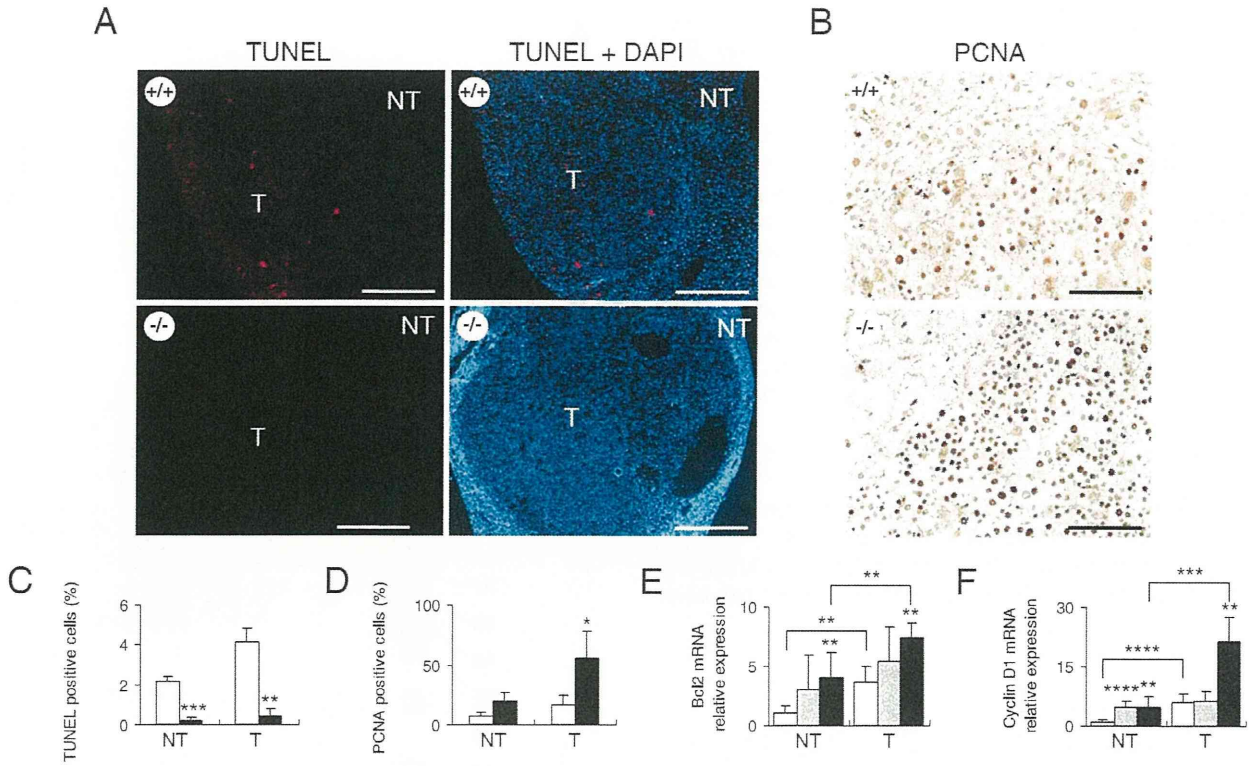

Figure 5. Tumor-bearing *Cygb*-deficient mice are associated with increased cancer cell proliferation and reduced apoptosis. **A:** Paraffin-embedded liver sections from wild-type (+/+) and homozygous (−/−) mice treated with 25-ppm DEN for 25 weeks were TUNEL labeled (**left**) and counterstained with DAPI (**right**). Apoptotic cells were present in the tumor (T) area in wild-type mice. NT, nontumor area. Scale bar = 400 μm. **B:** Paraffin-embedded liver sections were stained with PCNA. Scale bar = 100 μm. The frequency of apoptotic (**C**) or proliferate (**D**) cells was determined by counting TUNEL- or PCNA-positive cells, respectively (cells with the nucleus stained dark brown in the case of PCNA), in at least 1000 cells from each liver ($n = 3$). Expression levels of Bcl-2 (**E**) and cyclin D1 (**F**) mRNA in the NT ($n = 7$ to 12) and T ($n = 3$ to 5) areas from 25-ppm DEN-treated mice were determined by RT-qPCR and normalized to GAPDH. $Cygb^{+/+}$ (white bars), $Cygb^{+/-}$ (gray bars), and $Cygb^{-/-}$ (black bars) mice. Values are given as the mean ± SD of all experiments. $^{*}P < 0.05$, $^{**}P < 0.01$, $^{***}P < 0.001$, and $^{****}P < 0.0001$.

amined the effects of *Cygb* deficiency on the major pathways implicated in liver cancer.[30] As expected, *Cygb* loss was associated with an increase in both Akt phosphorylation and abundance in the livers (Figure 6A). This observation was also evident for Erk signaling (Figure 6, A and B). Consistent with increased Erk phosphorylation, *Cygb*-deficient mice exhibited increased expression of cyclin D1 (Figure 6A), and Jun and Fos mRNA in nontumor and tumor areas, relative to wild type (Figure 6C). These results suggested that the Akt and Erk pathways are activated in response to *Cygb* deficiency. The increased levels of Akt and Erk activation correlated with a marked elevation of IL-6 mRNA in both nontumor and tumor areas in *Cygb*-deficient mice (Figure 6D). IL-6 is a tumor-promoting cytokine that is required for Erk activation and contributes to alterations in Akt signaling.[31] Knowing that IL-6 functions as a downstream mediator for both IL-1 and tumor necrosis factor-α,[32] we examined the expression of these two cytokines. Remarkably, IL-1β and Tnfα levels (Figure 6D) increased 10- and 30-fold, respectively, at the mRNA level in the nontumor area of the liver and increased further in the tumors, relative to wild type. *Cygb*-deficient mice also had increased expression of Tgfβ3 mRNA (Figure 6D). These data suggest that *Cygb* loss can trigger inflammation and lead to the long-term elevation of tumor-promoting cytokines, resulting in the development of tumors.

Nitrotyrosine Accumulation in the Livers of DEN-Treated Cygb*-Deficient Mice*

Long-term administration of DEN has induced the expression of the inducible isoform of NO synthase and 3-nitrotyrosine, a marker of peroxynitrite formation, in preneoplastic and neoplastic rat liver tissues.[33] In this study, we detected the overproduction of nitrotyrosine in tumor and nontumor liver tissues of *Cygb*-deficient mice, compared with wild-type mice, as shown by IHC (Figure 7A) and immunoblot analyses (Figure 7B). These results indicate the high production of NO, together with superoxide, in *Cygb*-deficient mice.

Dysregulation of Genes Associated with Cell Proliferation and Differentiation in Cygb*-Deficient Mice*

To further screen for cellular alterations caused by *Cygb* gene disruption, we compared gene expression profiles between *Cygb*-deficient mice and their wild-type counterparts after 25-ppm DEN treatment for 25 weeks. We

observed the altered expression of cancer genes, including p53, cyclin D2, Pak1 (p21-activated kinase), Src, Cdkn2a, and Cebpa (CCAAT/enhancer-binding protein α) (data not shown). We examined in detail the mRNA levels of these genes by RT-qPCR. Consistent with the high rate of cellular proliferation in the liver of *Cygb*-deficient mice (Figure 5, B and D), we observed overexpression of cyclin D2 (Figure 8A) and p53 (Figure 8B), which have displayed high expression in astrocytomas, a type of brain tumor.[34] Pak1 promotes malignant tumor progression, and the Src proto-oncogene has shown increased expression in human skin tumors and leukemia.[35–38] In this study, we found that the mRNA expression of Pak1, in addition to Src, increased fivefold in the livers of $Cygb^{-/-}$ mice, relative to the wild type (Figure 8, C and D).

Cdkn2a, a tumor suppressor that negatively regulates the cell cycle, displayed increased expression at the mRNA level in the livers of *Cygb*-deficient mice (Figure 8E), consistent with other studies[39,40] on sarcomas and lung tumors.

Cebpa has the ability to inhibit proliferation, particularly in hepatocytes.[41,42] Down-regulation of CEBPA has been reported in human myeloid leukemia.[43] Consistent with these studies, our results showed decreased expression of Cebpa mRNA in the liver of *Cygb*-deficient mice, relative to the wild type (Figure 8F).

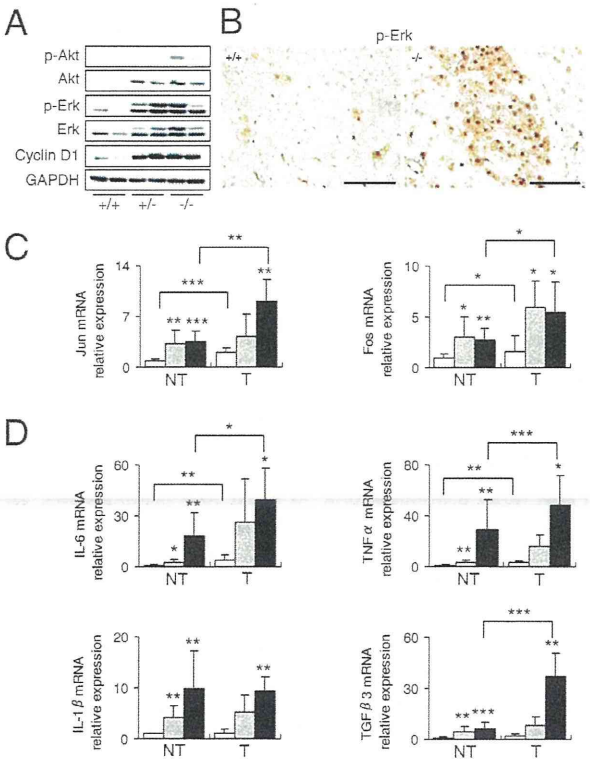

Figure 6. Tumor-bearing *Cygb*-deficient mice exhibited elevated phosphorylated Akt (p-Akt), phosphorylated Erk (p-Erk), and inflammation. *Cygb*-deficient mice from Figure 2 were subjected to additional biochemical and gene expression analyses. **A:** The liver was lysed and gel separated, and the levels of p-Akt, p-Erk, total Akt, total Erk, and cyclin D1 were examined by immunoblot analyses. All blots were reprobed with anti-GAPDH as a loading control. **B:** Paraffin-embedded liver sections were stained for phosphorylated Erk. Scale bar = 100 μm. **C** and **D:** Relative mRNA levels of Jun and Fos (**C**) and IL-6, Tnfα, IL-1β, and Tgfβ3 (**D**) in the nontumor (NT; n = 7 to 12) and tumor (T; n = 3 to 5) areas of the liver were determined by RT-qPCR and normalized to GAPDH. $Cygb^{+/+}$ (white bars), $Cygb^{+/-}$ (gray bars), and $Cygb^{-/-}$ (black bars) mice. Values are given as the mean ± SD of all experiments. $^{*}P < 0.05$, $^{**}P < 0.01$, and $^{***}P < 0.001$.

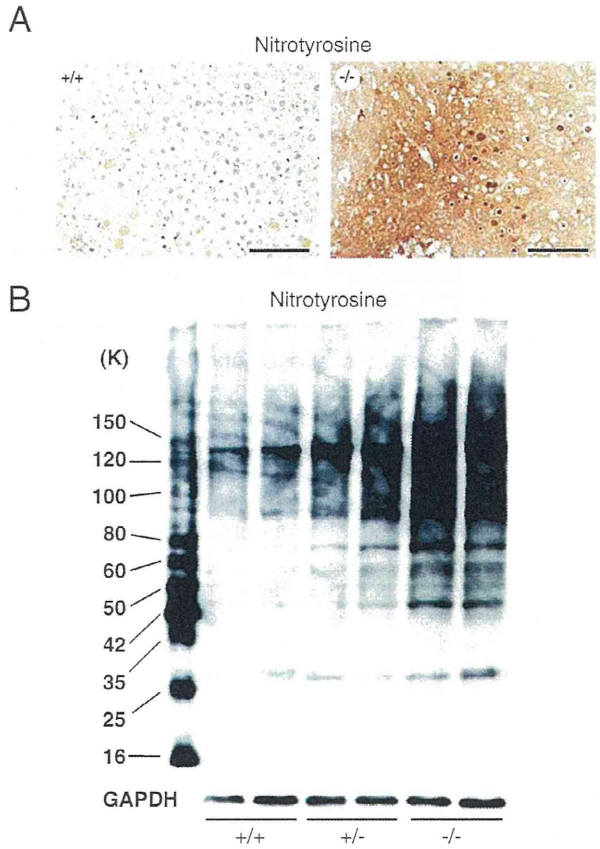

Figure 7. Peroxynitrite formation in the livers of *Cygb*-deficient mice. **A:** Paraffin-embedded liver sections from wild-type (+/+) and homozygous (−/−) mice treated with 25-ppm DEN for 25 weeks were stained with antinitrotyrosine. Nitrotyrosine-containing proteins were strongly expressed in the cytoplasm and nuclei of cancer cells in the tumor area, particularly in the inclusions of cancer cells. Scale bar = 100 μm. **B:** Protein homogenates of liver tissues from $Cygb^{+/+}$, $Cygb^{+/-}$, and $Cygb^{-/-}$ mice treated with 25-ppm DEN for 25 weeks were subjected to immunoblot detection for nitrotyrosine. GAPDH was used as a loading control. K, kDa (molecular mass).

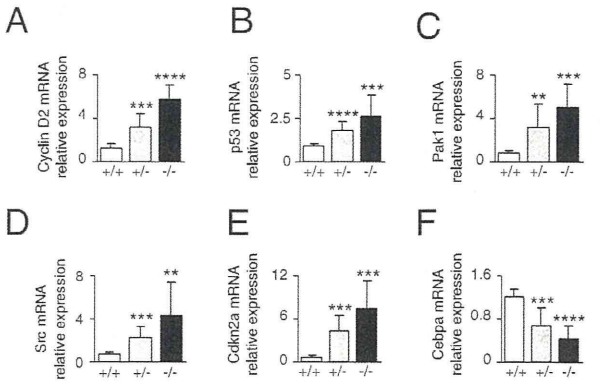

Figure 8. Altered regulation of cancer genes in *Cygb*-deficient mice. RT-qPCR analysis of cell growth–related gene transcripts cyclin D2 (**A**), p53 (**B**), and Pak1 (**C**) and cell differentiation and apoptosis-related gene transcripts Src (**D**), Cdkn2a (**E**), and Cebpa (**F**) in liver from mice treated with 25-ppm DEN for 25 weeks (n = 7 to 12). Levels are normalized to GAPDH. $Cygb^{+/+}$ (white bars), $Cygb^{+/-}$ (gray bars), and $Cygb^{-/-}$ (black bars) mice. Values are given as the mean ± SD of all experiments. $^{**}P < 0.01$, $^{***}P < 0.001$, and $^{****}P < 0.0001$.

Discussion

In the present study, we showed that loss of *Cygb* in C57BL/6J mice markedly increased their susceptibility to DEN-induced tumorigenesis. In the absence of *Cygb*, liver tumors developed earlier, were larger, and were more numerous compared with wild-type mice. By administering low-dose DEN to adult mice (0.05 ppm), which failed to induce liver cancer in wild-type mice, we observed the tumor-promoting effects of *Cygb* deficiency.

We observed high levels of Cygb expression in hepatic stellate cells, a liver-specific pericyte, from which Cygb was originally discovered by proteomic analysis of primary cultured rat cells and other stromal cells in the visceral organs, including the pancreas, gut, spleen, lung, and kidney.[1,4] These stromal cells are pericytes localized around the capillaries of the organs that are capable of vitamin A storage. Thus, we propose that Cygb may be an indicator of a vitamin A–storing phenotype of myofibroblasts of endoderm origin. However, as previously reported,[1,4,5] Cygb is ubiquitously expressed in all body organs in human, as in mice and rats. At the mRNA level, high expression is evident in the adult human heart and liver; modest expression is evident in the brain, kidney, trachea, and placenta; and low expression is evident in the adult skeletal muscle.[44] Several cancer cell lines, including HepG2 cells,[44] the NCI-H2228 lung cancer cell line, and HCC 1569 breast cancer cells,[19] also display CYGB mRNA expression. These observations indicate the role of Cygb in the regulation of cellular function originating from the epithelia. In this context, cancer development in the liver and lungs in $Cygb^{-/-}$ mice is anticipated. However, the role of mesenchymal cells that express Cygb highly in tumor development should be further evaluated because these myofibroblasts represent important environmental factors during tumor formation.

Cygb expression is augmented under hypoxia in the liver, heart, brain, and skeletal muscle and in HN33 cells (an immortalized mouse hippocampal cell line), BEAS-2B cells (a transformed human bronchial epithelial cell line), and HeLa cells (a human cervix carcinoma cell line).[16] Overexpression of Cygb protects mouse neuroblastoma N2a cells and human neuroblastoma SH-SY5Y cells under H_2O_2 exposure and the human neuronal cell line TE671 under prooxidant Ro19-8022 stimulation.[11,12,44] Overexpression of Cygb in the liver, induced by adeno-associated–virus-induced transfection, protects the liver from oxidative injury.[13] Conversely, the role of Cygb as an NO scavenger in rat hepatocytes and NIH3T3 fibroblasts may protect cells from NO-induced toxicity.[8,33] These reports and our findings regarding the accumulation of nitrotyrosine protein adducts in *Cygb*-deficient mice indicate the cytoprotective and antioxidative properties of Cygb.

Several tumor suppressor genes are located in both arms of chromosome 17. *TP53*, a known tumor suppressor gene at 17p13.1, is one of the most frequently mutated genes in cancers, including hepatocellular carcinoma.[45] *BRCA1* (breast cancer 1, early onset) at 17q12 is a human tumor suppressor gene encoding the breast cancer type 1 susceptibility protein,[46] which is present in the breast and other tissues, aiding the repair of damaged DNA and the destruction of the cell when DNA cannot be repaired. If *BRCA1* is damaged, cells duplicate uncontrollably, leading to cancer. Other known breast cancer–associated genes include *septin*, *DMC1*, and *HER2/ErbB2*.[47,48] Because *CYGB* exists on chromosome 17q25, genes on this chromosome appear commonly in the tumorigenesis of epithelial cells and mutation or epigenetic modification of these genes appears to trigger malignant transformation.

Clinically, liver cancer develops from a fibrotic liver, with chronic trauma induced by alcohol abuse and hepatitis virus B/C infection.[49] Chronic inflammation offers an appropriate environment for cancer development, by producing multiple growth factors, extracellular matrices, and neovascularization involving local hypoxia.[50] In this context, the augmented occurrence of pericellular fibrosis and fibrotic reactions (Figure 4, C–E) in *Cygb* deficiency may be involved in the development of liver cancer.

In conclusion, to our knowledge, this is the first report that *Cygb* deficiency induces susceptibility to cancer development in the liver and lungs of mice receiving DEN treatment. Thus, *Cygb*-deficient mice may provide a useful animal model to study cancer development in the liver and lungs; globins, such as Cygb, may shed new light on the biological features of organ carcinogenesis.

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Rapid Emergence of Telaprevir Resistant Hepatitis C Virus Strain from Wildtype Clone *In Vivo*

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Telaprevir is a potent inhibitor of hepatitis C virus (HCV) NS3-4A protease. However, the emergence of drug-resistant strains during therapy is a serious problem, and the susceptibility of resistant strains to interferon (IFN), as well as the details of the emergence of mutant strains *in vivo*, is not known. We previously established an infectious model of HCV using human hepatocyte chimeric mice. Using this system we investigated the biological properties and mode of emergence of mutants by ultra-deep sequencing technology. Chimeric mice were injected with serum samples obtained from a patient who had developed viral breakthrough during telaprevir monotherapy with strong selection for resistance mutations (A156F [92.6%]). Mice infected with the resistant strain (A156F [99.9%]) developed only low-level viremia and the virus was successfully eliminated with interferon therapy. As observed in patients, telaprevir monotherapy in viremic mice resulted in breakthrough, with selection for mutations that confer resistance to telaprevir (e.g., a high frequency of V36A [52.2%]). Mice were injected intrahepatically with HCV genotype 1b clone KT-9 with or without an introduced resistance mutation, A156S, in the NS3 region, and treated with telaprevir. Mice infected with the A156S strain developed lower-level viremia compared to the wildtype strain but showed strong resistance to telaprevir treatment. Although mice injected with wildtype HCV showed a rapid decline in viremia at the beginning of therapy, a high frequency (11%) of telaprevir-resistant NS3 V36A variants emerged 2 weeks after the start of treatment. *Conclusion:* Using deep sequencing technology and a genetically engineered HCV infection system, we showed that the rapid emergence of telaprevir-resistant HCV was induced by mutation from the wildtype strain of HCV *in vivo*. (HEPATOLOGY 2011;54:781-788)

Chronic hepatitis C virus (HCV) infection is a leading cause of cirrhosis, liver failure, and hepatocellular carcinoma.[1,2] The current standard treatment for patients chronically infected with HCV is the combination of peg-interferon (PEG-IFN) and ribavirin (RBV).[3-5] However, this treatment results in sustained viral response (SVR), defined as negative for HCV RNA 24 weeks after cessation of the therapy, in only about 50% of patients with genotype 1 HCV infection with high viral loads.[3-5] Given the low

Abbreviations: HCV, hepatitis C virus; HSA, human serum albumin; PEG-IFN, peg-interferon; RBV, ribavirin; RT-PCR, reverse transcript-polymerase chain reaction; SCID, severe combined immunodeficiency; SVR, sustained viral response; uPA, urokinase-type plasminogen activator.

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Potential conflict of interest: E.I., N.K., I.Y. are employees of Mitsubishi Tanabe Pharma Corp. The other authors have nothing to declare.

effectiveness of the current therapy, many molecules have been screened for antiviral activity against HCV for use in development of novel anti-HCV therapies. A number of new selective inhibitors of HCV proteins, the so-called STAT-C (specifically targeted antiviral therapy for HCV) inhibitors, are currently under development. Telaprevir is a reversible, selective, specific inhibitor of the HCV NS3-4A protease that has shown potent antiviral activity in HCV replicon assays.[6] Although the antiviral effect of telaprevir is quite potent, monotherapy using these drugs results in rapid emergence of drug-resistant strains.[7,8] Accordingly, these drugs are used in combination with pegylated-IFN and ribavirin for chronic hepatitis C patients. Because the HCV virus replicates rapidly and RNA polymerase lacks a proofreading system, HCV viral quasispecies can emerge *de novo*, and some of these variants may confer resistance. Although a resistant variant is initially present at low frequency, it may quickly emerge as the dominant species during antiviral treatment.[9,10] Resistant clones against HCV NS3-4A protease inhibitors have reportedly been induced in replicon systems.

The immunodeficient urokinase-type plasminogen activator (uPA) mouse permits repopulation of the liver with human hepatocytes, resulting in human hepatocyte chimeric mice that are able to develop HCV viremia after injection of serum samples positive for the virus.[11] We and other groups have reported that the human hepatocyte chimeric mouse is useful for evaluating the effect of NS3-4A protease inhibitor.[12,13] Using this mouse model, we developed a reverse genetics systems for HCV.[14,15] This system is useful to study characteristics of HCV strains with various substitutions of interest because the confounding effects of quasispecies can be minimized. Using ultra-deep sequencing technology, we demonstrate the rapid emergence of telaprevir resistance in HCV as a result of mutation from wildtype strain using genetically engineered HCV-infected human hepatocyte chimeric mice.

Materials and Methods

Animal Treatment. Generation of the uPA$^{+/+}$/SCID$^{+/+}$ mice and transplantation of human hepatocytes were performed as described recently by our group.[16] All mice were transplanted with frozen human hepatocytes obtained from the same donor. Mice received humane care and all animal protocols were performed in accordance with the guidelines of the local committee for animal experiments. Infection, extraction of serum samples, and sacrifice were performed under ether anesthesia. Mice were injected either intravenously with HCV-positive human serum samples or intrahepatically with *in vitro*-transcribed genotype 1b HCV RNA. HCV-infected mice were administered either perorally with 200-300 mg/kg of telaprevir (VX950; MP424; Mitsubishi Tanabe Pharma, Osaka, Japan) twice a day or intramuscularly with 1,500 IU/g of IFN-alpha (Dainippon Sumitomo Pharma, Tokyo). The telaprevir dose was determined in a previous study in which this dosage range was found to yield serum concentrations equivalent to treated human patients.[13]

Human Serum Samples. After obtaining written informed consent, human serum samples containing genotype 1b HCV were obtained from two patients with chronic hepatitis. The individual serum samples were divided into aliquots and stored separately in liquid nitrogen until use. The study protocol conforms to the ethical guidelines of the 1975 Declaration of Helsinki and was approved *a priori* by the Institutional Review Committee.

HCV RNA Transcription and Inoculation into Chimeric Mice. We have previously established an infectious genotype 1b HCV clone HCV-KT9 derived from a Japanese patient with severe acute hepatitis (GenBank access. no. AB435162).[15] We cloned this HCV complementary DNA (cDNA) into plasmid pBR322 under a T7 RNA promoter to create the plasmid pHCV-KT9. Ten μg of plasmid DNA, linearized by *Xba*I (Promega, Madison, WI) digestion, were transcribed in a 100 μL reaction volume with T7 RNA polymerase (Promega) at 37°C for 2 hours and analyzed by agarose gel electrophoresis. Each transcription mixture was diluted with 400 μL of phosphate-buffered saline (PBS) and injected into the livers of chimeric mice.[15] The QuikChange site-directed mutagenesis kit (Stratagene, Foster City, CA) was used to introduce a substitution at amino acid 156 of the NS3 region (A156S).

RNA Extraction and Amplification. RNA was extracted from serum samples by Sepa Gene RV-R (Sankojunyaku, Tokyo), dissolved in 8.8 μL RNase-free H_2O, and reverse transcribed using a random primer (Takara Bio, Shiga, Japan) and M-MLV reverse transcriptase (ReverTra Ace, Toyobo, Osaka, Japan) in a 20-μL reaction mixture according to the instructions provided by the manufacturer. Nested polymerase chain reaction (PCR) and quantitation of HCV by Light Cycler (Roche Diagnostic, Japan, Tokyo) were performed as reported.[15]

Ultra-Deep Sequencing. We adapted multiplex sequencing-by-synthesis to simultaneously sequence

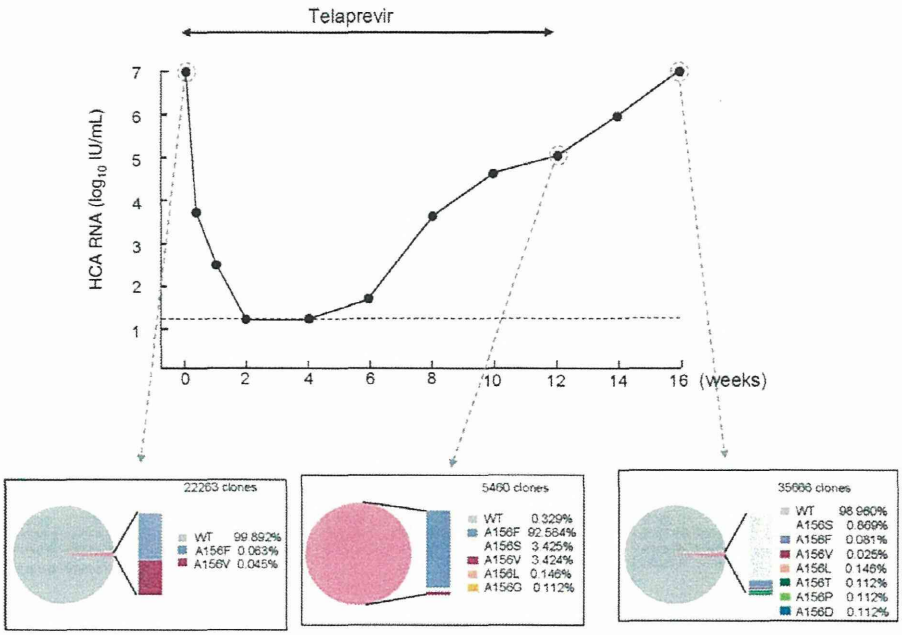

Fig. 1. Changes in serum HCV RNA levels in a telaprevir-treated chronic hepatitis C patient. A 55-year-old woman infected with genotype 1b HCV was treated with 750 mg of telaprevir every 8 hours for 12 weeks. Serum HCV RNA (upper panel) and the amino acid (aa) frequencies at aa156 in the HCV NS3 region by ultra-deep sequencing at the indicated times are shown. The horizontal dotted line indicates the detectable limit (1.2 log copy/mL).

multiple genomes using the Illumina Genome Analyzer. Briefly, cDNA was fragmented using sonication and the resultant fragment distribution was assessed using the Agilent BioAnalyzer 2100 platform. A library was prepared using the Multiplexing Sample Preparation Kit (Illumina, CA). Imaging analysis and base calling were performed using Illumina Pipeline software with default settings.[17-23] The N-terminal 543 nucleotides of NS3 protease were analyzed. This technique revealed an average coverage depth of over 1,000 sequence reads per basepair in the unique regions of the genome. Read mapping to a reference sequence was performed using Bowtie.[24] Because of the short 36 nucleotide read length, mapping hypervariable regions with multiple closely spaced variants against a reference sequence yields poor coverage. Therefore, common variants were identified by relaxing the mismatch settings as well as using *de novo* assembly using ABySS.[25] Multiple alternative reference sequences were included to improve coverage in variable regions. Codon counts were merged and analyzed using R v. 2.12.

Results

Emergence of a Telaprevir-Resistant Variant in a Hepatitis C Patient Treated with Telaprevir and Analysis of the A156F Mutation. A 55-year-old woman infected with genotype 1b HCV was treated with 750 mg of telaprevir every 8 hours for 12 weeks (Fig. 1). After 1 weeks of treatment, serum HCV RNA titer decreased below the detectable limit (1.2 log copy/mL). However, HCV RNA titer became positive by week 4. By week 12, HCV RNA titer had increased to 4.8 log copy/mL and telaprevir treatment was discontinued. Because direct sequence analysis showed an A156F mutation in the NS3 region in the serum samples at 12 weeks, we performed ultra-deep sequence analysis and confirmed the high frequency (92.5%) of A156F mutation. Four weeks after cessation of treatment (at 16 weeks), sequence analysis revealed that the major strain had reverted to wildtype (99%). To analyze the replication ability and the susceptibility of the A156F mutation to telaprevir, 100 μL serum samples containing 10^4 copies of HCV obtained at week 12 were injected into human hepatocyte chimeric mice. Two wildtype HCV-inoculated mice became positive for HCV RNA 2 weeks after inoculation and serum HCV RNA titer increased to high levels (7.6 and 7.8 log copy/mL, respectively) at 6 weeks after inoculation (Fig. 2). In contrast to wildtype HCV-infected mice, a mouse inoculated with serum containing the A156F mutant developed measurable viremia at 4 weeks postinoculation, although serum HCV RNA titer remained low at 6 weeks (5.2 log copy/mL). Eight weeks after inoculation ultra-deep sequence analysis showed a high frequency (99.9%) of A156F mutation. From this point the mouse was administrated 200 mg/kg of telaprevir perorally twice a day for 4 weeks. However, this treatment resulted in no reduction in serum HCV RNA level. During the observation period the A156F mutation remained at

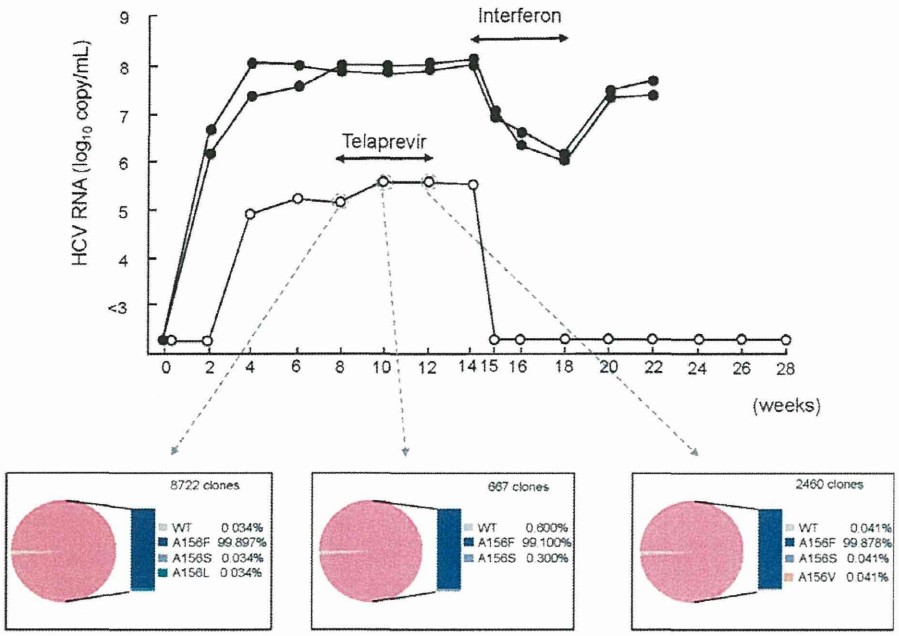

Fig. 2. Changes in serum virus titers in HCV-infected mice. Mice were injected with either wildtype (closed circles) or A156F-mutated HCV serum samples (obtained from an HCV-infected patient who received telaprevir monotherapy for 12 weeks; see Fig. 1) (open circles). Six weeks after injection the A156F mutant mouse was treated with 200 mg/kg of telaprevir orally twice a day for 4 weeks and injected intramuscularly with 1,500 IU/g/day of interferon-alpha for 4 weeks. Serum HCV RNA (upper panel) and amino acid (aa) frequencies at aa156 in the HCV NS3 region by ultra-deep sequencing at the indicated times are shown.

high frequency (>99%). To analyze the susceptibility of the A156F mutation to IFN, wildtype or A156F-mutated HCV-infected mice were treated with 1,500 IU/g/day of IFN-alpha for 4 weeks. Treatment resulted in only a two log reduction in HCV RNA level in wildtype HCV-infected mice. In contrast, serum HCV RNA titer decreased below the detectable limit 1 week after treatment in an A156F-infected mouse. Ten weeks after cessation of IFN-treatment (at week 28), HCV RNA in the mouse serum remained undetectable, suggesting that HCV RNA was eliminated. These results demonstrate that the A156F variant is associated with telaprevir-resistance, but the mutant has low replication ability and a high susceptibility to IFN.

Effect of Telaprevir on HCV-Infected Mice and Sequence Analysis of NS3 Region. Next we investigated the effect of telaprevir on wildtype HCV-infected mice. Two chimeric mice were inoculated intravenously with serum samples containing 10^5 copies of HCV obtained from an HCV-positive patient (Fig. 3). Six weeks after inoculation both mice were administered 200 mg/kg of telaprevir perorally twice a day for 4 weeks. Serum HCV RNA titer in both mice rapidly decreased; however, in one of the mice HCV RNA titer increased again 3 weeks after the start of treatment. Ultra-deep sequence analysis of the NS3 region showed that following the start of telaprevir administration the frequency of the V36A mutation increased from 18% at 2 weeks to 52% at 4 weeks, at which point it was accompanied by an increase in the HCV RNA titer. Two weeks after cessation of telaprevir treatment (at week 12), ultra-deep sequence analysis revealed that the frequency of the V36A mutant had decreased to 13% and the frequency of the wildtype HCV had increased to 84%, although the HCV RNA titer increased only slightly.

Intrahepatic Injection of HCV-KT9-Wild RNA and KT9-NS3-A156S RNA into Human Hepatocyte Chimeric Mice. We previously established an infectious genotype 1b HCV clone, HCV-KT9 (HCV-KT9-wild).[15] We created a telaprevir-resistant HCV clone by introducing an A156S amino acid substitution in the NS3 region of HCV-KT9 (KT9-NS3-A156S) (Fig. 4A). Using wildtype and telaprevir-resistant clones we investigated the replication ability *in vivo*. Mice were injected intrahepatically with 30 μg of *in vitro*-transcribed HCV-KT9-wild RNA or KT9-NS3-A156S RNA. Mice injected with HCV-KT9-wild developed measurable viremia at 2 weeks postinoculation and by 4 weeks postinoculation HCV RNA had reached 10^7 copy/mL (Fig. 4B). On the other hand, mice injected with KT9-NS3-A156S developed measurable viremia at 4 weeks postinoculation but maintained only low levels of viremia. These results suggest that the telaprevir-resistant HCV clone has a lowered replication ability compared to the wildtype HCV clone *in vivo*.

Treatment with Telaprevir and Analysis of Mutagenesis in Mice. Two mice infected with HCV-KT9-wild and one mouse infected with KT9-NS3-A156S were treated with 200 mg/kg of telaprevir twice a day for 2 weeks (Fig. 5A), resulting in 1.4 and 2.7 log

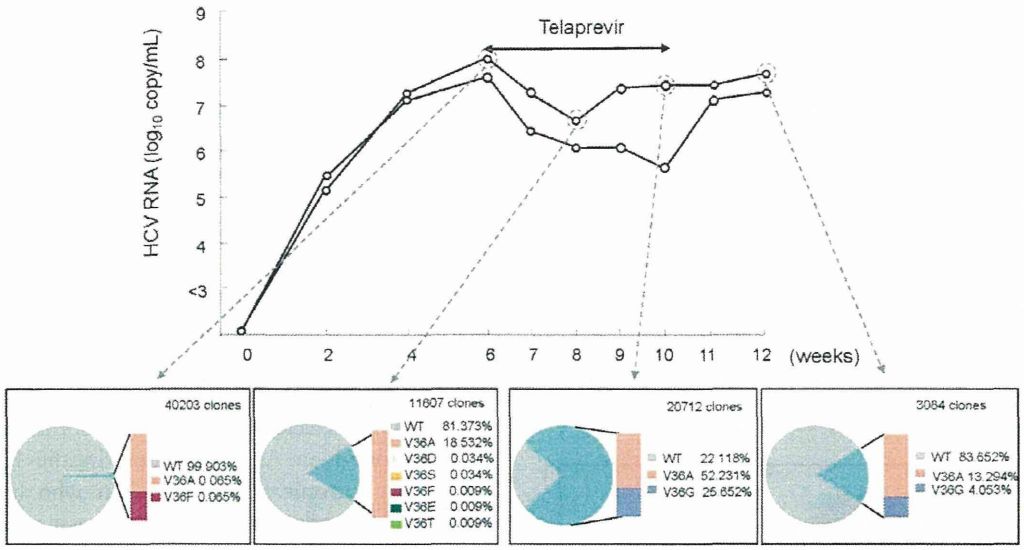

Fig. 3. Treatment with telaprevir in wildtype HCV-infected mice. Two mice were injected intravenously with 50 μL of HCV-positive human serum samples. Six weeks after HCV injection mice were treated with 200 mg/kg of telaprevir orally twice a day for 4 weeks. Serum HCV RNA (upper panel) and amino acid (aa) frequencies at aa36 in the HCV NS3 region by ultra-deep sequencing at the indicated times are shown.

reductions in HCV RNA level in the two wildtype HCV-infected mice. In contrast, only a 0.6 log reduction was observed in the KT9-NS3-A156S-infected mouse. These results demonstrate that our human hepatocyte chimeric mouse model infected with *in vitro*-transcribed HCV RNA provides an effective system for analysis of the susceptibility of HCV mutants to antiviral drugs. Interestingly, ultra-deep sequence analysis showed a rapid emergence of a V36A variant in the NS3 region in mouse serum 2 weeks after treatment (Fig. 5B). Four weeks after cessation of treatment (at week 6) the frequency of the V36A variant had decreased. Mice were then treated with 300 mg/kg of telaprevir twice a day for 4 weeks, which resulted in an elevated frequency of V36A variants at 1 (at week 7, 5.4%) and 4 weeks (at 10 week, 41.8%) after treatment and no reduction in serum HCV RNA level. These results suggest that telaprevir-resistant mutations emerged *de novo* from the wildtype strain of HCV, presumably through error-prone replication and potent selection for telaprevir escape mutants. During the telaprevir treatment period no increases of HCV RNA titers in these mice were observed, probably due to the low frequency of the resistant strain.

Discussion

Telaprevir is a peptidomimetic inhibitor of the NS3-4A serine protease that is currently undergoing clinical evaluation. Despite its effectiveness against HCV, some patients have shown a rapid viral breakthrough during the first 14 days of treatment.[26] Population sequencing of the viral NS3 region identified a number of mutations near the NS3 protease catalytic

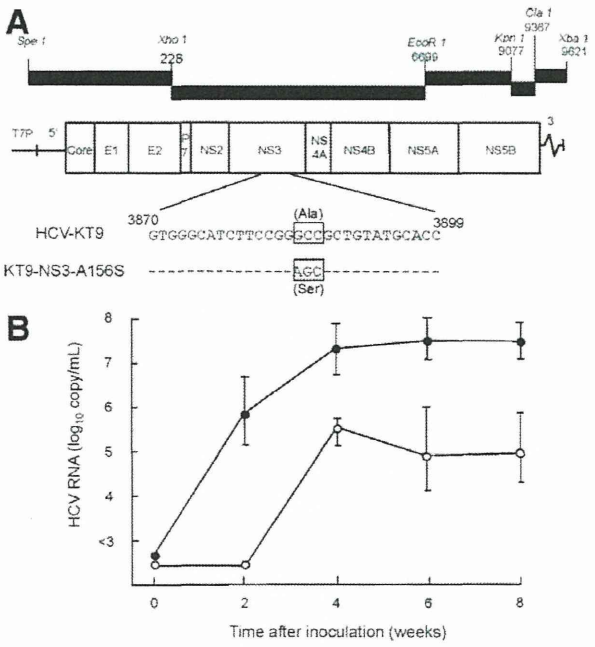

Fig. 4. Intrahepatic injection of *in vitro* transcribed HCV-KT9 RNA and KT9-NS3-A156S RNA into human hepatocyte chimeric mice. (A) The schematic of infectious genotype 1b HCV clones, HCV-KT9 and KT9-NS3-A156S. Boxes indicate codons at amino acid 156 in HCV NS3 region. Ala, alanine; Ser, serine. (B) Changes in serum levels of HCV RNA in mice intrahepatically injected with either HCV-KT9 RNA (closed circles) or KT9-NS3-A156S RNA (open circles). Data are represented as the mean ± SD of three mice.

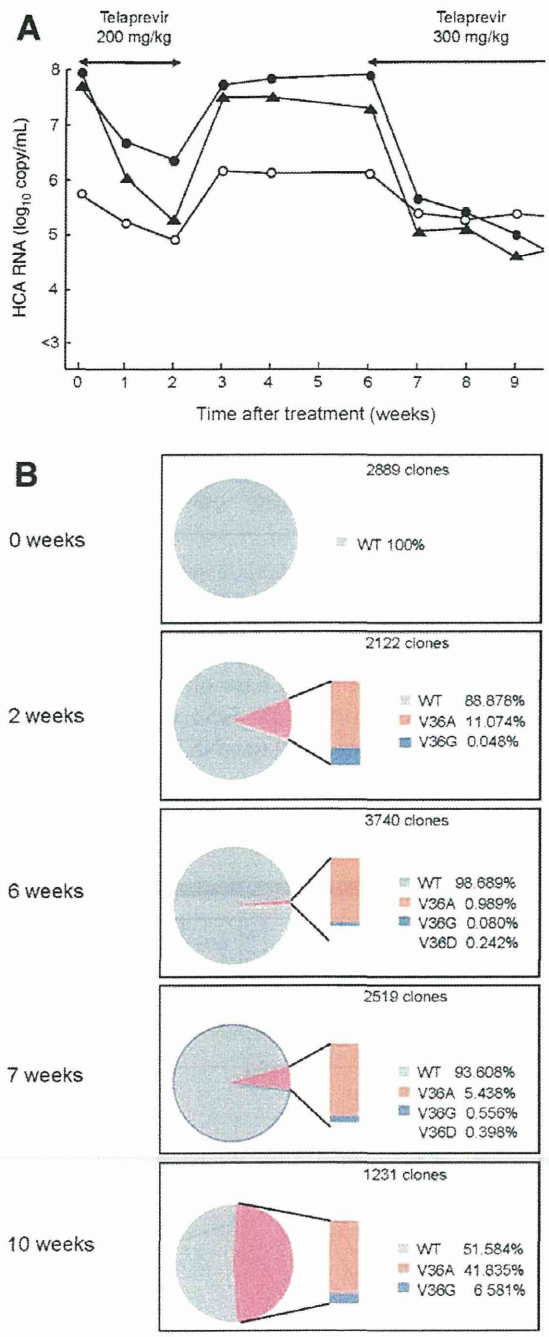

Fig. 5. The effect of telaprevir on mice infected with *in vitro*-transcribed HCV. Mice were injected with *in vitro*-transcribed HCV-KT9 RNA (closed circles and closed triangles) or KT9-NS3-A156S RNA (open circles). Six weeks after HCV RNA injection, mice were treated perorally with 200 mg/kg of telaprevir twice a day for 2 weeks. Four weeks after cessation of treatment mice were treated with 300 mg/kg of telaprevir twice a day for 4 weeks. (A) Mice serum HCV RNA titers at the indicated times are shown. Serum samples obtained from one of two HCV-KT9-infected mice (closed triangles) were used for ultra-deep sequencing. (B) Amino acid (aa) frequencies at aa36 in the HCV NS3 region based on ultra-deep sequencing are shown.

domain.[26] In particular, variants at NS3 residues 36, 54, 155, and 156 were shown to confer reduced sensitivity to telaprevir.[27]

In this study we analyzed the association between the antiviral efficacy of telaprevir and sequence variants within the NS3 region using chimeric mice infected with serum samples obtained from an HCV genotype 1b-infected patient. One of two HCV-infected mice had a viral breakthrough during the dosing period (Fig. 3). Ultra-deep sequence analysis of the NS3 region showed an increase of the V36A mutant, which has been reported to confer telaprevir resistance.[26] Consequently, our results show evidence of emergence of a telaprevir-resistant variant previously detected in human clinical trials.

We detected an A156F mutant in the HCV NS3 region in a chronic hepatitis patient who had experienced viral breakthrough during telaprevir monotherapy (Fig. 1). Likewise, HCV RNA titer in mice infected with the A156F variant showed no reduction following 2 weeks of telaprevir treatment (Fig. 2). However, 2 weeks of treatment with IFN-alpha rapidly suppressed serum HCV RNA titer below the detectable limit. These results demonstrate that A156F is telaprevir-resistant but has a high susceptibility to IFN.

Interestingly, ultra-deep sequencing revealed that the wildtype strain was present at low frequency (0.3%) in the serum inoculum (Fig. 2). However, the frequency of the wildtype failed to increase over time (Fig. 3), suggesting that the very small number of wildtype viral RNA (about 30 copies) may be incomplete or defective, as a large proportion of viral genomes are thought to be defective due to the virus's high replication and mutation rates.[9] Further analysis is necessary in order to interpret the significance of the presence of very low frequency variants detected by ultra-deep sequencing.

The short read lengths used in next generation sequencing also complicates the detection of rare variants, especially when variants are clustered within a region smaller than an individual read length (e.g., 36 basepairs). Relaxing the matching criteria allows mapping of more diverse reads but increases the error rate, whereas default settings may be geared toward more genetically homogenous haploid or diploid genomes. In this study we used *de novo* assembly to identify more diverse variants that failed to map to the reference sequence. Examining the variation in codon frequencies among samples, we created alternative reference sequences containing a sufficient range of variants to provide more uniform coverage of variable regions.

Using our previously established infectious HCV-KT9 genotype 1b HCV clone, we investigated the antiviral efficacy of telaprevir and the effect of