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Involvement of autophagy in alcoholic liver injury and hepatitis C pathogenesis

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Abstract

This review describes the principal pathways of macroautophagy (i.e. autophagy), microautophagy and chaperone-mediated autophagy as they are currently known to occur in mammalian cells. Because of its crucial role as an accessory digestive organ, the liver has a particularly robust autophagic activity that is sensitive to changes in plasma and dietary components. Ethanol consumption causes major changes in hepatic protein and lipid metabolism and both are regulated by autophagy, which is significantly affected by hepatic ethanol metabolism. Ethanol exposure enhances autophagosome formation in liver cells, but suppresses lysosome function. Excessive ethanol consumption synergizes with hepatitis C virus (HCV) to exacerbate liver injury, as alcohol-consuming HCV patients frequently have a longer course of infection and more severe manifestations of chronic hepatitis than abstinent HCV patients. Alcohol-elicited exacerbation of HCV infection pathogenesis is related to modulation by ethanol metabolism of HCV replication. Additionally, as part of this mechanism, autophagic proteins have been shown to regulate viral (HCV) replication and their intracel-

lular accumulation. Because ethanol induces autophagosome expression, enhanced levels of autophagic proteins may enhance HCV infectivity in liver cells of alcoholics and heavy drinkers.

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INTRODUCTION

Alcohol is known to exacerbate the pathogenesis of hepatitis C virus (HCV) infection and makes chronic hepatitis C patients less sensitive to antiviral treatment. Recent investigations indicate that autophagy is involved in the regulation of HCV replication and infectivity. Here, we provide basic information about the role of autophagy in liver and how ethanol modifies the autophagic response in liver cells. In addition, to underline a link between autophagy and viral replication, we review the data about HCV structure, replication cycle and autophagy in HCV-infected liver cells. Since alcohol consumption exacerbates HCV pathogenesis, we propose possible mechanisms that lead to liver failure in HCV-infected patients who drink

excessively, which may in part be regulated *via* autophagy-mediated accumulation of HCV in liver cells.

AUTOPHAGIC MACROMOLECULAR DIGESTION IN THE LIVER

Lysosomes and autophagy

In most tissues, the majority of intracellular proteins are degraded by the proteasome, an integral component of the ubiquitin-proteasome system (UPS)^[1]. In tissues such as liver that respond quickly to the composition of the plasma, the lysosome has a large part in degrading extracellular proteins (e.g. obsolete plasma proteins) brought by endocytosis into the hepatocyte. Lysosomes also degrade the remaining fraction of intracellular proteins that are not proteasome substrates and break down complex lipids (e.g. triglycerides), complex carbohydrates (e.g. glycogen) and nucleic acids. All the latter hydrolytic steps are done by autophagy, which literally means “self eating”^[2]. While autophagy always terminates by degrading macromolecular substrates in lysosomes, it can begin *via* one of three distinct cellular pathways. The most well-characterized process by which autophagy is defined is macroautophagy, the vacuolar sequestration by endoplasmic reticulum (ER) membranes of bulk portions of cytoplasm, forming a double membrane-enclosed body known as an autophagosome or autophagic vacuole (AV). The nascent AV, which contains both soluble constituents and particulate organelles, fuses with existing lysosomes to form a hydrolytic organelle called an autolysosome. Here, the sequestered substrates are hydrolyzed and the degradation products are released. Microautophagy, which is less well characterized than macroautophagy, is the uptake of smaller cytoplasmic particles by the lysosomal membrane followed by their degradation in the lysosome interior. Chaperone-mediated autophagy (CMA) is the uptake and degradation by lysosomes of single protein substrates that bear a KFERQ peptide motif. The latter is recognized by soluble chaperonins of which the most prominent is the heat shock constitutive protein 70 (HSC 70), which binds to and “directs” the protein substrate to lysosome-associated membrane proteins (LAMP). Most significant is LAMP-2A, which recognizes substrate chaperonin complexes and facilitates entry of the protein substrate into the lysosomal matrix for degradation. CMA was formerly considered a minor autophagic pathway, but recent findings indicate its heightened importance in liver cell maintenance and hepatic performance. CMA activity declines with age due to a gradual loss of LAMP-2A on the lysosome surface. Artificial restoration of this protein in aged LAMP-2A transgenic mice significantly improves liver function^[3]. CMA also has a compensatory function when macroautophagy in liver cells declines after artificial knock-down of macroautophagy gene products^[4].

Autophagy is important for liver cell survival, particularly in times of nutrient deprivation, when autophagy swiftly responds to fasting. The short half-life of autophagosomes (< 10 min)^[5] indicates that the protein compo-

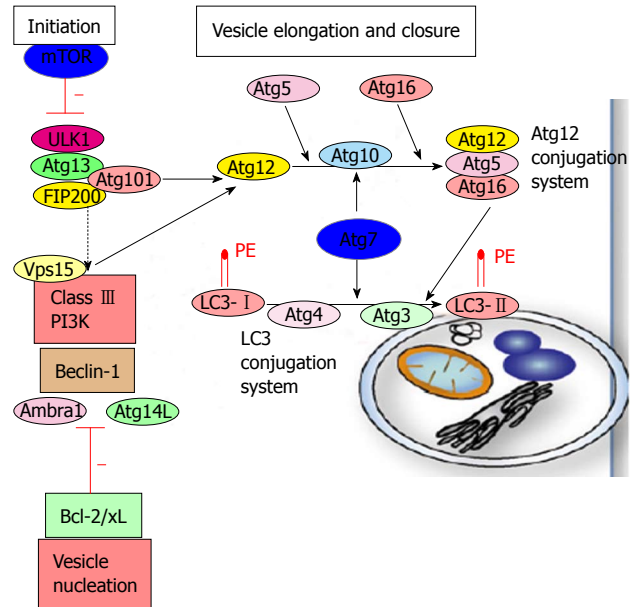


Figure 1 Molecular aspects of autophagosome formation. Reproduced with permission from^[11].

nents required for their formation are readily available for recruitment. Like the proteasome, autophagy has a key housekeeping and backup function as it degrades misfolded, aggregated proteins that are resistant to proteasome-catalyzed degradation^[6]. The importance of removing such aggregated proteins is clearly illustrated by the association of aggregate accumulation with disease pathogenesis. Patients with α -1-antitrypsin (A-1AT) deficiency are more susceptible to cirrhosis and liver cancer because of a propensity of the mutated, unsecreted A-1AT protein to aggregate within hepatocytes^[7].

Mechanism of autophagy

Identification of the major autophagy genes in yeast^[7-10] designated “Atg” has contributed significantly to our understanding of how autophagy proceeds in mammals. In all eukaryotic cells, nutrient deprivation is an inducer of autophagy. The mechanism of autophagy is described below in three steps and depicted in Figure 1.

Initiation of autophagosome formation: Initiation of autophagosome formation is regulated by the class III phosphoinositol-3-kinase (PI-3K) which triggers an upstream signaling cascade to inhibit the activity of the mammalian target of rapamycin (mTOR), a major anabolic kinase and a potent suppressor of autophagy. Inhibition of mTOR triggers the autophagic response by activating Atg proteins. In mammals, a complex is formed among the serine/threonine-protein kinase, ULK1 (a homolog of the yeast Atg1), the focal adhesion kinase family interacting protein 200, (FIP200), Atg17-like protein and Atg13, to begin the process of AV nucleation^[11]. Autophagosome (autophagic vacuole) formation begins when Beclin-1 (Atg6) forms a complex with Atg14. This subsequently

brings about formation of a double membrane vesicle that is likely derived from the ER^[12]. Coordinated complexes of Atg proteins catalyze vacuole (vesicle) elongation, notably the Atg12 ubiquitin-like conjugation system, consisting of Atg 5, 12 and 16, catalyze cleavage of Atg8, the microtubule light chain-3 (LC3I), and its conjugation to phosphatidylethanolamine (PE) to form the autophagic marker, LC3 II. The latter subsequently localizes to the autophagosome membrane, while its unlipidated precursor, LC3I remains in the cytoplasm (Figure 1).

Docking and fusion of cargo-filled autophagosomes:

Docking and fusion of cargo-filled autophagosomes with lysosomes follows autophagosome formation to form the hydrolytic autolysosome. Fusion is believed to be highly dependent upon the lysosomal membrane protein, LAMP-2.

Breakdown of the autolysosome contents occurs: The mechanism that triggers this hydrolysis is incompletely understood but it is likely that the collective action of lysosomal hydrolases brings about autolysosome dissolution.

Lysosomal proteolysis during ethanol consumption:

Liver enlargement (hepatomegaly) is common in alcoholics and in alcohol-fed laboratory animals. The rise in hepatic protein and fat each accounts for half the net increase in liver mass^[13]. The net protein gain very likely contributes to the more severe alcohol-induced liver pathologies, because some of the accumulated proteins are damaged by oxidants generated from ethanol metabolism, from mitochondrial leakage and from secondary reactions that enhance production of reactive species^[14,15]. In early studies, we showed that ethanol-induced protein accumulation reflects slower degradation of long-lived proteins, which are generally degraded in lysosomes^[16]. We later confirmed that ethanol feeding diminishes the proteolytic capacity of liver lysosomes^[17]. This is due to a reduced capacity for their acidification^[18] and lower contents of cathepsins B and L^[19]. The latter deficiency results from disruption of cathepsin precursor trafficking to lysosomes^[20], owing to declines in the ligand-binding activity, content, and synthesis rate of the mannose-6-phosphate receptor^[21,22]. This protein recognizes and binds cathepsin precursors for placement into the lysosomal compartment^[23].

Because lysosomes degrade the contents of autophagic vacuoles, we considered it likely that ethanol suppresses the initial stages of autophagy. Others demonstrated that livers of ethanol-fed rats exhibit volume densities of autophagosomes and autolysosomes substantially lower than controls^[24]. Other lines of evidence support autophagic suppression, including ethanol-induced down-regulation of AMP kinase, a catabolic regulator^[25] and ethanol-elicited disruption of cytoskeletal proteins^[26] that are essential for delivery of AV cargo to lysosomes.

Ethanol effects on intracellular autophagosome content in vitro and ex vivo

Using the marker, LC3- II we quantified autophagosomes

in recombinant HepG2 (VL-17A) cells which metabolize ethanol *via* ADH and CYP2E1. Parental HepG2 cells express neither enzyme^[27]. Contrary to our expectations, exposure of VL17A cells to 25 or 100 mmol/L ethanol for 12 to 72 h enhanced autophagosome content over that of untreated cells. AV elevation by ethanol was blocked by simultaneous exposure to 4-methyl-pyrazole (4MP), an inhibitor of ethanol oxidation. Furthermore, exposure to ethanol of non-metabolizing HepG2 cells showed no differences from untreated controls in autophagosome content, to suggest that the initiation of autophagy depends on the generation of ethanol metabolites^[28]. These results are consistent with those reported recently^[29]. Interestingly, they contrast with another report^[30] demonstrating that in CYP2E1-expressing E-47 (HepG2 recombinant) cells, ethanol exposure enhances steatosis but only slightly increases autophagy by 50%. In non-metabolizing C3A cells (similar to HepG2 cells) ethanol exposure causes a four-fold rise in autophagy but only a slight elevation of steatosis. The apparent disparity may be explained by differences in the duration of ethanol exposure (12 to 72 h reported here, compared with 120 h in the Wu *et al.*^[30] study) and the high degree of cellular steatosis, which is reciprocally regulated with autophagy in liver cells^[31].

We further tested the autophagic response in control and ethanol-exposed precision-cut rat liver slices (PCLS)^[32]. LC3 II levels in PCLS exposed to 50 mmol/L ethanol were increased two-fold over controls after 24 h of incubation. Simultaneous exposure to 4MP blocked this response^[28].

In vivo studies: After acute ethanol administration to mice, we observed a 35% enhancement in autophagosome content. This coincided with a decline in reduced glutathione (GSH) and a significant elevation in hepatic lipid peroxides, both indicators of oxidant stress. Chronic ethanol feeding to transgenic LC3-green fluorescent protein (GFP) mice caused a five-fold increase over controls of fluorescent puncta, indicating enhanced autophagosome formation. It is noteworthy that ethanol-fed mice in this study exhibited hepatomegaly and elevated liver protein over pair-fed controls^[28] consistent with our previous findings in rats^[16,33].

Summary

Our results are consistent with those recently published^[29] but are inconsistent with our hypothesis that ethanol suppresses the autophagic pathway. An obvious paradox emerges from these recent findings in view of our previous work, showing slower protein degradation in livers of ethanol-fed animals because of a disruption of lysosome function and biogenesis^[17,22]. An explanation for this disparity is that our recent investigations focused on autophagosome formation while our earlier studies emphasized lysosome function. We now postulate that ethanol metabolism enhances autophagosome formation while it disrupts the distal, degradative step of autolysosome formation. Previous work in alcohol/endotoxin-induced

pancreatitis, revealed that LAMP-2 protein is severely reduced in pancreata of ethanol-fed/endotoxin-treated rats. This alteration reduces autolysosome formation and subsequent degradation of autophagosome cargo^[34]. We postulate that this also occurs in liver during ethanol metabolism. Finally, we do not know the exact mechanism by which ethanol metabolism induces autophagosome content but we surmise that acetaldehyde, the primary oxidation product of ethanol metabolism and/or other reactive species generated by reactions secondary to ethanol metabolism, is/are probably responsible for this activation. Further, chronic alcohol consumption causes oxidant stress, which enhances the unfolded protein response (UPR) in the ER^[35]. Because AV membranes are derived from this organelle^[12], ER stress could enhance the formation of autophagosomes during ethanol oxidation.

HCV, ETHANOL AND AUTOPHAGY

Ethanol-induced oxidative stress and HCV infection

HCV is a well-established second hit, which drives the progression of alcoholic liver disease. Worldwide, 170 million people (about 2.2% of the world's population) are infected with HCV, and in about 80% of cases, infection persists for many years. Chronic viral hepatitis provides the potential risk for cirrhotic liver disease and life-threatening complications of portal hypertension and hepatocellular carcinoma^[36]. The ability of HCV proteins to induce oxidative stress *via* generation of reactive oxygen species (ROS) by mitochondrial electron transport complex I plays an important role in HCV infection pathogenesis. Therefore, ROS release results in decreased mitochondrial GSH and mitochondrial depolarization, which can be augmented by simultaneous ER oxidative stress^[37-39]. Cytochrome P450 (including CYP2E1) is involved in evolution of hepatitis to HCV-associated hepatocarcinoma^[40]. Furthermore, alcohol abuse associated with CYP2E1 activation strongly accelerates the progression of HCV infection by increasing fibrosis as well as the risk of death from cirrhosis in HCV patients. It is believed that immunosuppressive effects of alcohol impair viral clearance^[41,42]. The main mechanisms of HCV infection development, including immune dysfunction, apoptosis, steatosis and hepatic iron overload, can be triggered by heavy alcohol consumption in HCV patients^[43,44].

Hepatitis C virus and viral proteins

HCV, an enveloped virus of Flaviviridae family, has a positive-sense and single-stranded RNA. Its genome is 9.6 kb, encodes a polyprotein of 3010 amino acids and consists of a single open reading frame (ORF) flanked by untranslated regions^[45]. The NH₂-terminal part of the polyprotein includes three structural proteins: core (capsid protein) and two envelope proteins, E1 and E2^[46]. The polyprotein is processed by cellular and viral proteases into distinct structural and non-structural viral proteins. The COOH-terminal portion of the polyprotein consists of the non-structural (NS) proteins (p7, NS2, NS3, NS4A, NS4B, NS5A, NS5B) that form the replication complex for syn-

thesis of viral RNA and regulate virion assembly^[47-49]. The release of structural proteins from the nascent polyprotein is catalyzed by cellular proteases, while NS proteins are produced by viral proteases^[50].

The HCV replication cycle

To initiate the viral life cycle, HCV binds to specific cell receptors on the hepatocyte surface and is internalized by clathrin-dependent endocytosis. Although the exact mechanism of HCV cell entry is unknown, it is believed to be a multi-step process involving at least the tetraspanin CD81^[51], tight junction molecules, claudin 1 and occludin 1, as well as scavenger receptor SR-B1^[52,53]. Since extracellular HCV also circulates bound to lipids and very-low-density lipoproteins (VLDLs)^[54], the low density lipoprotein receptor may have a role in facilitating viral attachment. Initial capture of HCV particles by lipoprotein receptors is followed by interactions with SR-B1, CD81 and tight junction receptors leading to uptake and intracellular penetration of HCV *via* low-pH endosomes^[55]. Most receptors for HCV entry are species specific, which prevents infection of mouse tissue with human virus, thereby limiting or preventing cross-species infections. After attachment to the receptors and penetration inside the cells, HCV viral and cellular membranes are fused at the acidic compartment and an HCV RNA is released into cytoplasm. Viral RNA replication requires the formation of a complex contacting NS proteins, replicating RNA and cellular membranes, and an enveloped HCV virion carrying a newly-synthesized viral genome is formed by budding into the ER lumen. After assembly of the viral particle on lipid droplets (LDs), HCV leaves the cells through a secretory (VLDL) pathway^[56].

Association of HCV with lipid droplets

HCV core protein released from the polyprotein after host signal peptidase cleavage undergoes further maturation by proteolytic processing by signal peptidase^[57,58]. *In vitro* expression of core protein is associated with ER membranes and the surface of LD^[59]. The immature form of core protein cannot attach to LD. After maturation, core protein is directed from the ER to LD, and it attaches *via* a D2 domain, which includes a 55 amino acid protein containing two amphipathic α -helices (H I and H II) separated by a hydrophobic loop^[60]. D2 is important for core protein stability and its subsequent associations with cell membranes. The neighboring core segment, D1, has important functions in RNA binding and protein-protein interactions^[46]. LDs are directly involved in the production of infectious HCV particles^[61]. They are surrounded by unique membranes called "membraneous web", allowing a high amount of plus- and minus-strand HCV RNA as well as NS proteins (NS5A) to attach to LD covered with HCV core protein. NS5A-core interactions require the serine phosphorylation toward the C-terminal end of NS5A and are essential for the association of replication complex to the periphery of LDs, which is a pre-requisite for infectious virion assembly^[56]. Importantly, disruption of the core protein-LD association causes defects in HCV RNA and NS localization

and results in a loss of infectious viral particle assembly^[61], demonstrating that core protein is responsible for recruitment of NS proteins to LD. Attachment of core protein to LDs leads their aggregation toward the periphery of the nucleus, suggesting that the core modifies the microtubule-dependent mobility of LDs; it also displaces adipocyte differentiation-related protein (ADRP), the major LD surface protein^[62]. The modulation of the microtubule network by core protein is extremely important, as microtubule disruption reduces virus production. Thus, core protein changes the intracellular localization of LDs, securing the contacts between the sites of RNA synthesis and LDs. Due to core-NS5A protein-protein complex formation, these two proteins form a bridge between LDs and the sites of HCV RNA replication^[63]. The targeting of the viral components to LDs establishes the link between assembly and release of HCV virions, VLDL production and apoprotein B lipidation^[63].

HCV and autophagy

Some viruses, including HBV and HCV, subvert autophagy and use it to their own benefit. The link between autophagy and HCV replication is supported by several studies. Knockdown of autophagic proteins, beclin-1, Atg4B, Atg5 and Atg12 suppresses HCV replication at the onset of infection^[64]. Specifically, Atg7 knockdown decreases the production of infectious viral particles without affecting HCV viral protein expression^[65]. By inducing ER stress, HCV infection stimulates autophagosome formation regardless of HCV genotype^[64,66]. Recently, we have shown that this autophagosome formation and specifically, LC3 lipidation can be further enhanced by exposure to ethanol of JFH1-infected ethanol-metabolizing hepatoma cells (unpublished observations). Nevertheless, a co-localization of LC3-II protein in autophagosome and HCV proteins has not been found^[65,67]. However, a recent study of Guevin *et al.*^[68] demonstrated a transient link between Atg5 and HCV NS5B (RNA-dependent RNA polymerase) protein at a very early stage of infection. This study was conducted in the frame of yeast two-hybrid analysis on the cells co-expressing Atg5 and NS5B. Interaction between these proteins is required for the onset of viral replication. Atg5 is indeed involved in other positive-strand RNA virus replications *via* formation of a double membrane vesicle^[69]. This Atg5-NS5B interaction suggests that autophagy proteins play some additional, autophagy-unrelated role. Induction of autophagosome formation in HCV infection does not necessarily mean activation of autophagic protein degradation because HCV induces an incomplete autophagic response by impairing autolysosome function^[66,70]. One of the possible reasons is either defective autophagosome-lysosome fusion or impaired postfusion proteolytic degradation of autophagosome contents induced by alkalization of lysosome due to HCV p7 protein^[71]. The reduced capacity for lysosomal digestion may further prolong HCV survival.

HCV replication and ethanol

As revealed from numerous studies, exposure of liver cells

to ethanol affects HCV replication. Zhang *et al.*^[72] demonstrated that ethanol produces a concentration-dependent increase in HCV replication and related that effect to the activation of NF- κ B promoter. In addition, exposure of Huh7 cells and primary human hepatocytes to increasing concentrations of ethanol up-regulates intracellular and extracellular HCV RNA^[73]. However, the role of ethanol metabolism in HCV replication is still controversial. Recent studies in full genomic and subgenomic HCV replicon cells have shown that alcohol increases HCV replication 4-fold in a CYP2E1-dependent manner and these effects are blocked by N-acetyl cysteine^[74]. As demonstrated by Seronello *et al.*^[75], replication of both HCV genotypes 1b and 2a depends on lipid metabolism, is enhanced by acetaldehyde and requires elevated NADH/NAD⁺ ratio. On the other hand, extracellular and intracellular ROS suppress HCV replication. In addition, the effect of ethanol on HCV RNA replication in ethanol-metabolizing JFH1-infected Huh7.5 CYP2E1-expressing (RLW 2-9) cells depended on when ethanol was applied to the cells; application of ethanol before infection of cells with JFH1 enhanced HCV RNA replication, while exposure of RLW 2-9 cells to ethanol 3 d after infection suppressed HCV RNA levels^[76].

The mechanisms by which ethanol interferes with or activates the HCV replication cycle are not clear. While the literature on viral entry develops rapidly, very little is known about how ethanol affects the expression of receptors for HCV entry. These effects may depend on the ability of cells to metabolize ethanol. Thus, by using ethanol non-metabolizing cells, it has been shown that the expression of CD81 is up-regulated on monocytes of HCV-infected alcohol-consuming patients^[77], while ethanol exposure decreases claudin1 expression on alveolar epithelial cells^[78]. Recently, we showed that ethanol exposure did not affect CD81, but enhanced claudin 1 expression on ethanol-metabolizing CYP2E1⁺ HCV replicon and JFH1-infected hepatoma cells^[76,79]. Other mechanisms explaining the enhancement of HCV replication/expression by ethanol exposure to hepatocytes, including the regulation of autophagy, are under investigation.

HCV, fatty liver and autophagy

Expression of PPAR α , a nuclear receptor that modulates the expression of oxidative enzymes and fatty acid import into mitochondria, is impaired by HCV^[80]. HCV core protein reduces expression of PPAR α as well as its transcriptional activity. In addition, HCV core protein activates fatty acid synthesis by affecting SREBP1c. Sterol response element-binding proteins (SREBPs) are transcription factors that are bound to ER and regulate the activity of enzymes that support cholesterol and fatty acid synthesis. Genes for these proteins are transcriptionally induced by HCV^[81]. The phosphorylation and activation of these proteins *via* the MAP kinase or PI3-K-Akt pathways leads to induction of fatty acid synthase. Activation of SREBP1 by HCV core protein requires the participation of PA28 γ , a nuclear protea-

some activator^[82]. Lipid droplets accumulate fat and are the place of HCV full particle assembly^[83]. Since lipid droplet content is regulated in part by autophagy^[84] and autophagic degradation of the substrates (including lipids) is compromised by HCV and ethanol, this defect in autophagy may further promote fat deposition in the liver of HCV alcohol-consuming patients.

CONCLUSION

Autophagy is mediated by autophagosomes that “capture” autophagic substrates (proteins and lipids) and deliver them to the lysosome for further degradation. Ethanol up-regulates the upstream part of autophagy (autophagosome formation), but it suppresses lysosomal function, thereby negatively affecting protein degradation. By creating ER stress, HCV also enhances autophagosome formation; however, some HCV proteins (p7) interfere with normal lysosome function. In addition, autophagic proteins are involved in regulation of HCV replication. Autophagosome content hepatoma cells can be further increased by exposure to ethanol. The effects of ethanol on HCV replication are redox-dependent (require elevated NADH/NAD⁺ ratio). Thus, HCV- and alcohol-modified autophagy apparently plays a role in enhanced viral replication, intracellular virus accumulation and steatosis progression in HCV-infected alcohol-consuming patients.

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