence (Bukh et al. 2002). It is, however, important to stress here that REMs do not necessarily lead to inactivation of virus production. This is exemplified by one of the most potent adaptive changes within the Con1 replicase (i.e., the K1846T exchange within the NS4B protein of Con1) that does not interfere with production of infectious particles (Pietschmann et al. 2009). Even more striking, an adapted H77 genome designated H77S has been generated that carries multiple mutations which substantially enhance virus production and at the same time permit production of infectious virus (Yi et al. 2006; Yi and Lemon 2009). Thus, there are apparently different modes of increasing replication fitness of HCV consensus genomes in tissue culture, some of which interfere with production of virus particles. Certainly, gaining a deeper understanding of how REMs enhance replication in tissue culture is an important challenge for future research.

When Kato and colleagues in 2001 reported construction of a subgenomic replicon termed JFH1 which replicated with very high efficiency and without the requirement of adaptive mutations (Kato et al. 2001; Kato et al. 2003b; Date et al. 2004), this observation was a major finding itself. However, it turned out to be the prelude to a yet more important major breakthrough in HCV research: A few years later, three groups reported that the complete wild-type JFH1 genome or chimeras consisting of the JFH1 replicase genes NS3-NS5B and Core to NS2 regions of alternative HCV genomes replicated efficiently in Huh-7 cells and produced infectious viral progeny both in tissue culture and in animal models (Lindenbach et al. 2005; Wakita et al. 2005; Zhong et al. 2005). These particles were designated cell culture-derived HCV (HCVcc) and they are now routinely used in many laboratories. Each step of the viral life cycle can be studied with this system including viral entry, replication, and also the late events like genome packaging, virion assembly, maturation, and release. Immunoelectron microscopy with E2-specific antibodies demonstrated the presence of spherical particles with 50–65 diameter and cell culture viruses had a density profile comparable to serum-derived viruses (Lindenbach et al. 2005; Wakita et al. 2005; Zhong et al. 2005) (for detailed description of HCV particles see chapter by "Virion Assembly and Release" Lindenbach, this volume). The authenticity of recombinant virus particles was confirmed by demonstrating HCVcc infectivity in chimpanzees and in mice containing human liver xenografts (Lindenbach et al. 2005; Wakita et al. 2005; see also chapter "Animal Models for Hepatitis C" by Billerbeck et al., this volume). Interestingly, the specific infectivity of HCVcc recovered after passage in vivo was increased in comparison to cell culture produced viruses (Lindenbach et al. 2006). The highly infectious nature of the animal-derived viruses correlated with a lower buoyant density compared to cell culture-derived HCV. Interestingly, these features (lower density and higher infectivity) were lost after a single round of passaging in cell culture, suggesting that modifications that were not fixed within the viral genome were responsible for these alterations. Infection could be neutralized with patient sera or E2 and CD81-specific antibodies. Importantly, HCVcc were sensitive

to inhibitors targeting the viral protease and polymerase as well as to interferon-α (Lindenbach et al. 2005; Wakita et al. 2005; Zhong et al. 2005).

As the JFH1-based infection system belongs to genotype 2a, a major challenge is still the generation of molecular clones from other genotype supporting production of infectious virus in cell culture. As alluded to above, Yi et al. (2006) reported in 2006 an infectious clone of the genotype 1a designated H77S that contains five REMs. These mutations were selected through a tedious and iterative process of adaptation of subgenomic H77 replicons and are located therefore in the non-structural genes (Yi and Lemon 2004). However, virus titers that were recovered from transfected Huh-7.5 cells were about 100–1,000-fold lower compared to the JFH1 system. Passaging of the full-length H77S genome did not result in increased viral titers as observed for JFH1, probably due to a lower replication efficiency of H77S (Yi et al. 2006).

As mentioned above, transfection of a full-length wild-type Con1 clone resulted in a transient release of virus particles which was blocked by cell culture adaptive mutations in NS5A or NS3 (Pietschmann, Zayas et al. Pietschmann et al. 2009). Recently, another genotype 1b isolate (NC1) from a patient with acute severe hepatitis was described that shares 91 % nucleotide and 94 % amino acid sequence homology with the Con1 isolate (Date et al. 2012). The replication efficiency of a NC1 subgenomic replicon was lower compared to JFH1 but could be enhanced with the introduction of REMs. After transfection of full-length RNA only cells harboring genomes with NS5A mutations S2197 or S2204G showed significant amounts of core protein secreted into the cell culture supernatant. Next, the authors combined the identified REMs with previously described mutations in NS3 (Krieger et al. 2001) and NS4B (Lohmann et al. 2003) to increase replication and virus production. Enhanced production of infectious particles was observed, however, the efficiency was not sufficient for autonomous virus propagation in cell culture and for infectivity studies in vivo (Date et al. 2012).

4.1 JFH1 and Chimeric Genomes

Although these infection models described so far are an important achievement permitting studies of the complete HCV replication cycle in cell culture, these systems are restricted to specific isolates and limit comparable studies of all HCV genotypes. To overcome this restraint, a comprehensive panel of chimeric genomes was constructed by combining the JFH1 isolate with heterologous strains of all major HCV genotypes (Table 1). In most cases, the replicase proteins necessary for generating the membrane-bound replicase complex and nontranslated regions are derived from the highly efficient JFH1 strain. The proteins Core to NS2 which are required for viral morphogenesis (chapter "Virion Assembly and Release", this volume) are derived from another genotype. With this strategy the yield of HCVcc particles was subsequently enhanced by creating an intragenotypic chimera using the C-NS2 part of a different genotype 2a isolate, J6 (Yanagi et al. 1997; Lindenbach et al. 2005).

To analyze whether it is also possible to generate intergenotypic chimeras, an analogous chimeric genome that carried the Core to NS2 part of the GT 1b Con1 isolate was constructed (Pietschmann et al. 2006). However, although this genome produced infectious HCV, virus titers were very low probably due to incompatibilities between the Con1 (GT1b) and JFH1 (GT2a) proteins. Therefore, a series of intergenotypic reporter chimeras were generated with different cross-over sites varying from the C-terminus of E2 to the NS2-NS3 cleavage site. The results of this mapping analysis identified a cross-over site located right after the first trans-membrane domain of NS2 as the best choice for construction of infectious JFH1-Con1 chimeras JFH-J6 and JFH1-H77 chimeras (Pietschmann et al. 2006). Similar studies describing the generation of chimeric genomes of genotype 3a, 4a, 5a and finally all major seven genotypes have been reported (Pietschmann et al. 2006; Gottwein et al. 2007; McMullan et al. 2007; Yi et al. 2007; Jensen et al. 2008; Scheel et al. 2008; Gottwein et al. 2009; Gottwein et al. 2011a; Scheel et al. 2011a). These chimeric genomes were shown to be highly useful to study entry, neutralization, and virus assembly of all seven known HCV genotypes. They have been further validated to be infectious in vivo as human liver-chimeric mice developed high-titer infections after inoculation with HCV of genotypes 1–6 (Bukh et al. 2010). Highest virus titers could be achieved with a J6-JFH1 chimera designated Jc1 that allows the production of virus particles of about 10^6 infectious units per ml (Pietschmann et al. 2006).

Further improvements were the construction of reporter genomes of different HCV chimeric genomes (luciferase or GFP) for rapid and sensitive detection of replication or infection (Koutsoudakis et al. 2006; Tscherne et al. 2006; Schaller et al. 2007; Gottwein et al. 2011a; Reiss et al. 2011) (recently summarized in (Vieyres and Pietschmann 2012).

The idea of chimeric genomes was further expanded to also include non-structural proteins. As mentioned above, HCV replicons have only been described for genotypes 1 and 2 and efficiency or resistance of direct acting antiviral agents (DAAs) targeting non-structural proteins could not be tested for all genotypes. Recently, the construction of viable JFH1-based chimeras in which sequences encoding NS3/4A or NS5A were replaced with homologous sequences of other genotypes were described (Gottwein et al. 2011b; Scheel et al. 2011a, b). These technical developments that are based on adaptation approaches allow analyzing effects of antiviral compounds against NS3/4A and NS5A and antiviral resistance for all HCV genotypes in the context of infectious full-length HCV RNAs.

4.2 Adaptation of Infectious HCV Genomes to Cell Culture

The generation of chimeric genomes as discussed in the previous section is one way to increase viral yields in cell culture. However, genetic incompatibility between JFH1 and the alternative HCV genome segment fused to it often limits production of infectious virus This restriction can be overcome by serial passage of the chimeras in cell culture which over time results in the accumulation of adaptive changes

compensating the genetic differences between the fused genomes and thus increases virus yields (Abe et al. 2007; Gottwein et al. 2007; McMullan et al. 2007; Yi et al. 2007; Jensen et al. 2008; Scheel et al. 2008; Bungyoku et al. 2009; Gottwein et al. 2009; Gottwein et al. 2011a; Koutsoudakis et al. 2011; Chan et al. 2012). For instance, Yi and colleagues demonstrated that mutations in E1, p7, NS2, and NS3 contribute to the ability of a H77/JFH1 chimeric genome to assemble and release high amounts of virus particles (Yi et al. 2007). These mutations act independent of any detectable effect on viral RNA replication or polyprotein processing indicating a crucial role of these proteins in virus assembly and relase (Yi et al. 2007).

It is important to realize that the process of adapting inter- or intra-genotypic chimeric genomes is fundamentally different from the selection process which yields REM in replicons. In the former, functional incompatibility between JFH1 and the fused non-JFH1 derived proteins is overcome. In other words, the selection process "shapes" these specific partners to better cooperate in the viral replication cycle. In the latter, however, the monogenetic replicon is modified to better fit to the host cell environment (e.g., Huh-7). Likely as a consequence, most of the changes adapting a given non-JFH1 strain to the JFH1-derived NS3 to NS5B replicase in full-length chimeras are strictly chimera-specific and cannot be transferred to other chimeras. In contrast, there is a certain degree of flexibility with REMs which can be successfully transferred from Con1 to H77 and even to genotype 2a replicons (Grobler et al. 2003; Kato et al. 2003a; Maekawa et al. 2004; Ikeda et al. 2005; Abe et al. 2007; Mori et al. 2008).

Cell culture adaptations of JFH1-chimeras were mostly conducted in the highly permissive cell line Huh-7.5 and are based on the passage of JFH1 infected cells or by serial passages of viral supernatants. Due to this strategy, the selection process optimizes viral fitness of the chimera across the entire replication cycle and not only the processes of RNA translation and RNA replication are in the selection scheme of subgenomic replicons. Over time, viral variants emerge that harbor adaptive mutations leading to increased viral titers up to 100–1,000-fold over the parental genome.

Interestingly, several groups found that also the JFH1 wild-type genome can be efficiently adapted in cell culture with an increase in viral titers from 10^3 tissue culture infectious doses ($TCID_{50}$) per milliliter (mL) to 10^5–10^6 $TCID_{50}$/mL (Zhong et al. 2005; Delgrange et al. 2007; Russell et al. 2008; Kang et al. 2009; Kaul et al. 2007). This indicates that also JFH1 *per se* is not optimally suited for replication and propagation in Huh-7 cells. However, compared to all other known HCV isolates the degree of replication competence of this particular isolate in these cells is certainly unprecedented.

Titer-enhancing mutations were identified throughout the HCV genome (Core, E2, p7, NS2, NS3, NS5A, NS5B) and interestingly, repetition of an adaptation process showed that none of the mutations identified in the first experiment reappeared in the second selection (Zhong et al. 2005; Delgrange et al. 2007; Russell et al. 2008; Kang et al. 2009; Kaul et al. 2007). Thus, there are likely varying independent options to adapt JFH1 to cell culture replication in Huh-7-derived cells. Notably, adaptation of JFH1 itself yielded one of the few adaptive changes

(V2440L within domain III of NS5A) which boosts virus production not only of the construct it was selected with but also of other JFH1-based chimeras including GT1a, 1b, and 3a (Kaul et al. 2007). Therefore, this adaptive change likely optimize JFH1-based virus assembly in a manner that is compatible with divergent viral structural proteins—possibly by acting on properties of the viral replicase that generally favor assembly of infectious progeny. Notably, this mutation which is located at the P3 position of the NS5A-NS5B cleavage site was shown to delay polyprotein processing at this junction (Kaul et al. 2007). Although this alteration did not measurably change RNA replication, a subtle change in polyprotein processing could modulate interaction of the replicase with viral structural proteins and in turn efficiency of virus production. Interestingly, the very same mutation was later shown to confer partial resistance against drugs inhibiting cyclophilin A, a crucial replication co-factor of HCV (Kaul et al. 2009). Therefore, it is possible that not only RNA replication but also the efficiency of HCV assembly is modulated by cyclophilin A, possibly via modulation of polyprotein processing and folding. In many cases, however, the underlying mechanisms by which adaptive mutations facilitate production of infectious JFH1 or JFH1-chimeras are the beginning to emerge. First evidence suggests that enhanced physical interactions between the structural and non-structural proteins as well as within non-structural proteins during virus morphogenesis may be in part responsible for increased virus yields (Murray et al. 2008a; Jiang and Luo 2012). Alternatively, mutations were described which reduced cytotoxicity JFH1 (Kang et al. 2009) or increased specific infectivity of released particles likely by altered recognition of CD81 (Zhong et al. 2005; Russell et al. 2008). Notably, the G451R mutation within E2 of JFH1 falls into the latter category of mutations: First described as adaptive mutation for JFH1 by Zhong et al. (2006) additional work by Grove and Bitzegeio revealed that this mutation reduces dependence on SR-BI and increases exposure of the CD81 binding site on the virus particle (Grove et al. 2008; Bitzegeio et al. 2010). While these changes optimize cell entry in cell culture they are unlikely to confer a gain of fitness in vivo as these modification increase virus neutralization through a number of neutralizing antibodies (Grove et al. 2008; Bitzegeio et al. 2010). This example illustrates how cell culture adaptive changes increase viral fitness in tissue culture but at the same time skew viability in vivo. While such subtle changes facilitate in vitro experimentation and can give important and unique clues to the function and interplay of viral factors among themselves as well as with host determinants, this example also highlights the urgent need for better replication models based on primary HCV isolates.

4.3 HCV Trans-Complemented Particles

It is known from other plus-strand RNA viruses that assembly of progeny virus can be achieved when structural proteins are expressed in *trans* and independently from the RNA molecule that encodes the replicase proteins. This flexibility

has been widely used to generate viral vectors for gene delivery and immunization approaches (Lundstrom 2004). Subgenomic replicons of HCV contain all genetic elements needed for replication in human liver cells, while lacking the coding region of the viral structural proteins, p7 and NS2 (Lohmann et al. 1999). Consequently, these RNAs replicate in cells but are unable to produce infectious progeny virus. It was reported by several groups that this defect can be rescued by expression of the HCV structural proteins in *trans* via helper viruses or varying DNA-based expression systems in so-called in packaging cell lines (Ishii et al. 2008; Steinmann et al. 2008; Adair et al. 2009). With the production of these *trans*-complemented JFH1 particles (referred to as HCV_{TCP}) virus entry and replication can be studied independently from the late steps of the viral life cycle and thus from secondary rounds of infection. Moreover, due to the inability of HCV trans-complemented particles (HCV_{TCP}) to spread, this model has improved biosafety (Steinmann et al. 2008). Naturally occurring HCV subgenomic RNAs with different deletions in the structural proteins have been found in several patients and could also be *trans*-complemented in vitro (Pacini et al. 2009) highlighting that HCV_{TCP} can circulate in vivo and may modulate disease progression and outcome.

4.4 Permissive Host Cells

HCV replicates primarily in human hepatocytes, but multiple reports suggest that also extrahepatic reservoirs exist which may include the lymphatic system, gut, and the brain (Zignego et al. 2007; Weissenborn et al. 2009). Besides mutations that affect viral fitness in cell culture, also the host cell plays a crucial role in HCV replication. The most permissive cell line for efficient RNA replication in vitro is the human hepatoma cell line Huh-7 and its clonal descendants. Studies with HCV replicons demonstrated that only a subpopulation of Huh-7 cells allowed high levels of replication and efficiency was dependent on the cell passage number (Lohmann et al. 2003) and cell density (Guo et al. 2001; Pietschmann et al. 2001; Miyamoto et al. 2006). In fact the observation that during the replicon selection process a cell population which sustains elevated replication fitness emerges was utilized to create the most HCV-permissive cell lines currently available. Using IFN-α or a selective HCV inhibitor numerous highly permissive Huh-7-descendant cell clones were established including Huh-7.5 (Blight et al. 2002; Murray et al. 2003) and Huh-7-Lunet cells (Friebe et al. 2005) as well as other derivatives (Murray et al. 2003; Maekawa et al. 2004; Ikeda et al. 2005; Lanford et al. 2006). (Blight et al. 2002; Lohmann et al. 2003). The often dramatic differences between the permissiveness of individual Huh-7-derived cell clones including individual cell passages of the same polyclonal Huh-7 cell population highlights the strong host factor dependence of HCV the high variability of these cultured cells. As mentioned above, the molecular mechanisms that govern differential permissiveness of these cells are poorly defined. However, it is assumed that the abundance of crucial

host cell factors critical for replication plays an important role (Blight et al. 2002; Murray et al. 2003). Interestingly, in case of Huh-7.5 cells a lesion in the innate antiviral defence signaling pathway caused by a mutation in RIG-I has been implicated in the phenotype of high permissiveness of these cells (Sumpter et al. 2005). Although another group has not been able confirm a tight correlation between HCV-permissiveness and RIG-I status in these cells (Binder et al. 2007), this observation nevertheless illustrates that also lack antiviral restrictions may substantially increase permissiveness for HCV (for further details see chapter "Innate Immune Responses to Hepatitis C Virus" by Schoggins and Rice, this volume).

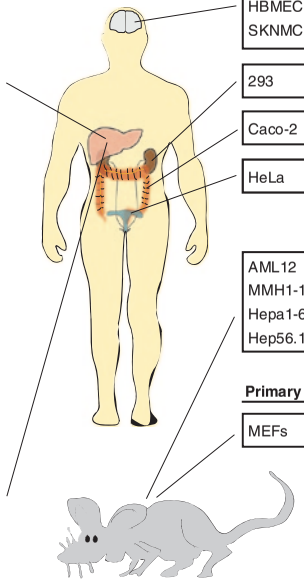
Initial approaches to establish robust HCV replication in cells other than Huh-7 were difficult. A first report that HCV replication is possible in human non-liver cells and even in non-human, mouse liver cells was published by Zhu et al. (2003) who described moderate replication of subgenomic replicons of the HCV N-isolate in Hela and the murine hepatoma cells Hepa1-6 cells. Interestingly, these cell lines were transfected with RNA isolated from stable Huh-7 cells instead of in vitro transcribed RNA to have a higher genetic variability (Zhu et al. 2003). However, unlike with selection of replicons in Huh-7 cells, in the mouse context no conserved mutations were identified that increase viral replication fitness in these non-human cells. Although the reason for this remains unclear, it is possible that the genetic barrier to adapt HCV proteins to murine replication co-factors was too high to permit selection of adaptive changes. Importantly, these findings provided formal proof that the essential host factors needed for HCV RNA replication can be found outside of human liver cells. Meanwhile numerous authors have described various alternative human liver-derived HCV-permissive cells including HuH-6 (Windisch et al. 2005), HepG2, IMY-N9 (Date et al. 2004), and LH86 (Zhu et al. 2007). Moreover, several human cells of non-liver origin are well established (Ali et al. 2004; Kato et al. 2005; Mee et al. 2009). Finally, a spectrum of non-human cells have been reported that sustain HCV replication (Zhu et al. 2003; Chang et al. 2006; Uprichard et al. 2006; Long et al. 2011) (Fig. 2).

However, it is important to note that RNA replication is in general lower in these cells, particularly in transient replication assays, compared to Huh-7-derived cell clones. HCV RNA replication has also been demonstrated in mouse embryonic fibroblast (MEFs) using JFH1 replicons (Chang et al. 2006). This study could be confirmed and extended by Lin and colleagues who showed that expression of the liver-specific miR-122 in MEFs stimulated the synthesis of HCV replicons in the rodent fibroblasts and that the combined effects of miR-122 expression and deletion of IRF-3 lead to cooperative stimulation of HCV subgenome replication (Lin et al. 2010). Therefore, MEFs now provide an important opportunity to utilize the powerful mouse genetic systems and the available mouse strains to unravel host factors that determine or preclude efficient HCV replication in these animals.

Similar to what has been observed in the replicon system, the identification of highly permissive Huh-7 cell lines is a prerequisite of a robust infection system. Huh-7.5 and Huh-7-Lunet/CD81 cells are two examples that support high levels of RNA replication and infection (Blight et al. 2002; Koutsoudakis et al. 2007). It was shown that some Huh-7 cell clones express low levels of the important HCV

Cell line	Origin	HCV isolate
Huh7-derived cell lines:		
Huh7.5 *	Hepatocellular carcinoma	Con1, H77, HCV-N, IB-1, IB-2, HCV-BK, JFH1
Huh7.5.1 *	Hepatocellular carcinoma	like in Huh7.5
Huh7-Lunet *	Hepatocellular carcinoma	Con1, JFH1
DMSO-treated Huh7 *	Hepatocellular carcinoma	JFH1
3D Huh7 culture *	Hepatocellular carcinoma	JFH1
Other human hepatoma cell lines:		
HuH6	Hepatocellular carcinoma	Con1, JFH1
HuH6-CLDN1 *	Hepatocellular carcinoma	JFH1
HepG2	Hepatocellular carcinoma	JFH1
HepG2-CD81-miR122 *	Hepatocellular carcinoma	JFH1
IMY-N9	Hepatocellular carcinoma	JFH1
LH86	Hepatocellular carcinoma	JFH1

Primary cells	Origin	HCV isolate
Fetal hepatocytes	Fetal liver	JFH1
Adult hepatocytes	Human adult liver	JFH1
Ault hepatoctes (MPCC)	Human adult liver	JFH1
Induced hepatocyte-like cells	Pluripotent stem cells	JFH1
Induced hepatocyte-like cells	Embryonic stem cells	JFH1
Human liver slices	Human adult liver	JFH1



Cell line	Origin	HCV isolate
hCMEC/D3 *	Brain microvascular endothelium	JFH1
HBMEC *	Brain microvascular endothelium	JFH1
SKNMC	Peripheral neuroblastom	JFH1
293	Embryonic kidney cells	Con1, JFH1
Caco-2	Colon adenocarcinoma	JFH1
HeLa	Cervical carcinoma	Con1, JFH1
AML12	Hepatoma cell line	JFH1
MMH1-1	Hepatoma cell line	JFH1
Hepa1-6	Hepatoma cell line	Con1, JFH1, HCV-N
Hep56.1D	Hepatocellular carcinoma	JFH1

Primary cells	Origin	HCV isolate
MEFs	Embryonic fibroblast	JFH1

Fig. 2 Primary cells and cell lines supporting HCV replication. The origin of human and murine cell lines permissive for HCV replication is given. Cells reported to support the complete HCV replication cycle including cell entry, RNA replication, and de novo production of infectious viral progeny are marked by an asterisk. Note that permissiveness between cells varies greatly and is generally highest in Huh-7-derived cell clones. References to the individual reported cell lines are given in the text

entry factor CD81 and that ectopic expression of this tetraspanin leads to much higher viral spread and infection events (Akazawa et al. 2007; Koutsoudakis et al. 2007). Conversely, selection of Huh-Lunet cell clones essentially lacking CD81 expression permitted receptor complementation studies for this important entry factor and the analysis of HCV cell-to-cell spread in the presence or absence of CD81. In a similar fashion, we have now HCV-permissive cell lines available permitting receptor complementation assays for SR-BI (Dreux et al. 2009; Catanese et al. 2010), CLDN1 (Haid et al. 2010), and OCLN (Ciesek et al. 2011b), thus greatly facilitating HCV cell entry studies with HCVcc. In parallel, a novel human hepatoma cell line, named LH86, was demonstrated to be permissive and susceptible to HCVcc (Zhu et al. 2007) and overexpression of CD81 and miR122 rendered HepG2 cells which were initially refractory to HCVcc infection fully permissive to HCV propagation (Narbus et al. 2011). Since the latter cells are known to polarize in cell culture HepG2-CD81-miR122 cells provide a unique opportunity to assess HCV infection and replication in polarized cells.

Instead of construction of reporter viruses, host cells can be modified for rapid and sensitive scoring of HCV infection events especially in a high-throughput format. One reported assay is based on a reporter cell line stably expressing the enhanced green fluorescent protein (EGFP) fused in-frame to the secreted alkaline phosphatase (SEAP) via a recognition sequence of the viral NS3/4A serine protease (Iro et al. 2009). Upon HCV infection and cleavage of the NS3/4A protease SEAP is released into the cell culture supernatant. Cell lines were also engineered to express the pro-apoptotic factor n4mBid, where NS3-dependent cleavage and activation led to an easily measurable cytopathic effect (Chockalingam et al. 2010).

Although HCV infects mainly hepatocytes, there is evidence for the existence of non-hepatic reservoirs suggesting that the virus might have a broader cell tropism. Genomic viral RNA could be detected in peripheral blood mononuclear cells (PBMCs) and negative-strand RNA and HCV were reported in brain autopsies of HCV-infected patients with neuropathological abnormalities [reviewed in (Morgello 2005; Weissenborn et al. 2009)]. Additionally, microscope techniques and strand-specific detection of HCV showed that microglia and macrophages are the dominant brain cell population positive for HCV (Wilkinson et al. 2009). Interestingly, there seemed to be differences between HCV sequences in the brain and those circulating in plasma (Radkowski et al. 2002; Fishman et al. 2008; Murray et al. 2008b) strengthening the possibility of HCV replication in cells of CNS origin. Direct detection of HCV antigens in the brain remains technically challenging as reported for the liver probably due to low HCV replication. However, it could recently be shown by in vitro studies that two neuroepithelioma cell lines express all HCV receptors essential for viral entry (Fletcher et al. 2010; Burgel et al. 2011) and support RNA replication (Fletcher et al. 2010). These cell lines were the first extrahepatic cells that sustain HCV infection without ectopic expression of cellular factor required for viral entry (Lindenbach 2010). HCV tropism for the brain is further supported by a recent study by Fletcher et al. (2012) demonstrating productive HCV infection of brain microvascular endothelial cells (BMEC), a major component of the blood/brain barrier. In this study, two independent-derived brain microvascular

endothelial cell lines were described to express all HCV receptor molecules and could be infected with HCVpp and HCVcc.

Collectively, the cell tropism of HCV could be expanded to several other human liver cell lines plus murine hepatoma cells and non-liver cell lines. With the discovery of novel HCV-specific dependency and restriction factors and genetic modifications of host cells further in vitro systems that sustain the entire HCV life cycle in cell culture are in development.

5 HCV Replication Models in Primary Cells and Patient Isolates

Studies on virus–host interactions have been hampered by limited in vivo and ex vivo models that mimic the natural environment of the liver. Due to the narrow host tropism of HCV small animal models are challenging and primary HCV isolates show a poor ability to replicate in tissue culture.

One drawback of human hepatoma cell lines like Huh-7 and its derivatives is that they do not polarize or express markers of mature hepatocytes and therefore may not fully recapitulate the polarized status of human hepatocytes in vivo (Decaens et al. 2008). However, chemical treatment or ectopic expression of host factors required for viral propagation may overcome some of these hurdles. Interestingly, treatment of human hepatoma cells with 1 % dimethyl sulfoxide was shown to differentiate cells in culture, induce the expression of hepatocyte-specific genes, and arrest cell growth (Sainz and Chisari 2006). These more hepatic-like cell cultures were still highly permissive for HCV infection and represent a more physiological relevant system compared to dividing Huh-7 cells and allow studies, e.g., of HCV persistence (Bauhofer et al. 2012) HepG2 cells can also grow in a polarized manner that mimics the bile canalicular configuration of hepatocytes. After ectopic expression of CD81 these cells have been used as a model of polarized culture to study HCV, however, these cells weakly support HCV RNA replication (Lindenbach et al. 2005; Flint et al. 2006; Mee et al. 2009). Overcoming this bottleneck, it was recently reported that the ectopic expression of miR122 in HepG2 cells permitted efficient RNA replication and support the entire HCV life cycle (Narbus et al. 2011). Furthermore, the growth of hepatoma cells in 3D cultures can also resemble the natural host cells of HCV in vivo and can be used to study HCV infections (Sainz et al. 2009; Molina-Jimenez et al. 2012). A human liver progenitor cell line, named HepaRG, can be differentiated into hepatocytes with specific cell culture conditions (Parent et al. 2004) and has been widely used for HBV infection experiments. It could now be shown that these cells are also susceptible to serum-derived HCV particles and support long-term production of viral particles, albeit at very low levels (Ndongo-Thiam et al. 2011).

Primary human hepatocytes (PHH) provide the closest in vitro model for the natural host cell of HCV. However, their use in HCV research is limited as PHH are difficult to obtain. In addition to limited availability, these cells have high donor variability, and the rapid loss of their differentiation status complicates tissue culture

experiments. Nevertheless, several groups reported infection of cultured PHH using sera from HCV-infected patients and could demonstrate CD81- and LDL receptor-dependent entry of serum-derived particles or inhibition of HCV replication by interferon. However, in general low-level replication was observed and results were difficult to reproduce (Carloni et al. 1993; Iacovacci et al. 1993; Fournier et al. 1998; Rumin et al. 1999; Lazaro et al. 2007; Buck 2008; Molina et al. 2008). Recently, a study by Podevin et al. (2010) described a method of culturing PHH with hepatocyte-specific gene expression for up to 2 weeks. Importantly, under these conditions PHH supported the complete infectious cycle of HCV, including production of new progeny virus, termed primary culture-derived HCV (HCVpc). The authors further could show that HCVpc had a lower average buoyant density and a higher specific infectivity than HCVcc particles produced in Huh-7 cells (Podevin et al. 2010). A limitation of this study is still that this model is restricted to cell culture-derived viruses and it is unclear if also patient-derived viruses can be propagated in this system. A very recent study which is based on ex vivo human adult liver slices demonstrated a productive infection using human primary isolates of genotype 1b as well as JFH1 viruses and genotype 1 JFH1 chimeric genomes (Lagaye et al. 2012). This new experimental model system in which viral titers above 10^5 ffu/ml were achieved allows in addition the validation of antiviral drugs.

Improvements of PHH cultivation were also made with the addition of non-parenchymal feeder cells to hepatocytes in micopatterned co-cultures (MPCC) (Ploss et al. 2010). MPCCs displayed hepatic function for several weeks, could be adapted to high-throughput format and were susceptible to HCV infection with limited virus spread for cell culture- and patient-derived viruses (Ploss et al. 2010). HCV detection techniques in PHH such as RNA quantification turned out to be sensitive but at the same time limited due to high background of input RNA. Detecting HCV infection events can be facilitated with a novel cell-based reporter system, in which the NS3/4A protease cleaves a fluorescent substrate that then relocated the reporter signal from a mitochondrial localization to the nucleus (Jones et al. 2010). This method permits visualizing HCV infection events in Huh-7 cells as well as PHH and could be extended to several other cell culture systems (Jones et al. 2010; Ploss et al. 2010).

Robust experimental model systems to study the role of host genetics like *IL-28B* polymorphism are restricted to needle biopsies, surgical resections, and organ donation. Two recent studies by Schwartz et al. (2012) and Wu et al. (2012) reported that hepatocyte-like cells derived from induced pluripotent stem cells (iPSC) allowed the productive infection with HCV, including inflammatory responses to infection. This novel development of an iPSC model can have the potential to study the impact of host genetics on hepatitis viral pathogenesis (Schwartz et al. 2012; Wu et al. 2012). Furthermore, these pluripotent stem cells can be genetically modified prior to differentiation and used to generate, e.g., HCV-resistant hepatocytes. Importantly, these hepatic-like cells also permitted direct infection by patient sera. Similar findings were also recently reported with human embryonic stem cells (hESC)-derived hepatocytes demonstrating that these cells could be infected with JFH1 viruses and supported the complete HCV replication cycle (Roelandt et al. 2012).

In conclusion, recent advances in the development of more physiologically relevant infection systems will advance our understanding of host–pathogen interactions in the liver.

6 Future Perspectives and Conclusions

After the molecular cloning of the HCV genome, it took more than a decade to establish functional cell culture systems for this human pathogen. Since then, step-by-step improvements were achieved that finally led to an infection system covering every step of the viral life cycle. Further improvements allow now to apply all virological techniques to study viral replication facilitating drug discovery. Chimeric genomes were created in which the structural proteins of all genotypes were fused to the JFH1 replicase, however, the challenge remains to propagate additional genotypes in vitro. Moreover, development of cell-based models to culture primary HCV isolates across different genotypes would open novel and unique perspectives to investigate viral determinants responsible for the different natural course and treatment outcome of hepatitis C. As Huh-7-derived cell lines do not recapitulate the functional liver tissue including differentiation and polarization more relevant host cell system are needed. Along these lines, a robust supply of primary human cells with differentiated hepatocyte function and morphology would greatly facilitate our ability to study the relevance of host factors for replication and pathogenesis of HCV. The recent exciting reports about HCV replication in human stem cell-derived cells raise hopes that these models are within reach and will permit robust molecular studies of pathogenesis and replication mechanisms. These achievements will further close the gap between in vitro studies and the clinical situation of HCV infections.

Acknowledgments The authors thank Gisa Gerold for critical reading of the manuscript and Dorothea Bankwitz for helping with the preparation of the figures. Work in the authors' laboratory is supported by grants from the European Research Council (VIRAFRONT), the Deutsche Forschungsgemeinschaft (DFG) (SFB 900, Teilprojekt A6; PI 734/1-1 and PI734/2-1), and by grants from the Initiative and Networking Fund of the Helmholtz Association SO-024 and HA-202 to T.P. E.S. is supported by DFG (STE 1954/1-1).

Financial and competing interest disclosure The authors declare no conflict of interest. T.P. has received consulting fees from Biotest AG and from Janssen Global Services, LLC.

References

Abe K, Ikeda M et al (2007) Cell culture-adaptive NS3 mutations required for the robust replication of genome-length hepatitis C virus RNA. Virus Res 125(1):88–97

Adair R, Patel AH et al (2009) Expression of hepatitis C virus (HCV) structural proteins in trans facilitates encapsidation and transmission of HCV subgenomic RNA. J Gen Virol 90(Pt 4):833–842

Aizaki H, Morikawa K et al (2008) Critical role of virion-associated cholesterol and sphingolipid in hepatitis C virus infection. J Virol 82(12):5715–5724

Akazawa D, Date T et al (2007) CD81 expression is important for the permissiveness of Huh7 cell clones for heterogeneous hepatitis C virus infection. J Virol 81(10):5036–5045
Ali S, Pellerin C et al (2004) Hepatitis C virus subgenomic replicons in the human embryonic kidney 293 cell line. J Virol 78(1):491–501
Appel N, Herian U et al (2005) Efficient rescue of hepatitis C virus RNA replication by trans-complementation with nonstructural protein 5A. J Virol 79(2):896–909
Appel N, Zayas M et al (2008) Essential role of domain III of nonstructural protein 5A for hepatitis C virus infectious particle assembly. PLoS Pathog 4(3):e1000035
Baldick CJ, Wichroski MJ et al (2010) A novel small molecule inhibitor of hepatitis C virus entry. PLoS Pathog 6(9):e1001086
Bartenschlager R (2006) Hepatitis C virus molecular clones: from cDNA to infectious virus particles in cell culture. Curr Opin Microbiol 9(4):416–422
Bartenschlager R, Lohmann V (2000) Replication of hepatitis C virus. J Gen Virol 81(Pt 7):1631–1648
Bartosch B, Dubuisson J et al (2003) Infectious hepatitis C virus pseudo-particles containing functional E1–E2 envelope protein complexes. J Exp Med 197(5):633–642
Bauhofer O, Ruggieri A et al. (2012) Persistence of HCV in quiescent hepatic cells under conditions of an interferon-induced antiviral response. Gastroenterology 143(2):429–38e8
Baumert TF, Ito S et al (1998) Hepatitis C virus structural proteins assemble into viruslike particles in insect cells. J Virol 72(5):3827–3836
Binder M, Kochs G et al (2007) Hepatitis C virus escape from the interferon regulatory factor 3 pathway by a passive and active evasion strategy. Hepatology 46(5):1365–1374
Bitzegeio J, Bankwitz D et al (2010) Adaptation of hepatitis C virus to mouse CD81 permits infection of mouse cells in the absence of human entry factors. PLoS Pathog 6:e1000978
Blanchard E, Belouzard S et al (2006) Hepatitis C virus entry depends on clathrin-mediated endocytosis. J Virol 80(14):6964–6972
Blight KJ, Kolykhalov AA et al (2000) Efficient initiation of HCV RNA replication in cell culture. Science 290(5498):1972–1974
Blight KJ, McKeating JA et al (2002) Highly permissive cell lines for subgenomic and genomic hepatitis C virus RNA replication. J Virol 76(24):13001–13014
Blight KJ, McKeating JA et al (2003) Efficient replication of hepatitis C virus genotype 1a RNAs in cell culture. J Virol 77(5):3181–3190
Brimacombe CL, Grove J et al (2011) Neutralizing antibody-resistant hepatitis C virus cell-to-cell transmission. J Virol 85(1):596–605
Buck M (2008) Direct infection and replication of naturally occurring hepatitis C virus genotypes 1, 2, 3 and 4 in normal human hepatocyte cultures. PLoS One 3(7):e2660
Bukh J, Pietschmann T et al (2002) Mutations that permit efficient replication of hepatitis C virus RNA in Huh-7 cells prevent productive replication in chimpanzees. Proc Natl Acad Sci USA 99(22):14416–14421
Bukh J, Meuleman P et al (2010) Challenge pools of hepatitis C virus genotypes 1–6 prototype strains: replication fitness and pathogenicity in chimpanzees and human liver-chimeric mouse models. J Infect Dis 201(9):1381–1389
Bungyoku Y, Shoji I et al (2009) Efficient production of infectious hepatitis C virus with adaptive mutations in cultured hepatoma cells. J Gen Virol 90(Pt 7):1681–1691
Buonocore L, Blight KJ et al (2002) Characterization of vesicular stomatitis virus recombinants that express and incorporate high levels of hepatitis C virus glycoproteins. J Virol 76(14):6865–6872
Burgel B, Friesland M et al (2011) Hepatitis C virus enters human peripheral neuroblastoma cells - evidence for extra-hepatic cells sustaining hepatitis C virus penetration. J Viral Hepat 18(8):562–570
Cai Z, Zhang C et al (2005) Robust production of infectious hepatitis C virus (HCV) from stably HCV cDNA-transfected human hepatoma cells. J Virol 79(22):13963–13973
Calland N, Albecka A et al (2012) (−)-Epigallocatechin-3-gallate is a new inhibitor of hepatitis C virus entry. Hepatology 55(3):720–729

Carloni G, Iacovacci S et al (1993) Susceptibility of human liver cell cultures to hepatitis C virus infection. Arch Virol Suppl 8:31–39
Catanese MT, Ansuini H et al (2010) Role of scavenger receptor class B type I in hepatitis C virus entry: kinetics and molecular determinants. J Virol 84(1):34–43
Chan K, Cheng G et al (2012) An adaptive mutation in NS2 is essential for efficient production of infectious 1b/2a chimeric hepatitis C virus in cell culture. Virology 422(2):224–234
Chang KS, Cai Z et al (2006) Replication of hepatitis C virus (HCV) RNA in mouse embryonic fibroblasts: protein kinase R (PKR)-dependent and PKR-independent mechanisms for controlling HCV RNA replication and mediating interferon activities. J Virol 80(15):7364–7374
Chockalingam K, Simeon RL et al (2010) A cell protection screen reveals potent inhibitors of multiple stages of the hepatitis C virus life cycle. Proc Natl Acad Sci USA 107(8):3764–3769
Ciesek S, von Hahn T et al (2011a) The green tea polyphenol, epigallocatechin-3-gallate, inhibits hepatitis C virus entry. Hepatology 54(6):1947–1955
Ciesek S, Westhaus S et al (2011b) Impact of intra- and inter-species variation of occludin on its function as coreceptor for authentic hepatitis C virus particles. J Virol 85(15):7613–7621
Coller KE, Berger KL et al (2009) RNA interference and single particle tracking analysis of hepatitis C virus endocytosis. PLoS Pathog 5(12):e1000702
Date T, Morikawa K et al. (2012) Replication and infectivity of a novel genotype 1b hepatitis C virus clone. Microbiol Immunol 56(5):308–317
Date T, Kato T et al (2004) Genotype 2a hepatitis C virus subgenomic replicon can replicate in HepG2 and IMY-N9 cells. J Biol Chem 279(21):22371–22376
Decaens C, Durand M et al (2008) Which in vitro models could be best used to study hepatocyte polarity? Biol Cell 100(7):387–398
Delgrange D, Pillez A et al (2007) Robust production of infectious viral particles in Huh-7 cells by introducing mutations in hepatitis C virus structural proteins. J Gen Virol 88(Pt 9):2495–2503
Dreux M, Dao Thi VL et al (2009) Receptor complementation and mutagenesis reveal SR-BI as an essential HCV entry factor and functionally imply its intra- and extra-cellular domains. PLoS Pathog 5(2):e1000310
Evans MJ, Rice CM et al (2004) Phosphorylation of hepatitis C virus nonstructural protein 5A modulates its protein interactions and viral RNA replication. Proc Natl Acad Sci USA 101(35):13038–13043
Evans MJ, von Hahn T et al (2007) Claudin-1 is a hepatitis C virus co-receptor required for a late step in entry. Nature 446(7137):801–805
Fishman SL, Murray JM et al (2008) Molecular and bioinformatic evidence of hepatitis C virus evolution in brain. J Infect Dis 197(4):597–607
Fletcher NF, Wilson GK et al. (2012) Hepatitis C virus infects the endothelial cells of the blood-brain barrier. Gastroenterology 142(3):634–643 e6
Fletcher NF, Yang JP et al (2010) Hepatitis C virus infection of neuroepithelioma cell lines. Gastroenterology 139(4):1365–1374
Flint M, Thomas JM et al (1999) Functional analysis of cell surface-expressed hepatitis C virus E2 glycoprotein. J Virol 73(8):6782–6790
Flint M, Dubuisson J et al (2000) Functional characterization of intracellular and secreted forms of a truncated hepatitis C virus E2 glycoprotein. J Virol 74(2):702–709
Flint M, von Hahn T et al (2006) Diverse CD81 proteins support hepatitis C virus infection. J Virol 80(22):11331–11342
Fournier C, Sureau C et al (1998) In vitro infection of adult normal human hepatocytes in primary culture by hepatitis C virus. J Gen Virol 79(Pt 10):2367–2374
Frese M, Schwarzle V et al (2002) Interferon-gamma inhibits replication of subgenomic and genomic hepatitis C virus RNAs. Hepatology 35(3):694–703
Friebe P, Boudet J et al (2005) Kissing-loop interaction in the 3′ end of the hepatitis C virus genome essential for RNA replication. J Virol 79(1):380–392
Gottwein JM, Scheel TK et al (2007) Robust hepatitis C genotype 3a cell culture releasing adapted intergenotypic 3a/2a (S52/JFH1) viruses. Gastroenterology 133(5):1614–1626

Gottwein JM, Scheel TK et al (2009) Development and characterization of hepatitis C virus genotype 1–7 cell culture systems: role of CD81 and scavenger receptor class B type I and effect of antiviral drugs. Hepatology 49(2):364–377

Gottwein JM, Jensen TB et al (2011a) Development and application of hepatitis C reporter viruses with genotype 1–7 core-nonstructural protein 2 (NS2) expressing fluorescent proteins or luciferase in modified JFH1 NS5A. J Virol 85(17):8913–8928

Gottwein JM, Scheel TK et al (2011b) Differential efficacy of protease inhibitors against HCV genotypes 2a, 3a, 5a, and 6a NS3/4A protease recombinant viruses. Gastroenterology 141(3):1067–1079

Grobler JA, Markel EJ et al (2003) Identification of a key determinant of hepatitis C virus cell culture adaptation in domain II of NS3 helicase. J Biol Chem 278(19):16741–16746

Grove J, Nielsen S et al (2008) Identification of a residue in hepatitis C virus E2 glycoprotein that determines scavenger receptor BI and CD81 receptor dependency and sensitivity to neutralizing antibodies. J Virol 82(24):12020–12029

Gu B, Gates AT et al (2003) Replication studies using genotype 1a subgenomic hepatitis C virus replicons. J Virol 77(9):5352–5359

Guo JT, Bichko VV et al (2001) Effect of alpha interferon on the hepatitis C virus replicon. J Virol 75(18):8516–8523

Haid S, Pietschmann T et al (2009) Low pH-dependent hepatitis C virus membrane fusion depends on E2 integrity, target lipid composition, and density of virus particles. J Biol Chem 284(26):17657–17667

Haid S, Windisch MP et al (2010) Mouse-specific residues of claudin-1 limit hepatitis C virus genotype 2a infection in a human hepatocyte cell line. J Virol 84(2):964–975 Recently, claudin-1 (CLDN1) was identified as a host protein essential

Hsu M, Zhang J et al (2003) Hepatitis C virus glycoproteins mediate pH-dependent cell entry of pseudotyped retroviral particles. Proc Natl Acad Sci USA 100(12):7271–7276

Iacovacci S, Sargiacomo M et al (1993) Replication and multiplication of hepatitis C virus genome in human foetal liver cells. Res Virol 144(4):275–279

Ikeda M, Yi M et al (2002) Selectable subgenomic and genome-length dicistronic RNAs derived from an infectious molecular clone of the HCV-N strain of hepatitis C virus replicate efficiently in cultured Huh7 cells. J Virol 76(6):2997–3006

Ikeda M, Abe K et al (2005) Efficient replication of a full-length hepatitis C virus genome, strain O, in cell culture, and development of a luciferase reporter system. Biochem Biophys Res Commun 329(4):1350–1359

Iro M, Witteveldt J et al (2009) A reporter cell line for rapid and sensitive evaluation of hepatitis C virus infectivity and replication. Antiviral Res 83(2):148–155

Ishii K, Murakami K et al (2008) Trans-encapsidation of hepatitis C virus subgenomic replicon RNA with viral structure proteins. Biochem Biophys Res Commun 371(3):446–450

Jensen TB, Gottwein JM et al (2008) Highly efficient JFH1-based cell-culture system for hepatitis C virus genotype 5a: failure of homologous neutralizing-antibody treatment to control infection. J Infect Dis 198(12):1756–1765

Jiang J, Luo G (2012) Cell culture adaptive mutations promote viral protein–protein interactions and morphogenesis of infectious Hepatitis C Virus. J Virol 86(17):8987–8997

Jones CT, Murray CL et al (2007) Hepatitis C virus p7 and NS2 proteins are essential for production of infectious virus. J Virol 81(16):8374–8383

Jones DM, Patel AH et al (2009) The hepatitis C virus NS4B protein can trans-complement viral RNA replication and modulates production of infectious virus. J Virol 83(5):2163–2177

Jones CT, Catanese MT et al (2010) Real-time imaging of hepatitis C virus infection using a fluorescent cell-based reporter system. Nat Biotechnol 28(2):167–171

Kang JI, Kim JP et al (2009) Cell culture-adaptive mutations in the NS5B gene of hepatitis C virus with delayed replication and reduced cytotoxicity. Virus Res 144(1–2):107–116

Kato T, Furusaka A et al (2001) Sequence analysis of hepatitis C virus isolated from a fulminant hepatitis patient. J Med Virol 64(3):334–339

Kato N, Sugiyama K et al (2003a) Establishment of a hepatitis C virus subgenomic replicon derived from human hepatocytes infected in vitro. Biochem Biophys Res Commun 306(3):756–766
Kato T, Date T et al (2003b) Efficient replication of the genotype 2a hepatitis C virus subgenomic replicon. Gastroenterology 125(6):1808–1817
Kato T, Date T et al (2005) Nonhepatic cell lines HeLa and 293 support efficient replication of the hepatitis C virus genotype 2a subgenomic replicon. J Virol 79(1):592–596
Kaul A, Worez I et al (2007) Cellculture adaptation of hepatitis C virus and in vivo viability of an adapted variant. J Virol 81(23):13168–13179
Kaul A, Stauffer S et al (2009) Essential role of cyclophilin A for hepatitis C virus replication and virus production and possible link to polyprotein cleavage kinetics. PLoS Pathog 5(8):e1000546
Khromykh AA, Westaway EG (1997) Subgenomic replicons of the flavivirus Kunjin: construction and applications. J Virol 71(2):1497–1505
Kishine H, Sugiyama K et al (2002) Subgenomic replicon derived from a cell line infected with the hepatitis C virus. Biochem Biophys Res Commun 293(3):993–999
Kobayashi M, Bennett MC et al (2006) Functional analysis of hepatitis C virus envelope proteins, using a cell–cell fusion assay. J Virol 80(4):1817–1825
Kolykhalov AA, Agapov EV et al (1997) Transmission of hepatitis C by intrahepatic inoculation with transcribed RNA. Science 277(5325):570–574
Koutsoudakis G, Kaul A et al (2006) Characterization of the early steps of hepatitis C virus infection by using luciferase reporter viruses. J Virol 80(11):5308–5320
Koutsoudakis G, Herrmann E et al (2007) The level of CD81 cell surface expression is a key determinant for productive entry of hepatitis C virus into host cells. J Virol 81(2):588–598
Koutsoudakis G, Perez-del-Pulgar S et al (2011) Cell culture replication of a genotype 1b hepatitis C virus isolate cloned from a patient who underwent liver transplantation. PLoS ONE 6(8):e23587
Krey T, d'Alayer J et al (2010) The disulfide bonds in glycoprotein E2 of hepatitis C virus reveal the tertiary organization of the molecule. PLoS Pathog 6(2):e1000762
Krieger N, Lohmann V et al (2001) Enhancement of hepatitis C virus RNA replication by cell culture-adaptive mutations. J Virol 75(10):4614–4624
Lagaye S, Shen H et al (2012) Efficient replication of primary or culture hepatitis C virus isolates in human liver slices: a relevant ex vivo model of liver infection. Hepatology 56(3):861–872
Lagging LM, Meyer K et al (1998) Functional role of hepatitis C virus chimeric glycoproteins in the infectivity of pseudotyped virus. J Virol 72(5):3539–3546
Lambot M, Fretier S et al (2002) Reconstitution of hepatitis C virus envelope glycoproteins into liposomes as a surrogate model to study virus attachment. J Biol Chem 277(23):20625–20630
Lanford RE, Guerra B et al (2003) Antiviral effect and virus-host interactions in response to alpha interferon, gamma interferon, poly(i)-poly(c), tumor necrosis factor alpha, and ribavirin in hepatitis C virus subgenomic replicons. J Virol 77(2):1092–1104
Lanford RE, Guerra B et al (2006) Hepatitis C virus genotype 1b chimeric replicon containing genotype 3 NS5A domain. Virology 355(2):192–202
Lavillette D, Bartosch B et al (2006) Hepatitis C virus glycoproteins mediate low pH-dependent membrane fusion with liposomes. J Biol Chem 281(7):3909–3917
Lavillette D, Pecheur EI et al (2007) Characterization of fusion determinants points to the involvement of three discrete regions of both E1 and E2 glycoproteins in the membrane fusion process of hepatitis C virus. J Virol 81(16):8752–8765
Lazaro CA, Chang M et al (2007) Hepatitis C virus replication in transfected and serum-infected cultured human fetal hepatocytes. Am J Pathol 170(2):478–489
Liang C, Rieder E et al (2005) Replication of a novel subgenomic HCV genotype 1a replicon expressing a puromycin resistance gene in Huh-7 cells. Virology 333(1):41–53
Lin LT, Noyce RS et al (2010) Replication of subgenomic hepatitis C virus replicons in mouse fibroblasts is facilitated by deletion of interferon regulatory factor 3 and expression of liver-specific microRNA 122. J Virol 84(18):9170–9180

Lindenbach BD (2010) New cell culture models of hepatitis C virus entry, replication, and virus production. Gastroenterology 139(4):1090–1093
Lindenbach BD, Evans MJ et al (2005) Complete replication of hepatitis C virus in cell culture. Science 309(5734):623–626
Lindenbach BD, Meuleman P et al (2006) Cell culture-grown hepatitis C virus is infectious in vivo and can be recultured in vitro. Proc Natl Acad Sci USA 103(10):3805–3809
Lohmann V, Korner F et al (1999) Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell line. Science 285(5424):110–113
Lohmann V, Korner F et al (2001) Mutations in hepatitis C virus RNAs conferring cell culture adaptation. J Virol 75(3):1437–1449
Lohmann V, Hoffmann S et al (2003) Viral and cellular determinants of hepatitis C virus RNA replication in cell culture. J Virol 77(5):3007–3019
Long G, Hiet MS et al (2011) Mouse hepatic cells support assembly of infectious hepatitis C virus particles. Gastroenterology 141(3):1057–1066
Lundstrom K (2004) Gene therapy applications of viral vectors. Technol Cancer Res Treat 3(5):467–477
Ma Y, Yates J et al (2008) NS3 helicase domains involved in infectious intracellular hepatitis C virus particle assembly. J Virol 82(15):7624–7639
Maekawa S, Enomoto N et al (2004) Introduction of NS5A mutations enables subgenomic HCV replicon derived from chimpanzee-infectious HC-J4 isolate to replicate efficiently in Huh-7 cells. J Viral Hepat 11(5):394–403
Matsuura Y, Tani H et al (2001) Characterization of pseudotype VSV possessing HCV envelope proteins. Virology 286(2):263–275
McCaffrey K, Gouklani H et al (2011) The variable regions of hepatitis C virus glycoprotein E2 have an essential structural role in glycoprotein assembly and virion infectivity. J Gen Virol 92(Pt 1):112–121
McMullan LK, Grakoui A et al (2007) Evidence for a functional RNA element in the hepatitis C virus core gene. Proc Natl Acad Sci USA 104(8):2879–2884
Mee CJ, Harris HJ et al (2009) Polarization restricts hepatitis C virus entry into HepG2 hepatoma cells. J Virol 83(12):6211–6221
Meertens L, Bertaux C et al (2006) Hepatitis C virus entry requires a critical postinternalization step and delivery to early endosomes via clathrin-coated vesicles. J Virol 80(23):11571–11578
Michalak JP, Wychowski C et al (1997) Characterization of truncated forms of hepatitis C virus glycoproteins. J Gen Virol 78(Pt 9):2299–2306
Mittelholzer C, Moser C et al (1997) Generation of cytopathogenic subgenomic RNA of classical swine fever virus in persistently infected porcine cell lines. Virus Res 51(2):125–137
Miyamoto M, Kato T et al (2006) Comparison between subgenomic replicons of hepatitis C virus genotypes 2a (JFH-1) and 1b (Con1 NK5.1). Intervirology 49(1–2):37–43
Molina S, Castet V et al (2008) Serum-derived hepatitis C virus infection of primary human hepatocytes is tetraspanin CD81 dependent. J Virol 82(1):569–574
Molina-Jimenez F, Benedicto I et al (2012) Matrigel-embedded 3D culture of Huh-7 cells as a hepatocyte-like polarized system to study hepatitis C virus cycle. Virology 425(1):31–39
Morgello S (2005) The nervous system and hepatitis C virus. Semin Liver Dis 25(1):118–121
Mori K, Abe K et al (2008) New efficient replication system with hepatitis C virus genome derived from a patient with acute hepatitis C. Biochem Biophys Res Commun 371(1):104–109
Murray EM, Grobler JA et al (2003) Persistent replication of hepatitis C virus replicons expressing the beta-lactamase reporter in subpopulations of highly permissive Huh7 cells. J Virol 77(5):2928–2935
Murray CL, Jones CT et al (2008a) Architects of assembly: roles of Flaviviridae non-structural proteins in virion morphogenesis. Nat Rev Microbiol 6(9):699–708
Murray J, Fishman SL et al (2008b) Clinicopathologic correlates of hepatitis C virus in brain: a pilot study. J Neurovirol 14(1):17–27

Narbus CM, Israelow B et al (2011) HepG2 cells expressing microRNA miR-122 support the entire hepatitis C virus life cycle. J Virol 85(22):12087–12092

Ndongo-Thiam N, Berthillon P et al (2011) Long-term propagation of serum hepatitis C virus (HCV) with production of enveloped HCV particles in human HepaRG hepatocytes. Hepatology 54(2):406–417

Owsianka A, Tarr AW et al (2005) Monoclonal antibody AP33 defines a broadly neutralizing epitope on the hepatitis C virus E2 envelope glycoprotein. J Virol 79(17):11095–11104

Pacini L, Graziani R et al (2009) Naturally occurring hepatitis C virus subgenomic deletion mutants replicate efficiently in Huh-7 cells and are trans-packaged in vitro to generate infectious defective particles. J Virol 83(18):9079–9093

Parent R, Marion MJ et al (2004) Origin and characterization of a human bipotent liver progenitor cell line. Gastroenterology 126(4):1147–1156

Peng B, Xu MYS, Han B, Lee Y-J, Chan K, Tian Y, Pagratis N, Mo H, McHutchison J, Delaney W, Cheng G (2012) Development and molecular characterization of a robust genotype 4 Hepatitis C virus subgenomic replicon. J Hepatol 56(Suppl 2):S322

Phan T, Beran RK et al (2009) Hepatitis C virus NS2 protein contributes to virus particle assembly via opposing epistatic interactions with the E1–E2 glycoprotein and NS3-NS4A enzyme complexes. J Virol 83(17):8379–8395

Pietschmann T, Lohmann V et al (2001) Characterization of cell lines carrying self-replicating hepatitis C virus RNAs. J Virol 75(3):1252–1264

Pietschmann T, Lohmann V et al (2002) Persistent and transient replication of full-length hepatitis C virus genomes in cell culture. J Virol 76(8):4008–4021

Pietschmann T, Kaul A et al (2006) Construction and characterization of infectious intragenotypic and intergenotypic hepatitis C virus chimeras. Proc Natl Acad Sci USA 103(19):7408–7413

Pietschmann T, Zayas M et al (2009) Production of infectious genotype 1b virus particles in cell culture and impairment by replication enhancing mutations. PLoS Pathog 5(6):e1000475

Pileri P, Uematsu Y et al (1998) Binding of hepatitis C virus to CD81. Science 282(5390):938–941

Ploss A, Evans MJ (2012) Hepatitis C virus host cell entry. Curr Opin Virol 2(1):14–19

Ploss A, Khetani SR et al (2010) Persistent hepatitis C virus infection in microscale primary human hepatocyte cultures. Proc Natl Acad Sci USA 107(7):3141–3145

Podevin P, Carpentier A et al (2010) Production of infectious hepatitis C virus in primary cultures of human adult hepatocytes. Gastroenterology 139(4):1355–1364

Radkowski M, Wilkinson J et al (2002) Search for hepatitis C virus negative-strand RNA sequences and analysis of viral sequences in the central nervous system: evidence of replication. J Virol 76(2):600–608

Reiss S, Rebhan I et al (2011) Recruitment and activation of a lipid kinase by hepatitis C virus NS5A is essential for integrity of the membranous replication compartment. Cell Host Microbe 9(1):32–45

Roelandt P, Obeid S et al. (2012) Human pluripotent stem cell derived hepatocytes support complete replication of hepatitis C virus. J Hepatol 57(2):246–251

Rumin S, Berthillon P et al (1999) Dynamic analysis of hepatitis C virus replication and quasispecies selection in long-term cultures of adult human hepatocytes infected in vitro. J Gen Virol 80(Pt 11):3007–3018

Russell RS, Meunier JC et al (2008) Advantages of a single-cycle production assay to study cell culture-adaptive mutations of hepatitis C virus. Proc Natl Acad Sci USA 105(11):4370–4375

Sainz B Jr, Chisari FV (2006) Production of infectious hepatitis C virus by well-differentiated, growth-arrested human hepatoma-derived cells. J Virol 80(20):10253–10257

Sainz B Jr, TenCate V et al (2009) Three-dimensional Huh7 cell culture system for the study of Hepatitis C virus infection. Virol J 6:103

Sainz B Jr, Barretto N et al (2012) Identification of the Niemann-Pick C1-like 1 cholesterol absorption receptor as a new hepatitis C virus entry factor. Nat Med 18(2):281–285

Sarrazin C, Mihm U et al (2005) Clinical significance of in vitro replication-enhancing mutations of the hepatitis C virus (HCV) replicon in patients with chronic HCV infection. J Infect Dis 192(10):1710–1719

Scarselli E, Ansuini H et al (2002) The human scavenger receptor class B type I is a novel candidate receptor for the hepatitis C virus. EMBO J 21(19):5017–5025

Schaller T, Appel N et al (2007) Analysis of hepatitis C virus superinfection exclusion by using novel fluorochrome gene-tagged viral genomes. J Virol 81(9):4591–4603

Scheel TK, Gottwein JM et al (2008) Development of JFH1-based cell culture systems for hepatitis C virus genotype 4a and evidence for cross-genotype neutralization. Proc Natl Acad Sci USA 105(3):997–1002

Scheel TK, Gottwein JM et al (2011a) Efficient culture adaptation of hepatitis C virus recombinants with genotype-specific core-NS2 by using previously identified mutations. J Virol 85(6):2891–2906

Scheel TK, Gottwein JM et al (2011b) Recombinant HCV variants with NS5A from genotypes 1–7 have different sensitivities to an NS5A inhibitor but not interferon-alpha. Gastroenterology 140(3):1032–1042

Schwartz RE, Trehan K et al (2012) Modeling hepatitis C virus infection using human induced pluripotent stem cells. Proc Natl Acad Sci USA 109(7):2544–2548

Schwarz AK, Grove J et al (2009) Hepatoma cell density promotes claudin-1 and scavenger receptor BI expression and hepatitis C virus internalization. J Virol 83(23):12407–12414

Sieczkarski SB, Whittaker GR (2002) Dissecting virus entry via endocytosis. J Gen Virol 83(Pt 7):1535–1545

Spaete RR, Alexander D et al (1992) Characterization of the hepatitis C virus E2/NS1 gene product expressed in mammalian cells. Virology 188(2):819–830

Steinmann E, Penin F et al (2007) Hepatitis C virus p7 protein is crucial for assembly and release of infectious virions. PLoS Pathog 3(7):e103

Steinmann E, Brohm C et al (2008) Efficient trans-encapsidation of hepatitis C virus RNAs into infectious virus-like particles. J Virol 82(14):7034–7046

Sumpter R Jr, Loo YM et al (2005) Regulating intracellular antiviral defense and permissiveness to hepatitis C virus RNA replication through a cellular RNA helicase, RIG-I. J Virol 79(5):2689–2699

Tarr AW, Owsianka AM et al (2007) Cloning, expression, and functional analysis of patient-derived hepatitis C virus glycoproteins. Methods Mol Biol 379:177–197

Timpe JM, Stamataki Z et al (2008) Hepatitis C virus cell–cell transmission in hepatoma cells in the presence of neutralizing antibodies. Hepatology 47(1):17–24

Triyatni M, Saunier B et al (2002) Interaction of hepatitis C virus-like particles and cells: a model system for studying viral binding and entry. J Virol 76(18):9335–9344

Tscherne DM, Jones CT et al (2006) Time- and temperature-dependent activation of hepatitis C virus for low-pH-triggered entry. J Virol 80(4):1734–1741

Uprichard SL, Chung J et al (2006) Replication of a hepatitis C virus replicon clone in mouse cells. Virol J 3:89

Vieyres G, Pietschmann T (2012) Entry and replication of recombinant hepatitis C viruses in cell culture. Methods pii: S1046-2023(12)00245-9[Epub ahead of print]

Vieyres G, Angus AG et al (2009) Rapid synchronization of hepatitis C virus infection by magnetic adsorption. J Virol Methods 157(1):69–79

Wakita T, Pietschmann T et al (2005) Production of infectious hepatitis C virus in tissue culture from a cloned viral genome. Nat Med 11(7):791–796

Weissenborn K, Tryc AB et al (2009) Hepatitis C virus infection and the brain. Metab Brain Dis 24(1):197–210

Wellnitz S, Klumpp B et al (2002) Binding of hepatitis C virus-like particles derived from infectious clone H77C to defined human cell lines. J Virol 76(3):1181–1193

Whidby J, Mateu G et al (2009) Blocking hepatitis C virus infection with recombinant form of envelope protein 2 ectodomain. J Virol 83(21):11078–11089

Wilkinson J, Radkowski M et al (2009) Hepatitis C virus neuroinvasion: identification of infected cells. J Virol 83(3):1312–1319
Windisch MP, Frese M et al (2005) Dissecting the interferon-induced inhibition of hepatitis C virus replication by using a novel host cell line. J Virol 79(21):13778–13793
Witteveldt J, Evans MJ et al (2009) CD81 is dispensable for hepatitis C virus cell-to-cell transmission in hepatoma cells. J Gen Virol 90(Pt 1):48–58
Wu X, Robotham JM et al (2012) Productive Hepatitis C Virus Infection of Stem Cell-Derived Hepatocytes Reveals a Critical Transition to Viral Permissiveness during Differentiation. PLoS Pathog 8(4):e1002617
Yanagi M, Purcell RH et al (1997) Transcripts from a single full-length cDNA clone of hepatitis C virus are infectious when directly transfected into the liver of a chimpanzee. Proc Natl Acad Sci USA 94(16):8738–8743
Yi M, Lemon SM (2004) Adaptive mutations producing efficient replication of genotype 1a hepatitis C virus RNA in normal Huh7 cells. J Virol 78(15):7904–7915
Yi M, Lemon SM (2009) Genotype 1a HCV (H77S) infection system. Methods Mol Biol 510:337–346
Yi M, Bodola F et al (2002) Subgenomic hepatitis C virus replicons inducing expression of a secreted enzymatic reporter protein. Virology 304(2):197–210
Yi M, Villanueva RA et al (2006) Production of infectious genotype 1a hepatitis C virus (Hutchinson strain) in cultured human hepatoma cells. Proc Natl Acad Sci USA 103(7):2310–2315
Yi M, Ma Y et al (2007) Compensatory mutations in E1, p7, NS2, and NS3 enhance yields of cell culture-infectious intergenotypic chimeric hepatitis C virus. J Virol 81(2):629–638
Zhong J, Gastaminza P et al (2005) Robust hepatitis C virus infection in vitro. Proc Natl Acad Sci USA 102(26):9294–9299
Zhong J, Gastaminza P et al (2006) Persistent hepatitis C virus infection in vitro: coevolution of virus and host. J Virol 80(22):11082–11093
Zhu Q, Guo JT et al (2003) Replication of hepatitis C virus subgenomes in nonhepatic epithelial and mouse hepatoma cells. J Virol 77(17):9204–9210
Zhu H, Dong H et al (2007) Hepatitis C virus triggers apoptosis of a newly developed hepatoma cell line through antiviral defense system. Gastroenterology 133(5):1649–1659
Zignego AL, Giannini C et al (2007) Hepatitis C virus lymphotropism: lessons from a decade of studies. Dig Liver Dis 39(Suppl 1):S38–S45

http://www.springer.com/978-3-642-27339-1

Hepatitis C Virus: From Molecular Virology to Antiviral Therapy

Bartenschlager, R. (Ed.)

2013, VIII, 346 p. 34 illus., 20 illus. in color., Hardcover
ISBN: 978-3-642-27339-1