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Inhibition of Hepatitis C Virus Replication by IFN-Mediated ISGylation of HCV-NS5A

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ISG15 is a ubiquitin-like molecule whose expression is induced by type I IFN (IFN-α/β) or in response to virus or bacterial infection. ISG15 or conjugation of ISG15 to target proteins was reported to play critical roles in the regulation of antiviral responses. IFN restricts replication of hepatitis C virus (HCV). However, molecular mechanism of IFN-α/β that inhibits HCV replication is not clear yet. In the current study, we demonstrated that replication of HCV was inhibited by overexpression of ISG15 and ISG15-conjugation enzymes in the HCV subgenomic replicon cells. Among various nonstructural proteins of HCV, NS5A was identified as the substrate for ISGylation. Furthermore, protein stability of NS5A was decreased by overexpression of ISG15 or ISG15-conjugating enzymes. The inhibitory effect of ISG15 or ISGylation on NS5A was efficiently blocked by substitution of lysine at 379 residue to arginine within the C-terminal region, suggesting that ISGylation directly controls protein stability of NS5A. Finally, the inhibitory effect of IFN-α/β on HCV replication was further enhanced by ISGylation, suggesting ISG15 as a therapeutic tool for combined therapy with IFN against HCV.

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Hepatitis C virus (HCV) is an enveloped RNA virus that belongs to the genus Hepacivirus, family Flaviviridae (1). The HCV genome is a single-stranded, 9.6-kb–long RNA molecule. It encodes a 3000-aa polypeptide that undergoes posttranslational processing to yield at least 10 functionally distinct viral proteins: core, envelope protein 1 (E1), envelope protein 2 (E2), p7, and nonstructural protein (NS)2, NS3, NS4A, NS4B, NS5A, and NS5B (2–4). Unlike other HCV nonstructural proteins, NS5A does not have enzymatic activity. Instead, HCV-NS5A physically interacts with various cellular proteins, such as p53, IFN-induced, dsRNA-activated protein kinase, or a novel transcription factor SNF2-related CBP activator protein, to elicit modulator roles in cell-cycle regulation, cellular transformation, and antiviral immune responses (5–7). HCV-NS5A is a membrane-associated protein that uses its N-terminal amphipathic helix domain and is usually found in the HCV RNA replication complex (8, 9). HCV-NS5A is indispensable for HCV RNA replication, because HCV genome replicates in the lipid droplet-associated membrane of the endoplasmic reticulum (ER) (10).

Chronic infection of HCV is a leading cause of liver disease, including chronic hepatitis, liver cirrhosis, and hepatocellular carcinoma (11). With the absence of effective vaccines to prevent HCV infection, combined treatment of pegylated IFN-α with ribavirin is the most favorable choice for therapy. However, resistance to IFN is often observed in patients with HCV infection (12, 13). Interestingly, mutations in HCV-NS5A were reported to correlate with responsiveness to IFN therapy in patients, although its precise mechanism is not conclusive (14). To overcome IFN resistance in patients with HCV infection, the development of chemicals that inhibit HCV-specific enzymatic activities or antisense oligomers that inhibit HCV replication has been undertaken (15–17).

Pathogen-associated molecular patterns of replicating HCV RNA genomes, such as 5′-triphosphate RNA or dsRNA, are recognized by the product of RIG-I in the cytoplasm. It triggers the activation of intracellular signaling pathways and transcription factors, such as NF-κB and IFN regulatory factors (18–22). An outcome of these events is the production of type I IFN (IFN-α/β) (23, 24). Secreted IFN-α/β induces the activation of the IFN-stimulated gene factor 3 complex, which translocates to the nucleus, where it binds to the IFN-stimulated response element regions of target genes to direct the expression of IFN-stimulated genes (ISGs). Among the genes induced by IFN, IFN-induced, dsRNA-activated protein kinase, MxA, and ISG15 function as effector molecules in the host cell response to viral infection (24). Multiple studies have shown a clear absence or low level of IFN-α/β in the hepatocytes of patients with chronic HCV infection. In addition, patients with chronic HCV infection show no significant level of ISG induction upon treatment with IFN (25). Based on these findings, it has been suggested that HCV viral proteins disturb the innate immune response of the host and that altered hepatic ISG expression is associated with liver pathology.

ISG15 is a type 1 IFN-inducible, ubiquitin-like protein. Most components for ISG15 conjugation (ISGylation), including UbeIL (E1, ISG15-activating enzyme), UbcH8 (E2, ISG15-conjugating enzyme), and HERC (E3, ISG15 ligase), are highly responsive to IFN-α/β–induced signal transduction (26, 27). Expression of ISG15 and the conjugation of ISG15 to target proteins are strongly promoted by IFN-α/β treatment, dsRNA, and viral or bacterial infection (28). Production of ISG15 or ISGylation is believed to play an important role in establishing the antiviral state of an infected cell. ISG15-deficient mice are highly susceptible to influenza, herpes, and Sindbis viral infections (29), whereas the protective role of overexpressed ISG15 in Sindbis virus-infected IFN-α/βR-deficient mice has been reported (30). It was also reported that ISGylation of cellular proteins...
can be suppressed by infection with influenza B virus through the interaction of ISG15 with the NS1B viral protein (31). In the current study, we investigated the role of ISGylation on HCV-NSSA and its implication for viral replication in subgenomic HCV replicon cells.

Materials and Methods
Cell culture and transfection
HuH-7 and COS7 cells were maintained in DMEM (Invitrogen, Grand Island, NY), supplemented with 10% FBS (HyClone, Logan, UT) and 1% penicillin/streptomycin (Invitrogen). HuH-5-15 and Huh-luc.neo-ET HCV (genotype 1b) subgenomic replicon cells (gift of R. Bartenschlager, University of Heidelberg, Heidelberg, Germany) were maintained in G418 (600 μg/ml; Calbiochem, San Diego, CA)-containing media. Cells were treated with EGF (50 ng/ml), 1% FBS (HyClone, Logan, UT), and were cloned into pDESt mammalian expression vectors (Invitrogen). For the HCV-NSSA expression vector, coding regions for NSSA of HCV genotype 1b were amplified by PCR using pGX10-NS5 as the template (gift of Y.C. Sung of POSTECH), digested with KpnI and XhoI, and inserted into the pcDNA3.1/myc or subsequently cloned into the pFlag/CMV plasmid.

Plasmid construction
The coding regions for HCV-NS2-, NS3-, NS4-, and NS5B of HCV genotype 1b were obtained by PCR amplification using pGX10-ΔNS, pGX10-NS3A, and pGX10-NS5 plasmids as templates, respectively (gift of Y.C. Sung, Pohang University of Science and Technology [POSTECH], Pohang, South Korea), and were cloned into pDEST mammalian expression vectors (Invitrogen). For the HCV-NSSA expression vector, coding regions for NSSA of HCV genotype 1b were amplified by PCR using pGX10-NS5 as the template (gift of Y.C. Sung of POSTECH), digested with KpnI and XhoI, and inserted into the pcDNA3.1/myc or subsequently cloned into the pFlag/CMV plasmid. Deletion mutants of HCV-NSSA were generated by PCR and were cloned into the pFlag/CMV plasmid. Point mutations in NSSA were generated using the QuickChange site-directed mutagenesis kit (Stratagene, La Jolla, CA), according to the manufacturer’s instructions. DNA sequences of the constructed plasmids were verified by automated sequencing. The expression plasmids were digested with KpnI and XhoI, and inserted into the pFlag/CMV plasmid. The coding region of the ΔK379R point mutation was introduced into NS5A of NK5.1 plasmid (gift of Y.C. Sung, POSTECH), digested with KpnI and XhoI, and inserted into the pFlag/CMV plasmid. Deletion mutants of HCV-NSSA were generated by PCR and were cloned into the pFlag/CMV plasmid. Point mutations in NSSA were generated using the QuickChange site-directed mutagenesis kit (Stratagene, La Jolla, CA), according to the manufacturer’s instructions. DNA sequences of the constructed plasmids were verified by automated sequencing. The expression plasmids were digested with KpnI and XhoI, and inserted into the pFlag/CMV plasmid.

Generation of mutant HCV subgenomic replicon cells

Immunoblot analysis
Cells were harvested in lysis buffer (50 mM Tris-HCl [pH 7.4], 150 mM NaCl, 1% Triton X-100, 0.5% deoxycholic acid, 0.1% SDS) containing 1 mM DTT, 0.57 mM PMSF, 5 μg/ml leupeptin, 2 μg/ml pepstatin A, 1 mM benzamidine, and 1 mM benzamidine. Total-cell lysates were separated by SDS-PAGE and transferred to a nitrocellulose membrane (Bio-Rad, Hercules, CA). Immuno blotting was performed using the indicated Abs. Cells were then incubated with Alexa Fluor 568- or Alexa Fluor 488-conjugated secondary Abs (both from Invitrogen). Slides were mounted and analyzed using a fluorescence microscope.

Immunofluorescence staining
Cells on glass cover slips were fixed with 4% paraformaldehyde solution and permeabilized with 0.2% Triton X-100. Cells were blocked with 3% goat serum/2.5% BSA and incubated with anti-HCV-NSSA (Virotek) or anti-Flag (Sigma-Aldrich, St. Louis, MO) Abs for 2 h. Cells were then incubated with Alexa Fluor 568- or Alexa Fluor 488-conjugated secondary Abs (both from Invitrogen). Slides were mounted and analyzed using a fluorescence microscope.

Results
Replication of HCV was inhibited by the overexpression of ISG15-conjugation components in the HCV subgenomic replicon cells

ISG15 is an IFN-inducible gene that is strongly induced by virus infection in immune and nonimmune cells. ISG15 was shown to negatively regulate the replication, assembly, and budding of Sindbis virus, HIV, and Ebola virus, respectively, which strongly suggests that it functions as an antiviral agent (30, 33). We wondered whether ISG15 or ISG15 conjugation had similar inhibitory effect on the replication of HCV. To explore the effect of ISGylation, we transfected Huh-luc.neo-ET replicon cells with ISG15, Ube1L, and UbcM8 expression plasmids and monitored the replication of subgenomic HCV replicons. Huh-luc.neo-ET replicon cells harbor the luciferase reporter gene in the HCV replicon construct (34). Therefore, it can be used to quantitatively analyze the effect of ISG15 conjugation on HCV replication (Fig. 1). Quite surprisingly, overexpression of ISG15 in HCV replicon cells significantly inhibited the replication of the HCV subgenomic replicon to up to 65% of that observed in the empty vector-transfected control cells.

Immunoprecipitation
Cells were harvested in lysis buffer, and 1 mg total-cell lysate was precleared with normal IgG and protein A/G agarose beads. Lysates were incubated for 12 h at 4°C with the appropriate Ab, followed by an additional 2 h of incubation with protein A/G agarose beads.

Luciferase assay
Cells carrying the Huh-luc.neo-ET HCV subgenomic replicon construct were transfected with empty vectors or expression vectors for the ISGylation-conjugation system. Cells were lysed 48 h posttransfection, and luciferase activity was measured using a dual-luciferase assay kit (Promega, Madison, WI). To ensure that equal amounts of cell lysates were used for luciferase assay, protein quantification using the Bradford method was performed prior to the assay.

Statistics
Data are represented as mean ± SD, and differences between groups were analyzed by the t test.

RNA isolation and analysis
Total RNA was extracted using TRIzol reagent (Invitrogen) and subjected to real-time RT-PCR. The primer sequences used for PCR were as follows: HCV-NS4, 5′-ACAACAGGACGCTTGTAT-3′ and 5′-TCTCTATTTGGGAATGATG-3′; HCV-NS5A, 5′-CTATGAGGGAAGTTGACAGTTAT-3′ and 5′-CCTAAGACGGTTTGGCCAGATG-3′.

FIGURE 1. Overexpression of the ISGylation system inhibits HCV replication in the HCV subgenomic replicon cells. Huh-luc.neo-ET replicon construct used in this study (34) (top panel). Cells were transfected with the indicated expression plasmids, and replication was measured by luciferase assay (bottom panel). Graph shows mean ± SD of triplicate experiment set. Representative data repeated in at least three independent experiments.
**HCV-NS5A is a target protein for ISG15 conjugation**

To understand the molecular mechanism of the inhibitory effect of ISG15 on HCV replication, we examined whether ISG15 conjugation exhibited a direct effect on HCV viral proteins. We cloned individual nonstructural proteins of HCV (HCV-NS3, -NS4, -NS5A, and -NS5B) and HCV-E2 structural protein in the mammalian expression vectors, and the result of ISG15 overexpression was investigated in the transfected COS7 monkey epithelial cells. In the cells overexpressing ISG15, cellular levels of HCV-E2, -NS3, and -NS4 protein were not significantly altered compared with equal amounts of empty vector-transfected cells (Fig. 2A). In contrast, protein levels of HCV-NS5A were dramatically reduced with cotransfection of ISG15 (Fig. 2B) or with components of ISG15-conjugation system: Ube1L and UbcM8 (Supplemental Fig. 1). To mimic the effect of intracellular RNA virus infection, which enhances the expression of ISG15-conjugation system, poly-IC was transfected into cells previously transfected with empty vector or expression vectors for ISGylation component. Stimulating cells with intracellular poly-IC further decreased the cellular levels of HCV-NS5A protein in the ISG15-transfected COS7 cells (Fig. 2C).

To test whether HCV-NS5A was a direct target of ISG15 conjugation, we next examined the ISGylation of NS5A in the COS7 cells. ISGylation of the total cellular proteins was strongly induced by poly-IC or IFN-β treatment in the COS7 cells (Fig. 2D), indicating that COS7 cells are equipped with an intact ISG15-conjugation system. For strong induction of ISGylation, cells were transfected with expression vectors for ISGylation enzymes, along with Flag-HCV-NS5A. Total cellular lysates were subjected to immunoprecipitation using an anti-Flag Ab, followed by immunoblot analysis using an anti-Myc Ab to detect ISGylated HCV-NS5A. In the cells overexpressing Myc-ISG15/E1/E2, slowly migrating forms of ISGylated Flag-HCV-NS5A were clearly visible (Fig. 2E). In contrast, ISG15 conjugation to other HCV viral proteins, such as HCV-NS3 or -NS5B, was not detected in the transfected COS-7 cells (Fig. 2F), nor in the cells stimulated with poly-IC or IFN-β (Supplemental Fig. 2).

**Lys379 in the polyproline-cluster motif of HCV-NS5A is the target site for ISG15 conjugation**

In the earlier study using subgenomic replicon systems, HCV-NS5A was suggested to be involved in HCV RNA replication (8, 35–38). Because HCV-NS5A contains multiple domains with specific functions, we attempted to determine the responsible domain(s) for regulation by ISG15 conjugation. We constructed deletion mutants of HCV-NS5A and examined ISGylation effect on the protein level. Protein levels of the deletion mutant NS5A (I del) lacking an N-terminal amphipathic helix (Fig. 3A) was similarly reduced by cotransfection with ISGylation components. In contrast, deletion mutant of NS5A (IV del) lacking a carboxy-terminal domain with poly-proline cluster motifs was not affected by the coexpression of the ISGylation components, indicating that ISGylation site(s) might reside in the C-terminal regions of HCV-NS5A. To test this possibility, we conducted immunoprecipitation assay of NS5A (IV del) protein in the ISG15/E1/E2-cotransfected COS7 cells (Fig. 3B). As predicted, ISGylation of NS5A (IV del) mutant was not observed, suggesting that the C-terminal domain that spans aa 309–447 of the HCV-NS5A is required for regulation by ISG15 conjugation. To identify the responsible site(s) for ISG15 conjugation in HCV-NS5A, we subsequently constructed various KR mutants of NS5A, in which lysine residues in the C-terminal domain have been individually substituted for arginine residue. Five lysine residues (K309, K331, K349, K359, and K379) were in the C-terminal domain of HCV-NS5A. In the earlier study using subgenomic replicon systems, HCV-NS5A was suggested to be involved in HCV RNA replication (8, 35–38). Because HCV-NS5A contains multiple domains with specific functions, we attempted to determine the responsible domain(s) for regulation by ISG15 conjugation. We constructed deletion mutants of HCV-NS5A and examined ISGylation effect on the protein level. Protein levels of the deletion mutant NS5A (I del) lacking an N-terminal amphipathic helix (Fig. 3A) was similarly reduced by cotransfection with ISGylation components. In contrast, deletion mutant of NS5A (IV del) lacking a carboxy-terminal domain with poly-proline cluster motifs was not affected by the coexpression of the ISGylation components, indicating that ISGylation site(s) might reside in the C-terminal regions of HCV-NS5A. To test this possibility, we conducted immunoprecipitation assay of NS5A (IV del) protein in the ISG15/E1/E2-cotransfected COS7 cells (Fig. 3B). As predicted, ISGylation of NS5A (IV del) mutant was not observed, suggesting that the C-terminal domain that spans aa 309–447 of the HCV-NS5A is required for regulation by ISG15 conjugation. To identify the responsible site(s) for ISG15 conjugation in HCV-NS5A, we subsequently constructed various KR mutants of NS5A, in which lysine residues in the C-terminal domain have been individually substituted for arginine residue. Five lysine residues (K309, K331, K349, K359, and K379) were in the C-terminal domain of HCV-NS5A, and lysines on 309, 331, 359, and 379 were found to be well conserved in the
diverse HCV isolates (Fig. 3C). Among the tested KR mutants of HCV-NS5A, only the K379R mutant remained unchanged after the overexpression of ISGylation components (Fig. 3D). Furthermore, ISGylation on HCV-NS5A was completely blocked in the K379R mutant compared with normal ISGylation in the wild-type (WT) or other KR mutants (Fig. 3E), suggesting that lysine 379 on HCV-NS5A is critical for protein regulation by ISGylation.

Reduction of HCV-NS5A protein by ISG15 conjugation in the subgenomic HCV replicon cells

We demonstrated that HCV-NS5A was a target protein of ISG15 conjugation, which led to decreased protein levels in COS7 cells. Based on these observations, we hypothesized that the reduction of HCV-NS5A by ISG15 conjugation may be responsible for the decreased replication of HCV observed in the Huh-luc/neo-ET replicon cells (Fig. 1). To investigate the molecular mechanism of HCV replication controlled by ISG15, we examined whether ISGylated NS5A can be degraded by 26S proteasome. For this purpose, we measured ISGylation of HCV-NS5A in the cells treated with 26S proteasome inhibitor MG132 (Fig. 5A). As previously reported (32), ISGylation was strongly enhanced in the MG132-treated total-cell lysates, and ISG15 conjugation to HCV-NS5A was correspondingly increased. Consequently, cellular levels of unconjugated NS5A protein were further decreased by MG132 treatment. Intriguingly, migrating patterns of ISGylated HCV-NS5A in SDS-PAGE were different from the untreated control, indicating that NS5A can be subject to further modification, such as ubiquitination. To prove this idea, ubiquitination of HCV-NS5A protein was separately assessed by immunoprecipitation in the ubiquitin-overexpressing COS7 cells (Fig. 5B). As expected, ubiquitin-conjugated forms of HCV-NS5A were observed in the MG132-treated cells. Interestingly, the ubiquitinated form of NS5A was also detected in the absence of MG132, suggesting that HCV-NS5A protein is a heavily ubiquitinated protein. It is noteworthy that zinc mesoporphyrin, which suppresses HCV replication, also prevented ISGylation of HCV-NS5A (Fig. 5C).
replication, exhibited enhanced ubiquitination of HCV-NS5A (39). To determine whether ISGylation of NS5A affects ubiquitination of NS5A, which leads to the protein degradation via 26S proteasome, we examined ubiquitination of HCV-NS5A (K379R) mutant protein.

Although basal ubiquitination of HCV-NS5A (K379R) was diminished, ubiquitination of WT and K379R mutant NS5A protein was similarly increased when 26S proteasome activity was blocked by MG132, indicating that HCV-NS5A might be ubiquitinated on the lysine residue other than K379 (Fig. 5C, Supplemental Fig. 3). However, despite MG132’s effect on the ubiquitination of NS5A, it is noteworthy that cellular levels of HCV-NS5A and NS5A (K379R) proteins were not changed (Fig. 5B, 5C). We speculated that the protein-synthesis rate of NS5A might be fast enough to counterbalance the degradation rate. To prove this idea, cells were treated with cycloheximide to block new protein synthesis, and the effect of MG132 on protein degradation was examined (Fig. 5D, Supplemental Fig. 4). Interestingly, expression of ubiquitin alone increased cellular levels of HCV-NS5A and NS5A (K379R) proteins. However, the cellular levels of the proteins were not affected by MG132 treatment, in the absence or presence of cycloheximide treatment. These results indicate that protein stability of HCV-NS5A is subject to control that involves ISGylation and ubiquitination.

ISG15-conjugation system as a potential combined therapy with type I IFNs

Finally, we examined whether ISG15 or the ISG15-conjugation system could be used as combined treatment with type I IFN. In the Flag-HCV-NS5A–transfected COS7 cells, cellular levels of HCV-NS5A protein were slightly suppressed by treatment with IFN-β, which was dramatically reduced by cotreatment of ISG15/E1/E2 overexpression (Fig. 6A). In the HCV replicon cells, IFN-β–mediated inhibition of HCV replication was further suppressed by cotransfection of ISGylation components (Fig. 6B). In addition, equivalent levels of the inhibitory effect of IFN-β (100 U/ml) on HCV replication were obtained using combined treatment with a lower dose of IFN-β (50 U/ml) and ISG15/E1/E2 overexpression in the HCV subgenomic replicon cells (Fig. 6C). In contrast, ISGylation-mediated inhibition of HCV replication was not observed in the mutant HCV replicon cells with NS5A (K379R), demonstrating that HCV-NS5A might be the only target for ISG15 conjugation (Fig. 6D). In conclusion, effective control of HCV replication can be achieved by ISG15 or ISG15-conjugation system, in combination with IFN-β.

**FIGURE 4.** ISGylation-mediated downregulation of HCV-NS5A protein in the HCV replicon cells. A, The replicon construct (I389/NS3-3/WT5-15) (top panel) (36). Huh-5-15 replicon cells (bottom panel) or Huh-luc/neot/ET replicon cells (B) were transfected with indicated expression vectors. Endogenous HCV-NS5A protein levels were examined by immunoblot assay. C, Huh-5-15 replicon cells were transfected with Mtv-ISG15 and Flag-UbcM8/HA-Ube1L plasmids and were analyzed by immunofluorescence staining using anti-Flag (green) and anti-HCV-NS5A (red) Abs and DAPI (blue). D, Huh-5-15 replicon cells were transfected with expression vectors for the ISG15-conjugation system, and ISGylation of the endogenous HCV-NS5A was examined by immunoprecipitation using anti-HCV-NS5A Abs, followed by immunoblot analysis.

**FIGURE 5.** HCV-NS5A protein regulation by ISGylation and ubiquitination. A–C, Transfected COS7 cells were treated with MG132 (5 μM) for 12 h before analysis. Total lysates (1 mg) were subjected to immunoprecipitation using anti-Flag Abs. **ISGylated HCV-NS5A; #ubiquitinated HCV-NS5A.** D, COS-7 cells were transfected with indicated expression plasmids and were treated with cycloheximide (30 μg/ml) for 6 h before analysis.
FIGURE 6. Effect of the combined treatment consisting of ISG15 conjugation plus IFN-β. A, Transfected COS7 cells were stimulated with IFN-β (1500 U/ml) for 24 h or left untreated. Protein levels of HCV-NS5A were analyzed by immunoblot assay. B, Huh-5-15 replicon cells and Huh-NS5A-K379R replicon cells were transfected with ISG15-conjugating enzymes and stimulated with IFN-β (100 U/ml) for the indicated times. Amplification of HCV replicons was investigated by real-time RT-PCR using PCR primers specific for HCV-NS4. Graphs show mean ± SD obtained from three separate experiments. C, Huh-5-15 replicon cells were transfected, as indicated, and amplification of the HCV replicon was examined by conventional RT-PCR after treatment with IFN-β (50 or 100 U/ml) for 24 h.

Discussion

In the current study, we demonstrated that the overexpression of ISG15 and ISGylation components induces ISGylation in the C-terminal regions of HCV-NS5A, reduces cellular levels of NS5A protein, and, hence, inhibits replication in the HCV subgenomic replicon cells.

The antiviral potential of ISG15 and ISGylation has been reported in various viral systems. Overexpression of ISG15 was shown to inhibit viral packing and replication of HIV, Ebola virus, and Sindbis virus in type I IFN-deficient mice (30, 33, 40). Mice with a defect in the production of ISG15 are hyperresponsive to viral infection by influenza A and B, herpes, and Sindbis viruses (29, 41). Viral proteins that specifically target ISG15 to inhibit ISGylation have been reported (31). Among the viruses that cause acute and chronic infection, HCV is notorious for evading host-immune mechanisms and developing resistance to current IFN-based therapy tools. An internal domain that determines sensitivity to IFN has been identified in HCV-NS5A proteins, although the exact mechanism for regulation is not clear (14). Although there is strong evidence that ISG15 can function as an antiviral mediator, its role in regulating HCV replication has not been extensively explored. Silencing UBP43, which specifically cleaves ISGylated residues, potentiates antiviral activity of IFN against HCV replication (42), indicating that IFN-dependent ISGylation of NS5A does play a critical role in regulating anti-HCV replication.

We showed that treating cells with intracellular poly-IC and overexpressed ISG15 synergistically suppressed the cellular levels of HCV-NS5A protein, suggesting that IFN-induced ISG15 conjugation may be involved in the negative regulation of HCV replication. Although ISGylation does not directly target substrates for degradation by 26S proteasome complex (43), it inhibits normal functions of target protein by reducing the amounts of unmodified forms (32). Alternatively, it is possible that ISG15 conjugation could lead to altered subcellular localization of target proteins, thereby inhibiting their physiological functions. HCV viral genomes are replicated in the vicinity of ER membranes and form a lipid droplet-associated replication complex (10). ER membrane association mediated by the N-terminal amphipathic helix domain of HCV-NS5A is a critical step in HCV RNA replication, and a mutant form of HCV-NS5A lacking the N-terminal domain does not support HCV viral replication (8). Recently, it was reported that E2-conjugating enzymes for ISGylation suppress ubiquitination of cellular protein (44), presenting a competition mechanism between ISGylation and ubiquitination or cross-talk between ubiquitination and ISGylation (45). Therefore, future studies addressing the regulatory role of ubiquitinated NS5A and its cross-talk to ISGylation will be a key to our understanding of the underlying mechanism of ISGylation-mediated regulation of HCV-NS5A protein.

HCV-NS5A is composed of four functional regions: an N-terminal amphipathic helix domain, a hyperphosphorylation cluster, the interferon sensitivity-determining region (ISDR), and a polyproline cluster in the C-terminal region (46). Although internal ISDR in the HCV-NS5A is known to determine sensitivity to IFN therapy (14), mutant forms of NS5A lacking ISDR exhibited similar levels of ISGylation, indicating that IFN-dependent ISGylation of NS5A does not require ISDR region (Supplemental Fig. 5). Instead, we identified a lysine residue, K379, in the polyproline cluster of HCV-NS5A as the target site for ISGylation. Because K379 residue on HCV-NS5A is conserved in most HCV genotypes, it is likely that the negative effect of ISG15 conjugation on HCV-NS5A may be universal. Although we now know that ISG15 conjugation of HCV-NS5A at Lys 379 is critical for ISGylation-mediated negative control of HCV-NS5A, the molecular link between ISGylation and its effect on target protein regulation is still elusive.

We did not observe a similar inhibitory effect of HCV replication by ISG15 or ISGylation in the Huh-7.5 cells infected with the JFH strain of HCV (Supplemental Fig. 6). Similarly, ISG15 was recently reported to promote HCV replication in the HCV J6/JFH1-infected Huh-7.5 cells (47). There are several possible explanations for this difference. First, the effect of ISG15 or ISGylation on HCV replication may be specific to the genotypes. To confirm the inhibitory effect of ISGylation, we examined two HCV subgenomic replicon constructs, with all of the HCV genome sequence derived from genotype 1b, whereas the HCV J6/JFH1 strain used for cellular infection was derived from genotype 2a. HCV-NS5A from genotypes 1b and 2a showed only 64% amino
acid identity. In addition, it is possible that accumulated mutations in the HCV J6/JFH1 RNA genome during replication provides an evasion mechanism against ISGylation. Finally, the effect of ISG15 or ISGylation on HCV-NS5A may be compromised by HCV viral proteins that are not present in the replicon construct. The HCV subgenomic replicon used in this study contained coding sequences covering NS3, NS4A/BS, NS5A, and NS5B. Therefore, it lacked core, E1, E2, p7, and NS2 proteins.

Currently available treatment of HCV infection is restricted to pegylated IFN-α and ribavirin (48, 49). However, limited efficacy and side effects in patients treated with IFN-α demand the development of new therapeutic tools. Based on the focal replication of virus-infected regions in the liver are required. Aiming at the effective delivery of ISG15-conjugation system to the liver in patients with genotype 1 nonresponders. Gastroenterology 138: 1909–1919.


Supplementary Figure 1. Protein levels of HCV-NS5A was decreased by overexpression of the ISG15 conjugation system. COS7 cells were co-transfected with indicated expression vectors, and total cellular lysates were analyzed at 48 h after transfection by immunoblot assay.

Supplementary Figure 2. Both HCV-NS3 and HCV-NS5B proteins were not ISGylated. COS7 cells were transfected with the indicated expression plasmids and were stimulated with polyI:C (25μg/ml) or IFNβ (100 U/ml) for 24 h. Total lysates (1 mg) was subjected to immunoprecipitation using anti-V5 antibody, and immune complexes were analyzed by immunoblot using the indicated antibodies. For whole cell extract (WCE), 1/20th volume of total cell lysates was analyzed.

Supplementary Figure 3. HCV-NS5A (K379R) mutant was subject to ubiquitination. Total lysates (1 mg) of transfected COS7 cells was subjected to immunoprecipitation using anti-Flag antibody and and immune complexes were analyzed by immunoblot using the indicated antibodies. #, ubiquitinated HCV-NS5A (K379R).

Supplementary Figure 4. Protein levels of both wild type and mutant forms of NS5A were upregulated by ubiquitin overexpression. COS7 cells were transfected with the indicated expression plasmids and treated with CHX (30μg/ml) for 6 hours before analysis.

Supplementary Figure 5. Mutant forms of NS5A lacking ISDR was ISGylated, similar to wild type NS5A. COS7 cells were transfected with the indicated expression plasmids and treated with MG-132. Total lysates (1 mg) was subjected to immunoprecipitation using anti-Flag antibody, and immune complexes were analyzed by immunoblot assay using the anti-Myc and anti-Flag antibodies. For whole cell extract (WCE), 1/20th volume of total cell lysates was used. **, ISGylated HCV-NS5A.

Supplementary Figure 6. Replication of JFH strain of HCV was not regulated by ISGylation. Huh-7.5 cells were transfected with the indicated expression plasmids. 24 h after transfection, cells were infected with the JFH strain of HCV and its replication was measured by luciferase assay.
Kim et al., Supplementary Figure 1

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Blot: Myc (NS5A)
Blot: Myc (ISG15)
Blot: HA (Ube1L)
Blot: Gapdh

COS-7 Cells
Kim et al., Supplementary Figure 2

A

B
<table>
<thead>
<tr>
<th>MG132</th>
<th>WT</th>
<th>K379R</th>
</tr>
</thead>
<tbody>
<tr>
<td>-</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>Flag-NS5A</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>HA-Ub</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>

IB: aHA

IB: aFlag

IB: aGapdh

+ CHX (30mg/ml)
Kim et al., Supplementary Figure 5
Kim et al., Supplementary Figure 6