

5. Boulant, S., P. Targett-Adams, and J. McLauchlan. 2007. Disrupting the association of hepatitis C virus core protein with lipid droplets correlates with a loss in production of infectious virus. *J. Gen. Virol.* **88**:2204–2213.
6. Brass, V., E. Bieck, R. Montserret, B. Wolk, J. A. Vellings, H. E. Blum, F. Penin, and D. Moradpour. 2002. An amino-terminal amphipathic alpha-helix mediates membrane association of the hepatitis C virus nonstructural protein 5A. *J. Biol. Chem.* **277**:8130–8139.
7. Bulgakov, O. V., J. T. Eggenschwiler, D. H. Hong, K. V. Anderson, and T. Li. 2004. FKBP8 is a negative regulator of mouse sonic hedgehog signaling in neural tissues. *Development* **131**:2149–2159.
8. Egger, D., B. Wolk, R. Gosert, L. Bianchi, H. E. Blum, D. Moradpour, and K. Bienz. 2002. Expression of hepatitis C virus proteins induces distinct membrane alterations including a candidate viral replication complex. *J. Virol.* **76**:5974–5984.
9. Elazar, M., K. H. Cheong, P. Liu, H. B. Greenberg, C. M. Rice, and J. S. Glenn. 2003. Amphipathic helix-dependent localization of NS5A mediates hepatitis C virus RNA replication. *J. Virol.* **77**:6055–6061.
10. Enomoto, N., I. Sakuma, Y. Asahina, M. Kurosaki, T. Murakami, C. Yamamoto, N. Izumi, F. Marumo, and C. Sato. 1995. Comparison of full-length sequences of interferon-sensitive and resistant hepatitis C virus 1b. Sensitivity to interferon is conferred by amino acid substitutions in the NS5A region. *J. Clin. Invest.* **96**:224–230.
11. Evans, M. J., C. M. Rice, and S. P. Goff. 2004. Phosphorylation of hepatitis C virus nonstructural protein 5A modulates its protein interactions and viral RNA replication. *Proc. Natl. Acad. Sci. USA* **101**:13038–13043.
12. Fernandes, F., D. S. Poole, S. Hoover, R. Middleton, A. C. Andrei, J. Gerstner, and R. Striker. 2007. Sensitivity of hepatitis C virus to cyclosporine A depends on nonstructural proteins NS5A and NS5B. *Hepatology* **46**:1026–1033.
13. Gao, L., H. Aizaki, J. W. He, and M. M. Lai. 2004. Interactions between viral nonstructural proteins and host protein hVAP-33 mediate the formation of hepatitis C virus RNA replication complex on lipid raft. *J. Virol.* **78**:3480–3488.
14. Geller, R., M. Vignuzzi, R. Andino, and J. Frydman. 2007. Evolutionary constraints on chaperone-mediated folding provide an antiviral approach refractory to development of drug resistance. *Genes. Dev.* **21**:195–205.
15. Gosert, R., D. Egger, V. Lohmann, R. Bartenschlager, H. E. Blum, K. Bienz, and D. Moradpour. 2003. Identification of the hepatitis C virus RNA replication complex in Huh-7 cells harboring subgenomic replicons. *J. Virol.* **77**:5487–5492.
16. Hamamoto, I., Y. Nishimura, T. Okamoto, H. Aizaki, M. Liu, Y. Mori, T. Abe, T. Suzuki, M. M. Lai, T. Miyamura, K. Moriishi, and Y. Matsuura. 2005. Human VAP-B is involved in hepatitis C virus replication through interaction with NS5A and NS5B. *J. Virol.* **79**:13473–13482.
17. Ho, S. N., H. D. Hunt, R. M. Horton, J. K. Pullen, and L. R. Pease. 1989. Site-directed mutagenesis by overlap extension using the polymerase chain reaction. *Gene* **77**:51–59.
18. Horton, R. M., H. D. Hunt, S. N. Ho, J. K. Pullen, and L. R. Pease. 1989. Engineering hybrid genes without the use of restriction enzymes: gene splicing by overlap extension. *Gene* **77**:61–68.
19. Huang, L., E. V. Sineva, M. R. Hargittai, S. D. Sharma, M. Suthar, K. D. Raney, and C. E. Cameron. 2004. Purification and characterization of hepatitis C virus nonstructural protein 5A expressed in *Escherichia coli*. *Protein. Expr. Purif.* **37**:144–153.
20. Inoue, K., K. Sekiyama, M. Yamada, T. Watanabe, H. Yasuda, and M. Yoshida. 2003. Combined interferon alpha2b and cyclosporin A in the treatment of chronic hepatitis C: controlled trial. *J. Gastroenterol.* **38**:567–572.
21. Kanda, T., A. Basu, R. Steele, T. Wakita, J. S. Rysse, R. Ray, and R. B. Ray. 2006. Generation of infectious hepatitis C virus in immortalized human hepatocytes. *J. Virol.* **80**:4633–4639.
22. Kapadia, S. B., and F. V. Chisari. 2005. Hepatitis C virus RNA replication is regulated by host geranylgeranylation and fatty acids. *Proc. Natl. Acad. Sci. USA* **102**:2561–2566.
23. Krieger, N., V. Lohmann, and R. Bartenschlager. 2001. Enhancement of hepatitis C virus RNA replication by cell culture-adaptive mutations. *J. Virol.* **75**:4614–4624.
24. Lamarre, D., P. C. Anderson, M. Bailey, P. Beaulieu, G. Bojger, P. Bonneau, M. Bos, D. R. Cameron, M. Cartier, M. G. Cordingley, A. M. Faucher, N. Goudreau, S. H. Kawai, G. Kukolj, L. Lagace, S. R. LaPlante, H. Narjes, M. A. Poupard, J. Rancourt, R. E. Sentjens, R. St. George, B. Simoneau, G. Steinmann, D. Thibeault, Y. S. Tsantrizos, S. M. Weldon, C. L. Yong, and M. Llinas-Brunet. 2003. An NS3 protease inhibitor with antiviral effects in humans infected with hepatitis C virus. *Nature* **426**:186–189.
25. Lindenhach, B. D., M. J. Evans, A. J. Syder, B. Wolk, T. L. Tellinghuisen, C. C. Liu, T. Maruyama, R. O. Hynes, D. R. Burton, J. A. McKeating, and C. M. Rice. 2005. Complete replication of hepatitis C virus in cell culture. *Science* **309**:623–626.
26. Liu, J., J. D. Farmer, Jr., W. S. Lane, J. Friedman, I. Weissman, and S. L. Schreiber. 1991. Calcineurin is a common target of cyclophilin-cyclosporin A and FKBP-FK506 complexes. *Cell* **66**:807–815.
27. Lohmann, V., F. Korner, J. Koch, U. Herian, L. Theilmann, and R. Bartenschlager. 1999. Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell line. *Science* **285**:110–113.
28. Macdonald, A., K. Crowder, A. Street, C. McCormick, and M. Harris. 2004. The hepatitis C virus NS5A protein binds to members of the Src family of tyrosine kinases and regulates kinase activity. *J. Gen. Virol.* **85**:721–729.
29. Macdonald, A., and M. Harris. 2004. Hepatitis C virus NS5A: tales of a promiscuous protein. *J. Gen. Virol.* **85**:2485–2502.
30. Manns, M. P., J. G. McHutchison, S. C. Gordon, V. K. Rustgi, M. Shiffman, R. Reindollar, Z. D. Goodman, K. Koury, M. Ling, and J. K. Albrecht. 2001. Peginterferon alpha-2b plus ribavirin compared with interferon alpha-2b plus ribavirin for initial treatment of chronic hepatitis C: a randomised trial. *Lancet* **358**:958–965.
31. Miyazaki, Y., K. Atsuzawa, N. Usuda, K. Watashi, T. Hishiki, M. Zayas, R. Bartenschlager, T. Wakita, M. Hijikata, and K. Shimotohno. 2007. The lipid droplet is an important organelle for hepatitis C virus production. *Nat. Cell Biol.* **9**:1089–1097.
32. Moradpour, D., F. Penin, and C. M. Rice. 2007. Replication of hepatitis C virus. *Nat. Rev. Microbiol.* **5**:453–463.
33. Moriishi, K., and Y. Matsuura. 2003. Mechanisms of hepatitis C virus infection. *Antivir. Chem. Chemother.* **14**:285–297.
34. Moriishi, K., R. Mochizuki, K. Moriya, H. Miyamoto, Y. Mori, T. Abe, S. Murata, K. Tanaka, T. Miyamura, T. Suzuki, K. Koike, and Y. Matsuura. 2007. Critical role of PA28gamma in hepatitis C virus-associated steatogenesis and hepatocarcinogenesis. *Proc. Natl. Acad. Sci. USA* **104**:1661–1666.
35. Moriya, K., H. Yotsuyanagi, Y. Shintani, H. Fujie, K. Ishibashi, Y. Matsuura, T. Miyamura, and K. Koike. 1997. Hepatitis C virus core protein induces hepatic steatosis in transgenic mice. *J. Gen. Virol.* **78**(Pt. 7):1527–1531.
36. Niva, H., K. Yamamura, and J. Miyazaki. 1991. Efficient selection for high-expression transfectants with a novel eukaryotic vector. *Gene* **108**:193–199.
37. Okamoto, T., Y. Nishimura, T. Ichimura, K. Suzuki, T. Miyamura, T. Suzuki, K. Moriishi, and Y. Matsuura. 2006. Hepatitis C virus RNA replication is regulated by FKBP8 and Hsp90. *EMBO J.* **25**:5015–5025.
38. Pawlowsky, J. M., and G. Germanidis. 1999. The nonstructural 5A protein of hepatitis C virus. *J. Viral Hepat.* **6**:343–356.
39. Randall, G., M. Panis, J. D. Cooper, T. L. Tellinghuisen, K. E. Sukhodolets, S. Pfeffer, M. Landthaler, P. Landgraf, S. Kan, B. D. Lindenbach, M. Chien, D. B. Weir, J. J. Russo, J. Ju, M. J. Brownstein, R. Sheridan, C. Sander, M. Zavolan, T. Tuschl, and C. M. Rice. 2007. Cellular cofactors affecting hepatitis C virus infection and replication. *Proc. Natl. Acad. Sci. USA* **104**:12884–12889.
40. Rieder, C. L., and S. S. Bowser. 1985. Correlative immunofluorescence and electron microscopy on the same section of Epon-embedded material. *J. Histochem. Cytochem.* **33**:165–171.
41. Robida, J. M., H. B. Nelson, Z. Liu, and H. Tang. 2007. Characterization of hepatitis C virus nonstructural replicon resistance to cyclosporine in vitro. *J. Virol.* **81**:5829–5840.
42. Sakamoto, H., K. Okamoto, M. Aoki, H. Kato, A. Katsume, A. Ohta, T. Tsukuda, N. Shimizu, Y. Aoki, M. Arisawa, M. Kohara, and M. Sudoh. 2005. Host sphingolipid biosynthesis as a target for hepatitis C virus therapy. *Nat. Chem. Biol.* **1**:333–337.
43. Shi, S. T., S. J. Polyak, H. Tu, D. R. Taylor, D. R. Gretchen, and M. M. Lai. 2002. Hepatitis C virus NS5A colocalizes with the core protein on lipid droplets and interacts with apolipoproteins. *Virology* **292**:198–210.
44. Shirane, M., and K. I. Nakayama. 2003. Inherent calcineurin inhibitor FKBP38 targets Bcl-2 to mitochondria and inhibits apoptosis. *Nat. Cell Biol.* **5**:28–37.
45. Tellinghuisen, T. L., J. Marcotrigiano, A. E. Gorbalenya, and C. M. Rice. 2004. The NS5A protein of hepatitis C virus is a zinc metalloprotein. *J. Biol. Chem.* **279**:48576–48587.
46. Tellinghuisen, T. L., J. Marcotrigiano, and C. M. Rice. 2005. Structure of the zinc-binding domain of an essential component of the hepatitis C virus replicase. *Nature* **435**:374–379.
47. Tu, H., L. Gao, S. T. Shi, D. R. Taylor, T. Yang, A. K. Mircheff, Y. Wen, A. E. Gorbalenya, S. B. Hwang, and M. M. Lai. 1999. Hepatitis C virus RNA polymerase and NS5A complex with a SNARE-like protein. *Virology* **263**:30–41.
48. Vignuzzi, M., J. K. Stone, J. J. Arnold, C. E. Cameron, and R. Andino. 2006. Quasispecies diversity determines pathogenesis through cooperative interactions in a viral population. *Nature* **439**:344–348.
49. Wakita, T., T. Pietschmann, T. Kato, T. Date, M. Miyamoto, Z. Zhao, K. Murthy, A. Habermann, H. G. Krausslich, M. Mizokami, R. Bartenschlager, and T. J. Liang. 2005. Production of infectious hepatitis C virus in tissue culture from a cloned viral genome. *Nat. Med.* **11**:791–796.
50. Wang, C., M. Gale, Jr., B. C. Keller, H. Huang, M. S. Brown, J. L. Goldstein, and J. Ye. 2005. Identification of FBL2 as a geranylgeranylated cellular protein required for hepatitis C virus RNA replication. *Mol. Cell* **18**:425–434.
51. Wasley, A., and M. J. Alter. 2000. Epidemiology of hepatitis C: geographic differences and temporal trends. *Semin. Liver Dis.* **20**:1–16.
52. Watashi, K., M. Hijikata, M. Hosaka, M. Yamaji, and K. Shimotohno. 2003.

- Cyclosporin A suppresses replication of hepatitis C virus genome in cultured hepatocytes. *Hepatology* **38**:1282-1288.
53. **Watashi, K., N. Ishii, M. Hijikata, D. Inoue, T. Murata, Y. Miyanari, and K. Shimotohno.** 2005. Cyclophilin B is a functional regulator of hepatitis C virus RNA polymerase. *Mol. Cell* **19**:111-122.
54. **Ye, J., C. Wang, R. Sumpter, Jr., M. S. Brown, J. L. Goldstein, and M. Gale, Jr.** 2003. Disruption of hepatitis C virus RNA replication through inhibition of host protein geranylgeranylation. *Proc. Natl. Acad. Sci. USA* **100**:15865-15870.
55. **Yi, M., and S. M. Lemon.** 2004. Adaptive mutations producing efficient replication of genotype 1a hepatitis C virus RNA in normal Huh7 cells. *J. Virol.* **78**:7904-7915.
56. **Yi, M., R. A. Villanueva, D. L. Thomas, T. Wakita, and S. M. Lemon.** 2006. Production of infectious genotype 1a hepatitis C virus (Hutchinson strain) in cultured human hepatoma cells. *Proc. Natl. Acad. Sci. USA* **103**:2310-2315.
57. **Zhong, J., P. Gastaminza, G. Cheng, S. Kapadia, T. Kato, D. R. Burton, S. F. Wieland, S. L. Uprichard, T. Wakita, and F. V. Chisari.** 2005. Robust hepatitis C virus infection in vitro. *Proc. Natl. Acad. Sci. USA* **102**:9294-9299.

Intramembrane Processing by Signal Peptide Peptidase Regulates the Membrane Localization of Hepatitis C Virus Core Protein and Viral Propagation[†]

Kiyoko Okamoto,^{1†} Yoshio Mori,^{1†} Yasumasa Komoda,¹ Toru Okamoto,¹ Masayasu Okochi,² Masatoshi Takeda,² Tetsuro Suzuki,³ Kohji Moriishi,¹ and Yoshiharu Matsuura^{1*}

Department of Molecular Virology, Research Institute for Microbial Diseases,¹ and Department of Post-Genomics and Diseases, Division of Psychiatry and Behavioral Proteomics, Graduate School of Medicine,² Osaka University, Osaka, and Department of Virology II, National Institute of Infectious Diseases, Tokyo,³ Japan

Received 12 February 2008/Accepted 11 June 2008

Hepatitis C virus (HCV) core protein has shown to be localized in the detergent-resistant membrane (DRM), which is distinct from the classical raft fraction including caveolin, although the biological significance of the DRM localization of the core protein has not been determined. The HCV core protein is cleaved off from a precursor polyprotein at the lumen side of Ala¹⁹¹ by signal peptidase and is then further processed by signal peptide peptidase (SPP) within the transmembrane region. In this study, we examined the role of SPP in the localization of the HCV core protein in the DRM and in viral propagation. The C terminus of the HCV core protein cleaved by SPP in 293T cells was identified as Phe¹⁷⁷ by mass spectrometry. Mutations introduced into two residues (Ile¹⁷⁶ and Phe¹⁷⁷) upstream of the cleavage site of the core protein abrogated processing by SPP and localization in the DRM fraction. Expression of a dominant-negative SPP or treatment with an SPP inhibitor, L685,458, resulted in reductions in the levels of processed core protein localized in the DRM fraction. The production of HCV RNA in cells persistently infected with strain JFH-1 was impaired by treatment with the SPP inhibitor. Furthermore, mutant JFH-1 viruses bearing SPP-resistant mutations in the core protein failed to propagate in a permissive cell line. These results suggest that intramembrane processing of HCV core protein by SPP is required for the localization of the HCV core protein in the DRM and for viral propagation.

The hepatitis C virus (HCV), which has infected an estimated 170 million people worldwide, leads to chronic hepatitis, which in turn causes severe liver diseases, including steatosis, cirrhosis, and eventually hepatocellular carcinoma (47). HCV possesses a positive-sense single-stranded RNA with a nucleotide length of 9.6 kb, which encodes a single large precursor polyprotein composed of about 3,000 amino acids. The viral polyprotein is processed by cellular and viral proteases into structural and nonstructural proteins (24). The development of efficient therapies for hepatitis C had been hampered by the lack of a reliable cell culture system, as well as by the absence of a small-animal model. Lohmann et al. established an HCV replicon, which consisted of an antibiotic selection marker and a genotype 1b HCV RNA, and showed that it replicated autonomously in the intracellular compartments of a human hepatoma cell line, Huh7 (16). The replicon system has been used as an important tool in the investigation of HCV replication, and it has served as a cell-based assay system for the evaluation of antiviral compounds. Recently, cell culture systems for *in vitro* replication and infectious-virus production were established based on the full-length HCV genome of a genotype 2a isolate, which was recovered from a fulminant hepatitis C pa-

tient (15, 45, 50). However, the molecular mechanism of the HCV life cycle in host cells has not been well characterized.

Several viruses have been reported to utilize a lipid raft composed of cholesterol and sphingolipids upon entry (34). The lipid raft is characterized by resistance to nonionic detergents at 4°C and includes caveolin, glycolipids, and other substances (40). Several nonenveloped viruses enter cells through a caveola/raft-mediated endosome, designated the caveosome, and then translocate to the endoplasmic reticulum (ER), endosome, or nucleus (34, 35), although enveloped viruses generally enter host cells through a clathrin-dependent pathway (18). HCV is enclosed by a host cell-derived membrane and belongs to the family *Flaviviridae*. Several reports suggest that HCV enters host cells through general endocytosis, such as by a clathrin-mediated pathway (5, 6, 22). However, HCV has been suggested to replicate on a detergent-resistant membrane (DRM), including some characteristic membrane structures such as lipid rafts and membranous webs (8, 9, 38). In a previous report, an HCV replication complex prepared from a cell fraction treated with a nonionic detergent was shown to be enzymatically active (2). HCV nonstructural proteins remodel the intracellular membrane to form a replication complex that includes several host proteins (8, 46). The HCV core protein has a C-terminal transmembrane region that is anchored on intracellular compartments such as the ER and mitochondria and on the surfaces of lipid droplets (10, 30, 42). Recent studies have indicated that assembly of HCV particles occurs around lipid droplets that are surrounded by the remodeled membranes (23). Although the HCV core protein functions as a capsid protein, it is found in the DRM fraction, which is

* Corresponding author. Mailing address: Department of Molecular Virology, Research Institute for Microbial Diseases, Osaka University, 3-1 Yamada-oka, Suita, Osaka 565-0871, Japan. Phone: 81-6-6879-8340. Fax: 81-6-6879-8269. E-mail: matsuura@biken.osaka-u.ac.jp.

† K. Okamoto and Y. Mori contributed equally to this work.

[†] Published ahead of print on 18 June 2008.

distinct from the classical lipid rafts (20). However, the biological function of the HCV core protein localized in the DRM has not been clarified.

The HCV core protein is cleaved from a precursor polyprotein by a signal peptidase (SP) to liberate it from the envelope protein E1 and is then further processed by a signal peptide peptidase (SPP) (21). However, the biological significance of the intramembrane processing of the HCV core protein by SPP remains largely unknown. Furthermore, the C-terminal end of the mature HCV core protein expressed in insect cells has been reported to be Phe¹⁷⁷ or Leu¹⁷⁹ (12, 29), while that in mammalian cells has not been determined. Expression of SPP enhanced the accumulation of nonenveloped nucleocapsid and reduced that of enveloped nucleocapsid in yeast cells, suggesting that maturation of core protein is carried out after the formation of enveloped particles (17). However, the effect of SPP cleavage on viral assembly in mammalian cells has not been well characterized. Randall et al. have reported that introduction of a small interfering RNA targeted to SPP reduced the production of infectious HCV particles (36), suggesting that SPP is required for the production of HCV particles. In this study, we determined the cleavage site of the mature HCV core protein expressed in human cells and examined the biological significance of the intramembrane processing of the core protein by SPP for the localization of the core protein in the DRM and the production of infectious particles.

MATERIALS AND METHODS

Cell lines and HCV infection. HCV subgenomic RNA was removed from the replicon cell line 9-13 (16) by treatment with alpha interferon. A cell line that was highly permissive for JFH-1 infection was cloned from the resulting crude populations by the limited-dilution method and designated Huh7OK1 (32). The Huh7OK1 cell line retained the ability to produce type I interferons through the RIG-I-dependent signaling pathway upon infection with RNA viruses and exhibited a cell surface expression level of human CD81 comparable to that of the parental cell line. The detailed characteristics of this cell line will be described in a future communication. The HuhOK1 and Huh7.5.1 cell lines (the latter was kindly provided by F. Chisari) and the human embryonic kidney cell line 293T were maintained in Dulbecco's modified Eagle's medium supplemented with 10% fetal calf serum and nonessential amino acids (Sigma, St. Louis, MO). Huh7OK1 or Huh7.5.1 cells were infected with HCV strain JFH-1 as described by Wakita et al. (45). The plasmid carrying strain JFH-1 cDNA under the control of the poly promoter (19) was transfected into Huh7OK1 or Huh7.5.1 cells, and propagation of the JFH-1 virus was determined by the production of HCV core protein (as described below) and by the titration of infectious particles (39). The persistently infected Huh7OK1 cells were maintained under normal conditions after 8 passages before use. The 9-13 cell line, which possesses an HCV subgenomic replicon (16), was cultured in Dulbecco's modified Eagle's medium supplemented with 10% fetal calf serum and 1 mg/ml G418.

Plasmids. Genes encoding the N-terminally FLAG-tagged and/or C-terminally hemagglutinin (HA)-tagged core proteins derived from the HCV genotype 1b strain J1 or its mutants were introduced into plasmid vector pCDNA3.1 (Invitrogen, Carlsbad, CA) as described previously (30). Each insert gene was transferred into a pCAGGS vector (28) at the PmeI site. The resulting plasmids encoded the HCV core protein (amino acid residues 1 to 191) with or without FLAG and HA tags at the N and C termini, respectively. All of the core proteins with these tags (FLAG-core-HA proteins) had a mutation of Ala¹⁹¹ to Arg in order to prevent cleavage by the SP (7). Plasmid pHH21/JFH-1, carrying a full genomic cDNA of strain JFH-1 under the control of the poly promoter, was used to produce the infectious JFH-1 virus (19). An adaptive mutation of Leu to Val at amino acid position 758 in the p7 region was introduced during a long-term passage of the JFH-1 virus into Huh7.5.1 cells (data not shown). To improve the replication efficiency of the JFH-1 virus, a mutation of Leu to Val was introduced into pHH21/JFH-1 by site-directed mutagenesis, and the resulting plasmid was designated pHH21/JFH-1/L758V. To generate plasmids encoding the mutant JFH-1 viruses, the following substitutions were introduced into pHH21/JFH-1/

L758V: Val¹³⁹, Val¹⁴⁰, and Leu¹⁴⁴ were replaced with Ala (JFH-1/VV/L3A); Ile¹⁷⁶ and Phe¹⁷⁷ were replaced with Ala and Leu, respectively (JFH-1/IF/AL); Ala¹⁸⁰, Ser¹⁸³, and Cys¹⁸⁴ were replaced with Val, Leu, and Val, respectively (JFH-1/ASC/VLV); and Asp²⁷³⁶ was replaced with Asn (JFH-1/GND).

Antibodies and reagents. Antisera against HCV genotype 1 or 2a core proteins were raised in rabbits by immunization with peptides corresponding to the region spanning residues 103 to 115, conserved among genotypes 1a and 1b, or to the region from residue 101 to 119 of genotype 2a (strain JFH-1). These peptides were synthesized and conjugated with keyhole limpet hemocyanin (Scrum Inc., Tokyo, Japan). Antisera were purified with an affinity column conjugated with the antigenic peptides. A monoclonal antibody to HCV NS5A (5A27) was prepared from BALB/c mice (CLEA Japan, Tokyo, Japan) immunized with the recombinant domain I of NS5A by a method described previously (31). Antibodies to caveolin-1, calreticulin, and the FLAG tag (M2) were purchased from Sigma. Antibodies to the HA tag and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) were purchased from Babco (Richmond, CA) and Santa Cruz Biotechnology (Santa Cruz, CA), respectively. The aspartic protease inhibitors (Z-LL)₂ ketone and L685,458 were purchased from the Peptide Institute (Osaka, Japan). These inhibitors were dissolved in dimethyl sulfoxide and stored at -20°C until use.

Transfection, SDS-PAGE, and Western blotting. Huh7.5.1 and 293T cells were transfected with plasmids by lipofection with Trans IT LT-1 (Mirus, Madison, WI) and Lipofectamine 2000 (Invitrogen), respectively, according to the manufacturers' protocols. Cells were lysed on ice in Triton lysis buffer (20 mM Tris-HCl [pH 7.4], 135 mM NaCl, 1% Triton-X 100, 10% glycerol) supplemented with a protease inhibitor mix (Nacalai Tesque, Kyoto, Japan) at 24 or 48 h after transfection and were then subjected to sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) using Tris-glycine buffer and Western blotting using appropriate antibodies as previously described (30). The stained protein bands were visualized using the SuperSignal West Femto enhanced-chemiluminescence substrate (Pierce, Rockford, IL) and an LAS3000 imaging system (Fuji Photo Film, Tokyo, Japan).

Determination of the expression of the C terminus of the mature HCV core protein in mammalian cells. Two million 293T cells cultured in a collagen-coated dish (diameter, 10 cm) were transfected with pCAGGS-FLAG-core (26) by lipofection, harvested at 20 h posttransfection with a rubber policeman after two washes with ice-cold phosphate-buffered saline (PBS), and collected by centrifugation at 1,000 × g for 5 min. The cells were lysed with 0.1 ml of triple-detergent lysis buffer (45 mM Tris-HCl [pH 7.4] containing 0.5% sodium deoxycholate, 0.1% SDS, 1% Triton X-100, 135 mM NaCl, and a protease inhibitor mix [Nacalai Tesque]) (24). The lysate was stored at -80°C until use. The lysate was thawed on ice and then centrifuged at 20,000 × g for 10 min at 4°C. The supernatant was mixed with 20 μl of 50% (vol/vol) anti-FLAG M2 affinity gel (Sigma) and then rotated at 4°C for 90 min. The gel beads were washed with the triple-detergent lysis buffer and then suspended in 30 μl of the loading buffer. The suspended gel beads were boiled for 5 min and then centrifuged at 20,000 × g for 5 min at room temperature. The resulting supernatant was subjected to SDS-PAGE, and the gel was stained with Sypro Ruby dye (Invitrogen). The portion of the gel including proteins with an expected molecular size of 20 kDa was excised from the stained gel, washed twice with 200 μl of 50 mM NH₄HCO₃ dissolved in 50% acetonitrile (vol/vol), and then immersed in 100 μl of 100% acetonitrile for dehydration. The dehydrated gel was incubated in 10 mM diethylenetriamine and 100 mM NH₄HCO₃ at 56°C for 1 h. To prevent the digestion of Cys residues at the C terminus by endoprotease Asp-N, alkylation of the gels was carried out in 55 mM iodoacetamide and 100 mM NH₄HCO₃ at 25°C for 45 min in the dark. Finally, gel pieces were washed twice with 100 mM ammonium carbonate dissolved in acetonitrile and were dried completely before digestion. An immersed volume of endoprotease Asp-N solution (10 μg/ml Asp-N and 50 mM NH₄HCO₃) was added to the dried gel and incubated at 37°C overnight, and the supernatant (the digested solution) after centrifugation was transferred to a new centrifuge tube. The precipitated gels were washed first with 20 μl of 20 mM NH₄HCO₃ and then with 20 μl of 50% (vol/vol) acetonitrile in 5% (vol/vol) formic acid, and the washed solutions were mixed with the digested solution and dried completely under a vacuum. The digested mixtures were applied to a ZipTip C₁₈ column (Millipore, Tokyo, Japan). After a wash with 0.1% (vol/vol) trifluoroacetic acid, the peptides were eluted with 1 μl of 0.1% (vol/vol) trifluoroacetic acid dissolved in 75% (vol/vol) acetonitrile. Samples with 10 mg of 2,5-dihydroxybenzoic acid per ml of 33% acetonitrile matrix were analyzed by matrix-assisted laser desorption/ionization-time-of-flight mass spectrometry (MALDI-TOF MS) using a MALDI-quadrupole-TOF tandem MS (MS-MS) QStar Pulsar i system (Applied Biosystems, Foster City, CA) in the linear positive-ion mode following the method of Hitachi Science Systems (Ibaraki, Japan).

Flotation assay. The flotation assay was carried out according to the method of Lecat et al. (14). Briefly, 10 million transfected or infected cells were washed with ice-cold PBS and then harvested with a rubber policeman. Collected cells were suspended in 0.6 ml of TNE buffer (25 mM Tris-HCl [pH 7.4] containing 150 mM NaCl, a protease inhibitor mix [Nacalai Tesque], and 5 mM EDTA) and then homogenized with a Dounce homogenizer or suspended with a 24-gauge needle. Each homogenate was incubated for 30 min on ice with or without 1% Triton X-100. The lysates were mixed with 0.4 ml of Optiprep (Sigma) to a final concentration of 40%. This mixture was overlaid with 1.2 ml of 30%, 1.2 ml of 25%, and 0.8 ml of 5% Optiprep and was then centrifuged at 42,000 rpm and 4°C for 5 h in an SW50 rotor (Beckman Coulter, Fullerton, CA). Each fraction was collected as 4 ml from the top of the centrifuging tube and was then precipitated with 4 volumes of cold acetone. The pellets were resolved in the loading buffer, boiled, and then subjected to SDS-PAGE and Western blotting. The fractions containing calreticulin, which is resident in the ER, in the absence and presence of the detergent were defined as the membrane and detergent-soluble fractions, respectively. In the presence of the detergent, the fractions with caveolin-1 were defined as the detergent-resistant fractions.

Quantitative real-time PCR. Total RNA was prepared from Huh7OK1 cells persistently infected with the JFH-1 virus or 9-13 cells by using an RNeasy minikit (Qiagen, Tokyo, Japan). The HCV genomic RNA was reverse transcribed and amplified by using a TaqMan EZ RT-PCR reagent kit (Applied Biosystems) with sense (5'-GAG TGT CGT GCA GCC TCC A-3') and anti-sense (5'-CAC TCG CAA GCA CCC TAT CA-3') primers corresponding to nucleotides 98 to 116 and 294 to 313, respectively. The kinetics of cDNA amplification were monitored by an ABI Prism 7000 sequence detection system (Applied Biosystems) using a reporter probe corresponding to nucleotides 238 to 267 of the 5'-conserved region of the HCV genotypes (5'-GCC CGC AAG ACT GCT AGC CGA GTA GTG TTG G-3') conjugated with 6-carboxyfluorescein and 6-carboxytetramethylrhodamine at the 5' and 3' termini, respectively. A serial dilution of the partial HCV RNA synthesized by *in vitro* transcription from plasmids encoding the 5'-terminal region of HCV cDNA under the control of a T7 promoter was used as the standard for HCV genomic RNA. Intracellular GAPDH mRNA was also amplified using the TaqMan Pre-Developed Assay Reagent human GAPDH (Applied Biosystems). The values for HCV genomic RNA were normalized to those for GAPDH mRNA.

Quantitative detection of HCV core protein by ELISA. HCV core protein was quantified by using an Ortho HCV antigen enzyme-linked immunosorbent assay (ELISA) (Ortho Clinical Diagnostics, Tokyo, Japan) according to the manufacturer's instructions. Huh7.5.1 cells were transfected with pFH21/JFH-1L758V or its mutants by lipofection. Cells and culture supernatants were harvested at 2, 4, 6, or 8 days after transfection. To determine the amounts of the intracellular core protein, cells were lysed with Triton lysis buffer on ice and subjected to the ELISA after 100- to 10,000-fold dilutions with PBS. Total protein levels were determined with a Micro BCA protein assay reagent kit (Pierce). Amounts of intracellular and extracellular core protein were normalized to total-protein amounts.

Immunofluorescent assay. Transfected Huh7.5.1 cells were fixed with a cold acetone-and-methanol mixture (50:50, vol/vol). After being blocked with 1% normal goat serum, cells were incubated with a mouse monoclonal antibody to NS5A at 4°C for 16 h, washed three times with PBS containing 0.5% Tween 20, and then incubated with an Alexa Fluor 594-conjugated antibody to mouse immunoglobulin G (Invitrogen). Cell nuclei were stained with Hoechst dye. The stained cells were washed three times with PBS containing 0.5% Tween 20 and then observed with a Fluoview FV1000 laser scanning confocal microscope (Olympus, Tokyo, Japan).

RESULTS

Mutation in the HCV core protein confers resistance to SPP cleavage. Amino acid residues Ala¹⁸⁰, Ser¹⁸³, and Cys¹⁸⁴ of the HCV core protein have been shown by others to be essential for intramembrane processing by SPP (10, 21), although our data suggested that Ile¹⁷⁶ and Phe¹⁷⁷, but not Ala¹⁸⁰, Ser¹⁸³, and Cys¹⁸⁴, were required for the processing of the HCV core protein by SPP (30). To clarify this discrepancy, we constructed an N-terminally FLAG-tagged and C-terminally HA-tagged wild-type HCV core protein and similarly tagged mutant core proteins in which Ala¹⁸⁰, Ser¹⁸³, and Cys¹⁸⁴ were replaced with Val, Leu, and Val, respectively (referred to below as Core

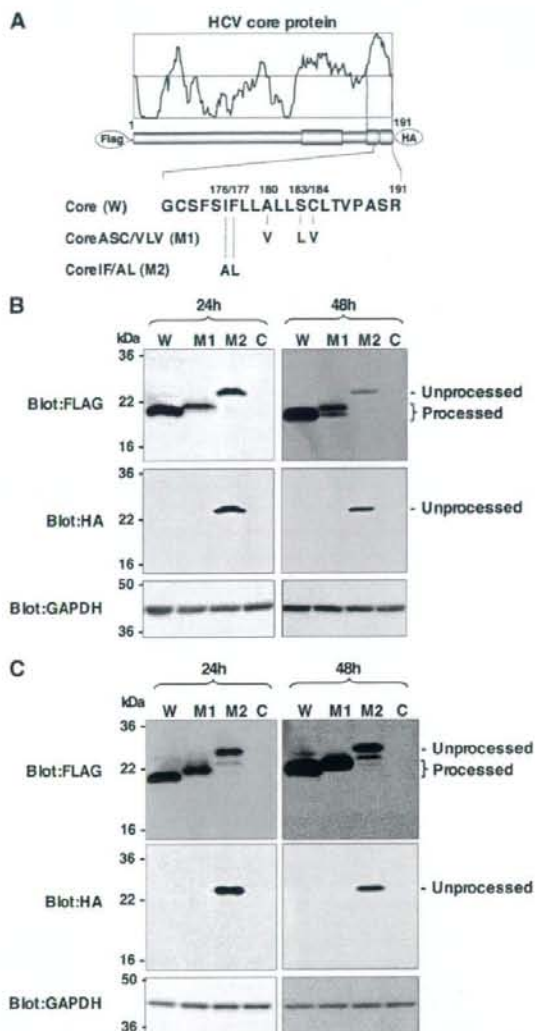
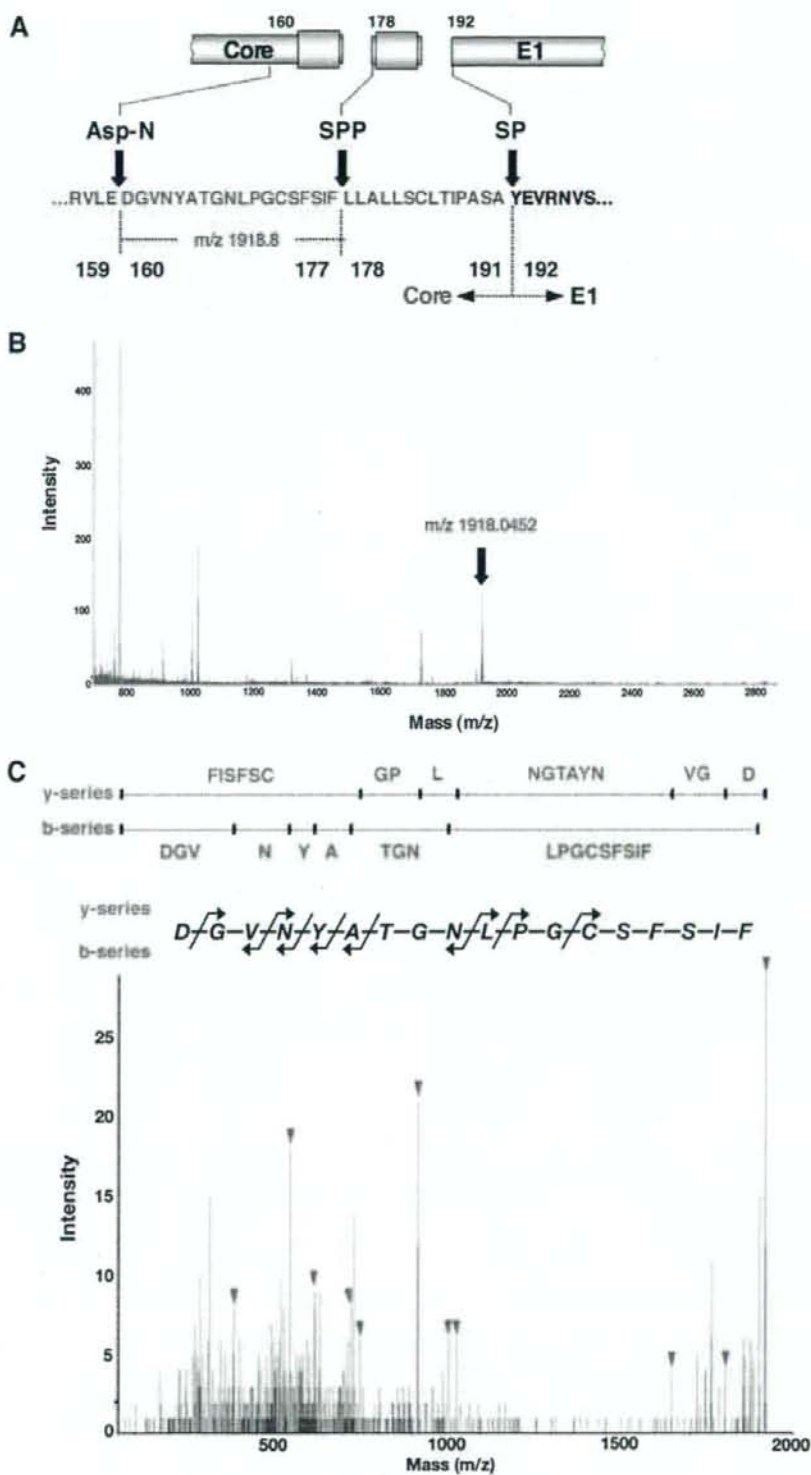


FIG. 1. Effects of mutations in the HCV core protein on cleavage by SPP. (A) cDNA constructs encoding the N-terminally FLAG- and C-terminally HA-tagged wild-type HCV core protein (W), Core ASC/VLV (M1), and Core IF/AL (M2). The Ala at amino acid residue 191 of all constructs was mutated to Arg in order to prevent the processing of an HA tag by SP. (B) Each of the core constructs or an empty vector (lane C) was transfected into 293T cells. Cell lysates harvested at 24 or 48 h posttransfection were subjected to Western blotting using antibodies against the indicated proteins. (C) Cells transfected with each of the core constructs or an empty vector were treated with 15 μM MG132 for 5 h and examined as described for panel B.

ASC/VLV, or M1) (21), or Ile¹⁷⁶ and Phe¹⁷⁷ were replaced with Ala and Leu, respectively (referred to below as Core IF/AL, or M2) (30). We then expressed these core proteins in 293T cells (Fig. 1). Ala¹⁹¹ was replaced with Arg in these FLAG-core-HA constructs to prevent cleavage by SP (7), and only the SPP-resistant core protein was detected by an anti-HA



antibody in this experimental setting. Core IF/AL was detected in cells by both anti-FLAG and anti-HA antibodies at 24 h and 48 h posttransfection, whereas the wild-type core and Core ASC/VLV were detected by an anti-FLAG antibody but not by an anti-HA antibody (Fig. 1B). These results indicate that Core IF/AL is resistant to SPP cleavage, in contrast to the complete processing of the wild-type core and Core ASC/VLV. Although Core ASC/VLV exhibited a single band that was slightly larger than the wild-type core protein at 24 h posttransfection, an extra band with the same mobility as the wild-type core protein appeared at 48 h posttransfection (Fig. 1B), suggesting that the introduction of mutations in Ala¹⁸⁰, Ser¹⁸³, and Cys¹⁸⁴ induces multiple processing in the signal sequence of the mutant core protein. To exclude the possibility that unprocessed Core ASC/VLV is degraded by a proteasome due to misfolding, each of the core constructs or the empty vector was transfected into 293T cells and treated with a proteasome inhibitor for 5 h. The unprocessed band of Core IF/AL, but not that of Core ASC/VLV, was detected by the anti-HA antibody (Fig. 1C). These results further support the notion that Core ASC/VLV is sensitive to SPP-dependent processing. Bands observed between unprocessed and processed proteins in cells expressing wild-type core or Core IF/AL in the presence of a proteasome inhibitor were not detected by the anti-HA antibody, suggesting that these products are generated by C-terminal truncation and are sensitive to proteasome degradation.

Identification of the C-terminal residue of the mature HCV core protein. Previous reports have suggested that the C terminus of the mature HCV core protein expressed in insect cells by using a baculovirus expression system is Phe¹⁷⁷ (29) or Leu¹⁷⁹ (12). To clarify the C-terminal amino acid residue of the mature HCV core protein expressed in human cells, a purified fragment of the HCV core protein was analyzed by MALDI-TOF MS. The FLAG-tagged HCV core protein was expressed under the control of a CAG promoter in 293T cells, purified by immunoprecipitation with beads conjugated with the anti-FLAG antibody, and then released from the beads by the addition of free FLAG peptide. The purified FLAG-tagged core protein was digested with Asp-N protease, and the final sample was subjected to MALDI-TOF MS for determination of the C-terminal residue. The N-terminal amino acid of the peptide fragment including the C terminus of the mature HCV core protein was expected to be Asp¹⁶⁰ (Fig. 2A). The peptide fragment with an m/z of 1,918.0452, which is close to the calculated value (m/z 1,918.8) of the sequence DGVNYATG NLPGCSFSIF (Fig. 2A), was detected, and no larger peak was evident (Fig. 2B). MS-MS analysis showed that the fragment has the amino acid sequence DGVNYATGNLPGCSFSIF (Fig. 2C). These results indicate that the C terminus of the

mature HCV core protein expressed in human cells is Phe¹⁷⁷. This is consistent with our previous observation (30) and with the data shown in Fig. 1, which indicate that the M2 mutation completely abrogated the processing of core protein by SPP. Both Ile¹⁷⁶ and Phe¹⁷⁷ may play crucial roles in recognition by SPP for intramembrane cleaving activity.

SPP processing is required for the localization of HCV core protein in the DRM. Based on confocal microscopy observations, Matto et al. reported that the HCV core protein associates with a DRM that is distinct from the classical raft fraction, as evidenced by the lack of colocalization of typical raft markers, including caveolin-1 and the B subunit of the cholera toxin, which binds to glycosphingolipid GM1 in the plasma membrane (20). We have previously suggested that intramembrane processing by SPP affects the intracellular localization of the HCV core protein, and the replacement of Leu¹³⁹, Val¹⁴⁰, and Leu¹⁴⁴ with Ala in the HCV core protein (Core LVL/3A [M3]) (Fig. 3A) abrogated SPP-mediated processing and ER retention (30). In this study, we examined the effect of SPP cleavage on the DRM localization of the HCV core protein. The wild-type or mutant HCV core protein was expressed in 293T cells, solubilized at 4°C in the presence or absence of 1% Triton X-100, and subjected to sucrose gradient centrifugation. Fractions were collected after ultracentrifugation and analyzed by immunoblotting. The wild-type core protein was partially detected in fraction 3, which corresponded to the DRM fraction, and was mainly detected in the detergent-soluble fraction (Fig. 3B). However, the mutant core proteins Core LVL/3A (M3) and Core IF/AL (M2) were localized in the membrane fraction but not in the DRM fraction (Fig. 3B). Although the M2 mutant exhibits clear resistance to SPP-dependent cleavage, as shown in Fig. 1B, processed core proteins of M2 and M3 mutants were detected by flotation analyses (Fig. 3B), suggesting that the M2 and M3 mutants are cleaved by unknown mechanisms during the concentration step. These results suggest that processing by SPP is required for the DRM localization of the HCV core protein.

A dominant-negative SPP mutant inhibits the intramembrane processing and DRM localization of the HCV core protein. SPP belongs to the family of aspartic proteases, which share two Asp residues for the active sites of protease activity. Asp²¹⁹ and Asp²⁶⁴ have been identified as active sites for the protease activity of SPP (48). Overexpression of the SPP mutant in which Asp²¹⁹ was replaced with Ala (SPPD219A) resulted in a dominant-negative activity that prevented the intramembrane processing of the HCV core protein (30). To examine the relationship between intramembrane processing by SPP and the localization of the HCV core protein in the DRM fraction, a C-terminally HA-tagged wild-type (SPP-HA)

FIG. 2. Determination of the C termini of the mature HCV core protein. (A) Schematic representation of the junction between the core and E1 proteins. The cleavage sites for the exogenous Asp-N protease and the host SPP were the N-terminal residue Asp¹⁶⁰ and the C-terminal residue Ala¹⁹¹, respectively. The cleavage site of the host SPP was determined to be the C-terminal residue Phe¹⁷⁷ in this study. The expected m/z of the peptide fragment (spanning residues 160 to 177) processed by the Asp-N protease and SPP is indicated. (B) The FLAG-core protein was purified with an anti-FLAG antibody, digested with Asp-N, and analyzed on a 2,5-dihydroxybenzoic acid matrix by MALDI-TOF MS in the linear positive-ion mode. The peak at m/z 1,918.0452 corresponded to the expected fragment (m/z 1,918.8) derived from the Asp-N- and SPP-digested core protein, DGVNYATGNLPGCSFSIF. (C) The peak at m/z 1,918.0452 was subjected to MS-MS analysis with a MALDI-Qq-TOF MS-MS QStar Pulsar *i* system. The resulting spectrum was applied to MASCOT to determine the amino acid sequence. The analyzed peak at m/z 1,918.0452 corresponded to the sequence DGVNYATGNLPGCSFSIF.

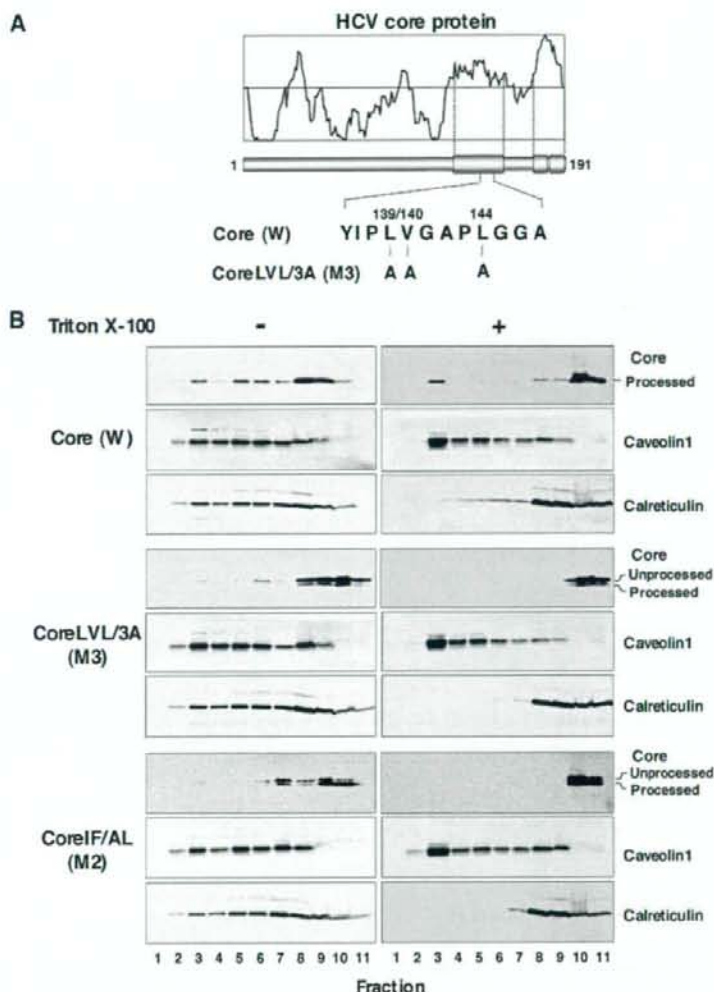


FIG. 3. HCV core protein partially migrates to the DRM after SPP processing. (A) cDNAs encoding authentic wild-type (W) and Core LVL/3A (M3) HCV core proteins. (B) Each plasmid was transfected into 293T cells, lysed with or without 1% Triton X-100, and then subjected to a flotation assay. Proteins in each fraction were concentrated with cold acetone and then subjected to Western blotting using antibodies against core protein, caveolin-1, and calreticulin. Membrane (left panels, lanes 1 to 9), DRM (right panels, lanes 1 to 7), and detergent-soluble (right panels, lanes 8 to 11) fractions were identified based on the localization of the marker proteins.

or D219A mutant (SPPD219A-HA) SPP was coexpressed with FLAG-core-HA in 293T cells (Fig. 4A). Overexpression of SPP-HA showed no effect on the localization of the HCV core protein, and the processed HCV core protein was partially localized in the DRM fraction (Fig. 4B, left). In contrast, overexpression of SPPD219A-HA inhibited the processing of the HCV core protein by endogenous SPP, and the level of unprocessed core protein, which was detected in the detergent-soluble fraction but not in the DRM fraction, was increased, whereas part of the processed core protein was localized in the DRM fraction (Fig. 4B, right). These results suggest that SPP cleavage is a prerequisite for the localization of HCV core protein in the DRM fraction. We have previously shown that

the HCV core protein is degraded through proteasome pathways (26, 39, 43). To rule out the possibility of proteasome-dependent degradation of the unprocessed HCV core protein in the DRM fraction, we examined the effect of the proteasome inhibitor MG132 on the localization of HCV core protein. The processed HCV core protein, but not the unprocessed core protein, was partially localized in the DRM fraction, irrespective of treatment with MG132 (Fig. 4C). These results indicate that the failure of the unprocessed HCV core protein to localize in the DRM fraction was not due to selective degradation of the unprocessed core protein by proteasomes.

An SPP inhibitor prevents the processing of HCV core protein and its localization in the DRM. To further assess the role

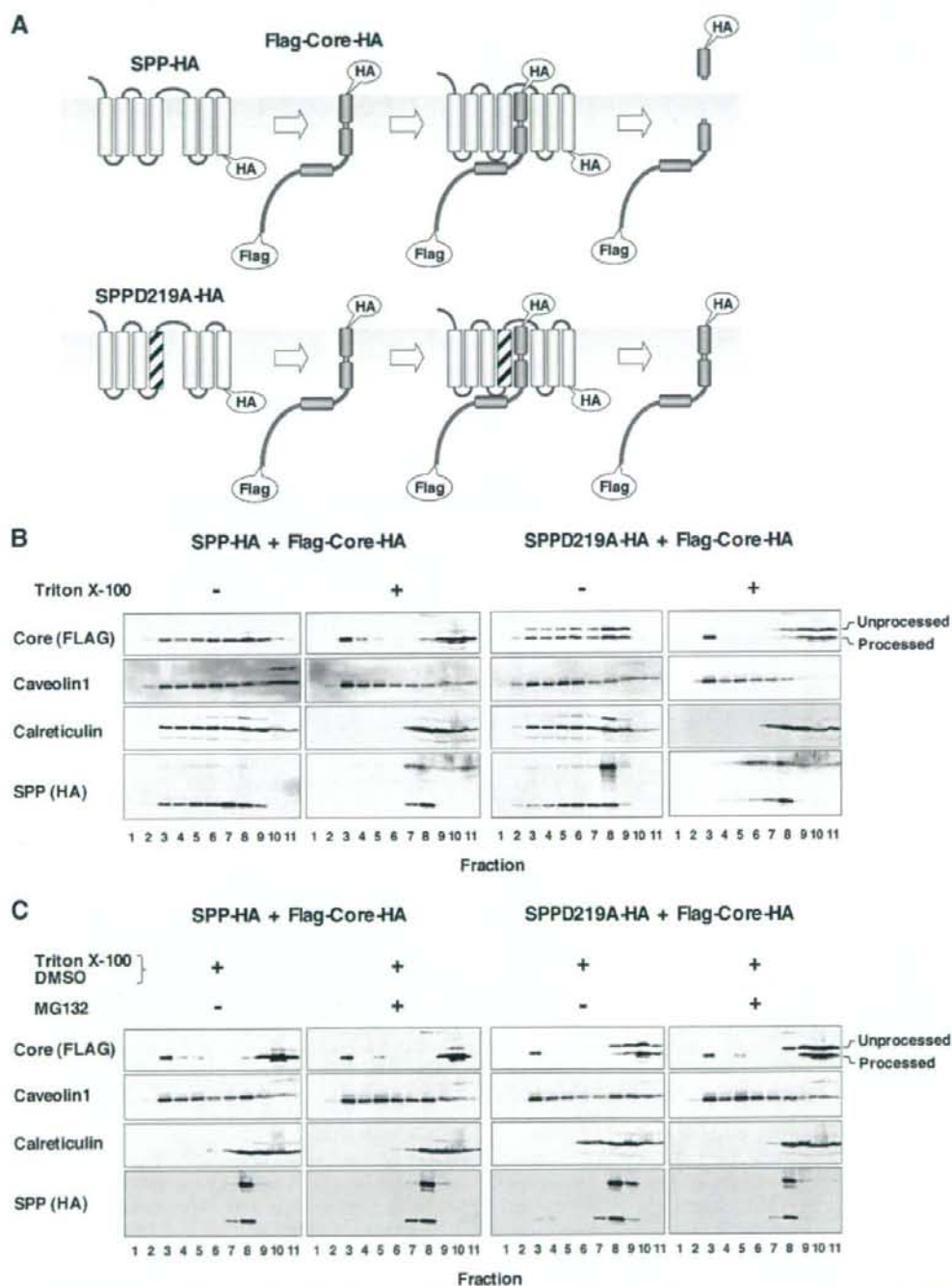


FIG. 4. The dominant-negative mutant of SPP prevents the cleavage of HCV core protein by SPP and its localization in the DRM. (A) Schematic representation of the processing of FLAG-core-HA by a wild-type SPP (SPP-HA) (top) and the dominant-negative effect of SPPD219A-HA (bottom). (B) FLAG-core-HA was coexpressed with SPP-HA or SPPD219A-HA in 293T cells, lysed in the presence or absence of detergent, and subjected to a flotation assay. (C) Effect of a proteasome inhibitor, MG132, on the DRM localization of the HCV core protein. Proteins in each fraction were concentrated with acetone and analyzed by immunoblotting using antibodies against the FLAG epitope tag, caveolin-1, calreticulin, and the HA epitope tag. The membrane (lanes 1 to 9 in the absence of Triton X-100), DRM (lanes 1 to 7 in the presence of Triton X-100), and detergent-soluble (lanes 8 to 11 in the presence of Triton X-100) fractions were identified based on the localization of the marker proteins.

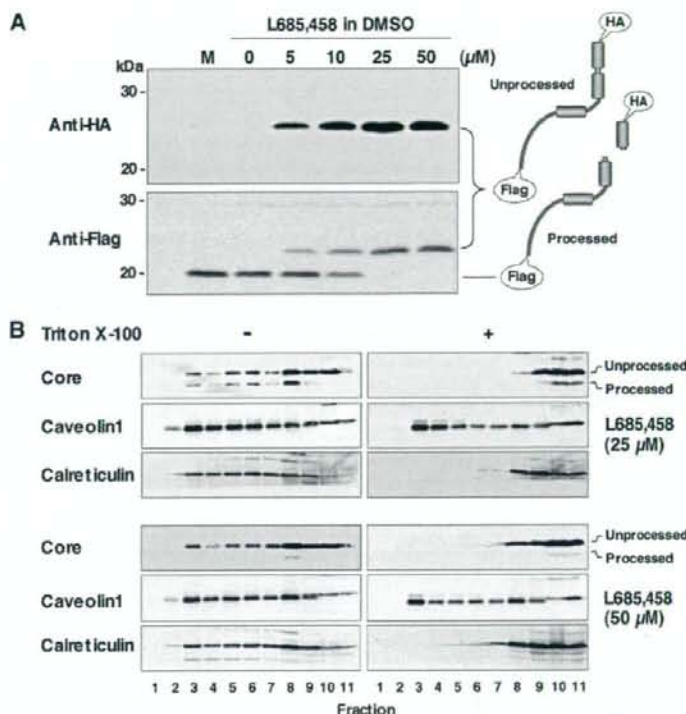


FIG. 5. Effect of an SPP inhibitor on the cleavage of HCV core protein by SPP. The HCV core protein was expressed in 293T cells, and L685,458 was added to the culture supernatant, at the indicated concentrations, at 5 h posttransfection. Cells harvested at 29 h posttransfection were lysed with 1% Triton X-100 and subjected to Western blotting (A) or a flotation assay (B). DMSO, dimethyl sulfoxide. In the flotation assay, proteins in each fraction were concentrated with acetone and analyzed by immunoblotting using antibodies against core protein, caveolin-1, and calreticulin. The membrane (left panels, lanes 1 to 9), DRM (right panels, lanes 1 to 7), and detergent-soluble (right panels, lanes 8 to 11) fractions were identified based on the localization of the marker proteins.

of intramembrane processing by SPP on the localization of HCV core protein in the DRM, we examined the effect of the SPP inhibitors (Z-LL)₂ ketone and L685,458 on the processing of the HCV core protein. Although (Z-LL)₂ ketone was insoluble at a concentration of 10 μ M and was highly toxic to 293T, Huh7, and Huh7-derived cell lines (data not shown), L685,458 was capable of penetrating the plasma membrane (49) and showed no visible cytotoxicity to the cell lines examined. Treatment with L685,458 inhibited the cleavage of the HCV core protein by SPP in a dose-dependent manner (Fig. 5A). As determined by flotation analyses of 293T cells expressing HCV core protein, the processed core protein was no longer localized in the DRM fraction following treatment with 25 or 50 μ M L685,458 (Fig. 5B). These results further support the notion that intramembrane processing by SPP is required for the localization of HCV core protein in the DRM.

Processing of the HCV core protein by SPP participates in viral propagation. To examine the effect of the processing of the HCV core protein by SPP on the propagation of strain JFH-1, Huh7OK1 cells persistently infected with the JFH-1 virus were treated with 25 μ M L685,458, and the cells were examined for processing of the HCV core protein and replication of viral RNA. The processed core protein of strain

JFH-1 was clearly detected in the DRM fraction in untreated control cells, whereas processing of the core protein was impaired by treatment with L685,458, corresponding to the decrease in the level of processed core protein in the DRM (Fig. 6A). In Huh7OK1 cells infected with strain JFH-1, intracellular viral RNA levels were reduced 30% by treatment with L685,458 at 2 days posttreatment but showed no reduction at 1 day (Fig. 6B, left), and viral RNA levels in the culture supernatant were reduced 60% to 70% by treatment with the compound at 1 and 2 days posttreatment (Fig. 6B, center). To exclude the possibility of deleterious effects of L685,458 on cellular proteins involved in viral replication, we determined the effect of L685,458 on viral RNA replication by using HCV subgenomic-replicon cells. The replication of the RNA lacking the region coding for structural proteins showed a slight enhancement rather than suppression at 1 and 2 days after treatment with L685,458 (Fig. 6B, right), suggesting that the SPP inhibitor treatment used in this study is not toxic to the cellular proteins involved in HCV RNA replication. The slight decrease in the level of intracellular HCV RNA in infected cells after treatment with L685,458 (Fig. 6B, left), but not in replicon cells, may be attributable to the ER stress induced by the accumulation of unprocessed core proteins in infected cells.

Although no effect of the inhibitor treatment on the expression of the intracellular core was observed, the secretion of core protein was slightly reduced (Fig. 6C). Furthermore, the production of infectious viral particles in the culture supernatants was clearly impaired by treatment with the SPP inhibitor (Fig. 6D).

The amino acid residues Val¹⁴⁰, Leu¹⁴⁴, Ile¹⁷⁶, Phe¹⁷⁷, Ala¹⁸⁰, Ser¹⁸³, and Cys¹⁸⁴ were conserved within the core proteins of the genotype 1b strain J1 and the genotype 2a strain JFH-1, while the hydrophobic amino acid residues Leu and Val were found at position 139 in the core proteins of strains J1 and JFH-1, respectively. In order to examine the role of SPP-mediated cleavage of the HCV core protein on the growth of HCV strain JFH-1, mutations of Val¹³⁹, Val¹⁴⁰, and Leu¹⁴⁴ to Ala (JFH-1/VVL/3A), of Ile¹⁷⁶ and Phe¹⁷⁷ to Ala and Leu (JFH-1/IF/AL), or of Ala¹⁸⁰, Ser¹⁸³, and Cys¹⁸⁴ to Val, Leu, and Val, respectively (JFH-1/ASC/VLV), in the core protein, or mutation of the Gly-Asp-Asp motif to Gly-Asn-Asp in NSS5 (JFH-1/GND) as a negative control, were introduced into cDNAs encoding strain JFH-1. The plasmid carrying each cDNA under the control of the polII promoter (19) was transfected into Huh7.5.1 cells, and the propagation of the JFH-1 viruses was determined. The expression of the core protein both in the culture medium and in cells transfected with the wild-type strain JFH-1 was increased during incubation, whereas it was severely impaired in the culture medium and cells transfected with JFH-1/VVL/3A, JFH-1/IF/AL, or the replication-deficient mutant JFH-1/GND. In contrast to JFH-1/VVL/3A and JFH-1/IF/AL, JFH-1/ASC/VLV was still capable of producing the core protein at a lower level than the wild-type strain JFH-1 (Fig. 6E). Furthermore, production of infectious particles was completely abrogated in the culture supernatants of cells transfected with JFH-1/VVL/3A, JFH-1/IF/AL, or the replication-deficient mutant JFH-1/GND, whereas JFH-1/ASC/VLV was still capable of producing infectious particles at a lower level than the wild-type strain JFH-1 (Fig. 6E, right). Expression of NS5A proteins was detected by immunofluorescent analyses in cells transfected with wild-type JFH-1, JFH-1/VVL/3A, JFH-1/IF/AL, or JFH-1/ASC/VLV but not in those transfected with JFH-1/GND, suggesting that JFH-1/VVL/3A and JFH-1/IF/AL are capable of replicating in cells but incapable of generating infectious particles (Fig. 6F). The propagation of JFH-1/ASC/VLV, bearing mutations in Ala¹⁸⁰, Ser¹⁸³, and Cys¹⁸⁴ residues that are suggested to be essential for the processing of the HCV core protein by SPP (10, 30), further supports our notion that mutation of these residues is unable to completely abrogate the intramembrane cleavage of the core protein (30). Collectively, these results suggest that the processing of the HCV core protein by SPP plays crucial roles in viral propagation.

DISCUSSION

A previous report has suggested that the amino acid residues Ala¹⁸⁰, Ser¹⁸³, and Cys¹⁸⁴ in the signal sequence are essential for the intramembrane proteolysis by SPP of the core protein of the HCV genotype 1a strain Glasgow expressed in the BHK and Huh7 cell lines by using the Semliki Forest virus expression system (21). However, we have shown that Leu¹³⁹, Val¹⁴⁰, and Leu¹⁴⁴ in the hydrophobic region and Ile¹⁷⁶ and Phe¹⁷⁷ in

the region upstream of the cleavage site, but not Ala¹⁸⁰, Ser¹⁸³, or Cys¹⁸⁴, are required for the ER retention and SPP cleavage of the core proteins derived from the genotype 1b strain J1 and the genotype 1a strain H77 expressed in 293T cells by transfection of expression plasmids (30). Subsequently, Hope et al. suggested that these discrepancies were attributable to differences in the SDS-PAGE systems used to separate the processed and unprocessed core proteins, not to any difference in the HCV strains or expression systems, indicating that the core protein cleaved by SPP could be separated by a Tris/Bicine-buffered system but not by a Tris/glycine system (10). In this study, we added an HA tag at the C terminus of each core protein in order to easily distinguish between the cleaved and uncleaved HCV core proteins, and we then examined the processing of the wild-type and mutant core proteins by SDS-PAGE using Tris/glycine buffer. The resistance of Core IF/AL to SPP cleavage was consistent with the finding that Ile¹⁷⁶ and Phe¹⁷⁷ are located just upstream of the SPP cleavage site identified in this study. In contrast, Core ASC/VLV was not detected by the anti-HA antibody, indicating that Ala¹⁸⁰, Ser¹⁸³, and Cys¹⁸⁴ in the signal sequence of the HCV core protein are not required for processing by SPP. A similar result was also obtained by immunoblotting using a Tris/Bicine-buffered system (data not shown). Furthermore, treatment with the SPP inhibitor L685,458 suppressed the cleavage of the core protein and abrogated both the localization of the mature core protein in the DRM and the propagation of strain JFH-1, suggesting that the intramembrane cleavage of the HCV core protein by SPP plays crucial roles in the DRM localization of the HCV core protein and the propagation of HCV. To further confirm the biological significance of the cleavage of the HCV core protein with respect to infectivity, we generated mutant viruses carrying mutations identical to each mutation of core protein described above. A JFH-1 mutant virus carrying the same mutation as Core ASC/VLV, but not other mutants, was still sufficiently viable to propagate in Huh7.5.1 cells. These findings clearly indicate that mutation of Ala¹⁸⁰, Ser¹⁸³, and Cys¹⁸⁴ to Val, Leu, and Val, respectively, in the signal sequence of the HCV core protein is not able to completely abrogate the cleavage of the core protein by SPP.

Interestingly, the Core ASC/VLV mutant exhibited an extra band that was identical in size to the band of the wild-type core protein, in addition to a slow-migrating band, on the SDS-PAGE gel at 48 h posttransfection (Fig. 1B). Vauloup-Fellous et al. also reported that the Core ASC/VLV mutant expressed by a recombinant Semliki Forest virus in mammalian cells or by a baculovirus in insect cells exhibited bands between the mature (21 kDa) and the immature (23 kDa) core protein (44). If Core ASC/VLV was cleaved at the same site as the wild-type core protein, the processed core protein should have the same molecular size as the processed wild-type core protein, because the mutations in Core ASC/VLV were introduced into the region downstream of the cleavage site. These results suggest that Core ASC/VLV is first processed downstream of the authentic SPP cleavage site and is then further processed at the residue close to Phe¹⁷⁷. Presenilins, which are involved in the cleavage of amyloid β protein precursor (APP), belong to the same aspartic protease family as SPP, which contains two Asp residues in the enzymatic active site (48). SPP might be able to cleave a substrate at multiple sites, as observed in the

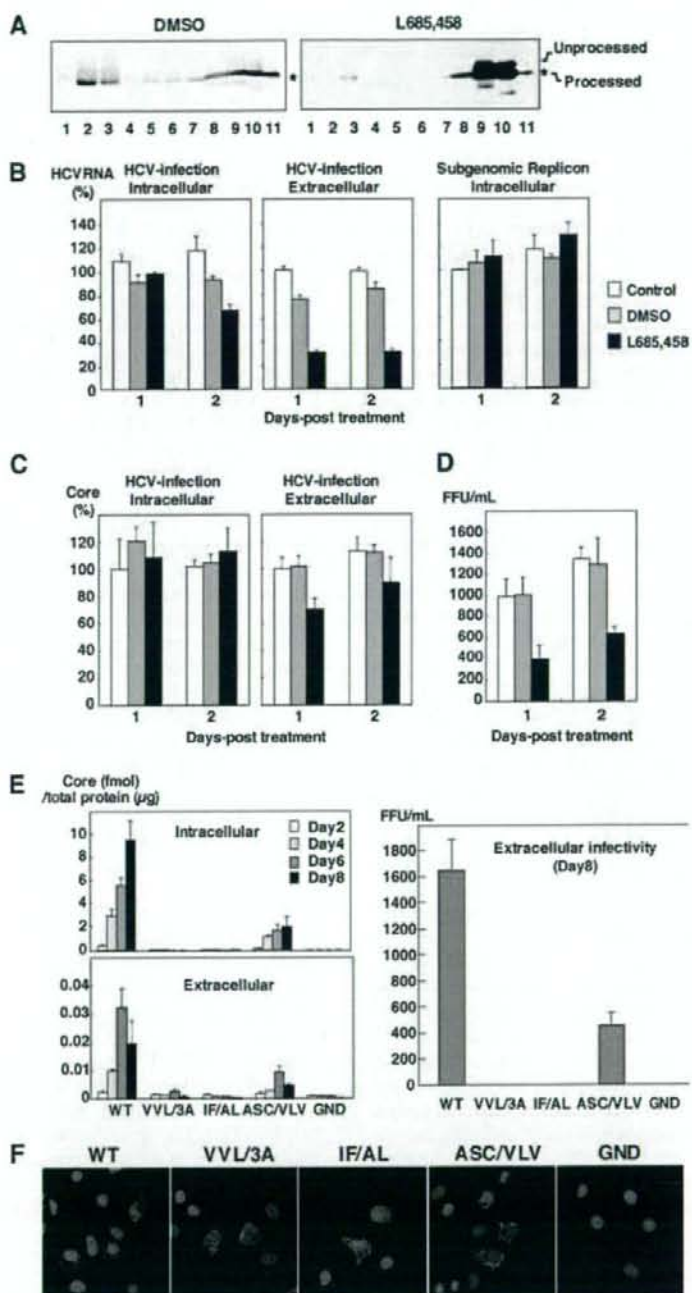


FIG. 6. Effect of the processing of HCV core protein by SPP on the propagation of JFH-1 virus. (A) L685,458 was added, at a concentration of 25 μ M, to the culture supernatant of Huh7OK1 cells persistently infected with HCV strain JFH-1. Cells harvested at 24 h after treatment were lysed with 1% Triton X-100 and subjected to a flotation assay. DRM (lanes 1 to 7) and detergent-soluble (lanes 8 to 11) fractions were identified based on the localization of the marker proteins (data not shown). Asterisks indicate processed core proteins. DMSO, dimethyl sulfoxide. (B to D) Cells persistently infected with HCV strain JFH-1 were harvested at 1 or 2 days after treatment with the inhibitor. The data shown in each panel are representative of three independent experiments. (B) Total RNA was prepared from the cells (left) and the culture supernatant (center). Levels of HCV viral RNA and GAPDH mRNA were determined by real-time quantitative PCR. Values for the levels of viral DNA were normalized to that for GAPDH mRNA as described in Materials and Methods. The subgenomic-replicon cell line 9-13 was treated with the inhibitor, and total

processing of APP by presenilins (33, 37). The Core ASC/VLV mutant may exhibit a preference for cleaving at the site between Asp¹⁷⁸ and Ala¹⁹¹ rather than at that between Phe¹⁷⁷ and Leu¹⁷⁸. However, we still do not know whether SPP can cleave multiple sites within the C-terminal transmembrane region of the wild-type HCV core protein, because our mass spectrometry data show that there was no peptide larger than m/z 1,918.0452, the size corresponding to the amino acid residues from position 160 to 177 (Fig. 2).

Although the wild-type HCV core protein is known to be partially localized in the DRM fraction (20), Core LVL/3A and Core IF/AL, which are resistant to cleavage by SPP, were detected in the detergent-soluble fraction. Furthermore, overexpression of a dominant-negative SPP mutant or treatment with an SPP inhibitor increased the amount of unprocessed core protein in the detergent-soluble fraction irrespective of the presence of the proteasome inhibitor. These results suggest that processing of the HCV core protein by SPP is a prerequisite for stable localization of the mature core protein in the DRM. Indeed, the biological significance of the DRM localization of the mature HCV core protein is still unclear. In addition, we still do not know how HCV core protein migrates into the DRM fraction, and we could not exclude the possibility of involvement of other cellular and viral proteins in the DRM localization of HCV core protein. The DRM fraction is suggested to consist of various membrane microdomains that include lipid rafts, which are enriched in cholesterol and sphingolipids. The immunofluorescent analyses by Matto et al. showed that the DRM fraction containing the HCV core protein in replicon cells harboring a full genomic HCV RNA was different from the classical lipid raft, as evidenced by the lack of colocalization of the typical lipid raft markers, including caveolin-1 and the cholera toxin B subunit (20). However, Aizaki et al. suggested that the HCV replication complex was localized in a lipid-raft-like DRM fraction that included sphingolipids (2). Previous studies have indicated that the HCV core protein is localized in lipid droplets (1, 10, 20, 21, 23) and that processing by SPP is essential for the localization of the HCV core protein in lipid droplets (21). Furthermore, it was shown that the HCV core protein of strain JFH-1 recruits the replication complex to the lipid-droplet-associated membranes, and HCV particles were detected in close proximity to the lipid droplets, suggesting that the lipid droplets and the lipid-droplet-associated membranes induced by the core protein participate in the assembly of HCV particles (23). In addition, lipid droplets including the core protein surrounded by nonstructural proteins were also detected in cells expressing the nonstructural proteins of strain JFH-1 (23). Based on these observations, it might be feasible to speculate that the HCV core protein is matured through processing by the SP and SPP and

is then translocated to the DRM and to the lipid droplets for viral assembly. A recent report by Aizaki et al. shows that HCV particles are enriched with cholesterol and sphingolipids (3), suggesting that the DRM is involved in viral assembly. On the other hand, some fraction of the core protein has been shown to migrate into the nucleus, where it is degraded by nuclear proteasomes (26, 41).

An alanine-scanning mutagenesis study of the HCV core protein has suggested that numerous residues within the carboxy-terminal two-thirds of the core protein are dispensable for RNA replication but essential for efficient infectious-virus production and that alanine substitution of the residues between positions 137 and 144 or 177 and 180 abrogated the extracellular release and intracellular stability of the mutant core proteins of chimeric JFH-1 viruses (27). This is consistent with the severe impairment of virus production by the JFH-1/VVL/3A mutant, in which Val¹³⁹, Val¹⁴⁰, and Leu¹⁴⁴ are all replaced with Ala, and by the JFH-1/IF/AL mutant, in which Ile¹⁷⁶ and Phe¹⁷⁷ are replaced with Ala and Leu, respectively, in spite of the substantial RNA replication in the cells (Fig. 6E and F). The impairment of viral assembly by the introduction of SPP-resistant mutations in the core protein and the reduction of viral production by treatment with an SPP inhibitor, without any effect on subgenomic-RNA replication, also support the notion that SPP-dependent cleavage of the HCV core protein is required for viral assembly rather than for viral replication. Furthermore, the lack of significant effects on viral production and on the stability of the core protein in cells infected with JFH-1 mutants in which residues from 181 to 190 were replaced with Ala (27) is also consistent with the incomplete inhibition of the replication of the JFH-1/ASC/VLV mutant, in which Ala¹⁸⁰, Ser¹⁸³, and Cys¹⁸⁴ are replaced with Val, Leu, and Val, respectively.

Increases in the levels of saturated and monounsaturated fatty acids enhance HCV RNA replication, in contrast to its suppression by polyunsaturated fatty acids (13), suggesting that enzymes associated with lipid biosynthesis are also involved in HCV replication. SREBP-1c regulates the transcription of acetyl coenzyme A carboxylase, fatty acid synthase, and stearoyl coenzyme A desaturase, leading to the production of saturated and monounsaturated fatty acids and triglycerides (11). Expression of the HCV core protein induces the production of lipid droplets composed mainly of triglycerides (4). Our recent study suggests that SREBP-1c was upregulated in the livers of transgenic mice expressing the HCV core protein through the LXR α /RXR α -dependent pathway, which leads to the development of fatty liver (25). The upregulation of SREBP-1c in the transgenic mice was required for the expression of PA28 γ , an HCV core-binding host protein involved in the activation of nuclear proteasome activity (26). The HCV core protein cleaved by SPP may

RNA was prepared from the cells (right). The amount of RNA is represented as a percentage of the amount in the untreated sample at 24 h after treatment (taken as 100%). (C) The amounts of intracellular (left) and extracellular (right) core protein were quantified by a quantitative ELISA. (D) Virus production in the culture supernatants was determined by a focus-forming assay. FFU, focus-forming units. (E) Plasmids coding for the full-length of the wild-type (WT) JFH-1 virus or a mutant (VVL/3A, IF/AL, ASC/VLV, or GND) were transfected into Huh7.5.1 cells. (Left) The amounts of intracellular and extracellular core protein were quantified by a quantitative ELISA at 2, 4, 6, and 8 days posttransfection. (Right) Virus production in the culture supernatants of Huh7.5.1 cells at 8 days after transfection with each plasmid was determined by a focus-forming assay. The data in each panel are representative of three independent experiments. (F) Detection of HCV RNA replication by NSSA immunofluorescence. At 6 days after transfection, NSSA and nuclei were stained red and blue, respectively.

play a role in the formation of lipid droplets associated with the core protein, leading to an enhancement of viral assembly.

In summary, we determined the C-terminal end of the mature HCV core protein expressed in human cells and demonstrated that SPP processing is essential for the DRM localization and stability of the mature core protein. Furthermore, both mutation in the core protein resistant to cleavage by SPP and treatment with an SPP inhibitor abrogated the propagation of strain JFH-1 in the permissive cell line. These results suggest that SPP is a promising target for the development of novel antiviral drugs for the treatment of chronic hepatitis C.

ACKNOWLEDGMENTS

We thank H. Murase for secretarial work. We also thank R. Bartschlagler and T. Wakita for providing cell lines and plasmids.

This work was supported in part by grants-in-aid from the Ministry of Health, Labor, and Welfare; the Ministry of Education, Culture, Sports, Science, and Technology; the 21st Century Center of Excellence Program; and the Foundation for Biomedical Research and Innovation.

REFERENCES

- Ait-Goughoulte, M., C. Hourieux, R. Patient, S. Trassard, D. Brand, and P. Roingeard. 2006. Core protein cleavage by signal peptide peptidase is required for hepatitis C virus-like particle assembly. *J. Gen. Virol.* 87:855–860.
- Aizaki, H., K. J. Lee, V. M. Sung, H. Ishiko, and M. M. Lai. 2004. Characterization of the hepatitis C virus RNA replication complex associated with lipid rafts. *Virology* 324:450–461.
- Aizaki, H., K. Morikawa, M. Fukasawa, H. Hara, Y. Inoue, H. Tani, K. Saito, M. Nishijima, K. Hanada, Y. Matsuura, M. Lal, T. Miyamura, T. Wakita, and T. Suzuki. 2008. A critical role of virion-associated cholesterol and sphingolipid in hepatitis C virus infection. *J. Virol.* 82:5715–5724.
- Barba, G., F. Harper, T. Harada, M. Kohara, S. Goulinet, Y. Matsuura, G. Eder, Z. Schaff, M. J. Chapman, T. Miyamura, and C. Brechot. 1997. Hepatitis C virus core protein shows a cytoplasmic localization and associates to cellular lipid storage droplets. *Proc. Natl. Acad. Sci. USA* 94:1200–1205.
- Blanchard, E., S. Belouzard, L. Goueslain, T. Wakita, J. Dubuisson, C. Wychowski, and Y. Rouille. 2006. Hepatitis C virus entry depends on clathrin-mediated endocytosis. *J. Virol.* 80:6964–6972.
- Codran, A., C. Royer, D. Jaeck, M. Bastien-Valle, T. F. Baumert, M. P. Kieny, C. A. Pereira, and J. P. Martin. 2006. Entry of hepatitis C virus pseudotypes into primary human hepatocytes by clathrin-dependent endocytosis. *J. Gen. Virol.* 87:2583–2593.
- Dubuisson, J., S. Duvert, J. C. Meunier, A. Op De Beeck, R. Cacan, C. Wychowski, and L. Cocquerel. 2000. Glycosylation of the hepatitis C virus envelope protein E1 is dependent on the presence of a downstream sequence on the viral polyprotein. *J. Biol. Chem.* 275:30605–30609.
- Gao, L., H. Aizaki, J. W. He, and M. M. Lai. 2004. Interactions between viral nonstructural proteins and host protein hVAP-33 mediate the formation of hepatitis C virus RNA replication complex on lipid raft. *J. Virol.* 78:3480–3488.
- Gosert, R., D. Egger, V. Lohmann, R. Bartschlagler, H. E. Blum, K. Bienz, and D. Moradpour. 2003. Identification of the hepatitis C virus RNA replication complex in Huh-7 cells harboring subgenomic replicons. *J. Virol.* 77:5487–5492.
- Hope, R. G., M. J. McElwee, and J. McLauchlan. 2006. Efficient cleavage by signal peptide peptidase requires residues within the signal peptide between the core and E1 proteins of hepatitis C virus strain J1. *J. Gen. Virol.* 87:623–627.
- Horton, J. D., J. L. Goldstein, and M. S. Brown. 2002. SREBPs: activators of the complete program of cholesterol and fatty acid synthesis in the liver. *J. Clin. Invest.* 109:1125–1131.
- Hussy, P., H. Langen, J. Mous, and H. Jacobsen. 1996. Hepatitis C virus core protein: carboxy-terminal boundaries of two processed species suggest cleavage by a signal peptide peptidase. *Virology* 224:93–104.
- Kapadia, S. B., and F. V. Chisari. 2005. Hepatitis C virus RNA replication is regulated by host geranylgeranylation and fatty acids. *Proc. Natl. Acad. Sci. USA* 102:2561–2566.
- Lecat, S., P. Verkade, C. Thiele, K. Fiedler, K. Simons, and F. Lafont. 2000. Different properties of two isoforms of annexin XIII in MDCK cells. *J. Cell Sci.* 113:2607–2618.
- Lindenbach, B. D., M. J. Evans, A. J. Syder, B. Wolk, T. L. Tellinghuisen, C. C. Liu, T. Maruyama, R. O. Hynes, D. R. Burton, J. A. McKeating, and C. M. Rice. 2005. Complete replication of hepatitis C virus in cell culture. *Science* 309:623–626.
- Lohmann, V., F. Korner, J. Koch, U. Herian, L. Theilmann, and R. Bartschlagler. 1999. Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell line. *Science* 285:110–113.
- Majeau, N., V. Gagne, M. Bolduc, and D. Leclerc. 2005. Signal peptide peptidase promotes the formation of hepatitis C virus non-enveloped particles and is captured on the viral membrane during assembly. *J. Gen. Virol.* 86:3055–3064.
- Marsh, M., and A. Helenius. 2006. Virus entry: open sesame. *Cell* 124:729–740.
- Masaki, T., R. Suzuki, M. Matsuda, T. Miyamura, T. Wakita, and T. Suzuki. 2006. Production of infectious hepatitis C virus by using RNA polymerase I-mediated transcription, abstr. 209, p. 59. In Abstracts of the 13th International Meeting on Hepatitis C Virus and Related Viruses. Nola Miles-Clark, Cairns, Australia.
- Matto, M., C. M. Rice, B. Aroeti, and J. S. Glenn. 2004. Hepatitis C virus core protein associates with detergent-resistant membranes distinct from classical plasma membrane rafts. *J. Virol.* 78:12047–12053.
- McLauchlan, J., M. K. Lemberg, G. Hope, and B. Martoglio. 2002. Intramembrane proteolysis promotes trafficking of hepatitis C virus core protein to lipid droplets. *EMBO J.* 21:3980–3988.
- Meertens, L., C. Bertaux, and T. Dragic. 2006. Hepatitis C virus entry requires a critical post-internalization step and delivery to early endosomes via clathrin coated vesicles. *J. Virol.* 80:11571–11578.
- Miyazari, Y., K. Atsuzawa, N. Usuda, K. Watahi, T. Hishiki, M. Zayas, R. Bartschlagler, T. Wakita, M. Hijikata, and K. Shimotohno. 2007. The lipid droplet is an important organelle for hepatitis C virus production. *Nat. Cell Biol.* 9:1089–1097.
- Moriishi, K., and Y. Matsuura. 2003. Mechanisms of hepatitis C virus infection. *Antivir. Chem. Chemother.* 14:285–297.
- Moriishi, K., R. Mochizuki, K. Moriya, H. Miyamoto, Y. Mori, T. Abe, S. Murata, K. Tanaka, T. Miyamura, T. Suzuki, K. Koike, and Y. Matsuura. 2007. Critical role of PA28 γ in hepatitis C virus-associated steatogenesis and hepatocarcinogenesis. *Proc. Natl. Acad. Sci. USA* 104:1661–1666.
- Moriishi, K., T. Okabayashi, K. Nakai, K. Moriya, K. Koike, S. Murata, T. Chiba, K. Tanaka, R. Suzuki, T. Suzuki, T. Miyamura, and Y. Matsuura. 2003. Proteasome activator PA28 γ -dependent nuclear retention and degradation of hepatitis C virus core protein. *J. Virol.* 77:10237–10249.
- Murray, C. L., C. T. Jones, J. Tasselto, and C. M. Rice. 2007. Alanine scanning of the hepatitis C virus core protein reveals numerous residues essential for production of infectious virus. *J. Virol.* 81:10220–10231.
- Niwa, H., K. Yamamura, and J. Miyazaki. 1991. Efficient selection for high-expression transfectants with a novel eukaryotic vector. *Gene* 108:193–199.
- Ogino, T., H. Fukuda, S. Imajoh-Ohmi, M. Kohara, and A. Nomoto. 2004. Membrane binding properties and terminal residues of the mature hepatitis C virus capsid protein in insect cells. *J. Virol.* 78:11766–11777.
- Okamoto, K., K. Moriishi, T. Miyamura, and Y. Matsuura. 2004. Intramembrane proteolysis and endoplasmic reticulum retention of hepatitis C virus core protein. *J. Virol.* 78:6370–6380.
- Okamoto, T., Y. Nishimura, T. Ichimura, K. Suzuki, T. Miyamura, T. Suzuki, K. Moriishi, and Y. Matsuura. 2006. Hepatitis C virus RNA replication is regulated by FKBP8 and Hsp90. *EMBO J.* 25:5015–5025.
- Okamoto, T., H. Omori, Y. Kaname, T. Abe, Y. Nishimura, T. Suzuki, T. Miyamura, T. Yoshimori, K. Moriishi, and Y. Matsuura. 2008. A single amino acid mutation in hepatitis C virus NS5A disrupting FKBP8 interaction impairs viral replication. *J. Virol.* 82:3480–3489.
- Okochi, M., S. Eimer, A. Botzcher, R. Baumeister, H. Romig, J. Walter, A. Capell, H. Steiner, and C. Haass. 2000. A loss of function mutant of the presenilin homologue SEL-12 undergoes aberrant endoproteolysis in *Caenorhabditis elegans* and increases A β 42 generation in human cells. *J. Biol. Chem.* 275:40925–40932.
- Pelkmans, L. 2005. Secrets of caveolae- and lipid raft-mediated endocytosis revealed by mammalian viruses. *Biochim. Biophys. Acta* 1746:295–304.
- Pelkmans, L., D. Puntener, and A. Helenius. 2002. Local actin polymerization and dynamin recruitment in SV40-induced internalization of caveolae. *Science* 296:535–539.
- Randall, G., M. Panis, J. Cooper, T. Tellinghuisen, K. Sukhodolet, S. Pfeffer, M. Landthaler, P. Landgraf, S. Kan, B. Lindenbach, M. Chien, D. Weir, J. Russo, J. Ju, M. Brownstein, R. Sheridan, C. Sander, M. Zavolan, T. Tuschl, and C. Rice. 2007. Cellular cofactors affecting hepatitis C virus infection and replication. *Proc. Natl. Acad. Sci. USA* 104:12884–12889.
- Sastre, M., H. Steiner, K. Fuchs, A. Capell, G. Multhaup, M. M. Condron, D. B. Teplow, and C. Haass. 2001. Presenilin-dependent γ -secretase processing of β -amyloid precursor protein at a site corresponding to the S3 cleavage of Notch. *EMBO Rep.* 2:835–841.
- Shi, S. T., K. J. Lee, H. Aizaki, S. B. Hwang, and M. M. Lai. 2003. Hepatitis C virus RNA replication occurs on a detergent-resistant membrane that cofractionates with caveolin-2. *J. Virol.* 77:4160–4168.
- Shirakura, M., K. Murakami, T. Ichimura, R. Suzuki, T. Shimoji, K. Fukuda, K. Abe, S. Sato, M. Fukasawa, Y. Yamakawa, M. Nishijima, K. Moriishi, Y. Matsuura, T. Wakita, T. Suzuki, P. M. Howley, T. Miyamura,

- and I. Shoji. 2007. E6AP ubiquitin ligase mediates ubiquitylation and degradation of hepatitis C virus core protein. *J. Virol.* **81**:1174-1185.
40. Simons, K., and E. Ikonen. 1997. Functional rafts in cell membranes. *Nature* **387**:569-572.
41. Suzuki, R., Y. Matsuura, T. Suzuki, A. Ando, J. Chiba, S. Harada, I. Saito, and T. Miyamura. 1995. Nuclear localization of the truncated hepatitis C virus core protein with its hydrophobic C terminus deleted. *J. Gen. Virol.* **76**:53-61.
42. Suzuki, R., S. Sakamoto, T. Tsutsumi, A. Rikimaru, K. Tanaka, T. Shimoike, K. Moriishi, T. Iwasaki, K. Mizumoto, Y. Matsuura, T. Miyamura, and T. Suzuki. 2005. Molecular determinants for subcellular localization of hepatitis C virus core protein. *J. Virol.* **79**:1271-1281.
43. Suzuki, R., K. Tamura, J. Li, K. Ishii, Y. Matsuura, T. Miyamura, and T. Suzuki. 2001. Ubiquitin-mediated degradation of hepatitis C virus core protein is regulated by processing at its carboxyl terminus. *Virology* **280**:301-309.
44. Vauloup-Fellous, C., V. Pene, J. Garaud-Aunis, F. Harper, S. Bardin, Y. Suire, E. Pichard, A. Schmitt, P. Sogni, G. Pierron, P. Briand, and A. R. Rosenberg. 2006. Signal peptide peptidase-catalyzed cleavage of hepatitis C virus core protein is dispensable for virus budding, but destabilizes the viral capsid. *J. Biol. Chem.* **281**:27679-27692.
45. Wakita, T., T. Pietschmann, T. Kato, T. Date, M. Miyamoto, Z. Zhao, K. Murthy, A. Habermann, H. G. Krausslich, M. Mizokami, R. Bartenschlager, and T. J. Liang. 2005. Production of infectious hepatitis C virus in tissue culture from a cloned viral genome. *Nat. Med.* **11**:791-796.
46. Wang, C., M. Gale, Jr., B. C. Keller, H. Huang, M. S. Brown, J. L. Goldstein, and J. Ye. 2005. Identification of FBL2 as a geranylgeranylated cellular protein required for hepatitis C virus RNA replication. *Mol. Cell* **18**:425-434.
47. Wasley, A., and M. J. Alter. 2000. Epidemiology of hepatitis C: geographic differences and temporal trends. *Semin. Liver Dis.* **20**:1-16.
48. Weihofen, A., K. Binns, M. K. Lemberg, K. Ashman, and B. Martoglio. 2002. Identification of signal peptide peptidase, a presenilin-type aspartic protease. *Science* **296**:2215-2218.
49. Weihofen, A., M. K. Lemberg, E. Friedmann, H. Rueeger, A. Schmitz, P. Paganetti, G. Rovelli, and B. Martoglio. 2003. Targeting presenilin-type aspartic protease signal peptide peptidase with γ -secretase inhibitors. *J. Biol. Chem.* **278**:16528-16533.
50. Zhong, J., P. Gastaminza, G. Cheng, S. Kapadia, T. Kato, D. R. Burton, S. F. Wieland, S. L. Uprichard, T. Wakita, and F. V. Chisari. 2005. Robust hepatitis C virus infection in vitro. *Proc. Natl. Acad. Sci. USA* **102**:9294-9299.

Manipulation of the peptide-binding specificity of an RNA in a rational manner by combinations of specificity-altering mutations

Kazuo Harada^{1*}, Maki Sugaya², Futoshi Nishimura¹ and Akira Katoh²

¹Department of Life Science, Tokyo Gakugei University, Koganei-shi, Tokyo 184-8501, Japan and Faculty of Science and Technology, Seikei University, Musashino-shi, Tokyo 180-8633, Japan

ABSTRACT

In this study, the potential to manipulate the peptide-binding specificity of an RNA in a rational manner was investigated. First, variants of the Rev-response element (RRE) RNA with different specificities towards the natural binding partner, Rev, and two RRE-binding aptamers, the RSG-1.2 and K1 peptides, were identified. Next, hybrid RRE mutants with combinations of two sets of specificity-altering substitutions were tested for peptide-binding specificity. It was shown that, in most cases, the results of the combination of individual mutations were of an additive nature, therefore providing a way to manipulate the peptide-binding specificity of an RNA in a predictable manner.

INTRODUCTION

Biochemical and structural studies on the interaction of arginine-rich peptides and their RNA sites has considerably increased our understanding of RNA-polypeptide interactions. In particular, the interaction of the HIV Rev peptide and the RRE has been extensively studied. The Rev peptide, a short peptide corresponding to the RNA-binding domain of the HIV Rev protein, has been shown to bind to an internal loop region of the RRE consisting of U45 to C51 and U66 to A75 of the RRE in an α -helical conformation (Fig. 1). Several peptides that bind to a similar region of the RRE, but with higher affinities and using a different binding strategy as the Rev peptide have been identified from random peptide libraries. The RSG-1.2 peptide,^{1,2} which binds to the RRE several times more strongly than the Rev peptide, and in a novel unstructured-turn-helix conformation,^{3,4} was selected from a relatively simple random library consisting of the three amino acids, arginine (R), serine (S), and glycine (G), followed by mutagenesis and reselection (Fig. 1B). In another selection of RRE-binding peptides from a complex polyarginine-based library, a putative α -helical high-affinity RRE-binding peptide, the K1 peptide, was identified (Fig. 1B).^{5,6}

On the other hand, we have previously shown that the nucleotide requirements for RRE-binding to the Rev and RSG-1.2 peptides are quite different.⁷ Strikingly, several nucleotide substitutions in the upper stem region of the RRE, where the nucleotide requirement for Rev- and RSG-

binding differed, were found to switch the peptide-binding specificity of the RRE from a bifunctional Rev- and RSG-1.2-binding mode to either a Rev-specific or a RSG-1.2-specific mode.

RESULTS AND DISCUSSION

In this study, in order to expand our studies on the peptide-binding specificity of RRE mutants to include the K1 peptide in addition to the Rev and RSG-1.2 peptides, we first determined the nucleotide requirements for the binding of RRE to the K1 peptide. This was carried out by selecting for K1-binding RRE variants from a doped RRE library using a bacterial reporter system, and comparing the selected sequences. When the clones with K1- and Rev-binding activities similar to those of the wild-type RRE were compared, the nucleotide requirements for K1-binding were found to be similar to those of the Rev peptide, except that the G48-G71 base pair did not covary to an A-A base pair as in the case of the Rev and RSG peptides. This suggested that the K1 peptide may be directly contacting the G-G base pair, unlike in the case of the Rev and RSG peptides, where the G-G to A-A base pair substitution is tolerated. Indeed, clone **G1***, a G-G to A-A variant identified in a previous study,⁷ was found to have considerably lower activity towards the K1 peptide. Next, when RRE variants with reduced activity towards the Rev peptide were compared the U45-A75 base-pair was not conserved. Indeed, further analysis resulted in the identification of a K1-specific RRE variant, **G16*** with a single nucleotide substitution (A75G).

Various Rev- and/or RSG-specific RRE variants **G1***, **G9**, **G30**, and **R26** that were identified in a previous study, as well as the K1-specific RRE variant **G16*** identified in this study were tested for their ability to bind to the Rev, RSG, and K1 peptides using the bacterial reporter system, and the results are summarized in Figure 1. In this system, β -galactosidase expression scored by intensity of colony color on tryptone/agar plates containing 5-bromo-4-chloro-3-indolyl β -D-galactopyranoside (Xgal) has been shown to correspond to binding affinity. Those colonies with blue color similar to that of the wild-type RRE and Rev peptide ($K_d = 60$ nM), the RSG peptide ($K_d = 12$ nM), and the K1 peptide ($K_d = 0.5$ nM) scored as 3+, 4+, and 6+, respectively.⁶ As a result, the mutants could be classified

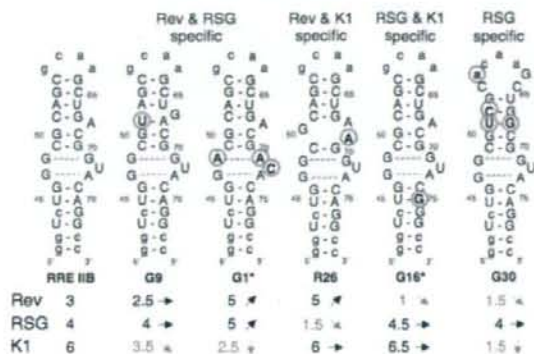


Fig. 1 *In vivo* peptide-binding activities of RRE mutants with arrows indicating the increase or decrease of activity relative to the wild-type RRE.

into a total of four peptide-specificity groups, the Rev- & RSG-specific **G9** and **G1***, the Rev- & K1-specific **R26**, the RSG-1.2- & K1-specific **G16***, and the RSG-specific **G30**.

To examine whether the base substitutions in clones **G9**, **G1***, **R26**, **G16***, and **G30** could be combined to create new specificities in a predictable way, hybrid RRE mutants with all possible combinations of two sets of substitutions were tested for peptide-binding specificity using the bacterial reporter system. Of the ten combination of two sets of mutations, the **G9** and **G30** mutations overlapped and could not be combined, leaving nine combinations that could be tested. In the **G9/R26** and **R26/G30** hybrids, the pairs of base substitutions both resulted in distinct secondary structural changes in the upper stem regions and would be expected to alter or destabilize the conformation of the other. Therefore, not surprisingly, an almost complete loss of binding to all three peptides was observed. Of the remaining seven hybrid RREs, the peptide-binding specificities of the five hybrids appeared to be of an additive nature, with the sum of the specificity change of the individual sets of substitutions agreeing well with the experimental values. For example, combination of the **G9** substitution, where the change in antitermination activity against the Rev, RSG, and K1 peptides was (-0.5, 0, -2.5), and the **G1** substitution, which was (2, 1, -3.5), resulted in a hybrid RRE **G9/G1*** with a specificity change of (1, 0.5, -5.5), which is similar to the calculated specificity of (1.5, 1, -6). Since both the **G9** and **G1*** substitutions were Rev & RSG-specific, combination of the two resulted in a hybrid RRE with reduced K1-binding, and as a consequence, improved Rev- and RSG-1.2-specificity. A similar additivity was observed for the remaining four hybrids **G9/G16***, **G1*/G16***, **R26/G16***, and **G16*/G30**, and the difference between the calculated values and the experimental values were almost all within 1 colony color unit. It is particularly worth noting that the combination of

the Rev & K1-specific mutation of **R26** with the RSG-1.2- & K1-specific mutation of **G16*** resulted in the creation of a novel highly K1-specific hybrid RRE. In addition, combination of the RSG-1.2- & K1-specific mutation of **G16*** with the RSG-1.2-specific mutation of **G30** resulted in a decrease in Rev- and K1-binding to yield a more specific RSG-1.2-binding hybrid RRE. The low binding affinity of the **G1*/G30** towards all three peptides may be due to the formation of a stable alternative secondary structure as predicted by an RNA folding algorithm, MulFold version 2.0. The **G1*/R26** hybrid, which was anticipated to yield a new Rev-specific hybrid, did not show activity towards all three peptides, suggesting that the two mutations, although separated by one base pair, are altering the conformation of the other mutants.

CONCLUSION

The results show that the peptide-binding specificity of an RNA can be manipulated in a semi-rational manner by combinations of specificity-altering base substitutions, provided that the pairs of substitutions are sufficiently separated in space and do not result in the formation of stable alternative structures.⁸ A similar strategy is also likely to be applicable to aptamers so that their ligand-binding specificity may be modified to create novel binding specificities or fine-tuned by reducing nonspecific binding. While further structural studies will be necessary to understand the exact nature of the changes in specificity observed in this study, the results demonstrate the multidimensionality of conformational space that RNA has for peptide binding was likely to have been utilized in the evolution of RNA-protein interactions.

REFERENCES

- Harada, K., Martin, S.S., Frankel, A.D. (1996) *Nature*, **380**, 175-179.
- Harada, K., Martin, S.S., Tan, R., Frankel, A.D. (1997) *Proc. Natl. Acad. Sci. USA*, **94**, 11887-11892.
- Gosser, Y., Hermann, T., Majumdar, A., Hu, W., Frederick, R., Jiang, F., Xu, W., Patel, D.J. (2001) *Nat. Struct. Biol.*, **8**, 146-150.
- Zhang, Q., Harada, K., Cho, H.S., Frankel, A.D., Wemmer, D.E. (2001) *Chem. Biol.*, **8**, 511-520.
- Peled-Zehavi, H., Horiya, S., Das, C., Harada, K., Frankel, A.D. (2003) *RNA*, **9**, 252-261.
- Sugaya, M., Nishimura, F., Katoh, A., Harada, K. (2008) *J. Pept. Sci.*, Mar 20. [Epub ahead of print]
- Iwazaki, T., Li, X., Harada, K. (2005) *RNA*, **11**, 1364-1373.
- Sugaya, M., Katoh, A., Harada, K. (2008) *Nucleosides Nucleotides Nucleic Acids*, in press.

*Corresponding author. E-mail: harada@u-gakugei.ac.jp

Analysis of the interaction between selected RNA-binding peptides and a target RNA containing a bulge and a GNRA-type tetraloop

Satoru Horiya¹, Chang-Song Koh², Senya Matsufuji¹, and Kazuo Harada^{2*}

¹Department of Molecular Biology, The Jikei University School of Medicine, Minato-ku, Tokyo 105-8461, Japan and ²Department of Life Science, Tokyo Gakugei University, Koganei-shi, Tokyo 184-8501, Japan

ABSTRACT

We have characterized the interaction between selected novel RNA-binding peptides and their target RNA. The RNA is comprised of two elements, a GCAA tetraloop, a member of the thermodynamically stable GNRA-type (where N is A or G, U, C; R is G or A) tetraloops, and a tri-purine bulge found in the frameshift stimulating structure on the human immunodeficiency virus type 1 (HIV-1) *gag-pol* mRNA. Peptides that bind specifically to the target RNA were selected from a combinatorial library based on arginine-rich motif (ARM) by a bacterial reporter system. We performed mutational studies using the reporter system and gel shift assays and found that the binding affinity and specificity of the RNA were mainly dependent on the GNRA-type tetraloop, and a modest contribution was also attributed to the bulge structure. Our finding reveals a novel mode of interaction by an RNA-peptide complex and expands our knowledge on the diversity of molecular recognition.

INTRODUCTION

We had been developing a system for selecting novel RNA-binding peptides from combinatorial libraries based on bacterial phenotypes of reporter gene expressed by a λ N-mediated transcription antitermination, and have isolated a number of unique peptides specifically binding to HIV Rev-response element (RRE) IIB from the libraries based on ARM (1, 2). In the present study, we identified novel peptides that specifically bind to a target RNA (designated FSL RNA) that is an RNA containing a functional bulge structure found in frameshift stimulator on HIV-1 *gag-pol* mRNA and capped with GCAA tetraloop (Fig. 1). HIV-1 *pol*, essential for viral replication in infected cells, is expressed as Gag-Pol fusion protein through -1 translational frameshifting at a shift site that possesses a slippery sequence of U-UUU-UUA (codons of *gag* in the original frame are separated by an hyphen) on *gag-pol* mRNA. Classically, a simple stem-loop starting 9 nts downstream from the shift site had been established as one of the essential elements for frameshifting. Subsequently, Brakier-Gingras and co-workers reported that a more complex structure forming an additional lower stem interrupted by a GGA bulge is required for efficient frameshifting (Fig. 1A) (3). Here, we report the characterization of the arginine-rich peptides identified as

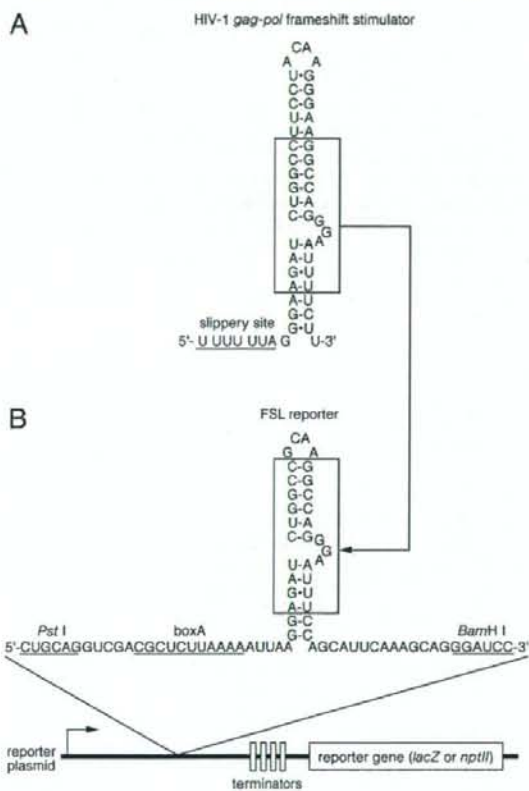


Fig. 1 (A) The sequence of the frameshift region of *gag-pol* on HIV-1 mRNA. (B) The targeted RNA (FSL) introduced in reporter plasmids used in this study. Generally, the activity of the reporter gene corresponds to the affinity of an introduced RNA-peptide complex in this system.

binders to the FSL RNA. Unexpectedly, based on mutational analysis, we found that the major determinant of the binding of the peptide to FSL RNA was affinity for an artificially replaced GCAA tetraloop. However, we also observed dependency of the bulge formation for peptide-binding, showing that the binding mode of the peptides to the FSL RNA constitutes a novel modular form of binding.

RESULTS AND DISCUSSION

First, we constructed a combinatorial peptide library based on the ARM. Previous studies have shown that a "doped" polyarginine library could be valid to yield RNA binding peptides, and we identified a number of strong binders to the RRE from one such library (2). Here, we used the polyarginine "doped" library whose prototype sequence encodes XXXXXXXXXXXXXXXXXXXX (where X denotes random amino acids encoded by an NNK codon; K is G or T), and the underlined Rs were doped by codon-based mutagenesis with a VVK codon (where V is A, G or C) at 50 % degeneracy. Using this library, we selected from $\sim 1.2 \times 10^8$ sequences and identified 4 unique clones that specifically bind to FSL RNA.

In order to investigate the essential regions of FSL RNA required for binding to the selected peptides, we prepared two additional reporters containing mutation at single-stranded regions of FSL. A mutation of GCAA to UUCG in tetraloop resulted in disruption of its antitermination activity, while a mutation of GGA to CCC in bulge did not affect activity, showing that the peptides specifically bound to the GCAA loop. The GCAA tetraloop is a member of the GNRA-type tetraloops that form thermodynamically stable stem-loop structures. The GNRA-fold RNA has been shown to bind to arginine-rich peptides. One well-studied example is the complex of boxB RNA and the N peptide of phage λ . λ boxB, which is comprised of 15 nts and forms a hairpin containing a pentaloop folds into GNRA-like conformation through binding to N peptide (4).

To characterize the tetraloop-binding mode of the selected peptides, we tested several loop mutants which included a number of GNRA hairpins as well as loop with mutations in the first and fourth position (ACAA and GCAG) using β -galactosidase colony color assay. As a result, all of the GNRA-type sequences exhibited similar activity and the non-GNRA tetraloops showed no detectable activity. We also tested the GAAAA pentaloop of boxB in the context of FSL to investigate the specificity towards loop size. Surprisingly, the GAAAA pentaloop showed higher activity than original target GCAA. Indeed, λ N also revealed activity against the GAAAA loop in the same context, suggesting that the selected peptides may recognize GNRA-loop in a manner similar to λ N. We therefore compared the sequence of the selected peptides with those of the N peptides. As expected, the alignment revealed high homology of the selected peptides with the N peptides. Although the C-terminal region of the selected peptides showed high homology with the N peptide, the sequences of the amino-terminal region were different from that of the N peptide in spite of their high conservation. Therefore, we investigated amino acid residues important for binding to the FSL RNA by scanning mutagenesis and compared the results with those reported for N binding to boxB, finding that the important residues in the C-terminal region of the selected peptides were fairly similar to those of the N peptide, while the amino-terminal region was also very important.

Although bulge mutations did not affect activity in the reporter system, the low sensitivity of *in vivo* might conceal the subtle effect of bulge mutations. To test this assumption, we carried out electrophoresis mobility shift assays (EMSA) with several RNA mutants and measured the binding affinity for RNAs as apparent K_D s in the presence of an excess amount of *Escherichia coli* tRNA. As a result, a GGA bulge deletion and a GGA to CCC substitution decreased binding affinity, revealing that RNA-binding by the selected peptides depends not only on the GCAA loop but also on the bulge. To further demonstrate the importance of the bulge, we analyzed mutations of the lower stem. As expected, in one of the selected peptides, disruption of the lower stem under the bulge decreased binding affinity, while restoring the disruption of the stem recovered binding affinity to the same level as wild-type FSL.

CONCLUSION

The binding affinity of selected peptides for the target RNA mainly depends on the GNRA-type tetraloops, however, the peptides also recognize the structure of the bulge fixed by the lower stem formation or the internal tri-purine sequence. This modular form of binding by an RNA and an ARM peptide expands our knowledge on the diverse modes of RNA-peptide interactions, and may be useful in the design of novel RNA-peptide complexes.

REFERENCES

1. Harada, K., Martin, S. S., Frankel, A. D. (1996) *Nature*, **380**, 175-179.
2. Peled-Zehavi, H., Horiya, S., Das, C., Harada, K., Frankel, A. D. (2003) *RNA* **9**, 252-261.
3. Dulude, D., Baril, M., Brakier-Gingras, L. (2002) *Nucleic Acids Res.* **30**, 5094-5102.
4. Legault, P., Li, J., Mogridge, J., Kay, L. E., Greenblatt, J. (1998) *Cell* **93**, 289-299.

*Corresponding author. E-mail: harada@u-gakugei.ac.jp.

Module Assembly for Protein-Surface Recognition: Geranylgeranyltransferase I Bivalent Inhibitors for Simultaneous Targeting of Interior and Exterior Protein Surfaces

Shinnosuke Machida,^[a] Kakeru Usuba,^[b] Michelle A. Blaskovich,^[c] Akiko Yano,^[b]
Kazuo Harada,^[b] Saïd M. Sebti,^[c] Nobuo Kato,^[a] and Junko Ohkanda*^[a]

