

Hepatitis C virus-related hepatocellular carcinoma: An insight into molecular mechanisms and therapeutic strategies

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Abstract

Hepatitis C virus (HCV) infects more than 170 million people worldwide, and thereby becomes a series global health challenge. Chronic infection with HCV is considered one of the major causes of end-stage liver disease including cirrhosis and hepatocellular carcinoma. Although the multiple functions of the HCV proteins and their impacts on the modulation of the intracellular signaling transduction processes, the drive of carcinogenesis during the infection with HCV, is thought to result from the interactions of viral proteins with host cell proteins. Thus, the induction of mutator phenotype, in liver, by the expression of HCV proteins provides a key mechanism for the development of HCV-associated hepatocellular carcinoma (HCC). HCC is considered one of the most common malignancies worldwide with increasing incidence during the past

decades. In many countries, the trend of HCC is attributed to several liver diseases including HCV infection. However, the development of HCC is very complicated and results mainly from the imbalance between tumor suppressor genes and oncogenes, as well as from the alteration of cellular factors leading to a genomic instability. Besides the poor prognosis of HCC patients, this type of tumor is quite resistance to the available therapies. Thus, understanding the molecular mechanisms, which are implicated in the development of HCC during the course of HCV infection, may help to design a general therapeutic protocol for the treatment and/or the prevention of this malignancy. This review summarizes the current knowledge of the molecular mechanisms, which are involved in the development of HCV-associated HCC and the possible therapeutic strategies.

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Key words: Hepatitis C virus; Hepatocellular carcinoma; Cirrhosis; Fibrosis; Inflammation; Carcinogenesis

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INTRODUCTION

Chronic infection with hepatitis C virus (HCV) is considered one of the major causes of end-stage liver disease including cirrhosis and hepatocellular carcinoma. HCV

infects more than 170 million people worldwide^[1], and thereby becomes a serious global health challenge. In the last decades, understanding the molecular pathogenesis of HCV infection was hampered by the lack of a suitable infection model, however, the establishment of both HCV replicons^[2,3] and small animal models^[3], helped to a better understanding the molecular mechanisms of both life cycle and the etiopathogenesis of the virus.

HCV is an enveloped virus with positive-sense RNA genome of 9.6 kb that encodes for a single polyprotein^[4]. This single polyprotein can be cleaved by both viral and cellular proteases into 10 mature proteins including, structural (Core, E1, E2/p7) and nonstructural (NS2, NS3, NS4A, NS4B, NS5A and NS5B) proteins (Figure 1).

The natural course of HCV infection is the progression to fibrosis and cirrhosis, and subsequently to hepatocellular carcinoma (HCC) in a significant proportion of HCV infected patients^[5-7]. Thus, beside its role in the cause of chronic infection that is mostly associated with the development of fibrosis and cirrhosis, HCV may play an integral role in the development of HCC *via* mechanisms mediated by viral proteins-host cell interaction^[8,9].

Because of the close association of cirrhosis with HCV-related HCC, the molecular mechanisms of HCV-mediated carcinogenesis are intensively discussed in the context of liver diseases, such as chronic inflammation, steatosis and fibrosis. However, these liver diseases seem to be the main cause for the development of cirrhosis^[10-12]. Although the multiple functions of the HCV proteins and their impacts on the modulation of the intracellular signaling transduction processes, the drive of carcinogenesis during HCV infection, is thought to result from the interactions of viral proteins with host cell proteins^[13-16]. Thus, the induction of mutator phenotype, in liver, by the expression of HCV proteins provides a key mechanism for the development of HCV-associated HCC.

MOLECULAR MECHANISMS OF ONCOGENIC PROTEINS OF HCV

Based on their proliferative potential that is widely documented *in vitro* and *in vivo*, some of HCV viral proteins including core, NS3, NS5A and NS5B have been shown to possess an oncogenic potential^[17-19]. These documented oncogenic potential results mainly from the interference of HCV viral proteins with cellular proteins, which are responsible for the regulation of cell cycle control^[20]. Under normal physiological conditions, the cell cycle progression is regulated by consecutive activation of cyclin and cyclin-dependent kinase (CDK) complexes^[21]. For example, active cyclin-CDK complexes in G1 results in the phosphorylation of the retinoblastoma family of proteins (pRb, p130 and p107), leading the activation of the members of transcription factor family E2F, and subsequently the upregulation of cellular genes, which are characteristic for the progression of G1 phase of the cell cycle^[22]. In addition to cyclin-CDK complexes, the regulation of these checkpoints are p53 and rb path-

ways-dependent activation^[23,24].

Up on the transcriptional activation of the cyclin-dependent kinase inhibitor p21, during G1/S transition, by p53, p21 becomes available to bind and to inhibit CDK2, leading to cell cycle arrest^[21]. Thus, anti-growth signals, such as checkpoint activation can play an essential role by limiting the replication of oncogenic viruses, in response to viral infection including HCV.

The interference of cellular proteins and HCV core protein is considered a major risk factor for the progression of HCC. As widely reported, the expression of HCV core protein in a transgenic mouse model was found to be sufficient to induce tumor formation in liver^[25]. In addition, HCV core can trigger the activation of peroxisome proliferator-activated receptor alpha that, in turn, may contribute to HCC^[26-28]. Also the expression of HCV core protein was found to promote the immortalization of primary human hepatocytes as well as to reverse replicative senescence^[29]. In addition to the activation of telomerase in the immortalized hepatocytes, the HCV core protein was found to increase the expression of interleukin (IL)-6, gp130, leptin receptor, and signal transducer and activator of transcription 3^[29]. However, the upregulation of these genes, in response to the expression of HCV core protein, thought to be involved in the regulation of c-myc and cyclin D1, and subsequently leading to the promotion of cellular transformation^[30].

The role of NS3 in the neoplastic transformation of hepatocytes *in vivo* and *in vitro*^[17,31-33]. Also, the enhancement of transformation and tumorigenicity upon transfection with HCV NS3 DNA has been reported in the non-tumorigenic mouse fibroblast cell line NIH 3T3 into nude mice^[34]. Moreover, the HCV NS3 C-terminal-deleted protein showed both transforming and oncogenic potential^[35]. The expression of the NS3 protein in human hepatocytes was found to induce transformed characters with reduced population doubling time as well as anchorage-independent growth and tumor development that is associated with the increased phosphorylation of extracellular regulated protein kinases and p38 proteins^[36]. Also, the NS3 protein has been shown to form complexes with p53^[19], and to inhibit p21 promoter activity^[37].

The oncogenic potential of HCV NS5A protein has been shown to be mediated by suppression of the cell cycle regulatory gene p21 in response to its interaction to p53^[38-40]. In addition, NS5A protein has been reported to suppress the expression of the mitotic spindle protein ASPM through the PKR-p38 signaling pathway, as well as the induction of aberrant mitoses, chromosome instability and HCC^[41].

In addition to its ability to form a cytoplasmic complex with Rb in infected cells^[42], the HCV NS5B-dependent downregulation of Rb results in the enhancement of E2F-dependent transcription as well as the promotion cellular proliferation^[21]. Also, the cell-cycle checkpoint, the mitotic spindle checkpoint, is a target for HCV NS5B. Since the interaction of the HCV polymerase NS5B with Rb results in the degradation of Rb and activates the MAD2 promot-

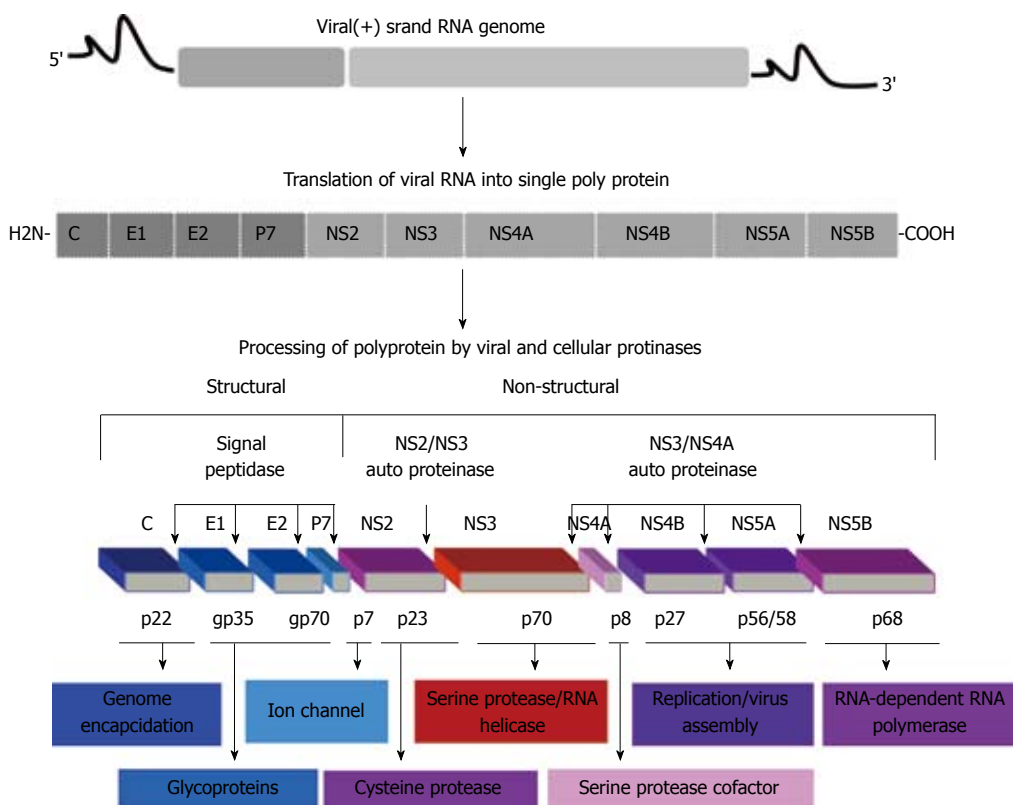


Figure 1 Hepatitis C virus genome including 5' and 3' noncoding regions, and the long open reading frame encoding for polyprotein precursor of 3010 amino acids. This polyprotein precursor can be cleaved functionally by co- and post-translationally processes mediated by cellular and viral proteases into ten different products, including structural and non-structural proteins. The structural proteins core (C), envelop 1 (E1) and E2 are located in the N-terminal third, whereas, the non-structural/replicative proteins (NS2, NS3, NS4A, NS4B, NS5A, NS5B) are located in the remainder of the polyprotein. Putative functions of the cleavage products are shown.

er^[43]. Thus, the loss of host-cell genomic stability due to deregulation of Rb pathway may result from viral infection.

MOLECULAR MECHANISM OF HCV-ASSOCIATED CHRONIC INFLAMMATION

Chronic inflammation, which generally associated with the increased proliferation of tissue cells, and an increased rate of random mutations, leads mostly to chromosomal instability^[44-48], and ultimately to both tumor progression and invasion^[8,49,50]. Also, the correlation between chronic inflammation and the promotion of carcinogenesis has been reported in several clinical studies dealing with HCV-associated liver cirrhosis and HCC^[51-53]. Accordingly, the interaction of viral proteins with cellular factors in host cells^[21,54], and the augmentation of chronic liver disease during the course of HCV infection, suggests a central role for viral proteins in the regulation of chronic inflammation leading to the initiation and subsequently progression of HCC^[55-59]. Thus, HCV-associated chronic inflammation seems to result from the dysregulation of cell cycle control^[60] and the loss of tumor-suppressor gene functions^[61], together with the induction of the proinflammatory cytokines, such as tumor necrosis factor (TNF)- α . Since the significant increase of proinflammatory cytokines was noted in HCV-expressing cells^[31,62], and in clinical samples including liver biopsies and sera

of HCV-infected patients^[54,63]. Therefore, the association between chronic inflammation and the development of HCC, during the infection with HCV is considered. Indeed, the chronic inflammatory process of HCV infection that is thought to be responsible for the promotion of the increased mutation rate in the regenerating hepatocytes, and thereby contributes to the development of HCC^[45-48]. In contrast, the rare occurrence of HCC in auto-immune hepatitis^[64,65], indicates that the inflammation alone cannot be the reason for a high incidence of HCC in HCV-infected patients^[66-68]. Although the role of HCV-associated chronic inflammation is considered to be the primary inducer of liver fibrosis and cancer, the molecular mechanisms whereby the chronic inflammation mediates the progression of liver fibrosis and subsequently HCC are not fully understood. As widely reported, chemokines produced in the liver during HCV infection are involved mainly in the regulation of migration of activated T cells from the periphery to infected parenchyma^[69]. More important, these chemokines and their receptors are associated not only with viral control, but also with immune-mediated liver inflammation^[70]. Accordingly, in a hepatotropic viral infection in humans, a marked intrahepatic non-specific mononuclear infiltrate during viral persistence was reported^[71], suggesting an essential role for the intrahepatic chemoattraction of non-specific T cells in the modulation of liver damage^[69]. Thus, besides their functional role in viral clearance,

chemokines and their receptors are implicated in the development of chronic tissue inflammation. In fact, the modulation of these pathways seems to be essential for generating an efficient immune response, as well as for the regulation of the inflammatory process during the course of the chronic infection with HCV, a viral strategy to escape from immune control^[72].

Generally, chemokines and their receptors are the main actor in the regulation of multistep pathway of inflammatory processes, which are responsible for the migration of lymphocytes to the liver^[73,74]. In chronic hepatitis C, the expression of different chemokines in the liver has been documented in several studies^[75-78]. The most reported chemokines include CXCL10 that is produced by hepatocytes and sinusoidal endothelial cells^[76,77], CXCL9 and CXCL11, which are increased in the serum and liver of patients with chronic hepatitis C^[76,79]; CCL5 that is elevated in chronic hepatitis C and it is produced by hepatocytes, sinusoidal endothelial cells and biliary epithelium^[80]. However, the expression of all these chemokines in the liver can be induced directly by HCV. Since the induction of CXCL10, CXCL9 and CCL5, in hepatocytes, by HCV proteins, including NS5A and core has been reported^[81]. Although the dominant role of chemokines in the modulation of HCV-associated inflammation, the precise mechanisms, which are involved in the regulation of HCV-associated chronic inflammation still remain to be discussed in detail. The mechanisms that thought to be involved in the regulation of HCV-associated chronic inflammation are induction of IL-1 β , IL-6 and TNF- α by HCV core and NS3 proteins, indirect induction of CXCL10 and CXCL9 by HCV core and NS5A proteins.

MOLECULAR MECHANISMS OF HCV-ASSOCIATED FIBROSIS

Generally, a variety of adverse stimuli including viruses such as HCV can trigger fibrogenesis. However, the ability of HCV and its proteins to induce fibrosis is mediated either direct by the interference of HCV proteins with various cellular pathways^[82-84], or indirect *via* steatosis^[26,85], or type 2 diabetes^[86-88] - dependent mechanisms, which finally lead to the deregulation of released cytokines^[89-91].

As widely recognized, the excess synthesis and deposition of extracellular matrix (ECM) that is mainly directed by the induction of cytokine release, is mostly associated with the increased severity of liver disease^[92,93]. As a result, the matrix metalloproteinase (MMPs) including, MMP-1, -2, -3, -8, -9, -12, -13 and -14, become inactive and fail to remove excess ECM^[94-96], and subsequently disturb the balance between fibrogenesis and fibrolysis in the liver^[97-100], an evidence for the development of liver fibrosis. Therefore, the inhibition of MMPs in response to repeated liver injury can lead to the dysfunction of ECM, and subsequently to undesired tissue remodeling, architectural disruption and a fibrogenic response.

As known, the source of fibrogenic cytokines and

growth factors in liver is activated liver macrophages, such as Kupffer cells, proliferating bile ductular epithelia, endothelia, mononuclear cells, and myofibroblasts^[101-103]. Therefore, the stimulation of hepatic stellate cells and provascular fibroblasts by fibrogenic cytokines and growth factors mediates their transformation into myofibroblasts, the main source of collagens, MMPs and tissue inhibitor of MMPs, resulting in the accumulation of ECM that is responsible for the balance between fibrogenesis and fibrolysis in the liver^[104-106]. However, a proposed model for the development of liver fibrosis during the course of HCV infection is outlined in Figure 2.

Transforming growth factor β 1 (TGF- β 1) is the most prominent profibrogenic cytokine that can be released from any cell type during inflammation, tissue regeneration and fibrogenesis^[107-111]. Thus, besides its multiple functions, the TGF- β 1 is strongly involved in the regulation of the production and deposition of the major ECM proteins^[112,113].

As known, fibrosis results from the deposition of ECM material around the liver parenchyma. This deposition is mediated by the promotion of liver fibrogenesis that results mainly from either the inflammation of liver stellate cells or from hepatocyte damage in response to the generated reactive oxygen species (ROS) by Kupffer cells^[114,115].

Besides the role of epithelial-mesenchymal transition paradigm in the development of fibrosis and HCC, epithelial cells are considered important mediators for progressive fibrosis and HCC^[116]. During the progression of chronic liver diseases, such as HCV infection, hepatocytes undergo transition from tumor-suppressive pSmad3C pathway, a characteristic pathway of epithelial cells, to JNK/pSmad3L pathway that is, in turn, mediates the activation of myofibroblasts leading to the promotion of liver fibrosis and subsequently increasing the risk of cancer^[117-119]. The loss of both epithelial homeostasis and acquisition of migratory mesenchymal phenotype are known to be essential for tumor invasion^[120-122]. In this context, the role of HCV-induced JNK pathway^[17,36,54], is thought to be essential for the regulation of Smad3L-dependent signaling^[36,123]. Thus, the possible interaction of Smad3L-dependent signaling with oncogenic pathways including, the activator protein 1 may be responsible for the augmentation of the mesenchymal phenotype of hepatocytes^[124]. Thus, the interaction of HCV core with Smad3^[125,126], and the subsequent inhibition of TGF- β -induced Smad3 transcriptional activity provides evidence for the contribution of HCV core protein in the regulation of TGF- β signaling and its downstream biological responses seem to be a possible mechanism for the development of HCV-associated HCC^[54,127].

The elevation of TGF- β 2 production in the sera of HCV-infected patients or in core-expressing liver cells^[54], in HCC biopsies^[128], besides the significant cell proliferation in HCV core-expressing cells^[36,54,123], suggest a central role for TGF- β signaling pathway in the regulation of HCV-associated HCC. Although the functional

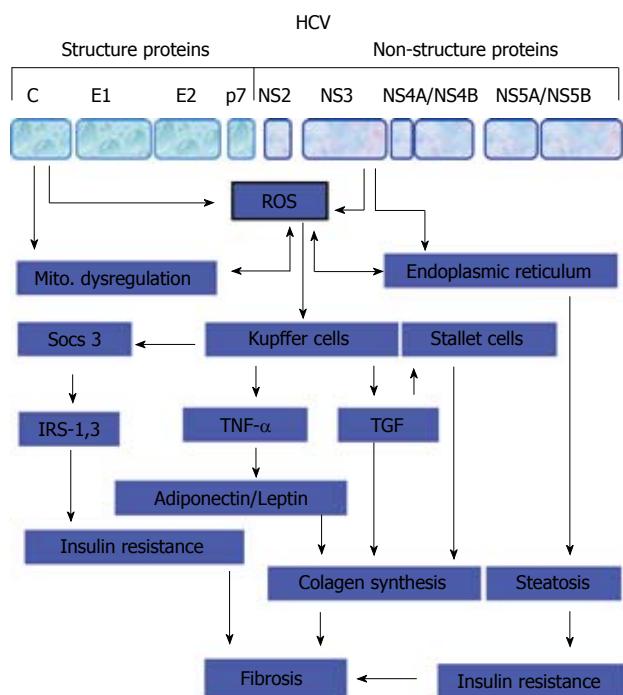


Figure 2 Pathogenesis of liver fibrosis in chronic hepatitis C infected patients. Potential mechanisms that thought be involved in the regulation of hepatitis C virus -associated hepatic fibrosis. HCV: Hepatitis C virus; ROS: Reactive oxygen species; IRS: Insulin receptor substrate; TNF: Tumor necrosis factor; TGF: Transforming growth factor.

role of TGF-β in liver tumorigenesis as well as the implication of EMT in HCC development is not well elucidated, the contribution of HCV oncogenic potential in the course of hepatocarcinoma is widely documented^[17,36,54,129]. However, the possible factors and mediators, which are thought to be involved in the regulation of HCV-associated fibrosis are ROS, TGF-β1, TNFα, epidermal growth factor (EGF), insulin-like growth factor, micro integral membrane protein (TIMP)-1, TIMP-3, MMP-1, MMP3, MMP-8.

MOLECULAR MECHANISMS OF HCV-ASSOCIATED HCC

HCC is the only malignancy whose occurrence in patients is associated with the appearance of risk factors, such as chronic liver inflammation and cirrhosis^[130-132]. However, the extensive epidemiological studies performed in the last decades led to the identification of major risk factors of HCC and thereby helped to understand the pathogenesis of HCC^[133-135]. Although the advances that made in the understanding of HCC pathogenesis, little is known about the molecular mechanisms of this malignancy. The most changes that occur in liver tissues are thought to result from either viral infection or the exposure to hepatotoxic agents leading to significant changes in the cellular signaling pathways and their target genes that are responsible in the regulation of tumor formation. These pathways include Wnt/β-catenin^[8,136], p53^[137,138], pRb^[139-141], mitogen-activated protein (MAP) kinases^[142,143], stress

signaling^[144-147], Ras^[148-150], epidermal growth factor receptor^[151-153], TGF-β^[54,154], and JAK/STAT^[155].

Wnt/β-catenin pathway has been reported to be involved in the regulation of HCC development in response to viral infection including HCV^[156]. Also, the up-regulation of frizzled-7 and dephosphorylation of β-catenin is frequently observed in HCC^[157-160]. Therefore, the targeted inactivation of Wnt pathway is considered a potential therapeutic target for the prevention or the ablation of HCV-associated HCC. Moreover, the increase of the mutation in β-catenin in HCC patients in response to either HCV infection^[161] or the exposure to aflatoxin^[162,163], provides evidence for the involvement of Wnt pathway in the regulation of HCV-associated HCC.

The tumor suppressor *P53* gene, which can be inactivated by single point mutation^[164,165], is one of the most studied proteins in the context of tumor development. Although the expression of this protein at normal levels in most tumors, under normal physiological conditions, the level of cellular p53 is low. The alteration of the expression level of p53 in response to either intracellular or extracellular stress signals can lead to significant changes that mostly vary from down regulation to up-regulation^[164-166]. However, the loss of p53 function as tumor suppressor protein is controlled by defects in p53 signaling.

Retinoblastoma, pRb1 is a major cellular barrier to cancer development that controls cell cycle progression through a mechanism including, the repression of the E2F transcription factor family of proteins^[167,168]. The phosphorylation of pRb and subsequently G1/S cell cycle transition is mainly correlated with activation of CDKs in different tumor types including, HCC^[20,169-173]. In according, HCV core protein-induced acceleration of liver cells was found to be associated with activation of CDKs, inhibition of pRb and the up regulation of E2F1^[20,54]. In addition, there is strong correlation between the loss of pRB and the inhibition of functional p53 in HCV core expressing cells^[21], as well as in different tumor types including HCC^[169-171]. The inhibition of CDK inhibitors p16INK4A, p21(WAF1/CIP1), and p27Kip1 in response to frequent mutation, or HCV infection was found to be associated with carcinogenesis of most HCC cases^[172,173]. Also, the disruption of pRb pathway in various tumor types including, HCC has been reported in several studies^[20,174], an evidence for the critical role of pRB in carcinogenesis.

Although HCV is a single-stranded RNA virus, and its genome is never integrated into the genome of hepatocytes^[175], and no known oncogenic properties have been reported for its genes, a significant portion of HCV-infected patients with induced cirrhosis has been shown to develop HCC^[20]. Thus, HCV-induced oncogenesis seems to result from the interference of HCV proteins with the intracellular signal transduction processes *via* mechanism includes dysregulation of cell cycle control.

Core protein, the most viral protein that is widely reported to interact with several intracellular signal transduction pathways, and thereby orchestrate their function,

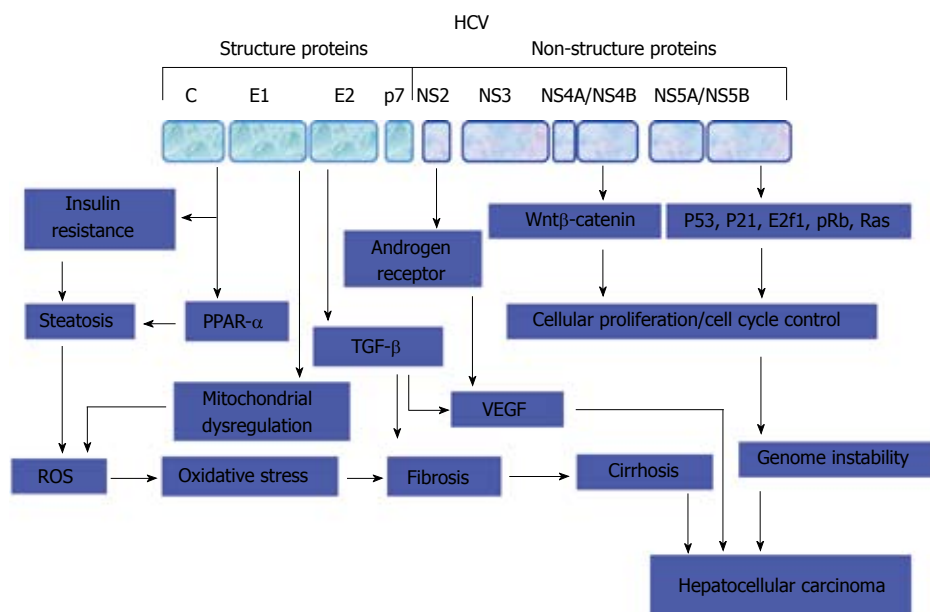


Figure 3 Molecular mechanisms of hepatitis C virus-mediated hepatocarcinogenesis. Key steps that thought to be involved in the development of hepatitis C virus-associated hepatocellular carcinoma. HCV: Hepatitis C virus; ROS: Reactive oxygen species; IRS: Insulin receptor substrate; TGF: Transforming growth factor; VEGF: Vascular endothelial growth factor; PPAR: Peroxisome proliferator-activated receptor.

as oncogenic mediator, by indirect activation of TNF- α receptor^[176,177], Raf-1 kinase^[173,178], MAP kinase^[36,179], E2F1/Rb^[21] and nuclear factor kappa B^[180,181] pathways. Also, the inhibition of TNF- α -induced apoptosis and the modulation of other cytokines activities during the course of HCV infection may prolong survival of infected hepatocytes, and subsequently leads to the accumulation of genetic damages that mediate the processes of the malignancy^[182-184].

Although the direct involvement of HCV core protein in the development of HCC has been demonstrated in transgenic mice^[25,185], the mechanism(s) whereby HCV core triggers HCC is not completely addressed in human. Apart from HCV core protein, the role of other viral proteins such as, nonstructural proteins NS5A and NS3 in the development of hepatocarcinogenesis is less clear^[17-19,38-41]. A suggested model for the development of HCV-associated HCC is outlined in Figure 3. Also, the possible mechanisms of HCV-associated HCC are: (1) activation of cellular oncogenes such as, Ras, c-Myc, E2F1 by HCV proteins; (2) inactivation of tumor suppressor genes such as p21, p53, Rb by HCV proteins; and (3) HCV proteins-induced dysregulation of Wnt/ β -catenin, MAPK, JAK/STAT, PI3K/Akt, EGF- β , TGF- β pathways.

THERAPEUTIC STRATEGIES OF HCV-ASSOCIATED HCC

Currently, the available HCC therapy is limited and usually with no clinical benefit for patients with advanced disease^[186-188]. Although surgery or liver transplantation can successfully cure small or slow-growing tumors, the success is hampered because of donor organ shortage as well as the rapid and frequent recurrence of HCC in the transplanted liver^[189-191].

Despite the potentially curative and palliative approaches are available for the treatment of HCC^[192,193],

there is no effective systemic chemotherapy for HCC treatment. Apart from limited benefit of the available therapies, the choice of the HCC treatment depends on several factors including, cancer stage, resources, and practitioner expertise.

Several anticancer agents including, sorafenib have shown promise in the treatment of patients with HCC^[194]. Sorafenib is a small molecule multikinase inhibitor with antiproliferative, antiangiogenic and pro-apoptotic properties. Although its limited benefit for patients with advanced HCC and compensated cirrhosis, the treatment with sorafenib is associated with the increase in overall survival^[195,196]. However, the relative success with sorafenib, despite the commonly reported side effects, has prompted its clinical utilization as a relevant therapeutic either alone or in combination with other treatments^[197,198]. In addition, the reliability of sorafenib as relevant therapeutic approaches for HCC encouraged to test other small molecules, such as brivanib and erlotinib^[199-202], and monoclonal antibodies, such as bevacizumab, and cetuximab^[203,204] for their therapeutic potential in patients with hepatocellular carcinoma. Based on the successful clinical development of sorafenib in HCC treatment, the era of the molecularly targeted agents undergoes active clinical development.

Although the efficacy of antiviral therapy on HCV viral status and underlying liver function in patients is still unclear, antiviral treatment may render patients with HCV-related HCC to tolerate HCC treatments and thereby may improve prognosis^[205,206]. However, based on its success, the clinical management of chronic HCV can improve the prevention of the late recurrence of HCC. Whereas, the high viral load has been shown to be an HCC recurrence risk that can be common to all HCV carriers-independent from their HCCAg status, alanine aminotransferase (ALT) levels, and stage of chronic infection^[207,208]. Interferon- α therapy was found to reduce significantly the risk for hepatocellular carcinoma, especially among virologic or

biochemical responders^[209]. For example, patients with sustained biochemical response, independent from viral load, were at reduced risk for HCC, when compared with patients with sustained virologic response^[210,211]. However, the degree of these reduced HCC risk is thought to be variable related to ALT levels^[212,213], suggesting that the reduced risk of HCC recurrence is not associated only with disappearance of viremia, but also with amelioration of hepatic inflammation.

The key signal transduction pathways, which are involved in the regulation of the pathogenesis of HCV-associated HCC are considered a roadmap for the development of clinical relevant approach for the treatment or the prevention of HCV-associated HCC. Currently, the targeted therapies, which are developed for the pathways that are mentioned in the context of HCV-mediated HCC development are either in clinical development or already proved for clinical use. These include therapies that target endothelial growth factor receptor, insulin growth factor 1^[214,215], vascular endothelial growth factor receptor 1-3^[216], in addition to those target c-MET^[217], Ras/Raf and MEK^[169,173], Akt/mTOR^[218], pathways. Other signaling pathways such as, Jak-STAT, and TGF- β ^[54], need more attention to investigate their clinical relevance and therapeutic potential in the treatment of HCC or HCV-associated HCC.

CONCLUSION

Chronic infection with HCV can lead to cirrhosis and hepatocellular carcinoma. Although the allegation of clinicians and researchers that the presence of cirrhosis is the main output for the development of HCC in individuals with chronic HCV infection, the direct role of HCV infection in the development of HCC in non-cirrhotic individuals has been suggested.

Generally, the induction of cancer is a multistep-dependent mechanism. In HCV infection, however, some of these steps might be bypassed during the development of HCV-associated HCC. Therefore, the overall effects that can be achieved by the expression of viral proteins including core protein, even in the absence of a complete set of genetic aberrations, are essential for carcinogenesis. Apart from conventional process of the induction of HCC, a plausible explanation might be given for many unusual events that take place in HCV-infected patients. The incidence of HCC in patients with HCV is known to correlate with the progression of liver fibrosis. However, the degree of liver fibrosis and the status of the infection may influence the risk of HCC occurrence in HCV-infected patients. Although HCC without cirrhosis in HCV-infected patients is rare, the direct implication of viral proteins in the development of HCC has been recently reported. Thus, the contribution of the viral infection to the development of HCC is thought to result from chronic hepatitis and/or cirrhosis.

Although there is no evidence that HCV by itself is oncogenic, the development of HCC in non-cirrhotic

HCV-infected individuals is less frequent, so that a direct oncogenic effect of viral proteins is considered.

Commonly, in patients with HCV-related HCC, the tumors seem to be solitary, smaller sized, and encapsulated, when compared to those of hepatitis B virus (HBV)-related HCC. Because of the most of HCC that occurs in patients with chronic hepatitis and liver cirrhosis, is associated with infection with HBV or HCV, the treatment of these hepatitis viruses with anti-viral agents and chemoprevention approaches may decrease the risk of HCC.

However, the key signal transduction pathways, which are involved in the regulation of the pathogenesis of HCV-associated HCC, are considered a roadmap for the development of clinical relevant approach for the treatment or the prevention of HCV-associated HCC.

Thus, the development of novel targeted therapies based on the inhibition of the signaling pathways, which are directly involved in the regulation HCV-mediated initiation, progression and invasion of HCC may provide a better picture of the clinical utility and treatment options for patients with HCV-associated HCC.

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