

Structural Proteins of HCV and Biological Functions

Kohji Moriishi and Yoshiharu Matsuura

Abstract Hepatitis C virus (HCV) is a major causative agent of liver disorders and a major risk factor for hepatocellular carcinoma. The induction of hepatocellular carcinoma by HCV is thought to involve not only chronic inflammation, but also the biological activity of HCV components. Structural proteins of HCV are composed of the core protein and two envelope proteins, E1 and E2. The HCV core protein has been reported to exhibit multiple biological functions involved in lipid synthesis, iron metabolism, insulin response, oxidative stress and cell growth, and to thereby contribute to the development of carcinogenesis and metabolic disorders. Moreover, several reports suggest that envelope proteins also play an important role in viral entry as well as HCV-related pathogenic events. However, the mechanism by which the structural proteins induce hepatitis C-related disorders has not been fully understood. This review focuses on the current status of biological responses mediated by HCV structural proteins.

Keywords HCV • Structural proteins • Core protein • Envelope protein • Oxidative stress • Insulin resistance • Lipid metabolism • Mitochondria

Hepatitis C virus (HCV) possesses a genome consisting of a single positive strand RNA with a nucleotide length of 9.6 kb, which encodes a single polyprotein. This polyprotein is matured by processing dependent on host and viral proteases, resulting in structural and nonstructural proteins (Grakoui et al. 1993a, b; Harada et al. 1991; Hijikata et al. 1991). Structural proteins consisting of the core protein and two envelope proteins E1 and E2 occupy one third of the N-terminal region of the polyprotein, while the remaining viral proteins consist of the viroporin p7 and nonstructural proteins which form a replication complex with host factors (Grakoui et al. 1993c). The structural proteins and host lipid components are employed for

K. Moriishi, D.V.M., Ph.D.

Department of Microbiology, Division of Medicine, Graduate School of Medicine and Engineering, University of Yamanashi, 409-3898 Chuo-shi, Yamanashi, Japan

Y. Matsuura, D.V.M., Ph.D. (✉)

Department of Molecular Virology, Research Institute for Microbial Diseases, Osaka University, 565-0871 Osaka, Japan

e-mail: matsuura@biken.osaka-u.ac.jp

formation of the viral particle (for review see (Moriishi and Matsuura 2012). The nucleocapsid consisting of mature core proteins and a viral genome is surrounded by an envelope composed of host lipids and viral envelope proteins.

The HCV core protein and envelope proteins are released from the viral polyprotein by host proteases. HCV structural proteins may provide a host for severe liver disorders over several decades of persistent infection. The HCV core protein is involved in formation of the viral particle as well as the induction of liver disorders, including metabolic diseases. In addition, it is more important that the core protein could induce hepatocellular carcinoma in mice regardless of other HCV viral proteins (Moriya et al. 1998). Accumulating evidence supports the notion that envelope proteins induce a stress response during persistent infection to lead to liver disorders. This review summarizes the biological functions of HCV structural proteins in the development of HCV-related disorders.

1 Maturation of HCV Structural Proteins for Assembly of Viral Particles

1.1 Processing and Modification of HCV Core Protein

Hepatitis C virus (HCV) belongs to the genus Hepacivirus of the *Flaviviridae* family. The *Flaviviridae* family is composed of four genera, Flavivirus, Pestivirus, Pegivirus and Hepacivirus. The viral genomic structures and the composition of viral proteins differ among these genera. The capsid, or core, protein is encoded in the 5'-regions of the viral genomes of three of the four genera, with the exception being Pegivirus. Pegivirus does not have a capsid protein, suggesting that unknown viral or host proteins may be involved in formation of the viral particle. The structure and processing of the capsid protein are variable in genera of the *Flaviviridae* family. The structural proteins of HCV were detected as processed proteins at the first time in mammal and insect cells (Matsuura et al. 1992), contributing to identification of their cleavage sites. The capsid proteins of HCV and GBV-B, which are classified into the genus Hepacivirus, are cleaved by signal peptide peptidase (SPP), following signal peptidase-dependent processing (McLauchlan et al. 2002; Targett-Adams et al. 2006), while the capsid protein of classical swine fever virus (CSFV), which belongs to the genus Pestivirus, is cleaved by SPP (Heimann et al. 2006). The C-terminal end of the mature HCV core protein expressed in insect cells was reported to be Phe177 or Leu179 (Hussy et al. 1996; Ogino et al. 2004). The C-terminal residue of the mature HCV core protein that was expressed in a human cell line was identified as Phe177 by mass spectrometry (Okamoto et al. 2008). Non-primate hepaciviruses have recently been identified in dogs, horses, rodents and bats (Burbelo et al. 2012; Drexler et al. 2013; Kapoor et al. 2011, 2013; Lyons et al. 2012; Tanaka et al. 2014). The C-terminal hydrophobic membrane-anchoring region of HCV core protein shows high

homology to the core protein of equine hepacivirus, which is the most closely related homologue of HCV among non-primate hepaciviruses (Burbelo et al. 2012; Kapoor et al. 2013; Lyons et al. 2012). We recently reported that the core protein of equine hepacivirus was cleaved by SPP and then localized on the lipid droplets and partially on lipid-raft like membranes in a manner similar to HCV core protein (Tanaka et al. 2014). The secondary structures and cis-acting elements of the equine hepacivirus genome also exhibit characteristics similar to those of the HCV genome (Tanaka et al. 2014). The mechanism of the viral propagation may thus be conserved between equine hepacivirus and HCV.

A hydrophobicity/hydrophilicity plot suggests that the core protein consists of three domains, domain 1 (2–118), 2 (119–174), and 3 (175–191) (Hope and McLauchlan 2000; McLauchlan 2000). The helix-loop-helix structure located in domain 2 is critical for association of the core protein with lipid droplets and shares common features with the core proteins of GBV-B (Hope et al. 2002). Three hydrophobic amino acid residues, Leu139, Val140, and Leu144, in domain 2 exhibit hydrophobic peaks within domain 2 and are responsible for SPP-dependent cleavage, membrane anchoring and virus production (Okamoto et al. 2004, 2008). Furthermore, comparative analysis between the JFH1 and Jc1 strains suggests that the efficiency of virus assembly is determined by the binding ability of domain 2 to lipid droplets (Shavinskaya et al. 2007). Cysteine residue 172 of HCV core protein is palmitoylated. Palmitoylation of the core protein is responsible for the virus production but not for SPP-dependent processing or LD localization of the core protein (Majeau et al. 2009). These results suggest that the hydrophobicity of domains 2 and 3 is critical for intracellular localization and SPP cleavage of the core protein and viral production.

Recently, herpesviruses and other pathogens have been reported to employ SPP for their life cycles and pathogenesis. Human cytomegalovirus protein US2 promoted dislocation of the class I major histocompatibility complex (MHC) heavy chain from the endoplasmic reticulum (ER) by direct interaction with SPP, resulting in proteasome-dependent degradation of the MHC class I heavy chain (Loureiro et al. 2006). Herpes simplex virus-1 exploited SPP by binding to the viral glycoprotein gK for its own replication (Allen et al. 2014). The human malaria *Plasmodium falciparum* expresses its own SPP on the cell surface. The malaria SPP recognizes Band3 in the red blood cells for invasion (Li et al. 2008). SPP inhibitors, L-685,458, NITD731 and LY411,575, were shown to block the growth of *P. falciparum* and the rodent malarial parasite *P. berghei* (Li et al. 2009c; Harbut et al. 2012; Parvanova et al. 2009). SPP or SPP-like proteases may be employed by other pathogens for their propagation and will be target molecules for the development of therapeutic compounds against several pathogens.

1.2 Structure of Envelope Proteins for the Viral Entry and Assembly

HCV envelope proteins E1 and E2 are cleaved from the polyprotein by signal peptidase (Hijikata et al. 1991). Both E1 and E2, each of which consists of a large ectodomain with a C-terminal transmembrane region, are classified into a group of type I membrane proteins and are reported to form non-covalent heterodimers (Deleersnyder et al. 1997). The envelope proteins are highly modified post-translationally at 6 and 11 potential sites for N-glycosylation (Goffard and Dubuisson 2003; Zhang et al. 2004), some of which are responsible for infectivity (Goffard et al. 2005). The core domain (the ectodomain E2 lacking HVR1) of the HCV E2 protein shares some basic characteristics with other class II fusion proteins, such as an immunoglobulin-like fold consisting of a β -sheet structure (Kong et al. 2013; Khan et al. 2014). However, the precise function of E1 and E2 in membrane fusion has not yet been fully clarified. Two hydrophobic regions spanning from 504 to 522 and from 604 to 624 in E2 are predicted to be potential fusion peptides (Khan et al. 2014; Lavillette et al. 2007; Krey et al. 2010), while the region spanning from 262 to 290 in E1 is reported to be important for membrane fusion (Li et al. 2009b). E2 should be responsible for the HCV entry step in cooperation with E1, but the mechanism underlying this step remains unclear.

The synthesized viral genome is wrapped with the core proteins to form a nucleocapsid on lipid droplets close to the ER, on which the viral genome is synthesized (Miyanari et al. 2007). A nucleocapsid egresses with envelope proteins into the ER membrane in close proximity to the lipid droplets. HCV particles in the patients' sera have been reported to exhibit densities of 1.03–1.25 g/ml (Thomssen et al. 1992, 1993). HCV particles with a density of lower than 1.06 g/ml are infectious to chimpanzees, while those with a higher density exhibit lower infectivity (Bradley et al. 1991; Hijikata et al. 1993). HCV particles interacting with lipoproteins in the sera of patients (Andre et al. 2002) were prepared from the fractions with very low to low buoyant densities (1.03–1.25 g/ml), and have been designated lipo-viro-particles (LVP) (Andre et al. 2002; Nielsen et al. 2006). LVP are composed of HCV particle components and very low-density lipoproteins (VLDL), including apolipoprotein B (ApoB) and apolipoprotein E (ApoE) (Andre et al. 2002). The HCV entry process on the surface of hepatocytes has been reported to be carried out by using entry factors including LDLR, CD81, scavenger receptor class B type I (SR-BI), and the tight junction proteins claudin-1 and occludin (Bartosch et al. 2003; Evans et al. 2007; Pileri et al. 1998; Ploss et al. 2009). Lectin receptors including DC-SIGN, L-SIGN, and langerin may be responsible for the invasive step from sinusoidal endothelial cells (Lozach et al. 2003; Pohlmann et al. 2003; Gardner et al. 2003; Chen et al. 2014). Envelope proteins with Man8/9 N-glycans exhibit higher binding to lectin receptors (DC-SIGN, L-SIGN and langerin) than to non-lectin receptors (CD81, SRBI, claudin-1, and occludin) in the presence of calcium ions, while HCV envelope proteins with Man5 N-glycans bound to non-lectin receptors at a higher affinity than lectin receptors (Chen

et al. 2014). The HCV viral particle may be captured by lectin receptors on sinusoidal endothelial cells at a high affinity followed by infection to hepatocytes via non-lectin receptors. HCV envelope proteins interact with ApoE and ApoB in ER (Boyer et al. 2014). Intracellular and extracellular infectious particles also associate with ApoE and ApoB (Boyer et al. 2014). ApoE, but not E2, on the surface of LVP mediates the SR-BI-dependent entry step via the lipid transfer activity of SR-BI, although the HVR1 of E2 affects this step (Dao Thi et al. 2012). These results suggest that E2 HVR1 enhances the SR-BI-ApoE interaction for HCV entry. Further study will be required to clarify the mechanism by which HCV utilizes SR-BI for its entry step.

2 Biological Functions of Structural Proteins

2.1 *Modulation of Lipid Metabolism by HCV Core Protein*

Liver steatosis is frequently found in persistent HCV infection and results in accumulation of triglyceride and fatty acids in hepatocytes (see Negro 2010). However, the involvement of HCV infection in the development of fatty liver has not yet been clarified completely. Several reports support the notion that HCV core protein contributes to the accumulation of lipid droplets and hepatic steatosis in transgenic mice and cultural cells (Barba et al. 1997; Hope and McLauchlan 2000; Moriya et al. 1997). The lipid profiling of a core transgenic mouse of genotype 1b showed a similar composition to that of a hepatitis C patient (Koike et al. 2010; Miyoshi et al. 2011). Syntheses of triglycerides and fatty acids are transcriptionally regulated by the sterol regulatory element-binding proteins (SREBPs) (Horton et al. 2002). An HCV cell culture system derived from the genotype 3a strain showed that lipid accumulation was enhanced in cells infected with HCV genotype 3a compared to those infected with the genotype 2a strain JFH-1 (Kim et al. 2014). Patients infected with HCV genotype 3a exhibited progression of steatosis at a significantly higher rate than those with genotype 1a or 1b (Adinolfi et al. 2011; Mihm et al. 1997). Expression of the HCV core protein derived from genotype 3a induced lipid accumulation in lipid-free cultured cells at a higher level than expression of other genotype core proteins (Abid et al. 2005). The HCV core protein of genotype 3a stimulated activity of the fatty acid synthetase promoter at a significantly higher level than that of genotype 1b (Abid et al. 2005).

HCV infection or expression of the genotype 3a core protein was found to enhance the cleavage of SREBPs, leading to posttranslational activation of SREBPs (Waris et al. 2007). The recent report by Bose et al. suggested that the forkhead box transcription factor FoxO1 was activated by the HCV core protein or infection followed by activation of sreb-1c promoter activity, leading to the accumulation of lipids (Bose et al. 2014). However, controversial results were reported from hepatitis C patients. McPherson reported that SREBP-1c was not involved in

HCV-related steatosis (McPherson et al. 2008), whereas Lima-Cabello et al. reported that LXR α , SREBP-1c and -2, and fatty acid synthetase were overexpressed in the livers of HCV patients with steatosis (Lima-Cabello et al. 2011), suggesting that LXR α transcriptionally upregulates SREBP-1c expression followed by fatty acid synthetase expression. It has been reported that most of the genes under the control of SREBPs were upregulated during the early stage of HCV infection in the livers of chimpanzees (Bigger et al. 2004). Our previous data indicated that the core protein potentiates the binding ability of the LXR α -RXR α complex to the *srebp-1c* promoter in cultured cells and in the livers of core-transgenic mice (Moriishi et al. 2007). Upregulation of *srebp-1c* promoter activity may be associated with direct interaction between the core protein and RXR α (Tsutsumi et al. 2002b). Cholesterol and ApoB were significantly reduced in patients with severe hepatitis C or core-transgenic mice (Perlemuter et al. 2002). The microsomal triglyceride transfer protein (MTP) positively regulates the formation and secretion of very low-density lipoproteins. In core-transgenic mice, MTP-specific activity is significantly decreased (Perlemuter et al. 2002), resulting in accumulation of lipids in the liver. The gene related to the synthesis and secretion of lipids may be regulated by HCV infection or the core protein at a transcriptional and/or post-translational step.

Peroxisome proliferator activated receptors are nuclear receptors that transcriptionally regulate metabolic signaling (Halilbasic et al. 2013). PPAR α regulates the genes encoding enzymes associated with peroxisomal microsomal and mitochondrial γ oxidation (Halilbasic et al. 2013). PPAR α is expressed in the liver and down-regulated in the HCV-infected liver and the core-expressing HepG2 cells (Dharancy et al. 2005). PPAR α was decreased in mice infected with adenovirus expressing the HCV core protein (Yamaguchi et al. 2005). In an earlier study, severe liver steatosis was induced in core-transgenic mice (Moriya et al. 1997). HCV replication transcriptionally induced the expression of miR-27 in cell culture and an in vivo mouse model (Singaravelu et al. 2014). Both the HCV core protein and NS4B promote the expression of miR-27 through a PI3-K-dependent pathway. Transfection of miR-27 enhances the size and volume of lipid droplets in cultured cells and also impairs PPAR α signaling. PPAR α transcriptionally increases the genes regulating mitochondrial and peroxisomal fatty acid oxidation (Desvergne and Wahli 1999). An increase in miR-27 in infected cells also downregulates ANGPTL3, which is an inhibitor of lipoprotein lipase responsible for fatty acid uptake (Mattijssen and Kersten 2012). These data suggest that induction of miR-27 by HCV infection downregulates fatty acid oxidation via impairment of PPAR α signaling and up-regulates fatty acid uptake via inhibition of ANGPTL3 expression, leading to development of liver steatosis. Unexpectedly, PPAR α -knockout core-transgenic mice did not show steatosis (Tanaka et al. 2008). Furthermore, PPAR α expression was required for induction of hepatocellular carcinoma by HCV core protein (Tanaka et al. 2008). Therefore, the HCV core protein may require a small amount of PPAR α for the development of liver disorders and may maintain PPAR α at a steady level.

PPAR γ is involved in adipocyte differentiation and energy storage by adipocytes mediating an anabolic energy state (Halilbasic et al. 2013). In addition, PPAR γ plays an important role in the development of liver steatosis (Gavrilova et al. 2003; Yu et al. 2003). The HCV core protein has been shown to potentiate PPAR γ activity and transcriptionally upregulate SREBP1 activity, resulting in lipid accumulation. Furthermore, HCV core protein expression induced leptin receptor activation in hepatic stellate cells and contributed to transcriptional upregulation of MMP-1, PAPR γ and SREBP-1c, leading to promotion of hepatic fibrogenesis (Wu et al. 2013). PPAR γ may thus be involved in HCV core-induced liver steatosis, in cooperation with PPAR α .

2.2 Regulation of Iron Metabolism by HCV Core Protein

Iron overload has been reported as a common hallmark of chronic hepatitis C infection (Bonkovsky 2002; Boucher et al. 1997; Di Bisceglie et al. 1992). Accumulation of iron in the liver by HCV infection promotes liver inflammation and interferon resistance due to inhibition of the JAK-STAT pathway by oxidative stress (Olynyk et al. 1995; Bassett et al. 1999; Nishina et al. 2008; Fujita et al. 2007). Iron is involved in induction of reactive oxygen species (ROS). Iron Fe²⁺ reacts with hydrogen peroxide (H₂O₂) to yield Fe³⁺, hydroxyl radical (\cdot OH), and hydroxide ion (OH⁻) (Fenton reaction) (Graf et al. 1984). Hydroxyl radical reacts with lipids, resulting in lipid peroxidation (Okada 1996). Iron concentration in the liver is regulated by an import protein transferrin receptor and an export protein ferroportin (Pantopoulos et al. 2012). Imported iron atoms are enclosed with ferritin in cells and stored as iron-ferritin complexes (Ganz and Nemeth 2012; Liu and Theil 2005). Another iron-regulating protein, hepcidin, which is encoded on the gene HAMP, is a short peptide inducing internalization and degradation of ferroportin and regulates plasma iron concentration and iron metabolism in the liver (Ganz and Nemeth 2012; Nemeth et al. 2004, 2006). Expression of hepcidin is stimulated by iron overload and inflammation, and is suppressed by anemia and hypoxia (Nemeth and Ganz 2006). BMP6 is produced and secreted by various cell types and is a main regulator of hepcidin expression (Andriopoulos et al. 2009). BMP6 binds and stimulates dimers of BMP-RI/II to cooperate with the coreceptor hemojuvelin (Andriopoulos et al. 2009; Meynard et al. 2009; Xia et al. 2008), leading to downstream signaling including dimerization of Smad4 with Smad1/5/8 (Wang et al. 2005). Smad dimers transcriptionally induce expression of hepcidin. Screening of a whole genome using an siRNA library revealed that hepcidin-knockdown reduced HCV replication significantly (Tai et al. 2009), suggesting that hepcidin expression is required for HCV replication and control of iron metabolism. Hepcidin was shown to be transcriptionally enhanced by the HCV core protein through Smad4, STAT3 and CK2 (Foka et al. 2014). Knockdown of hepcidin impaired HCV replication in a replicon cell line (Bartolomei et al. 2011). Iron upregulates HCV replication by enhancement of IRES-dependent translation

and expression of eIF3 and La (Cho et al. 2008; Theurl et al. 2004; Wang et al. 2012). However, knockdown of hepcidin suppressed IRES- as well as CAP-dependent translation (Tai et al. 2009). Hepcidin may contribute to translational regulations of the viral proteins and host proteins by accumulation of iron in HCV-infected cells.

2.3 *Quality Control of HCV Structural Proteins*

The core protein is modified with ubiquitin by host enzymes. The host E3 ligase E6AP catalyzes ubiquitination of the core protein to suppress viral production (Shirakura et al. 2007). The poly-ubiquitinated core protein is degraded in the cytosol in a proteasome-dependent manner. HCV core protein is also degraded in a ubiquitin-independent PA28 γ -dependent pathway, leading to upregulation of the viral production by suppression of cytosolic ubiquitin-dependent degradation of the core protein (Moriishi et al. 2003, 2007). The host mechanisms of protein degradation may regulate HCV production and control the quality of the core protein for viral propagation. Although qualitative limitations of HCV envelope proteins have been regulated by an ER-associated degradation (ERAD) system (Saeed et al. 2011), inhibition of ER enhanced the viral production (Saeed et al. 2011), suggesting that unfolded envelope proteins positively regulate the HCV production.

The unfolded protein response (UPR) is carried out by three pathways, an IRE1 α , a PERK and an ATF6-dependent pathway (Gardner et al. 2013). The luminal domains of the PERK, ATF6 and IRE1 α proteins interact with the ER resident chaperone BiP (Bertolotti et al. 2000). BiP renders PERK, ATF6 and IRE1 α inactive without accumulation of unfolded protein (Bertolotti et al. 2000), while the accumulation of unfolded proteins stimulates release of BiP from PERK, ATF6 or IRE1 α , leading to the induction of genes related to protein folding, cell survival, autophagy and so on (Bertolotti et al. 2000). UPR stimulates expression of both MAP1LC3B and ATG5 by ATF4 and CHOP, which are induced by activation of PARG and ATF6 (Rouschop et al. 2010; Wang et al. 2014). ATF4 also activates transcription of CHOP (Kojima et al. 2003). The HCV core protein was recently shown to activate both the PERK and ATF6 pathways, but not the IRE1 α pathway, to stimulate expression of MAP1LC3B, ATG12 and ATG5 (Wang et al. 2014), suggesting that autophagy is induced by the upregulation of ATG proteins through the UPR of HCV core protein. Expression of HCV envelope proteins induced the expression of CHOP through PERK and IRE1 α pathways (Chan and Egan 2005). CHOP stimulates IP3R through Ero1 α activation, followed by accumulation of Ca²⁺ in mitochondria (Li et al. 2009a). UPR-induced accumulation of Ca²⁺ in mitochondria may be associated with ROS production in HCV infected cells, as described later.

2.4 *Effect of HCV Infection on Mitochondria*

The HCV core protein can enhance the production of ROS by damaging the mitochondrial electron transport system, and thereby contribute to the emergence of hepatocellular carcinoma (Moriya et al. 2001; Nunez et al. 2004; Okuda et al. 2002), suggesting that accumulation of lipids advances the occurrence of hepatocellular carcinoma by enhancing ROS production. Expression of HCV polyproteins in cultured sarcoma cells promoted the production of ROS and nitrogen species and inhibited complex I activity, resulting in activation of mitochondrial calcium uptake (Piccoli et al. 2007). The HCV core protein is localized in the lipid droplets, ER and mitochondria (Okuda et al. 2002) and could induce ROS, leading to accumulation of lipid peroxidation products and enhancement of antioxidant gene expression (Okuda et al. 2002). Upregulation of lipid peroxidation was observed in core-transgenic mice but not in wild type mice following treatment with CCl₄ (Okuda et al. 2002). The mitochondria of transgenic mice expressing HCV polyprotein exhibited enhancement of glutathione oxidation, decrease in NADPH contents, impairment of complex I activity and promotion of ROS production (Korenaga et al. 2005). Glutathione oxidation and ROS upregulation were also found in isolated mitochondria in the presence of recombinant core protein (Korenaga et al. 2005). Ca²⁺ uptake was increased by the recombinant core protein in isolated mitochondria (Korenaga et al. 2005). HCV core protein induced ER stress via an unfolded protein response and then potentiated production of ER chaperone proteins and release of Ca²⁺ from the ER store (Benali-Furet et al. 2005; Bergqvist et al. 2003). In addition, the HCV core protein was found to enhance mitochondrial Ca²⁺ uptake via the Ca²⁺ uniporter, which is localized in the mitochondrial inner membrane (Li et al. 2007). Furthermore, HCV core protein interacted with the mitochondria chaperone prohibitin to upregulate prohibitin stability in cultured cells and the transgenic mouse liver (Tsutsumi et al. 2009). HCV core protein inhibited the interaction between prohibitin and COX, resulting in the impairment of COX activity (Tsutsumi et al. 2009). These reports suggest that HCV core protein induces ER stress and Ca²⁺ release from the ER and then stimulates mitochondrial Ca²⁺ uptake to upregulate ROS production. In addition, the HCV core protein may impair COX activity by both sequestering prohibitin and decreasing glutathione, leading to further enhancement of ROS production.

2.5 *Insulin Resistance*

Epidemiological studies have clearly established an association between type 2 diabetes mellitus and HCV infection (Cavaghan et al. 2000; Kahn 1998). Type 2 diabetes is a complex disease characterized by the high-level production of hepatic glucose due to insulin resistance, resulting in glucose tolerance hyperglycemia (Cavaghan et al. 2000; Kahn 1998). Insulin is ordinarily produced at a

sufficient level in type 2 diabetes mellitus patients; however, the glucose level cannot be decreased due to a disorder in insulin signaling. Insulin receptor is a tyrosine kinase composed of two subunits (Draznin 2006; Youngren 2007). Binding of insulin activates insulin receptor, which triggers Tyr phosphorylation of insulin receptor substrate 1 (IRS1) (Draznin 2006; Youngren 2007). The phosphorylated IRS1 and IRS2 positively regulate PI3K, which phosphorylates phosphatidylinositol 4, 5-bisphosphate into phosphatidylinositol-3,4,5-triphosphate (PIP3). PDK1 and PDK2 are recruited by the resulting PIP3 with Akt and then phosphorylate Akt at Thr308 and Ser 473 (Burgering and Coffey 1995; Taniguchi et al. 2006; Alessi et al. 1996; Manning and Cantley 2007), resulting in activation of Akt. Phosphorylated Akt itself phosphorylates a glucose transporter, GLUT-4, contributing to translocation of GLUT-4 to the plasma membrane for upregulation of glucose uptake (Taniguchi et al. 2006; Thirone et al. 2006).

Elevation of TNF α production is one of the risk factors for insulin resistance (Gurav 2012). TNF α can indirectly mediate phosphorylation of IRS1 at multiple sites through the activation of several Ser kinases, including JNK, IKK β and ERK (Gao et al. 2003; Solinas and Karin 2010). TNF α stimulates activation of MEKK1, ASK1 and TAK1, which phosphorylate MKK7 for activation (Nakajima et al. 2006). In the same study, phosphorylated MKK7 was able to phosphorylate JNK (Nakajima et al. 2006). JNK1 has been shown to interact with IRS1 through the region spanning from the residues 555–898 (Aguirre et al. 2000). Phosphorylation of IRS1 Ser307 was detected in cultured cells treated with a JNK agonist, resulting in a decrease in Tyr phosphorylation of IRS1 (Aguirre et al. 2000). Rui et al. suggested that a TNF α -dependent, JNK-independent mechanism may also be associated with phosphorylation of IRS1 Ser307 (Rui et al. 2001). Insulin was shown to stimulate the PI3K pathway to enhance phosphorylation of IRS1 Ser307 (Aguirre et al. 2002; Rui et al. 2001). Insulin-stimulated JNK phosphorylates IRS1 S307 may be a negative feedback pathway of insulin signaling (Lee et al. 2003). Phosphorylation of IRS1 Ser307 by JNK impairs the binding ability of IRS1 to insulin receptor (Aguirre et al. 2002), while phosphorylation of IRS1 Ser302 by JNK may also be involved in the negative feedback of insulin signaling (Werner et al. 2004). An increase in TNF α and a decrease in Tyr phosphorylation of IRS1 were observed in both the livers of HCV core gene transgenic mice and hepatitis C patients (Shintani et al. 2004; Miyamoto et al. 2007). Furthermore, JNK and its downstream factor AP-1 have been shown to be activated in core gene transgenic mice (Tsutsumi et al. 2002a). The HCV core protein also activated JNK and enhanced phosphorylation of IRS1 Ser312, leading to a decrease in Tyr phosphorylation of IRS1 and inhibition of insulin signaling (Banerjee et al. 2008). HCV core protein may activate JNK through upregulation of TNF α production, leading to insulin resistance through Ser phosphorylation of IRS1.

Evidence of the involvement of suppressor of cytokine signaling (SOCS) proteins in HCV-associated insulin resistance has been accumulating. SOCS-1 and SOCS-3 show relatively high homology and share similar functions. Both SOCS-1 and SOCS-3 can bind to insulin receptors irrespective of their phosphorylation status and impair Tyr phosphorylation of IRS-1 (Ueki et al. 2004). Further, SOCS-1

and SOCS-3 were shown to promote the degradation of IRS-1/2 via the ubiquitin-proteasome pathway (Rui et al. 2002). SOCS-1, but not SOCS-3, was decreased in the livers of core gene transgenic mice and hepatitis C patients, as well as in HepG2 cells expressing HCV core protein (Miyoshi et al. 2005). Expression of SOCS-3 was promoted after IFN treatment in HCV-infected chimpanzees, whereas the human liver showed variable responses to different treatments (Huang et al. 2007). SOCS-3 expression was significantly promoted in peripheral lymphocytes prepared from genotype 1b-infected IFN-non-responders (Persico et al. 2007). HCV core protein stimulated the expression of SOCS-3 and then enhanced ubiquitination of IRS1 and IRS2, leading to a decrease in IRS1/2 in a proteasome-dependent pathway (Kawaguchi et al. 2004). Induction of SOCS3 expression by the HCV core protein may be associated with the core protein mutations of Met70 and Leu91 (Funaoka et al. 2011), which are statistical predictors of low response to IFN/ribavirin therapy (Akuta et al. 2005, 2010). The regulation of IRS1 by HCV core protein may be accomplished by a genotype-specific pathway. Ubiquitin-dependent degradation of IRS1 was observed by the HCV core protein of genotypes 1b and 3a (Pazienza et al. 2007). In addition, IRS1 was decreased transcriptionally by downregulation of PPAR γ and post-translationally by upregulation of SOCS-7 (Pazienza et al. 2007), while the core protein of genotype 1b activated mTOR, which suppresses IRS1 by Ser/Thr phosphorylation (Pazienza et al. 2007). E2 transcriptionally promoted the expression of SOCS3 and ubiquitination-dependent downregulation of IRS1, resulting in the impairment of Akt and GSK3 (Hsieh et al. 2012). The HCV core protein may regulate SOCS proteins cooperating with E2 under infectious conditions.

2.6 Involvement of Envelope Proteins in Biological Functions

Envelope proteins may control tight junction and facilitate secondary invasion of HCV after primary infection. Occludin, claudin-1 and ZO-1, which are tight junction proteins, are localized in the baso-lateral membrane position of Huh7, while these tight junction proteins were defused in Huh7 harboring a full-genomic but not a sub-genomic HCV replicon (Benedicto et al. 2008). Exogenous expression of HCV structural proteins, but not core alone, resulted in the translocation of tight junction proteins irrespective of the viral replication (Benedicto et al. 2008). HCV envelope proteins may facilitate subsequent virus infection by disruption of tight junction.

HCV envelope proteins may regulate ROS production and cell death. HCV infection was shown to stimulate production of ROS and NO and to reduce mitochondrial transmembrane potential (Machida et al. 2006), leading to double-stranded DNA breaks and apoptosis. Although expression of core, E1, or NS3 could induce ROS production in cultured cells (Machida et al. 2006), regulation of

apoptosis by E2 is controversial. Chiou et al. reported that E2 induces apoptosis by cytoplasmic release of cytochrome c, upregulation of Bax and downregulation of Bcl-2 followed by activations of caspases-3, 8, and 9 (Chiou et al. 2006), whereas apoptosis induced by the death ligand TRAIL was suppressed by the expression of E2 (Lee et al. 2005). The expression of E2 may be capable of supporting the HCV replication by inhibiting apoptosis (Lee et al. 2005).

Phosphorylation and activation of STAT1 were enhanced by the expression of both HCV E2 and HIV gp120 (Balasubramanian et al. 2006). Lyn kinase, p38MAP kinase and protein kinase C δ are responsible for STAT1 phosphorylation (Balasubramanian et al. 2006). An increase in STAT1 might contribute to apoptosis in the hepatocytes of patients co-infected with HCV and HIV. HCV infection down-regulated the amounts of miR181c, which targets homeobox A1 (HOXA1), by modulating C/EBP- β (Mukherjee et al. 2014). In the same study, HOXA1 expression was potentiated in HCV-infected cells (Mukherjee et al. 2014). In addition, miR-181c was shown to bind directly to the E1 or NS5A gene (Mukherjee et al. 2014). Finally, HOXA1 promotes cell growth through upregulation of STAT3 and STAT5 (Mohankumar et al. 2007). These data suggest that the transcriptional and posttranscriptional down-regulation of miR-181c by HCV infection might contribute to activation of HOXA1 followed by upregulation of STA3 and STAT5.

3 Conclusions

The structural proteins of HCV are basically employed for formation of a viral particle like structural proteins of other enveloped viruses. The HCV core proteins is processed by host proteases, and then associated with lipid droplets and intracellular compartments for formation of nucleocapsid, while HCV glycoproteins, E1 and E2, are localized in ER membrane in close proximity to the lipid droplets. Both envelope proteins are classified into a group of type I membrane proteins, and are reported to form non-covalent heterodimers. The recent report of structural analysis revealed that HCV E2 protein is classified into the family of class II fusion protein. The envelope proteins play an important role in an entry step cooperating with several host entry factors, lectin and lipoproteins. In this text, we also summarized the biological functions of HCV structural proteins (Fig. 1). To date, it has not been fully clarified how HCV can cause hepatocellular carcinoma in humans. Persistent inflammation over a long period of time is expected to be associated with the development of hepatocellular carcinoma, due to both genomic alterations and biological functions of the HCV proteins. HCV core protein upregulates uptake of free fatty acids and the transcriptional activities of SREBPs, and down-regulates MTP function and β -oxidation, leading to liver steatosis. In addition, the structural proteins induce accumulation of mitochondrial Ca^{2+} and iron via ER stress and functions of hepcidin and Ca^{2+} uniporter, resulting in an increase in ROS. Oxidative stress induced by HCV infection may be one of the causative agents related to the

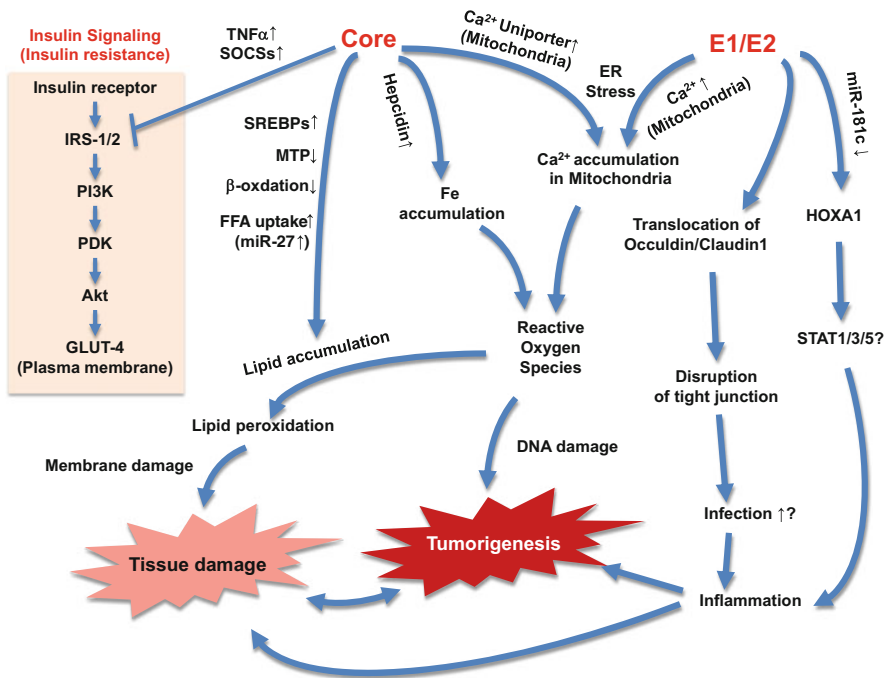


Fig. 1 Schematic diagram of the biological functions of HCV structural proteins. The biological and pathological actions induced by HCV structural proteins are summarized following the text

genetic alterations, including DNA double-strand breaks. In addition, retrotransposition targeting specific genes is predicted to be one of the potential causative agents of hepatocellular carcinoma in hepatitis B and C patients (Shukla et al. 2013). However, the mechanism by which HCV-related retrotransposition is induced has not been fully understood. Further study will be required to understand how carcinogenesis is related to hepatitis viruses and to develop antiviral agents for the eradication of these viruses in humans.

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