

FIG. 4. PA28 $\gamma$  participated in the enlargement of pancreatic islets induced by the HCV core protein. (A) Histological sections prepared from pancreas tissues of PA28 $\gamma^{+/+}$ , PA28 $\gamma^{+/+}$ CoreTg, PA28 $\gamma^{-/-}$ , and PA28 $\gamma^{-/-}$ CoreTg mice were stained with hematoxylin and eosin. Dotted circles indicate pancreatic islets. (B) The area occupied by pancreatic islets was measured by computer software in three different fields of every six randomly selected sections of 10 mice per genotype and is represented as a percentage of the total pancreatic area. \*\* $P < 0.01$ ; \*\*\* $P < 0.001$ . The scale bar indicates 100  $\mu$ m.

mice but not in PA28 $\gamma^{+/+}$  (normal littermates) or PA28 $\gamma^{-/-}$  mice. PA28 $\gamma$  was found at a similar level in PA28 $\gamma^{+/+}$ CoreTg and PA28 $\gamma^{+/+}$  mice but was not present in either PA28 $\gamma^{-/-}$  or PA28 $\gamma^{-/-}$ CoreTg mice (Fig. 1A). The expression of the HCV core protein in the livers of 2-month-old male mice was slightly higher in PA28 $\gamma^{-/-}$ CoreTg ( $1.36 \pm 0.44$  ng/mg of total protein;  $n = 7$ ) than in PA28 $\gamma^{+/+}$ CoreTg ( $1.23 \pm 0.22$  ng/mg of total protein;  $n = 7$ ) mice, but these values were not significantly different ( $P > 0.05$ ). Insulin sensitivity is dependent on several conditions such as body weight, obesity, and liver steatosis (26). PA28 $\gamma^{-/-}$  mice were slightly smaller than their normal littermates (PA28 $\gamma^{+/+}$ ) at more than 3 months old, as described previously (36), but this was not significantly different in 2-month-old mice (Fig. 1B). PA28 $\gamma^{+/+}$ CoreTg mice exhibited severe hepatic steatosis from 4 months of age (35). To avoid the influence of hepatic steatosis and body weight on the examination of insulin resistance, 2-month-old mice were

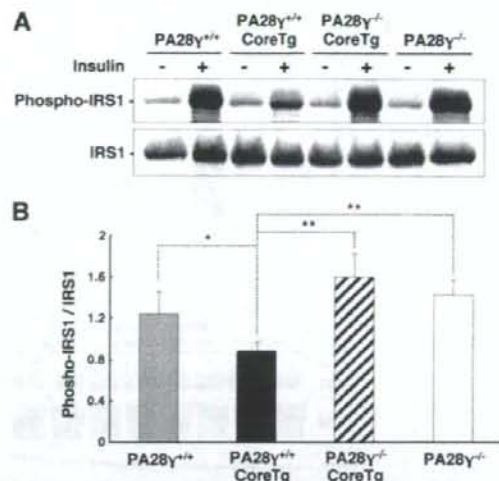


FIG. 5. PA28 $\gamma$  participated in the inhibition of the tyrosine phosphorylation of IRS1 induced by the HCV core protein. Liver tissues from PA28 $\gamma^{+/+}$ , PA28 $\gamma^{+/+}$ CoreTg, PA28 $\gamma^{-/-}$ , and PA28 $\gamma^{-/-}$ CoreTg mice were prepared after administration of insulin (+) or phosphate-buffered saline (-). The samples (100  $\mu$ g of total protein) were examined by immunoblotting with antibodies against IRS1 and phospho-Tyr608 of mouse IRS1 (A). Phosphorylated IRS1 was estimated from the density on the immunoblotted membrane by using computer software (B) ( $n = 5$  in each group). The data presented are representative of three independent experiments. \* $P < 0.05$ ; \*\* $P < 0.01$ .

used in this study. Figure 1B shows the body weights of 2-month-old mice. There were no significant differences in body weight among PA28 $\gamma^{+/+}$ CoreTg, PA28 $\gamma^{-/-}$ CoreTg, PA28 $\gamma^{-/-}$ , and PA28 $\gamma^{+/+}$  mice. Steatosis was not detected in the livers of the 2-month-old mice (data not shown).

**PA28 $\gamma$  is involved in the development of hyperinsulinemia and insulin resistance in PA28 $\gamma^{+/+}$ CoreTg mice.** In our previous study, we found a significant difference in serum insulin levels, but not in plasma glucose levels, between PA28 $\gamma^{+/+}$ CoreTg mice and normal littermates (47). To determine the involvement of PA28 $\gamma$  in the development of insulin resistance in PA28 $\gamma^{+/+}$ CoreTg mice, we examined here the plasma glucose and insulin levels in the mice under fasting and fed conditions. Although no significant difference in plasma glucose levels was observed in the mice under either fasting (Fig. 2A) or fed (Fig. 2B) conditions, serum insulin levels were significantly higher in PA28 $\gamma^{+/+}$ CoreTg mice than in PA28 $\gamma^{+/+}$  mice under both conditions (Fig. 2C and D), as described previously (47). In contrast, the serum insulin concentration in PA28 $\gamma^{-/-}$ CoreTg mice was recovered to a normal level similar to that of PA28 $\gamma^{+/+}$  and PA28 $\gamma^{-/-}$  mice under either fasting (Fig. 2C) or fed (Fig. 2D) conditions.

To determine the glucose intolerance among the mice, glucose was administered to the mice after fasting, and the plasma glucose level was then determined. There was no significant difference among the genotypes at any time point in the glucose tolerance test (Fig. 3A), suggesting that the volume of glucose was maintained at a normal level by the higher concentration of insulin in PA28 $\gamma^{+/+}$ CoreTg mice. In our previ-

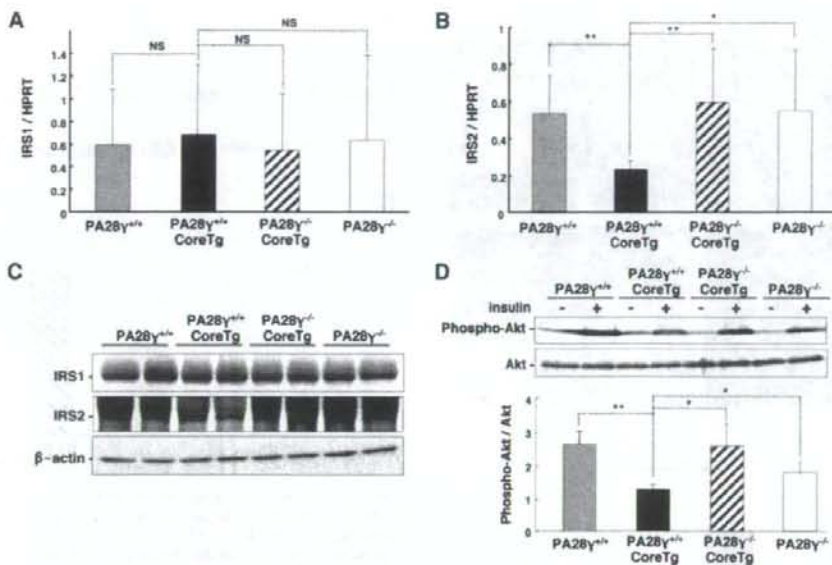


FIG. 6. PA28 $\gamma$  participated in the inhibition of the IRS2 expression and Akt phosphorylation induced by HCV core protein. The transcription of IRS1 (A) and IRS2 (B) was estimated by quantitative RT-PCR ( $n = 5$  in each group). (C) The expression levels of IRS1 and IRS2 in the livers of the mice were determined by immunoblotting with specific antibodies. (D) Phosphorylation of Akt in the livers of the mice was examined by immunoblotting with antibodies against Akt and phosphorylated Akt. The ratio of Akt phosphorylation was determined by computer software based on the densities of phosphorylated Akt and a total amount of Akt ( $n = 3$  in each group). The data presented are representative of three independent experiments. \* $P < 0.05$ ; \*\* $P < 0.01$ . NS, not statistically significant; HPRT, hypoxanthine phosphoribosyl transferase.

our study, the reduction in the plasma glucose concentration after insulin administration was impaired in PA28 $\gamma^{+/+}$  CoreTg mice (47). In this study, PA28 $\gamma^{-/-}$  CoreTg mice exhibited a normal insulin level comparable to those of PA28 $\gamma^{+/+}$  and PA28 $\gamma^{-/-}$  mice by an insulin tolerance test, in contrast to PA28 $\gamma^{+/+}$  CoreTg mice, in which a high concentration of plasma glucose was detected at all time points, as previously reported (Fig. 3B). These data suggest that hyperinsulinemia was induced in PA28 $\gamma^{+/+}$  CoreTg mice to compensate for insulin resistance and retain a physiological level of plasma glucose and that PA28 $\gamma$  participates in the development of hyperinsulinemia and insulin resistance in PA28 $\gamma^{+/+}$  CoreTg mice.

**Morphology of pancreatic islets.** Hyperinsulinemia and insulin resistance are expected to enlarge the pancreatic islet mass due to the overexpression of insulin. Our previous report showed the enlargement of the pancreatic islets in PA28 $\gamma^{+/+}$  CoreTg mice. To clarify whether a knockout of the PA28 $\gamma$  gene restores the enlarged pancreatic islets to their normal size, the morphology of the pancreatic islets of the mice was evaluated by histologic examination (Fig. 4A). The relative islet area in the pancreatic cells of the PA28 $\gamma^{-/-}$  CoreTg mice was smaller than that of PA28 $\gamma^{+/+}$  CoreTg mice and comparable to that of PA28 $\gamma^{+/+}$  and PA28 $\gamma^{-/-}$  mice (Fig. 4B). Infiltration of inflammatory cells within or surrounding the islets was not found in all genotypes of mice. These results suggest that PA28 $\gamma$  also participates in the enlargement of pancreatic islets induced in PA28 $\gamma^{+/+}$  CoreTg mice.

**PA28 $\gamma$  impairs the insulin-signaling pathway through the suppression of both tyrosine phosphorylation of IRS1 and expression of IRS2.** Insulin binds to insulin receptors, resulting in the activation of downstream signaling (26). The activated insulin receptors phosphorylate themselves, IRS1, and IRS2. Phosphorylated IRS1 and IRS2 can activate phosphatidylinositol 3 (PI3)-kinase signaling, leading to the activation of glucose metabolism and cell growth. Our previous report showed that tyrosine phosphorylation of IRS1 is suppressed in the livers of PA28 $\gamma^{+/+}$  CoreTg mice and that the administration of anti-TNF- $\alpha$  antibody restores insulin sensitivity (47). We examined whether a knockout of the PA28 $\gamma$  gene could restore the tyrosine phosphorylation of IRS1. Tyrosine phosphorylation of IRS1 was suppressed in the livers of PA28 $\gamma^{+/+}$  CoreTg mice in response to insulin stimulation, whereas it was recovered in PA28 $\gamma^{-/-}$  CoreTg mice to levels comparable to those in PA28 $\gamma^{+/+}$  and PA28 $\gamma^{-/-}$  mice (Fig. 5).

Chronic hyperinsulinemia downregulates the expression of IRS2, which is one of the essential components of the insulin-signaling pathway in the liver (46). However, in our previous study, we showed that there was no significant difference in the phosphorylation of IRS2 between PA28 $\gamma^{+/+}$  CoreTg mice and their normal littermates (47). To gain more insight into the mechanisms of regulation of IRS expression, we determined the transcription and translation of IRS1 and IRS2 in the livers of the mice by real-time PCR and Western blotting, respectively. Although there was no significant difference in IRS1 expression at either the transcriptional or translational level among the mice

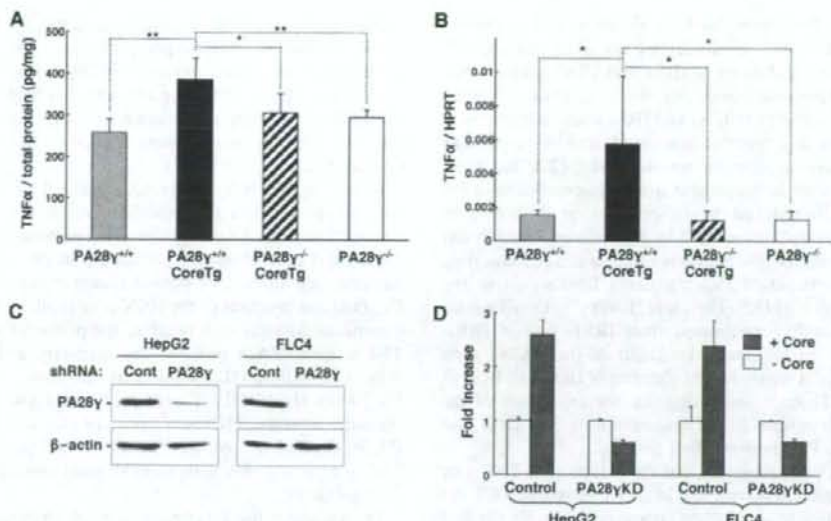


FIG. 7. PA28 $\gamma$  was required for activation of the TNF- $\alpha$  promoter by the HCV core protein. (A) Expression of TNF- $\alpha$  in the livers of mice was determined by ELISA ( $n = 5$  in each group). (B) TNF- $\alpha$  mRNA in the livers of mice was examined by quantitative RT-PCR ( $n = 5$  in each group). (C) Knockdown of the expression of PA28 $\gamma$  in the HepG2 and FLC-4 cell lines by the introduction of a plasmid encoding a short hairpin RNA (shRNA) targeted to the PA28 $\gamma$  gene. The expression levels of PA28 $\gamma$  and  $\beta$ -actin were determined by immunoblotting with specific antibodies. (D) Promoter activity of TNF- $\alpha$  in the presence or absence of the HCV core protein was determined by luciferase assay in the PA28 $\gamma$ -knockdown and control cell lines. The data presented are representative of three independent experiments. HPRT, hypoxanthine phosphoribosyl transferase.

(Fig. 6A and C), the expression of IRS2 was clearly impaired in PA28 $\gamma^{+/+}$ CoreTg mice at both the transcriptional and translational levels compared with that in other mice (Fig. 6B and C). The serine/threonine protein kinase Akt is phosphorylated by phosphoinositide-dependent kinase 1 (PDK1) under the activated condition of IRS family proteins (26). The insulin-induced phosphorylation of Akt was suppressed in the livers of PA28 $\gamma^{+/+}$ CoreTg mice but not in those of PA28 $\gamma^{+/+}$ , PA28 $\gamma^{-/-}$ , or PA28 $\gamma^{-/-}$ CoreTg mice (Fig. 6D). These results suggest that the expression of the HCV core protein in the livers of mice in the presence of PA28 $\gamma$  impairs the insulin-signaling pathway through the suppression of both the tyrosine phosphorylation of IRS1 and the expression of IRS2.

**PA28 $\gamma$  is required for activation of the TNF- $\alpha$  promoter by HCV core protein.** TNF- $\alpha$  is an adipokine (54) and suppresses the signaling pathway of IRS1 and IRS2 (14, 42). Several reports suggested that the serum TNF- $\alpha$  level is higher in HCV patients than in healthy individuals (19, 37). Elevations of TNF- $\alpha$  levels have also been demonstrated in the livers of PA28 $\gamma^{+/+}$ CoreTg mice (47). To determine the involvement of PA28 $\gamma$  in the enhancement of TNF- $\alpha$  expression, the expression of TNF- $\alpha$  in the livers of each genotype was determined by ELISA and real-time PCR (Fig. 7A and B). Transcription and translation of TNF- $\alpha$  were increased in the livers of PA28 $\gamma^{+/+}$ CoreTg mice but were restored in the livers of PA28 $\gamma^{-/-}$ CoreTg mice to levels comparable to those of PA28 $\gamma^{+/+}$  and PA28 $\gamma^{-/-}$  mice. To determine the effect of PA28 $\gamma$  expression on the promoter activity of TNF- $\alpha$  in human liver cells, PA28 $\gamma$ -knockdown human hepatoma cell lines HepG2 and FLC4 were

established by the introduction of a plasmid encoding a short hairpin RNA targeting the PA28 $\gamma$  gene in the cell lines. The expression of PA28 $\gamma$  was clearly suppressed in the cell lines (Fig. 7C). The expression of HCV core protein in the hepatoma cell lines potentiated TNF- $\alpha$  promoter activity, whereas the promoter activation by the HCV core protein was suppressed in the PA28 $\gamma$ -knockdown cell lines (Fig. 7D). These results suggest that PA28 $\gamma$  is required for the activation of the TNF- $\alpha$  promoter induced by the expression of the HCV core protein in human hepatoma cell lines.

## DISCUSSION

HCV infection has a close association with type 2 diabetes, which is a polygenic disease with a pathophysiology that includes a defect in insulin secretion, increased hepatic glucose production, and resistance to the action of insulin (2, 8, 18). Insulin binds to insulin receptors, which exhibit tyrosine kinase activity, leading to the autophosphorylation and phosphorylation of IRS (56). Tyrosine phosphorylation in IRS proteins leads to the interaction between IRS proteins and the regulatory subunit p85 of PI3-kinase, which enhances glucose uptake and inhibits lipolysis (21). Activated PI3-kinase phosphorylates phosphatidylinositol 4,5-bisphosphate to produce phosphatidylinositol 3,4,5-trisphosphate, which contributes to the activation of PDK1 (55). Activated PDK1 phosphorylates downstream substrates including Akt and other kinases (55). A diabetic phenotype that included insulin resistance was found in IRS2-knockout mice with normal growth (57), although a

knockout of the IRS1 gene has been shown to lead to growth retardation and insulin resistance but not overt diabetes (5, 52). The double knockdown of IRS1 and IRS2 genes in the liver induces hyperinsulinemia and insulin resistance in mice (53). The reduction of both IRS1 and IRS2 under conditions of insulin resistance and hyperinsulinemia (3) and in the livers of *ob/ob* mice, an obese diabetic mouse model (20), has been reported previously. In the present study, the expression of the HCV core protein reduced the phosphorylation of tyrosine on IRS1 and the production of IRS2 in the livers of mice but did not completely abolish the activities of these genes, suggesting that residual activities of IRS transfer a faint signal to the downstream region of IRS. Therefore, PA28 $\gamma^{+/+}$  CoreTg mice may exhibit a milder phenotype than IRS1- and/or IRS2-knockout mice. In this study, knockout of the PA28 $\gamma$  gene restored the insulin sensitivity and signaling of IRS1 and IRS2 in PA28 $\gamma^{+/+}$  CoreTg mice, suggesting that the expression of the HCV core protein leads to the dysfunction of both IRS1 and IRS2 through a PA28 $\gamma$ -dependent pathway.

Our previous study suggested that the induction of TNF- $\alpha$  by the HCV core protein plays a role in insulin resistance (47). An increase in TNF- $\alpha$  levels has been correlated with obesity and insulin resistance in animal models and humans (14, 42). However, the mechanism by which TNF- $\alpha$  induces insulin resistance is not completely known. The expression of TNF- $\alpha$  has been shown to be increased in PA28 $\gamma^{+/+}$  CoreTg mice, resulting in the suppression of phosphorylation of IRS1, and insulin sensitivity in PA28 $\gamma^{+/+}$  CoreTg was improved by the administration of an anti-TNF- $\alpha$  antibody (47). In the present study, the expression level of TNF- $\alpha$  in PA28 $\gamma^{-/-}$  CoreTg mice was similar to that in PA28 $\gamma^{-/-}$  mice or their normal littermates. The expression of the HCV core protein enhanced the promoter activity of the TNF- $\alpha$  gene in human liver cell lines but not in those with a knockdown of the PA28 $\gamma$  gene by RNA interference (Fig. 7D). These data suggest that PA28 $\gamma$  plays a crucial role in HCV core-induced expression of TNF- $\alpha$ . Sterol regulatory element-binding proteins (SREBPs) were shown to be increased at the stage of viremia in HCV-infected chimpanzees (49). SREBPs are known to regulate not only the biosynthesis of lipid but also the transcription of IRS2 and TNF- $\alpha$  (17, 45). Therefore, it might be feasible to speculate that the HCV core protein may cooperate with PA28 $\gamma$  to regulate the expression of SREBPs.

Houstis et al. previously reported that reactive oxygen species (ROS) are increased in both cellular and mouse models of insulin resistance induced by treatment with TNF- $\alpha$  or dexamethasone and that insulin sensitivity was restored by treatment with small antioxidant molecules (16). The HCV core protein potentiates ROS production in hepatoma cells and HCV core gene-transgenic mice (23, 34, 41). Accelerated production of ROS results in mitochondrial dysfunction, which contributes to a decrease in fatty acid oxidation. Defects in mitochondrial fatty acid oxidation enhance the production of intracellular fatty acyl coenzyme A (CoA) and diacylglycerol (48, 58). Mitochondrial dysfunction and accumulation of lipid droplets in mice expressing the HCV core or the full-length HCV polyprotein have been reported (27, 34). An increase in lipid droplets also leads to the accumulation of fatty acid CoA and diacylglycerol (48, 58). Fatty acyl CoA and diacylglycerol nonspecifically activate the Ser/Thr kinase cascade, leading to the enhancement of the serine phosphorylation of IRS1 (26). Serine phosphorylation on IRS1 blocks the tyrosine

phosphorylation of IRS1 by insulin receptors (26). In the present study, however, serine phosphorylation of IRS1 in PA28 $\gamma^{+/+}$  CoreTg mice was similar to that in PA28 $\gamma^{-/-}$  CoreTg mice (data not shown). TNF- $\alpha$  signaling pathways other than the accumulation of ROS and fatty acid intermediates may also participate in the inhibition of tyrosine phosphorylation on IRS1 in PA28 $\gamma^{+/+}$  CoreTg mice.

How does the HCV core protein induce TNF- $\alpha$  production? Our previous report suggests that the HCV core protein is degraded through a PA28 $\gamma$ -dependent pathway (32). Recently, PA28 $\gamma$  has been shown to participate in the proteasome-dependent degradation of steroid receptor coactivator 3 (28). Degradation products of the HCV core protein via the PA28 $\gamma$ -dependent pathway may regulate the promoter activity of the TNF- $\alpha$  gene. PA28 proteins are necessary and sufficient to fully reconstitute Hsp90-initiated refolding together with Hsc70 and Hsp40 (31). Therefore, it might also be feasible to speculate that the HCV core protein refolded by an Hsp90/PA28 $\gamma$ -dependent pathway activates the promoter of the TNF- $\alpha$  gene together with an unknown transcription factor(s) or regulator(s).

In conclusion, the data obtained in this study suggest that the expression of the HCV core protein enhances the production of TNF- $\alpha$  and suppresses the phosphorylation of tyrosine on IRS1 and the production of IRS2 through a PA28 $\gamma$ -dependent pathway, thereby leading to insulin resistance. PA28 $\gamma$  may be a novel target for the treatment of HCV-induced diabetes.

#### ACKNOWLEDGMENTS

We gratefully thank H. Murase for secretarial work.

This study 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 Program for the Promotion of Fundamental Studies in Health Sciences of the National Institute of Biomedical Innovation (NIBIO); the 21st Century Center of Excellence Program; and the Foundation for Biomedical Research and Innovation.

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**Critical role of PA28( $\gamma$ ) in hepatitis C virus-associated steatogenesis and hepatocarcinogenesis**

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PNAS published online Jan 18, 2007;  
doi:10.1073/pnas.0607312104

**This information is current as of January 2007.**

<b>Supplementary Material</b>	Supplementary material can be found at: <a href="http://www.pnas.org/cgi/content/full/0607312104/DC1">www.pnas.org/cgi/content/full/0607312104/DC1</a>  This article has been cited by other articles: <a href="http://www.pnas.org/otherarticles">www.pnas.org/otherarticles</a>
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Notes:

# Critical role of PA28 $\gamma$ in hepatitis C virus-associated steatogenesis and hepatocarcinogenesis

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Edited by Peter Palese, Mount Sinai School of Medicine, New York, NY, and approved December 1, 2006 (received for review August 23, 2006)

Hepatitis C virus (HCV) is a major cause of chronic liver disease that frequently leads to steatosis, cirrhosis, and eventually hepatocellular carcinoma (HCC). HCV core protein is not only a component of viral particles but also a multifunctional protein because liver steatosis and HCC are developed in HCV core gene-transgenic (CoreTg) mice. Proteasome activator PA28 $\gamma$ /REG $\gamma$  regulates host and viral proteins such as nuclear hormone receptors and HCV core protein. Here we show that a knockout of the PA28 $\gamma$  gene induces the accumulation of HCV core protein in the nucleus of hepatocytes of CoreTg mice and disrupts development of both hepatic steatosis and HCC. Furthermore, the genes related to fatty acid biosynthesis and *sreb-1c* promoter activity were up-regulated by HCV core protein in the cell line and the mouse liver in a PA28 $\gamma$ -dependent manner. Heterodimer composed of liver X receptor  $\alpha$  (LXR $\alpha$ ) and retinoid X receptor  $\alpha$  (RXR $\alpha$ ) is known to up-regulate *sreb-1c* promoter activity. Our data also show that HCV core protein enhances the binding of LXR $\alpha$ /RXR $\alpha$  to LXR-response element in the presence but not the absence of PA28 $\gamma$ . These findings suggest that PA28 $\gamma$  plays a crucial role in the development of liver pathology induced by HCV infection.

fatty acid | proteasome | sterol regulatory element-binding protein (SREBP) | RXR $\alpha$  | LXR $\alpha$

Hepatitis C virus (HCV) belongs to the Flaviviridae family, and it possesses a positive, single-stranded RNA genome that encodes a single polyprotein composed of  $\approx$ 3,000 aa. The HCV polyprotein is processed by host and viral proteases, resulting in 10 viral proteins. Viral structural proteins, including the capsid (core) protein and two envelope proteins, are located in the N-terminal one-third of the polyprotein, followed by nonstructural proteins.

HCV infects >170 million individuals worldwide, and then it causes liver disease, including hepatic steatosis, cirrhosis, and eventually hepatocellular carcinoma (HCC) (1). The prevalence of fatty infiltration in the livers of chronic hepatitis C patients has been reported to average  $\approx$ 50% (2, 3), which is higher than the percentage in patients infected with hepatitis B virus and other liver diseases. However, the precise functions of HCV proteins in the development of fatty liver remain unknown because of the lack of a system sufficient to investigate the pathogenesis of HCV. HCV core protein expression has been shown to induce lipid droplets in cell lines and hepatic steatosis and HCC in transgenic mice (4–6). These reports suggest that HCV core protein plays an important role in the development of various types of liver failure, including steatosis and HCC.

Recent reports suggest that lipid biosynthesis affects HCV replication (7–9). Involvement of a geranylgeranylated host protein, FBL2, in HCV replication through the interaction with NS5A suggests that the cholesterol biosynthesis pathway is also important for HCV replication (9). Increases in saturated and monounsaturated fatty acids enhance HCV RNA replication, whereas increases in polyunsaturated fatty acids suppress it (7). Lipid homeostasis is regulated by a family of sterol regulatory element-binding proteins (SREBPs), which activate the expression of >30 genes involved in

the synthesis and uptake of cholesterol, fatty acids, triglycerides, and phospholipids. Biosynthesis of cholesterol is regulated by SREBP-2, whereas that of fatty acids, triglycerides, and phospholipids is regulated by SREBP-1c (10–14). In chimpanzees, host genes involved in SREBP signaling are induced during the early stages of HCV infection (8). SREBP-1c regulates the transcription of acetyl-CoA carboxylase, fatty acid synthase, and stearoyl-CoA desaturase, leading to the production of saturated and monounsaturated fatty acids and triglycerides (15). SREBP-1c is transcriptionally regulated by liver X receptor (LXR)  $\alpha$  and retinoid X receptor (RXR)  $\alpha$ , which belong to a family of nuclear hormone receptors (15, 16). Accumulation of cellular fatty acids by HCV core protein is expected to be modulated by the SREBP-1c pathway because RXR $\alpha$  is activated by HCV core protein (17). However, it remains unknown whether HCV core protein regulates the *sreb-1c* promoter.

We previously reported (18) that HCV core protein specifically binds to the proteasome activator PA28 $\gamma$ /REG $\gamma$  in the nucleus and is degraded through a PA28 $\gamma$ -dependent pathway. PA28 $\gamma$  is well conserved from invertebrates to vertebrates, and amino acid sequences of human and murine PA28 $\gamma$ s are identical (19). The homologous proteins, PA28 $\alpha$  and PA28 $\beta$ , form a heteroheptamer in the cytoplasm, and they activate chymotrypsin-like peptidase activity of the 20S proteasome, whereas PA28 $\gamma$  forms a homoheptamer in the nucleus, and it enhances trypsin-like peptidase activity of 20S proteasome (20). Recently, Li and colleagues (21) reported that PA28 $\gamma$  binds to steroid receptor coactivator-3 (SRC-3) and enhances the degradation of SRC-3 in a ubiquitin- and ATP-independent manner. However, the precise physiological functions of PA28 $\gamma$  are largely unknown *in vivo*. In this work, we examine whether PA28 $\gamma$  is required for liver pathology induced by HCV core protein *in vivo*.

## Results

**PA28 $\gamma$ -Knockout HCV Core Gene Transgenic Mice.** To determine the role of PA28 $\gamma$  in HCV core-induced steatosis and the development of HCC *in vivo*, we prepared PA28 $\gamma$ -knockout core gene transgenic mice. The PA28 $\gamma$ -deficient, PA28 $\gamma$ <sup>-/-</sup> mice were born without

Author contributions: K. Moriishi, K.T., T.M., T.S., K.K., and Y. Matsuura designed research; K. Moriishi, R.M., K. Moriya, H.M., Y. Mori, and T.A. performed research; S.M. contributed new reagents/analytic tools; Y. Matsuura analyzed data; and K. Moriishi, K.K., and Y. Matsuura wrote the paper.

The authors declare no conflict of interest.

This article is a PNAS direct submission.

Freely available online through the PNAS open access option.

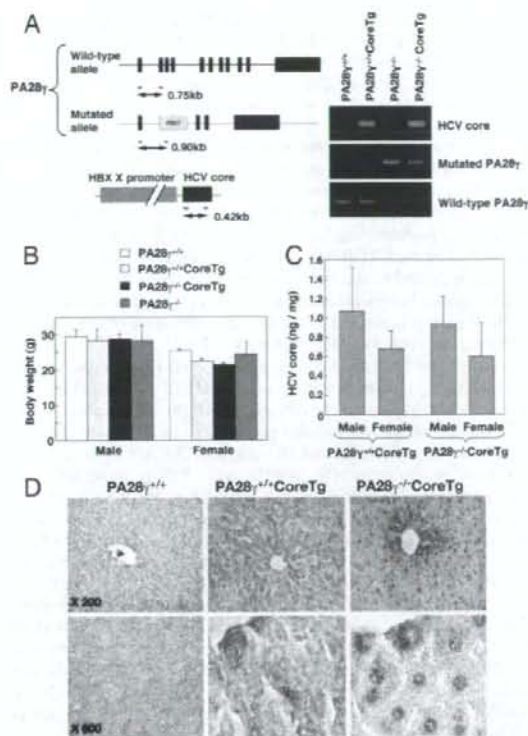
Abbreviations: CoreTg, HCV core gene-transgenic; HCC, hepatocellular carcinoma; HCV, hepatitis C virus; LXR, liver X receptor; LXRE, liver X receptor-response element; MEF, mouse embryonic fibroblast; ROS, reactive oxygen species; RXR, retinoid X receptor; SRC-3, steroid receptor coactivator-3; SREBP, sterol regulatory element-binding protein.

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This article contains supporting information online at www.pnas.org/cgi/content/full/0607312104DC1.

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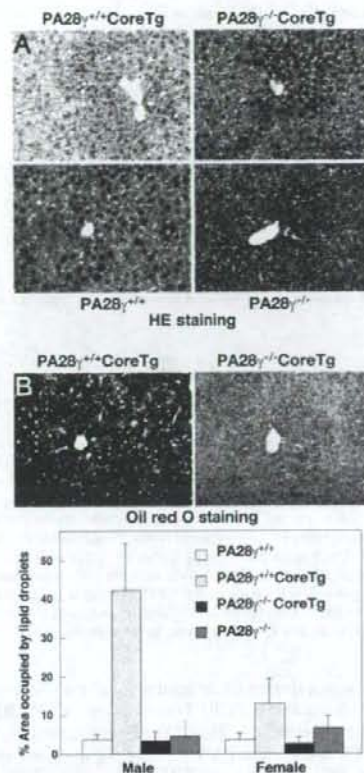




**Fig. 1.** Preparation and characterization of PA28 $\gamma$ -knockout HCV core-transgenic mice. (A) The structures of the wild-type and mutated PA28 $\gamma$  genes and the transgene encoding the HCV core protein under the control of the HBV X promoter were investigated. Positions corresponding to the screening primers and sizes of PCR products are shown. PCR products of the HCV core gene as well as wild-type and mutated PA28 $\gamma$  alleles were amplified from the genomic DNAs of PA28 $\gamma^{+/+}$ , PA28 $\gamma^{+/+}$ CoreTg, PA28 $\gamma^{-/-}$ , and PA28 $\gamma^{-/-}$ CoreTg mice. (B) Body weights of PA28 $\gamma^{+/+}$ , PA28 $\gamma^{+/+}$ CoreTg, PA28 $\gamma^{-/-}$ CoreTg, and PA28 $\gamma^{-/-}$  mice at the age of 6 months. (C) HCV core protein levels in the livers of PA28 $\gamma^{+/+}$ CoreTg and PA28 $\gamma^{-/-}$ CoreTg mice were determined by ELISA (mean  $\pm$  SD,  $n = 10$ ). (D) Localization of HCV core protein in the liver. Liver sections of PA28 $\gamma^{+/+}$ , PA28 $\gamma^{+/+}$ CoreTg, and PA28 $\gamma^{-/-}$ CoreTg mice at the age of 2 months were stained with anti-HCV core antibody.

appreciable abnormalities in all tissues examined, with the exception of a slight retardation of growth (22). HCV core gene-transgenic (PA28 $\gamma^{+/+}$ CoreTg) mice were bred with PA28 $\gamma^{-/-}$  mice to create PA28 $\gamma^{+/+}$ CoreTg mice. The PA28 $\gamma^{+/+}$ CoreTg offspring were bred with each other, and PA28 $\gamma^{-/-}$ CoreTg mice were selected by PCR using primers specific to the target sequences (Fig. 1A). No significant differences in body weight were observed among the 6-month-old mice, although PA28 $\gamma^{-/-}$  mice exhibited a slight retardation of growth (Fig. 1B). A similar level of PA28 $\gamma$  expression was detected in PA28 $\gamma^{+/+}$ CoreTg and PA28 $\gamma^{+/+}$  mice (see Fig. 5B). The expression levels and molecular size of HCV core protein were similar in the livers of PA28 $\gamma^{+/+}$ CoreTg and PA28 $\gamma^{-/-}$ CoreTg mice (Fig. 1C; see also Fig. 5B).

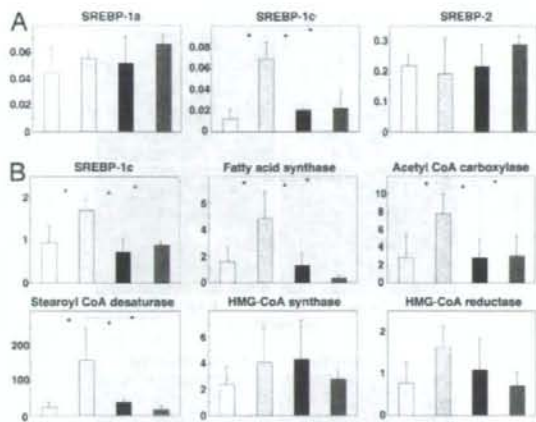
**PA28 $\gamma$  Is Required for Degradation of HCV Core Protein in the Nucleus and Induction of Liver Steatosis.** HCV core protein has been detected at various sites, such as the endoplasmic reticulum, mitochondria, lipid droplets, and nucleus of cultured cell lines, as well as in hepatocytes of PA28 $\gamma^{+/+}$ CoreTg mice and hepatitis C patients



**Fig. 2.** Accumulation of lipid droplets by expression of HCV core protein. (A) Liver sections of the mice at the age of 6 months were stained with hematoxylin/eosin (HE). (B) (Upper) Liver sections of PA28 $\gamma^{+/+}$ CoreTg and PA28 $\gamma^{-/-}$ CoreTg mice at the age of 6 months were stained with oil red O. (Lower) The area occupied by lipid droplets of PA28 $\gamma^{+/+}$  (white), PA28 $\gamma^{+/+}$ CoreTg (gray), PA28 $\gamma^{-/-}$ CoreTg (black), and PA28 $\gamma^{-/-}$  (dark gray) mice was calculated by Image-Pro software (MediaCybernetics, Silver Spring, MD) (mean  $\pm$  SD,  $n = 10$ ).

(6, 23, 24). Although HCV core protein is predominantly detected in the cytoplasm of the liver cells of PA28 $\gamma^{+/+}$ CoreTg mice, as reported in ref. 6, in the present study a clear accumulation of HCV core protein was observed in the liver cell nuclei of PA28 $\gamma^{-/-}$ CoreTg mice (Fig. 1D). These findings clearly indicate that at least some fraction of the HCV core protein is translocated into the nucleus and is degraded through a PA28 $\gamma$ -dependent pathway. Mild vacuolation was observed in the cytoplasm of the liver cells of 4-month-old PA28 $\gamma^{+/+}$ CoreTg mice, and it became more severe at 6 months, as reported in ref. 25. Hematoxylin/eosin-stained liver sections of 6-month-old PA28 $\gamma^{+/+}$ CoreTg mice exhibited severe vacuolating lesions (Fig. 2A), which were clearly stained with oil red O (Fig. 2B Upper), whereas no such lesions were detected in the livers of PA28 $\gamma^{-/-}$ CoreTg, PA28 $\gamma^{+/+}$ , or PA28 $\gamma^{-/-}$  mice at the same age. The areas occupied by the lipid droplets in the PA28 $\gamma^{+/+}$ CoreTg mouse livers were  $\sim$ 10 and 2–4 times larger than those of male and female of PA28 $\gamma^{+/+}$ , PA28 $\gamma^{-/-}$ , and PA28 $\gamma^{-/-}$ CoreTg mice, respectively (Fig. 2B Lower). These results suggest that PA28 $\gamma$  is required for the induction of liver steatosis by HCV core protein in mice.

**PA28 $\gamma$  Is Required for the Up-Regulation of SREBP-1c Transcription by HCV Core Protein in the Mouse Liver.** To clarify the effects of a knockout of the PA28 $\gamma$  gene in PA28 $\gamma^{+/+}$ CoreTg mice on lipid



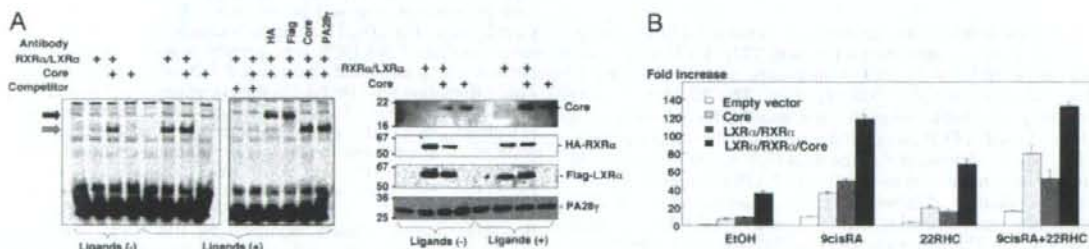
**Fig. 3.** Transcription of genes regulating lipid biosynthesis in the mouse liver. (A) Total RNA was prepared from the livers of 2-month-old mice; and the transcription of genes encoding SREBP-1a, SREBP-1c, and SREBP-2 was determined by real-time PCR. (B) The transcription of genes encoding SREBP-1c, fatty acid synthase, acetyl-CoA carboxylase, stearoyl-CoA desaturase, HMG-CoA synthase, and HMG-CoA reductase of 6-month-old mice was measured by real-time PCR. The transcription of the genes was normalized with that of hypoxanthine phosphoribosyltransferase, and the values are expressed as relative activity ( $n = 5$ ;  $\ast, P < 0.05$ ;  $\ast\ast, P < 0.01$ ). The transcription of each gene in PA28 $\gamma^{+/+}$ , PA28 $\gamma^{+/+}$ CoreTg, PA28 $\gamma^{-/-}$ CoreTg, and PA28 $\gamma^{-/-}$  mice is indicated by white, gray, black, and dark gray bars, respectively.

metabolism, genes related to the lipid biosyntheses were examined by real-time quantitative PCR. Transcription of SREBP-1c was higher in the livers of PA28 $\gamma^{+/+}$ CoreTg mice than in those of PA28 $\gamma^{+/+}$ , PA28 $\gamma^{-/-}$ , and PA28 $\gamma^{-/-}$ CoreTg mice at 2 months of age, but no such increases in SREBP-2 and SREBP-1a were observed (Fig. 3A). Although transcription of SREBP-1c and its regulating enzymes, such as acetyl-CoA carboxylase, fatty acid synthase, and stearoyl-CoA desaturase, was also enhanced in the livers of 6-month-old PA28 $\gamma^{+/+}$ CoreTg mice compared with the levels in PA28 $\gamma^{+/+}$ , PA28 $\gamma^{-/-}$ , and PA28 $\gamma^{-/-}$ CoreTg mice, no statistically significant differences were observed with respect to the transcription levels of cholesterol biosynthesis-related genes that are regulated by SREBP-2 (e.g., HMG-CoA synthase and HMG-CoA reductase) (Fig. 3B). These results suggest the

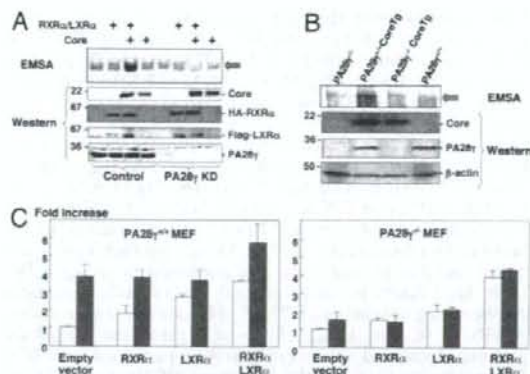
following: (i) the up-regulation of SREBP-1c transcription in the livers of mice requires both HCV core protein and PA28 $\gamma$ ; and (ii) the nuclear accumulation of HCV core protein alone, which occurs because of the lack of degradation along a PA28 $\gamma$ -dependent proteasome pathway, does not activate the *sreb-1c* promoter.

**HCV Core Protein Indirectly Potentiates *sreb-1c* Promoter Activity in an LXR $\alpha$ /RXR $\alpha$ -Dependent Manner.** LXR $\alpha$ , which is primarily expressed in the liver, forms a complex with RXR $\alpha$  and synergistically potentiates *sreb-1c* promoter activity (16). Activation of RXR $\alpha$  by HCV core protein suggests that cellular fatty acid synthesis is modulated by the SREBP-1c pathway, although HCV core protein was not included in the transcription factor complex in the electrophoresis mobility shift assay (EMSA) (17). To analyze the effect of HCV core protein and PA28 $\gamma$  on the activation of the *sreb-1c* promoter, we first examined the effect of HCV core protein on the binding of the LXR $\alpha$ /RXR $\alpha$  complex to the LXR-response element (LXRE) located upstream of the SREBP-1c gene (Fig. 4A). Although a weak shift of the labeled LXRE probe was observed by incubation with nuclear extracts prepared from 293T cells expressing FLAG-tagged LXR $\alpha$  and HA-tagged RXR $\alpha$ , a clear shift was obtained by the treatment of cells with 9-*cis*-retinoic acid and 22(*R*)-hydroxycholesterol, ligands for LXR $\alpha$  and RXR $\alpha$ , respectively. In contrast, coexpression of HCV core protein with LXR $\alpha$  and RXR $\alpha$  potentiated the shift of the probe irrespective of the treatment with the ligands. Addition of 500 times the amount of nonlabeled LXRE probe (competitor) diminished the shift of the labeled probe induced by the ligands and/or HCV core protein. Furthermore, coinubation of the nuclear fraction with antibody to FLAG or HA tag but not with antibody to either HCV core or PA28 $\gamma$  caused a supershift of the labeled probe. These results indicate that HCV core protein does not participate in the LXR $\alpha$ /RXR $\alpha$ -LXRE complex but indirectly enhances the binding of LXR $\alpha$ /RXR $\alpha$  to the LXRE.

The activity of the *sreb-1c* promoter was enhanced by the expression of HCV core protein in 293T cells, and it was further enhanced by coexpression of LXR $\alpha$ /RXR $\alpha$  (Fig. 4B). Enhancement of the *sreb-1c* promoter by coexpression of HCV core protein and LXR $\alpha$ /RXR $\alpha$  was further potentiated by treatment with the ligands for LXR $\alpha$  and RXR $\alpha$ . The cells treated with 9-*cis*-retinoic acid exhibited more potent enhancement of the *sreb-1c* promoter than those treated with 22(*R*)-hydroxycholesterol. HCV core protein exhibited more potent enhancement of the *sreb-1c* promoter in cells treated with both ligands than in those treated with either ligand alone. These results suggest that HCV core protein poten-



**Fig. 4.** Activation of the *sreb-1c* promoter by HCV core protein. (A) FLAG-LXR $\alpha$  and HA-RXR $\alpha$  were expressed in 293T cells together with or without HCV core protein. Ligands for LXR $\alpha$  and RXR $\alpha$  dissolved in ethanol [Ligands (+)] or ethanol alone [Ligands (-)] were added to the culture supernatant at 24 h posttransfection. Cells were harvested at 48 h posttransfection, and nuclear extracts were mixed with the reaction buffer for EMSA in the presence or absence of antibody (100 ng) against HA, FLAG, HCV core or PA28 $\gamma$ , or nonlabeled LXRE probe (Competitor). (Left) The resulting mixtures were subjected to PAGE and blotted with horseradish peroxidase/streptavidin. The mobility shift of the LXRE probe and its supershift are indicated by a gray and black arrow, respectively. (Right) Expression of HCV core, HA-RXR $\alpha$ , FLAG-LXR $\alpha$ , and PA28 $\gamma$  in cells was detected by immunoblotting. (B) Effects of ligands for RXR $\alpha$ , 9-*cis*-retinoic acid (9cisRA), and for LXR $\alpha$ , 22(*R*)-hydroxycholesterol (22RHC), on the activation of the *sreb-1c* promoter in 293T cells expressing RXR $\alpha$ , LXR $\alpha$ , and/or HCV core protein. Ligands were added into the medium at a concentration of 5  $\mu$ M, and the cells were harvested after 24 h of incubation.



**Fig. 5.** PA28 $\gamma$  is required for HCV core-dependent activation of the *srebp-1c* promoter. (A) Effect of PA28 $\gamma$  knockdown on the LXR $\alpha$ /RXR $\alpha$ -DNA complex. FLAG-LXR $\alpha$  and HA-RXR $\alpha$  were expressed in FLC4 (control) or PA28 $\gamma$ -knockdown (PA28 $\gamma$ KD) cells together with or without HCV core protein. Cells were harvested at 48 h posttransfection, and nuclear extracts were mixed with the reaction buffer for EMSA. (Upper) The resulting mixtures were subjected to PAGE and blotted with horseradish peroxidase-streptavidin. The mobility shift of the LXRE probe is indicated by an arrow. (Lower) Expression of HCV core, HA-RXR $\alpha$ , FLAG-LXR $\alpha$ , and PA28 $\gamma$  in cells was detected by immunoblotting. (B) Effect of PA28 $\gamma$  knockout on the LXR $\alpha$ /RXR $\alpha$ -DNA complex in the mouse liver. (Upper) Nuclear extracts were prepared from the livers of 2-month-old PA28 $\gamma$ <sup>-/-</sup>, PA28 $\gamma$ <sup>+/-</sup>CoreTg, PA28 $\gamma$ <sup>-/-</sup>CoreTg, and PA28 $\gamma$ <sup>+/-</sup> mice and subjected to EMSA. The mobility shift of the LXRE probe is indicated by an arrow. (Lower) The expression of HCV core, PA28 $\gamma$ , and  $\beta$ -actin in the livers of the mice was detected by immunoblotting. (C) Effect of HCV core protein on *srebp-1c* promoter activity in PA28 $\gamma$ -knockout fibroblasts. A plasmid encoding firefly luciferase under the control of the *srebp-1c* promoter was transfected into MEFs prepared from PA28 $\gamma$ <sup>+/-</sup> (Left) or PA28 $\gamma$ <sup>-/-</sup> (Right) mice together with a plasmid encoding a *Renilla* luciferase. An empty plasmid or plasmids encoding mouse RXR $\alpha$  or LXR $\alpha$  were also cotransfected into the cells together with (gray bars) or without (white bars) a plasmid encoding HCV core protein. Luciferase activity under the control of the *srebp-1c* promoter was determined, and it is expressed as the fold increase in relative luciferase activity after standardization with the activity of *Renilla* luciferase.

tiates *srebp-1c* promoter activity in an LXR $\alpha$ /RXR $\alpha$ -dependent manner.

**HCV Core Protein Activates the *srebp-1c* Promoter in an LXR $\alpha$ /RXR $\alpha$ - and PA28 $\gamma$ -Dependent Manner.** To examine whether PA28 $\gamma$  is required for HCV core-induced enhancement of *srebp-1c* promoter activity in human liver cells, a PA28 $\gamma$ -knockdown human hepatoma cell line (FLC4 KD) was prepared. Enhancement of binding of the LXRE probe to LXR $\alpha$ /RXR $\alpha$  by coexpression of HCV core protein and LXR $\alpha$ /RXR $\alpha$  in FLC4 cells was diminished by knockdown of the PA28 $\gamma$  gene (Fig. 5A). Furthermore, formation of the LXR $\alpha$ /RXR $\alpha$ -LXRE complex was enhanced in the livers of PA28 $\gamma$ <sup>+/-</sup>CoreTg mice but not in those of PA28 $\gamma$ <sup>-/-</sup>, PA28 $\gamma$ <sup>+/-</sup>, or PA28 $\gamma$ <sup>-/-</sup>CoreTg mice (Fig. 5B). The expression of the HCV core protein in the mouse embryonic fibroblasts (MEFs) of PA28 $\gamma$ <sup>+/-</sup> mice induced the activation of the mouse *srebp-1c* promoter through the endogenous expression of LXR $\alpha$  and RXR $\alpha$  (Fig. 5C Left). Further enhancement of the activation of the *srebp-1c* promoter by HCV core protein in PA28 $\gamma$ <sup>+/-</sup> MEFs was achieved by the exogenous expression of both LXR $\alpha$  and RXR $\alpha$ . However, no enhancing effect of HCV core protein on *srebp-1c* promoter activity was observed in PA28 $\gamma$ <sup>-/-</sup> MEFs (Fig. 5C Right). These results support the notion that HCV core protein enhances the activity of the *srebp-1c* promoter in an LXR $\alpha$ /RXR $\alpha$ - and PA28 $\gamma$ -dependent manner.

**Table 1. HCC in mice at 16–18 months of age**

Mouse and sex	Total no. of mice	No. of mice developing HCC	Incidence, %
<b>PA28<math>\gamma</math><sup>+/-</sup>CoreTg</b>			
Male	17	5	29.4
Female	28	3	10.7
<b>PA28<math>\gamma</math><sup>-/-</sup></b>			
Male	16	0	0
Female	4	0	0
<b>PA28<math>\gamma</math><sup>-/-</sup>CoreTg</b>			
Male	23	0	0
Female	13	0	0
<b>PA28<math>\gamma</math><sup>+/-</sup>CoreTg</b>			
Male	15	0	0
Female	21	0	0

**PA28 $\gamma$  Plays a Crucial Role in the Development of HCC in PA28 $\gamma$ <sup>+/-</sup>CoreTg Mice.** The incidence of hepatic tumors in male PA28 $\gamma$ <sup>+/-</sup>CoreTg mice older than 16 months was significantly higher than that in age-matched female PA28 $\gamma$ <sup>+/-</sup>CoreTg mice (6). We reconfirmed here that the incidence of HCC in male and female PA28 $\gamma$ <sup>+/-</sup>CoreTg mice at 16–18 months of age was 29.4% (5 of 17 mice) and 10.7% (3 of 28 mice), respectively. To our surprise, however, no HCC developed in PA28 $\gamma$ <sup>-/-</sup>CoreTg mice (males, 15; females, 21), although, as expected, no HCC was observed in PA28 $\gamma$ <sup>+/-</sup> (males, 16; females, 4) and PA28 $\gamma$ <sup>-/-</sup> mice (males, 23; females, 13) (Table 1). These results clearly indicate that PA28 $\gamma$  plays an indispensable role in the development of HCC induced by HCV core protein.

## Discussion

HCV core protein is detected in the cytoplasm and partially in the nucleus and mitochondria of culture cells and hepatocytes of transgenic mice and hepatitis C patients (6, 23, 24, 26). Degradation of HCV core protein was enhanced by deletion of the C-terminal transmembrane region through a ubiquitin/proteasome-dependent pathway (27). We previously reported (18) that PA28 $\gamma$  binds directly to HCV core protein and then enhances degradation of HCV core protein in the nucleus through a proteasome-dependent pathway because HCV core protein was accumulated in nucleus of human cell line by treatment with proteasome inhibitor MG132. In this work, accumulation of HCV core protein was observed in nucleus of hepatocytes of PA28 $\gamma$ <sup>-/-</sup>CoreTg mice (Fig. 1D). This result directly demonstrates that HCV core protein migrates into the nucleus and is degraded through a PA28 $\gamma$ -dependent pathway. However, HCV core protein accumulated in the nucleus because knockout of PA28 $\gamma$  gene abrogated the ability to cause liver pathology, suggesting that interaction of HCV core protein with PA28 $\gamma$  in the nucleus is prerequisite for the liver pathology induced by HCV core protein. We have previously shown (18) that HCV core protein is degraded through a PA28 $\gamma$ -dependent pathway, and Minami *et al.* (28) reported that PA28 $\gamma$  has a cochaperone activity with Hsp90. Therefore, degradation products of HCV core protein by means of PA28 $\gamma$ -dependent processing or correct folding of HCV core protein through cochaperone activity of PA28 $\gamma$  might be involved in the development of liver pathology. We do not know the reason why knockout of the PA28 $\gamma$  gene does not affect the total amount of HCV core protein in the liver of the transgenic mice. PA28 $\gamma$ -dependent degradation of HCV core protein may be independent of ubiquitination, as shown in SRC-3 (21), whereas knockdown of PA28 $\gamma$  in a human hepatoma cell line enhanced the ubiquitination of HCV core protein [supporting information (SI) Fig. 6], suggesting that lack of PA28 $\gamma$  suppresses a ubiquitin-independent degradation but enhances a ubiquitin-dependent degradation of HCV core protein. Therefore, the total amount of HCV

core protein in the liver of the mice may be unaffected by the knockout of the PA28 $\gamma$  gene.

Our results suggest that the interaction of HCV core protein with PA28 $\gamma$  leads to the activation of the *sreb-1c* promoter along an LXR $\alpha$ /RXR $\alpha$ -dependent pathway and the development of liver steatosis and HCC. HCV core protein was not included in the LXR $\alpha$ /RXR $\alpha$ -LXRE complex (Fig. 3A), suggesting that HCV core protein indirectly activates the *sreb-1c* promoter. Cytoplasmic HCV core protein was shown to interact with Sp110b, which is a transcriptional corepressor of RAR $\alpha$ -dependent transcription, and this interaction leads to the sequestering of Sp110b in the cytoplasm, resulting in the activation of RAR $\alpha$ -dependent transcription (29). The sequestration of an unidentified corepressor of the LXR $\alpha$ /RXR $\alpha$  heterodimer in the cytoplasm by HCV core protein may also contribute to the activation of the *sreb-1c* promoter. Although the precise physiological function of PA28 $\gamma$ -proteasome activity in the nucleus is not known, PA28 $\gamma$  has previously been shown (21) to regulate nuclear hormone receptors by means of the degradation of its coactivator SRC-3 and to participate in the fully Hsp90-dependent protein refolding (28). It appears reasonable to speculate that degradation or refolding of HCV core protein in a PA28 $\gamma$ -dependent pathway might be involved in the modulation of transcriptional regulators of various promoters, including the *sreb-1c* promoter. Saturated or monounsaturated fatty acids have been shown to enhance HCV RNA replication in Huh7 cells containing the full-length HCV replicon (7). The up-regulation of fatty acid biosynthesis by HCV core protein may also contribute to the efficient replication of HCV and to the progression of HCV pathogenesis.

Expression of HCV core protein was reported to enhance production of reactive oxygen species (ROS) (30), which leads to carbonylation of intracellular proteins (31). Enhancement of ROS production may trigger double-stranded DNA breaks and result in the development of HCC (30, 32, 33). HCV core protein could enhance the protein carbonylation in the liver of the transgenic mice in the presence but not in the absence of PA28 $\gamma$  (SI Fig. 7), suggesting that PA28 $\gamma$  is required for ROS production induced by HCV core protein. Development of HCC was observed in PA28 $\gamma^{+/+}$  CoreTg mice but not in PA28 $\gamma^{-/-}$  CoreTg mice (Table 1). Enhancement of ROS production by HCV core protein in the presence of PA28 $\gamma$  might be involved in the development of HCC in PA28 $\gamma^{+/+}$  CoreTg mice.

It is well known that resistant viruses readily emerge during the treatment with antiviral drugs targeting the viral protease or replicase, especially in the case of infection with RNA viruses. Therefore, antivirals targeting the host factors that are indispensable for the propagation of viruses might be an ideal target for the development of antiviral agents because of a lower rate of mutation than that of viral genome, if they have no side effects to patients. Importantly, the amino acid sequence of PA28 $\gamma$  of mice is identical to that of human, and mouse PA28 $\gamma$  is dispensable because PA28 $\gamma$  knockout mice exhibit no abnormal phenotype except for mild growth retardation. Therefore, PA28 $\gamma$  might be a promising target for an antiviral treatment of chronic hepatitis C with negligible side effects.

In summary, we observed that a knockout of the PA28 $\gamma$  gene from PA28 $\gamma^{+/+}$  CoreTg mice induced the accumulation of HCV core protein in the nucleus and disrupted the development of both steatosis and HCC. Activation of the *sreb-1c* promoter was up-regulated by HCV core protein both *in vitro* and *in vivo* through a PA28 $\gamma$ -dependent pathway, suggesting that PA28 $\gamma$  plays a crucial role in the development of liver pathology induced by HCV infection.

## Materials and Methods

Histology and immunohistochemistry, real-time PCR, and detection of proteins modified by ROS are discussed in *SI Materials and Methods*.

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**Plasmids and Reagents.** Human PA28 $\gamma$  cDNA was isolated from a human fetal brain library (18). The gene encoding HCV core protein was amplified from HCV strain J1 (genotype 1b) (34) and cloned into pCAG-GS (35). Mouse cDNAs of RXR $\alpha$  and LXR $\alpha$  were amplified by PCR from the total cDNAs of the mouse liver. The RXR $\alpha$  and LXR $\alpha$  genes were introduced into pEF-FLAGGspGBK (36) and pcDNA3.1 (Invitrogen, Carlsbad, CA), respectively. The targeting fragment for human PA28 $\gamma$  knockdown (GGATCCGGTGGATCAGGAAGTGAAGTTCAAGAGACCTTCACTTCCTGATCCACCTTTTTGGAAAAGCTT) was introduced into the BamHI and HindIII sites of pSilencer 4.1 U6 hygro vector (Ambion, Austin, TX). Mouse anti-FLAG (M2) and mouse anti- $\beta$ -actin antibodies were purchased from Sigma (St. Louis, MO). Rabbit polyclonal antibody against synthetic peptides corresponding to amino acids 70–85 of PA28 $\gamma$  was obtained from AFFINITI (Exeter, U.K.). Horseradish peroxidase-conjugated goat anti-mouse and anti-rabbit IgGs were purchased from ICN Pharmaceuticals (Aurora, OH). Rabbit anti-HCV core protein was prepared by immunization with recombinant HCV core protein (amino acids 1–71), as described in ref. 24. Mouse monoclonal antibody to HCV core protein was kindly provided by S. Yagi (37). The plasmid for expression of HA-tagged ubiquitin was described in ref. 27.

**Preparation of PA28 $\gamma$ -Knockout HCV CoreTg Mice.** The generation of C57BL/6 mice carrying the gene encoding HCV core protein genotype 1b line C49 and that of PA28 $\gamma^{-/-}$  mice have been reported previously (22, 25). Both strains were crossed with each other to create PA28 $\gamma^{-/-}$  CoreTg mice. PA28 $\gamma^{-/-}$  CoreTg mice were identified by PCR targeted at the PA28 $\gamma$  or HCV core gene (22, 25). Using 1  $\mu$ g of genomic DNA obtained from the mouse tail, the PA28 $\gamma$  gene was amplified by PCR with the following primers: sense, PA28-3 (AGGTGGATCAGGAAGTGAAGCTCAA); and antisense, PA28 $\gamma$ -5c (CACCTCACTTGTGATCCGCTCTT-GAAAGAATCAACC). The targeted sequence for the PA28 $\gamma$ -knockout mouse was detected by PCR using the PA28-3 primer and the PAKO-4 primer (TGCAGTTCATTCAGGGCACCAGG-CAG). The transgene encoding HCV core protein was detected by PCR as described in ref. 25. The expression of PA28 $\gamma$  and HCV core protein in the livers of 6-month-old mice was confirmed by Western blotting with mouse monoclonal antibody to HCV core protein, clone 11-10, and rabbit antibody to PA28 $\gamma$ . Mice were cared for according to the institutional guidelines. The mice were given ordinary feed, CRF-1 (Charles River Laboratories, Yokohama, Japan), and they were maintained under specific pathogen-free conditions.

All animal experiments conformed to the Guidelines for the Care and Use of Laboratory Animals, and they were approved by the Institutional Committee of Laboratory Animal Experimentation (Research Institute for Microbial Diseases, Osaka University).

**Preparation of Mouse Embryonic Fibroblasts.** MEFs were prepared as described in ref. 22. MEFs were cultured at 37°C under an atmosphere of 5% CO<sub>2</sub> in Dulbecco's modified Eagle's medium (Sigma) supplemented with 10% FBS, penicillin, streptomycin, sodium pyruvate, and nonessential amino acids.

**Transfection and Immunoblotting.** Plasmid vectors were transfected into the MEFs and 293T cells by liposome-mediated transfection by using Lipofectamine 2000 (Invitrogen). The amount of HCV core protein in the liver tissues was determined by an ELISA as described in ref. 37. The cell lysates were subjected to SDS/PAGE (12.5% gel), and they were then transferred onto PVDF membranes. Proteins on the membranes were treated with specific antibody and Super Signal Femto (Pierce, Rockford, IL). The results were then visualized by using an LAS3000 imaging system (Fuji Photo Film, Tokyo, Japan). The method of immunoprecipitation test is described in ref. 18.

**Reporter Assay for *srebp-1c* Promoter Activity.** The genomic DNA fragment encoding the *srebp-1c* promoter region (located from residues -410 to +24) was amplified from a mouse genome. The fragment was introduced into the KpnI and HindIII sites of pGL3-Basic (Promega, Madison, WI), and it was designated as pGL3-*srebp-1c*Pro. The plasmids encoding RXR $\alpha$  and LXR $\alpha$  were transfected into MEFs together with pGL3-*srebp-1c*Pro and a control plasmid encoding *Renilla* luciferase (Promega). The total DNA for transfection was normalized by the addition of empty plasmids. Cells were harvested at 24 h posttransfection. The ligand of RXR $\alpha$ , 9-*cis*-retinoic acid (Sigma), and that of LXR $\alpha$ , 22(*R*)-hydroxycholesterol (Sigma) were added at a final concentration of 5  $\mu$ M each to the culture medium of 293T cells transfected with pGL3-*srebp-1c*Pro together with expression plasmids encoding RXR $\alpha$ , LXR $\alpha$ , and HCV core protein at 24 h posttransfection. Cells were harvested 24 h after treatment. Luciferase activity was measured by using the dual-luciferase reporter assay system (Promega). Firefly luciferase activity was standardized with that of *Renilla* luciferase, and the results are expressed as the fold increase in relative luciferase units.

**Electrophoresis Mobility Shift Assay (EMSA).** EMSA was carried out by using a LightShift Chemiluminescent EMSA kit (Pierce) according to the manufacturer's protocol. Nuclear extract of the cell lines and liver tissue was prepared with an NE-PER nuclear

and cytoplasmic extraction reagent kit (Pierce). Briefly, double-stranded oligonucleotides for EMSA were prepared by annealing both strands of each LXRE of the *srebp-1c* promoter (5'-GGACGCCCTAGTAACCCCGGC-3') (16). Both strands were labeled at the 5' ends with biotin. The annealed probe was incubated for 20 min on ice with nuclear extract (3  $\mu$ g of protein) in a reaction buffer containing 10 mM Tris-HCl (pH 7.5), 50 mM KCl, 1 mM DTT, 0.05  $\mu$ g/ $\mu$ l poly(dI-dC), 2.5% glycerol, 0.05% Nonidet P-40, and 0.1 nM labeled probe, with or without 1 mM nonlabeled probe. The resulting mixture was subjected to PAGE (5% gel) at 120 V for 30 min in 0.5 $\times$  TBE. The DNA-protein complex was transferred to a Hybond N+ membrane (Amersham, Piscataway, NJ), incubated with horseradish peroxidase-conjugated streptavidin, and visualized by using a LAS3000 imaging system.

**Statistical Analysis.** The results are expressed as the mean  $\pm$  SD. The significance of differences in the means was determined by Student's *t* test.

We thank H. Murase for secretarial work and D. C. S. Huang for providing the 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.

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CASE REPORT

## Fatal liver failure caused by reactivation of lamivudine-resistant hepatitis B virus: A case report

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Received: 2006-07-05 Accepted: 2006-08-29

**Key words:** Hepatitis B virus; Lamivudine; Polymerase; Interferon; Tyrosine-methionine-aspartate-aspartate

Suzuki Y, Yotsuyanagi H, Okuse C, Nagase Y, Takahashi H, Moriya K, Suzuki M, Koike K, Iino S, Itoh F. Fatal liver failure caused by reactivation of lamivudine-resistant hepatitis B virus: A case report. *World J Gastroenterol* 2007; 13(6):

<http://www.wjgnet.com/1007-9327/13/.asp>

### INTRODUCTION

Lamivudine is a nucleoside analogue that interrupts the reverse transcription of hepatitis B viral (HBV) pregenomic RNA. Lamivudine is effective for controlling chronic hepatitis B and currently recommended as the first line of treatment for chronic active hepatitis B<sup>[1,2]</sup>. Even for patients with decompensated liver cirrhosis, lamivudine improves liver function and extends transplantation free intervals<sup>[3,10]</sup>. Since more than 10% of patients with chronic HBV infection are estimated to develop liver cirrhosis and may eventually suffer from decompensated liver cirrhosis or hepatocellular carcinoma, the role of lamivudine in the treatment of advanced liver disease caused by chronic HBV infection is large<sup>[11-14]</sup>.

The major problems concerning lamivudine treatment are the viral and biochemical breakthroughs caused by drug resistance. Amino acid mutation in the highly conserved tyrosine-methionine-aspartate-aspartate (YMDD) motif can occur six months after treatment and often increases alanine aminotransferase (ALT) level. Although the increase is usually mild, a marked increase in ALT level leading to fatal hepatic failure has been reported<sup>[15-17]</sup>. Factors other than the YMDD motif mutation that are associated with the worsening of liver function remain to be clarified.

Here, we report a case of fatal hepatic failure caused by lamivudine-resistant HBV. A serial analysis of viral amino acid sequences indicated that the acquisition of mutations outside the YMDD motif might be related to the deterioration of the patient's condition.

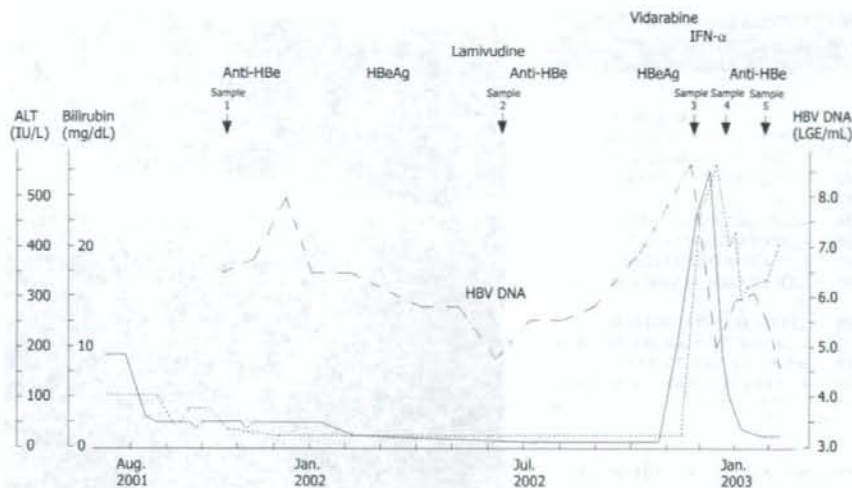
### CASE REPORT

A 57-year old man visited our hospital in September 2001 for the treatment of decompensated chronic hepatitis

### Abstract

We present a case of fatal liver failure caused by the activation of lamivudine-resistant hepatitis B virus (HBV) nine months after lamivudine treatment. A 57-year old man visited our hospital for the treatment of decompensated chronic hepatitis B. Lamivudine was started in December 2001. Subsequently, serum HBV was negative for HBV DNA with seroconversion from HBeAg to anti-HBe and improvement of liver function. However, HBV DNA and HBeAg were again detected in September 2002. He was complicated by breakthrough hepatitis and admitted to our hospital in November for severely impaired liver function. Vidarabine treatment was started and serum HBV DNA and alanine aminotransferase (ALT) decreased transiently. However, after the start of  $\alpha$ -interferon treatment, HBV DNA level increased and liver function deteriorated. He died 1 mo after admission. An analysis of amino acid sequences in the polymerase region revealed that rtM204I/V with rL80I/V occurred at the time of viral breakthrough. After the start of antiviral treatment, rL180M was detected in addition to rtM204I/V and rL80I/V, and became predominant in the terminal stage of the disease. HBV clone with a high replication capacity may be produced by antiviral treatment leading to the worsening of liver function. Antiviral therapy for patients with breakthrough hepatitis in advanced liver disease should be carefully performed.

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**Figure 1** Clinical course of our patient. HBV DNA level was quantified by transcription-mediated amplification assay. The levels of HBV DNA started to increase 8 mo after treatment with reappearance of HBeAg. Breakthrough hepatitis developed 12 mo after treatment. The timing of serum sample analysis for mutations is shown by the arrowhead.

B. In 1978, He was found to be positive for serum HBs antigen (HBsAg). In July 2001, he was admitted to a nearby hospital for ascites where he was diagnosed as having decompensated cirrhosis with exacerbated chronic hepatitis B. The symptomatic control of his ascites improved his general condition. For further treatment, he was referred to our hospital.

On his first visit, he showed no symptoms or signs of worsening hepatic failure or encephalopathy. No ascites or leg edema was observed. His bulbar conjunctiva was slightly jaundiced. Dilated vasculature was observed in his neck and chest. His ALT, total bilirubin and albumin were 50 IU/L, 3.1 mg/dL and 3.7 g/dL, and his prothrombin time was 76%. He was diagnosed as having liver cirrhosis with a Child-Pugh score of 8. He was negative for HBe antigen (HBeAg) and his HBV DNA level measured by transcription-mediated amplification and hybridization protection assay<sup>[18]</sup> was 106.5 genome copies/mL.

In November 2001, he was found to be positive for HBeAg and showed an increase in HBV DNA level. Because he had a history of decompensated chronic hepatitis B, lamivudine treatment (100 mg/d) was started in December. Figure 1 shows the clinical course. The high serum levels of bilirubin and ALT decreased and normalized within 6 mo after lamivudine treatment was started. The patient became negative for HBV DNA and HBeAg.

However, in September 2002, he was found to be positive for HBeAg again and showed an increase in HBV DNA level. In November 2002, he observed jaundice of his bulbar conjunctiva and was admitted to our hospital. Although he was alert, his bulbar conjunctiva and skin were jaundiced. His ALT, total bilirubin, were 474 IU/L, 11.4 mg/dL and 4.3 g/dL. His HBV DNA level was 108.6 genome copies/mL. He was diagnosed as having breakthrough hepatitis caused by lamivudine-resistant mutants of HBV. HBV with an amino acid substitution in the YMDD motif in the domain C of polymerase region was detected.

Because interferon is not indicated in patients with decompensated cirrhosis, vidarabine, which is effective for the control of active HBV infection<sup>[19-21]</sup>, was administered together with lamivudine under informed consent. Liver function improved transiently with a decrease in HBV DNA within 2 wk. As prolonged vidarabine administration may induce several complications<sup>[22]</sup>, vidarabine was switched to interferon- $\alpha$ . After the start of interferon- $\alpha$  treatment, HBV DNA level increased and liver function worsened. He died of hepatic failure and rupture of esophageal varices 1 mo after his admission.

The histopathology of the patient's liver after necropsy showed cirrhosis with zonal necrosis. Hepatocyte regeneration was scarce (Figure 2).

To elucidate the viral factors affecting early viral breakthrough and fatal outcome, amino acid sequences of the upstream polymerase region (aa 1-250) of HBV DNA in serum were examined at 5 points as shown in Figure 1. The methods were as follows.

First, DNA was extracted from 100  $\mu$ L of a serum sample using the QIAamp DNA blood mini kit (Qiagen Inc., Valencia, CA). Three fragments spanning the upper polymerase region of HBV DNA were amplified by nested PCR with the primers shown in Table 1. The first stage of amplification was carried out using a thermal cycler for 40 cycles (94°C for 1 min, 55°C for 1 min, 72°C for 1 min) in 100  $\mu$ L of reaction mixture containing 200 mmol/L dNTPs, 1.0 mmol/L each of the primers and 1  $\times$  PCR buffer [50 mmol/L KCl, 10 mmol/L Tris-HCl (pH 8.3), 1.5 mmol/L MgCl<sub>2</sub> and 0.001% (w/v) gelatin] and 2 units of Ampli-Taq polymerase gold (Perkin Elmer Cetus Corp., CT). Two microliters of the PCR products was subjected to the second stage of amplification under the same conditions as the first stage.

Second, PCR products were purified using Wizard PCR preps DNA purification resin (Promega, WI) and cloned into a plasmid vector using the TA cloning kit (PCR cloning kit Qiagen, CA). Four clones were selected from each plate, from which recombinant plasmid DNA was

**Table 1** Primers used for amplification and sequencing of polymerase region of HBV

Region 1		
Outer sense	nt 2222-2241	CTTACTTTTGGGAAGAGAAAC
Outer antisense	nt 2490-2509	CGACAGTAGAAGAATAAAG
Inner sense	nt 2222-2241	CTTACTTTTGGGAAGAGAAAC
Inner antisense	nt 2478-2497	GAATAAAGCCAGTAAAGTT
Region 2		
Outer sense	nt 2413-2434	GCGTCGCAGAAGATCTCAATC
Outer antisense	nt 2816-2835	GTCCCAAGAATATGGTGAC
Inner sense	nt 2434-2452	CTCGGAATCTCAATGTTAG
Inner antisense	nt 2816-2835	GTCCCAAGAATATGGTGAC
Region 3		
Outer sense	nt 2490-2509	CTTATTCTTCTACTGTACC
Outer antisense	nt 3121-3143	CGATTGGTGGAGGCAGGAGGAGG
Inner sense	nt 2637-2656	ATGCCTGCTAGGTTTTATCC
Inner antisense	nt 3121-3143	CGATTGGTGGAGGCAGGAGGAGG

purified using a commercially available kit (Plasmid midi kit, Qiagen, Valencia, CA). Nucleotide sequences were determined bidirectionally using the dye terminator cycle sequencing ready reaction kit (PE Applied Biosystems, CA) and the PCR primers. Sequencing was performed using an automated DNA sequencer (ABI 377; PE Applied Biosystems).

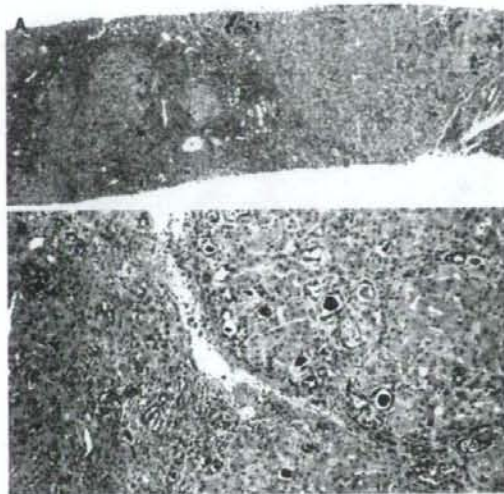
The determined amino acid sequences in the polymerase region are shown in Figure 3. No amino acid sequence changes were found at the start of lamivudine treatment. At the time of viral breakthrough, rtM204I with rtL80I became dominant. After the start of interferon treatment, rtM204I was replaced by rtM204V and rtL80I by rtL80V. At the final stage of the disease, mutation rtL180M appeared besides rtM204V and rtL80V.

## DISCUSSION

Lamivudine monotherapy is effective in suppressing HBV replication and ameliorating liver disease in chronic hepatitis B patients regardless of HBeAg positivity. A one-year study of HBeAg-positive chronic hepatitis B patients showed that 16% of these patients become seroconverted to anti-HBe and 72% of these patients showed normalization of their ALT levels<sup>[23]</sup>. Furthermore, treatment with lamivudine is associated with histologic improvement not only in terms of necroinflammatory score but also in terms of fibrosis score after long-term treatment<sup>[24]</sup>.

One advantage of lamivudine is that it can be used safely in patients with decompensated cirrhosis<sup>[5-10]</sup>. In contrast to IFN- $\alpha$ , lamivudine is well tolerated without any significant side effects even in patients with decompensated cirrhosis. Furthermore, lamivudine can improve liver function and survival prognosis.

However, the emergence of a drug-resistant mutant is a big problem in lamivudine treatment. A large-scale Asian study showed that lamivudine resistant HBV infection occurred in 23% of patients in year one and 65% of patients in year five. Hepatitis flares, which occurred more commonly in patients with lamivudine resistant mutations, occurred in 10% of patients in year one, and in 18% to 21% of patients in years two to five. Among patients with



**Figure 2** Histopathological findings of liver specimens. Irregularly-shaped parenchymal cells with massive necrosis (A) and scarce hepatocyte regeneration (B) surrounded by extensive fibrosis (A: HE  $\times$  20; B: HE  $\times$  80).

lamivudine resistant HBV infection, occurrence of hepatic decompensation increased significantly in patients with lamivudine resistant HBV infection for more than 4 years (from 0% to 6%)<sup>[25]</sup>. In this large-scale Asian study, liver-disease-related death occurred in two patients.

The prognosis of patients with lamivudine-resistant HBV infection, particularly those with advanced liver disease, may be determined by the timing and severity of breakthrough hepatitis. However, the viral factors that may influence the severity of this hepatitis remain to be clarified. A recent study indicated that patients with a normal ALT level even after the emergence of a YMDD motif mutant are characterized by HBeAg negativity during pretreatment, HBeAg loss during therapy, a longer duration from the commencement of therapy until the emergence of YMDD mutant, and lack of mixed-type YMDD mutants<sup>[26]</sup>. In contrast, patients with severely exacerbated hepatitis after the emergence of a YMDD mutant tend to have more substitutions in the reverse transcriptase (rt) region within the polymerase gene at the time of hepatitis exacerbation than those without hepatitis exacerbation<sup>[26]</sup>.

Our patient acquired amino acid mutations in the polymerase region one after the other. Amino acid changes in rtM204/I appeared at the time of viral breakthrough. After the initial treatment with vidarabine, rtM204/V substituted for rtM204/I in one of the four clones. During the interferon treatment, rtM204/V became predominant.

Another mutation observed in our patient was rtL80I/V. Ogata *et al.*<sup>[27]</sup> showed that rtL180M is accompanied with rtM204I in some patients with resistance to lamivudine. Because the mutation at aa position 80 was found at the same time as that at aa position 204 in our patient, it is not clear whether the mutation at aa position 80 affects the clinical course.

At the final stage of the disease with deterioration of





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S-Editor Wang GP L-Editor Wang XL E-Editor Lu W

## Review

# Drug resistance in antiviral treatment for infections with hepatitis B and C viruses

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Treatments for infections with hepatitis B and C viruses have recently developed markedly, and range from non-specific interferon-based treatments to specific antiviral treatments, such as those that inhibit hepatitis virus-coded protein production or activity. These developments have contributed to the achievement of excellent enhancement of the antiviral effect. On the other hand, the development of specific antiviral therapies has created unprecedented problems. Antiviral drug-resistant strains of viruses have emerged, leading to a poor prognosis for infected patients. Clarification of the mechanisms underlying the emergence of such resistance to drugs will be useful for the treatment of such patients. In this review, we outline pathological conditions associated with hepatitis B and C viruses and their treatments, and discuss the current situation and mechanisms underlying the emergence of antiviral drug-resistant strains.

**Key words:** Interferon, lamivudine, entecavir, adefovir, ribavirin

## Introduction

Infections with hepatitis B and C viruses (HBV and HCV, respectively) are a problem worldwide. Many patients are infected with HBV and HCV, and these infections are not only a major medical burden but also a socioeconomic burden because of their possible progression from chronic hepatitis to cirrhosis and hepatocellular carcinoma (HCC) if left untreated.<sup>1,2</sup> The treatments against these hepatitis viruses have been mainly nonspecific, based on the use of interferon (IFN). Specific antiviral drugs developed recently that inhibit

hepatitis viral replication, for example, by inhibition of reverse transcriptase in HBV, have shown remarkable efficacy.<sup>3,4</sup> However, these treatments have also turned out to be a double-edged sword because they have led to the emergence of strains resistant to these drugs. The emergence of antiviral drug-resistant strains of these viruses may hinder the development of treatments against them.

## HBV infection

HBV belongs to the family *Hepadnaviridae*. HBV is a DNA virus that has an approximately 3.2-kb circular incomplete double-stranded DNA genome. When it replicates, HBV forms DNA by using its own reverse transcriptase with RNA as a replicative intermediate. Worldwide, the distribution of HBV carriers and the incidence of HCC are closely correlated. The number of HBV carriers in Japan is estimated to be approximately one million, many of whom became infected via perinatal mother-to-child transmission. Hepatitis B e antigen (HBeAg) is a protein produced by the wild-type HBV strain as it replicates that appears in the blood. Generally, the presence of HBeAg indicates an abundance of the virus; and the detection of anti-HBe antibody often indicates a marked decrease in the HBV load.

HBV carriers are HBeAg-positive asymptomatic carriers (AsC) in the early stages of HBV infection. Their blood HBV level is very high in these stages. They can develop symptoms of hepatitis at any time of their life, but generally do between adolescence and their early 30s. At that time, the HBV load decreases markedly, and symptoms of hepatitis improve in 2 to 3 years in 80%–90% of HBV patients. Most of these patients then become negative for HBeAg and positive for the anti-HBe antibody. The annual incidence of seroconversion from being HBeAg-positive to anti-HBe antibody-

Received: February 21, 2007 / Accepted: February 25, 2007  
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positive has been reported to be approximately 5%.<sup>5,6</sup> However, symptoms of hepatitis persist in about 10%–20% of these patients even after seroconversion; such patients often develop cirrhosis and HCC.<sup>7</sup>

#### Treatment of HBV infection

There are several choices for treatment of chronic hepatitis B, but they all have limited efficacy. HBV elimination [i.e., serum HB surface antigen (HBsAg)-negative status] is difficult in HBV carriers. Seroconversion from HBeAg-positive to anti-HBe antibody-positive is generally the goal of HBV infection treatment. It should also be understood that many HBV AsCs do not need to or often must not undergo treatment with any anti-HBV agent.

In approximately 80% of patients with chronic hepatitis B, seroconversion occurs spontaneously. Consequently, chronic hepatitis B does not progress to cirrhosis in most chronic hepatitis B patients. The 15%–20% of HBV carriers who do not show seroconversion ultimately develop cirrhosis and/or HCC and should undergo antiviral treatment for chronic hepatitis B. IFN and reverse transcriptase inhibitors, including lamivudine, adefovir dipivoxil, and entecavir, have been approved for the treatment of chronic hepatitis B. Among these, lamivudine was the first used for chronic hepatitis B patients.

Lamivudine recipients are more likely than placebo recipients to show a histological response (52% vs. 23%,  $P < 0.001$ ), the disappearance of HBeAg in serum (32% vs. 11%,  $P = 0.003$ ), a sustained decrease in serum HBV DNA level to undetectable levels (44% vs. 16%,  $P < 0.001$ ), and a sustained normalization of the serum alanine aminotransferase (ALT) level (41% vs. 7%,  $P < 0.001$ ) after 52 weeks of treatment.<sup>8</sup>

Entecavir has an antiviral effect comparable to that of lamivudine. In one study of HBeAg-positive patients,<sup>9</sup> histological improvement after 48 weeks occurred in 226 of 314 patients in an entecavir-treated group (72%) and in 195 of 314 patients in a lamivudine-treated group (62%,  $P = 0.009$ ). More patients in the entecavir-treated group than in the lamivudine-treated group had undetectable serum HBV DNA levels according to a polymerase chain reaction (PCR) assay (67% vs. 36%,  $P < 0.001$ ), and normalization of ALT levels (68% vs. 60%,  $P = 0.02$ ). However, the seroconversion rate was not very high in either group.

#### Emergence of antiviral resistance in HBV infection

The treatment efficacy against HBV infection has improved, as mentioned above. The primary reason for chronic hepatitis B becoming resistant to treatment is the emergence of drug-resistant strains.

#### Mechanisms underlying development of resistance to IFN-based treatments

IFNs are administered in a wide range of doses according to various protocols for chronic hepatitis B. Such variation in protocols must be taken into account in determining the therapeutic efficacy of such drugs. Viral factors potentially involved in drug resistance include the HBV genotype and the presence of HBeAg, a precore gene mutation, or a core promoter mutation. HBeAg negativity, HBV genotypes C and D, precore gene 1896 mutation, and 1762/1764 mutations in the core promoter have been reported to be responsible for a poor response to IFN treatment. Strictly, these factors do not indicate "drug resistance" to IFN. The acquisition of the precore gene 1896 mutation also decreases the efficacy of IFN treatment.<sup>10</sup>

#### Mutation of the HBV polymerase domain

The HBV polymerase (*Pol*) gene is shown in Fig. 1. The Pol/RT region of this gene encodes HBV reverse transcriptase (RT). In HBV gene replication, reverse transcription from pregenomic RNA to viral gene DNA occurs, and reverse transcriptase is used in this process. The Pol/RT region is further divided into five domains from A to E. The Pol/RT active center is reported to be in domain C, domains B and E have been reported to be important for RNA template binding, and domains A and D for binding to nucleic acids.

Nucleic acid analog formulations are incorporated into the viral genome involved in reverse transcription instead of nucleic acids to inhibit viral replication competitively. However, if a Pol/RT gene mutation emerges, the nucleic acid analog formulation administered may be unable to inhibit viral replication because of interference with its binding to RT. Acquisition of this mutation of the Pol/RT gene thus results in the emergence of a drug-resistant viral strain. This mutation is shown in Fig. 1.

#### Resistance to lamivudine

Among nucleic acid analog formulations, lamivudine (LAM) has been used longest for the treatment of chronic hepatitis B, and its use continued until resistance to this drug emerged. Many factors underlying this resistance have been identified.

LAM resistance is caused by a mutation in which the 204th methionine (M) in the polymerase domain is replaced by valine (V) or isoleucine (I) (rtM204V/I). Because the site containing the 204th methionine is referred to as the YMDD motif, this mutation is also called the YVDD mutation or YIDD mutation. Another mutation associated with rtM204V/I is caused by replacement of the 180th leucine (L) by M (rtL180M).

rtM204V/I was detected in 10% of HBeAg-positive patients with chronic hepatitis B 24 weeks after the start