3. B型肝炎ウイルス(HBV)研究の進歩

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動　向

近年のB型肝炎ウイルス（HBV）研究は，大まかに2つの方向性で進歩を遂げてきた．一つはC型肝炎ウイルス（HCV）研究と同様の手法による成果であり，もう一つはHBV独自に展開された成果である．まず一つ目は，HCV同様にHBV研究でもGWAS解析が行われ，いくつかの宿主因子（HLA-DP/DQなど）が同定されてきた．また，B型慢性肝炎に対する効果が期待されるインターフェロン（IFN）治療の効果予測因子として，HCV同様にIL28BのSNPが報告された．さらに，次世代ゲノムシークエンサの技術革新により，HBVによる肝細胞癌の原因解明が進んできている．一方，HBV独自の研究としては，宿主側のウイルス受容体としてNTCP（Na^+-Taurocholate Cotransporting Polypeptide）が同定され，現在まで培養細胞を用いたHBV感染系が確立していない状況のなか，大変興味深い知見が蓄積されてきている．

これまでHBV研究進展の妨げとなっていた要因の一つは，HBV感染サイクルを再現する細胞培養系が確立されていなかったことである．しかし，そのような現状にあってもHBV感受性の動物の探索（チンパンジーのみでなく，小型原猿類のツパイ，さらにヒト肝細胞を移植したヒト肝キメラマウスなど）や初代肝細胞の性質を維持する細胞株の作成や肝臓の立体構造を模倣した3次元培養法など，いくつかの新しい試みがなされている．

近年報告された研究内容のうち，今回は特にヒトを対象とした新しい知見を中心に概説する．

A. GWASによるHLA class I関連分子の同定

近年，ゲノムワイドに均一に配置された約90万カ所の一塩基多型（SNP: single nucleotide polymorphism）を一括タイピングすることが可能となり，このゲノムワイド関連分析法（GWAS: genome-wide association study）を用いることにより様々な疾患の発症，病態，薬剤反応性，副作用に関連する要因が明らかになっている．肝炎領域においてもこの手法を用いることで，C型慢性肝疾患に対するインターフェロン治療反応性，C型肝炎ウイルス（HCV）感染自然排徐，ペグインターフェロン・リバビリン療法における貧血，HCV関連肝細胞癌，B型肝炎ウイルス（HBV）持続感染などに関連する遺伝子多型が同定されている．

2009年に鎌谷らのグループが日本人B型慢性

肝炎患者群179検体と対照群934検体を対象としたGWASを実施した結果，HLA-DPA1/DPB1遺伝子領域がB型肝炎慢性化に有意な関連を示すことを報告し[1]，さらに検体数を増やしたGWASからHLA-DQ遺伝子領域がHLA-DPと独立したB型慢性肝炎発症の関連因子であることが報告された[2]．また，独立した日本人集団と韓国人集団を対象としたGWAS研究により，HLA-DP遺伝子がB型肝炎慢性化のみならず，HBVの排除にも寄与することが報告された[3]．

一方，HBV感染ハイリスク群を主な対象とするHBVワクチン接種において，ある一定の割合で高い抗体価（HBs抗体価）が得られないことが知られていたが，この要因にもHLA領域（HLA-DR, HLA-DP, HLA class Ⅲ領域）が関連することが，インドネシア人集団約3,600人を対象としたGWASにより明らかとなった[4]．したがってHBV感染症に関連する遺伝的要因として，HLA領域の重要性が再認識された．

しかし，B型肝炎慢性化およびHBV排除に対するHLA-DP遺伝子の寄与は広く東アジアの集団（日本，韓国，タイ，中国）で再現されるものの[1-3,5-7]，欧米の集団で再現されたという報告は少ない．このことは，垂直感染によるHBV蔓延が主であるアジア諸国の特徴を反映しているのかもしれない．近年，HBV Genotype A感染が蔓延するわが国では，HBV遷延化や慢性化例が報告されるようになり，ウイルス要因のみならず宿主要因を明らかにする必要がある．

B. HBV制御に関するIL28B SNPの関与

C型慢性肝炎に対するPEG-IFN/RBV併用療法の治療効果およびHCV感染後の慢性化に寄与する宿主因子IL28BのSNPが，B型慢性肝炎のIFN治療効果に関連することを示唆する報告が相次いでいる．

HBe抗原陰性B型慢性肝炎のうち，IL28BのSNPsがC型慢性肝炎に対する治療反応良好群（メジャータイプ）と同じ遺伝子型の場合，治療中ないし治療終了後のウイルス学的および血清学的な反応性が高いことが報告された[8]．約2年間のIFN治療を受けた101例のHBe抗原陰性B型慢性肝炎の報告より，rs12979860メジャータイプ（CC）の症例ではヘテロ・マイナータイプ（CT＋TT）に比べて治療終了時HBV-DNA＜10^4 copies/mLを示す（EOT）割合が高く（69% vs 45%, p=0.01），治療終了6カ月後の効果（SVR）も高い（31% vs 13%, p=0.02）結果であった[8]．さらに興味深いことに，治療終了後平均11年間フォローした結果，HBs抗原陰性化率も有意にメジャータイプ（CC）で高率であった（29% vs 13%, p=0.039）．IL28BのSNPは，HBV-DNA低値，ALT高値，IFN治療期間とは独立してウイルス学的効果の予測因子として抽出された．さらにHBV genotypeをDのみ（n=93）に限定してIL28BのSNPで層別化した結果[9]も，同様にヘテロ・マイナータイプ（CT＋TT）に比べてメジャータイプ（CC）で良好な成績を示した（EOT; 69% vs 44%, p=0.014, SVR; 31% vs 12%, p=0.028, HBsAg陰性化; 29% vs 12%, p=0.048）．さらにrs12979860とrs8099917を比較した結果，rs8099917の方が治療効果予測に優れている可能性も報告された[9]．

一方，HBe抗原陽性例の治療効果におけるIL28B SNPの影響は，統一した見解が得られていない．台湾の報告では，6カ月間のPEG-IFN治療を行った115例のHBe抗原陽性例ではHBe抗原のセロコンバージョン（SC）率はIL28B遺伝子型による差を認めなかった[10]．一方，中国において1年間のPEG-IFN治療を行った512例のHBe抗原陽性B型肝炎例の成績では，治療終了後6カ月以降もHBV-DNA＜500 copies/mLを維持しHBe抗原のSCを認める割合はrs8099917のマ

イナーアレル（C）を有する群で高い割合を示していた（8.3% vs 3.9%, p=0.003）[11]．しかし，アジアとヨーロッパを含む11施設で行った他施設共同研究のうち，PEG-IFN治療を受けた205例のHBe抗原陽性例をIL28B SNP別に解析した結果[12]では，IFN治療終了時のHBe抗原SC率はrs12979860遺伝子型CCで50%，CTで29%，TTで10%（p=0.001）であった．さらに，IL28B遺伝子型はHBs抗原陰性化率の独立した因子であり，その危険率は3.47倍（95%信頼区間; 1.04-13.48, p=0.042）と報告された．HBe抗原陽性例では，免疫寛容から肝炎期に至る様々な症例が混在している時期であり，免疫応答への影響が示唆されるIL28B SNPで治療効果を予測するには限界があるのかもしれない．

C. NTCP同定

肝臓は独自の代謝系を有することが知られており，その一つとして物資の輸送が挙げられる．この物質輸送にトランスポーターが関与していることは古くから示唆されており，1990年代の初めから次々と新しいトランスポーターが分子レベルでクローニングされていた．肝細胞膜の類洞側と毛細胆管側には多数の異なるトランスポーターが発現し，胆汁産生および分泌に重要な役割を果たしている．基本的に物質は類洞側トランスポーターを介し血中より肝細胞内に取り込まれ，毛細胆管側トランスポーターを介し胆汁中に分泌される．これらは比較的広い基質認識性を持つことが知られており，HBV感染に関するレセプターの一つとなることが報告された．

肝類洞側膜に局在するNTCP（Na^+–Taurocholate Cotransporting Polypeptide）は，主に血液中から肝細胞内への胆汁酸の輸送に関与するトランスポーターとして知られていた．輸送のメカニズムは細胞外のNa^+との共輸送であり，通常は胆汁酸のNa^+依存的輸送に関与し，細胞外から細胞内への一方向のみに保たれている．

以前より，HBV感染やHDV感染がエンベロープ蛋白の一つであるLarge S蛋白のpre-S1ドメインと同じ配列のペプチドによりブロックされることが知られており，おそらくこのpre-S1ペプチドはウイルスレセプターとの結合をブロックするだろうと想定されていた．2012年にYanら[13]はzero-distance photo-affinity cross-linkingと呼ばれる手法[14]を用いて，pre-S1ペプチドが結合する受容体を単離し，質量分析を行った．解析に必要な十分量の結合蛋白質を得るためにツパイ初代肝細胞（PTH）[15,16]を用い，さらに次世代シークエンシングによる全RNA配列決定により得られたツパイ蛋白質データベースを作成し，この細胞側受容体がNTCP（SLC10A1）であることを同定した．また，NTCPとHBV Pre-S1との結合能について，変異体ペプチドによる結合能の低下やHEK293細胞およびHuH7細胞にNTCPの遺伝子導入により確認し，さらにPTH，HepaRG細胞[17]，ヒト初代肝細胞（PHH）を用いたNTCPノックダウン実験によるHBVとHDV感染性の低下を確認した．従来よりHBV感染が成立しないといわれていたHepG2やHuH7など肝細胞癌由来の細胞ではNTCPの発現は低く，これらの細胞にNTCPを強制発現させるとHBVやHDVの感染が確認された．

一方，初代肝細胞を用いたHBV類似ウイルス（ダックHBVウイルス）感染の感受性が*in vitro*培養後に喪失していくことがこれまでに知られていたが[18]，同様にNTCP発現が培養経過に伴い減少していくことが観察された．おそらくは，*in vitro*培養では維持できない肝組織特異的な転写因子が肝細胞のNTCP発現維持に必要であり，培養細胞の感染効率が低い要因ではないかと類推される．

他の多くのウイルス感染から明らかなように，

宿主側のウイルス受容体は単一の蛋白質である可能性は低く，ウイルスの吸着，細胞内侵入，細胞膜との融合といった，様々な行程をウイルス感染は必要とする．これまでにもHBV吸着には細胞膜上のヘパラン硫酸プロテオグリカンが候補として挙がっていたが[19-21]，実験的にHBV感染を再現することはできなかった．今回のNTCP同定は，HBV研究を大幅に進展させることが期待されるが，NTCPのノックダウンによりすべてのHBV感染が除去されるわけではなく，またNTCPによってすべての細胞にHBV感染が再現できるわけではないことから，今後さらなる共受容体の探索が脚光を浴びると予測される．

D. B型関連肝癌の全ゲノム解析

HBVによる癌化メカニズムの一つに宿主DNAへのHBVゲノム組み込みが想定されていたが，その組み込み位置はランダムであり一定の組み込みサイトはないものと考えられていた．2012年に，Sungらは次世代シークエンサーを用いて81例のB型関連肝細胞癌と7例のHBV陰性肝細胞癌の全ゲノム配列を解析し，HBVゲノムの組み込み部位を報告した[22]．81例中75例にHBVゲノムの組み込みを認め，癌部のみに組み込みがあるものが48例，癌部・非癌部の両方に認めるものが26例，非癌部のみに認めるものが1例のみであった．組み込みを認めた遺伝子はTERT（18例），MLL4（9例），CCNE1（4例）が多く，各遺伝子内部または近傍に組み込まれ遺伝子発現を誘導していた．さらに組み込まれたHBVゲノムは，Precore/core遺伝子領域およびX遺伝子領域の組み込みが多かった．また，HBVの組み込みが高頻度であるほど，宿主ゲノムのcopy number variation（ゲノムコピー変異）が多く，染色体の不安定を誘導し，HBVゲノムの組み込みが患者の予後と関連することが示唆された．

むすび

2013年より新たに厚生労働省のB型肝炎創薬研究事業が立ち上がり，これまでHCVに特化していた多くの肝炎研究者がHBV研究に参入している．近年のHBV研究の進歩を活用し多くの研究者が成果を上げ，日本発のB型肝炎治療創薬が実現することを期待したい．

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Genetic Characterization of Hepatitis C Virus in Long-Term RNA Replication Using Li23 Cell Culture Systems

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Abstract

Background: The most distinguishing genetic feature of hepatitis C virus (HCV) is its remarkable diversity and variation. To understand this feature, we previously performed genetic analysis of HCV in the long-term culture of human hepatoma HuH-7-derived HCV RNA-replicating cell lines. On the other hand, we newly established HCV RNA-replicating cell lines using human hepatoma Li23 cells, which were distinct from HuH-7 cells.

Methodology/Principal Findings: Li23-derived HCV RNA-replicating cells were cultured for 4 years. We performed genetic analysis of HCVs recovered from these cells at 0, 2, and 4 years in culture. Most analysis was performed in two separate parts: one part covered from the 5′-terminus to NS2, which is mostly nonessential for RNA replication, and the other part covered from NS3 to NS5B, which is essential for RNA replication. Genetic mutations in both regions accumulated in a time-dependent manner, and the mutation rates in the 5′-terminus-NS2 and NS3-NS5B regions were $4.0–9.0\times10^{-3}$ and $2.7–4.0\times10^{-3}$ base substitutions/site/year, respectively. These results suggest that the variation in the NS3-NS5B regions is affected by the pressure of RNA replication. Several in-frame deletions (3–105 nucleotides) were detected in the structural regions of HCV RNAs obtained from 2-year or 4-year cultured cells. Phylogenetic tree analyses clearly showed that the genetic diversity of HCV was expanded in a time-dependent manner. The GC content of HCV RNA was significantly increased in a time-dependent manner, as previously observed in HuH-7-derived cell systems. This phenomenon was partially due to the alterations in codon usages for codon optimization in human cells. Furthermore, we demonstrated that these long-term cultured cells were useful as a source for the selection of HCV clones showing resistance to anti-HCV agents.

Conclusions/Significance: Long-term cultured HCV RNA-replicating cells are useful for the analysis of evolutionary dynamics and variations of HCV and for drug-resistance analysis.

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Introduction

Hepatitis C virus (HCV) infection frequently causes chronic hepatitis, which progresses to liver cirrhosis and hepatocellular carcinoma. Such persistent infection has now become a serious health problem, with more than 170 million people worldwide infected with HCV [1]. HCV is an enveloped positive single-stranded RNA (9.6 kb) virus belonging to the *Flaviviridae* family, and the HCV genome encodes a large polyprotein precursor of approximately 3000 amino acid (aa) residues. This polyprotein is cleaved by a combination of host and viral proteases into at least 10 proteins in the following order: core, envelope 1 (E1), E2, p7, nonstructural protein 2 (NS2), NS3, NS4A, NS4B, NS5A, and NS5B [2,3].

The initial development of a cell culture-based replicon system [4] and a genome-length HCV RNA-replicating system [5] using genotype 1b strains led to rapid progress in investigations into the mechanisms underlying HCV replication [6,7]. HCV replicon RNA (approximately 8 kb) is a selectable, bicistronic HCV RNA with the first cistron, the neomycin phosphotransferase (Neo^R) gene, being translated under control of the HCV internal ribosome entry site (IRES) and the second cistron, the NS3-NS5B regions, being translated under control of the encephalomyocarditis virus (EMCV) IRES. Genome-length HCV RNA (approximately 11 kb) possesses the Core-NS5B regions in substitution for the NS3-5B regions of the replicon in addition to the replicon structure. It was reported that infectious HCV particles are not produced in genome-length HCV RNA-replicating cell systems using genotype 1b strains [6,8]. However, in 2005, an efficient virus production system using the JFH-1 strain of genotype 2a was developed using HuH-7-derived cells [9]. Since then, this infectious HCV system became a powerful tool to study the full viral life cycle [10].

The most distinguishing feature of the HCV RNA is its remarkable diversity and variation. To date, six major HCV genotypes, each having a large number of subtypes, have been found to show more than a 20% difference at the nucleotide level compared with any other genotypes [11,12]. An approximately 5–8% difference at the nucleotide level has been observed within a single genotype [3]. Furthermore, an approximately 1% difference at the nucleotide level is also observed among HCV genomes in an individual [13]. Although genetic analyses of HCV using *in vivo* specimens have estimated that the genetic mutation rate of HCV is $1.4–1.9\times10^{-3}$ base substitutions/site/year [14–16], the potential variability of HCV is not clear due to the selective pressure of immune system functions *in vivo* [17,18].

To define the actual genetic mutation frequency of HCV, we previously performed genetic analysis of HCV [19,20] using human hepatoma HuH-7 cell culture-based HCV replicon systems or genome-length HCV RNA-replication systems. In studies using the 1B-1 or O strain of genotype 1b, the accumulation of genetic mutations (mutation rate is $3.0–4.8\times10^{-3}$ base substitutions/site/year), the enlargement of genetic diversity, and an increase in GC contents of HCV RNA were observed in a time-dependent manner during a 2-year cell culture [19,20]. These results suggest that the long-term culture of HCV RNA-replicating cells is useful for understanding the evolutionary dynamics and variations of HCV. However, HuH-7-derived cells are the only cell culture system used thus far for robust HCV replication [6,7]. Therefore, it remains unclear whether our results obtained from HuH-7-derived HCV RNA-replicating cell culture systems reflect the general features of HCV's genetic diversity and variation. On the other hand, in 2009 we established four new human hepatoma Li23 cell-derived genome-length HCV RNA (O strain of genotype 1b; GenBank accession no. AB191333)-replicating cell lines, OL (polyclonal; a mixture of approximately 200 clones), OL8 (monoclonal), OL11 (monoclonal), and OL14 (monoclonal) [21], and have been culturing them for more than 4 years. Since we demonstrated that the gene expression profile of Li23 cells was distinct from those in HuH-7 cells [22], and that anti-HCV targets in Li23-derived cells were distinct from those in HuH-7-derived cells [23–25], we expected to find distinct HCV variability and diversity from those observed previously in HuH-7-derived cells. To clarify this point, we carried out comprehensive genetic analysis of HCVs obtained from 0-year, 2-year, and 4-year cultures of OL, OL8, OL11, and OL14 cells, and compared them with the original ON/C-5B/QR,KE,SR RNA [21].

Here, we report the evolutionary HCV dynamics occurring in the long-term replication of genome-length HCV RNAs using Li23-derived cell culture systems.

Materials and Methods

Cell Cultures

The human hepatoma Li23 cell line, which was established and characterized in 2009, consists of human hepatoma cells from a Japanese male (age 56) [21]. The Li23 cells were cultured in modified medium for human immortalized hepatocytes, as described previously [21,26]. Genome-length HCV RNA-replicating cells (Li23-derived OL, OL8, OL11, and OL14 cells) were cultured in the medium for the Li23 cells in the presence of 0.3 mg/ml of G418 (Geneticin, Invitrogen, Carlsbad, CA). These cells were passaged every 7 days for 4 years. HCV RNA-replicating cells possess the G418-resistant phenotype, because Neo^R as a selective marker was produced by the efficient replication of HCV RNA. Therefore, when HCV RNA is excluded from the cells or when its level decreases, the cells are killed in the presence of G418. In this study, OL, OL8, OL11, and OL14 cells were renamed OL(0Y), OL8(0Y), OL11(0Y), and OL14(0Y) cells, respectively, to specify the time at which the cells were established. These "0Y" cells of passage number 3 were used in this study. Two-year cultures of OL(0Y), OL8(0Y), OL11(0Y), and OL14(0Y) cells were designated OL(2Y), OL8(2Y), OL11(2Y), and OL14(2Y) cells, respectively. Four-year cultures of OL(0Y), OL8(0Y), OL11(0Y), and OL14(0Y) cells were designated OL(4Y), OL8(4Y), OL11(4Y), and OL14(4Y) cells, respectively.

Quantification of HCV RNA

Quantitative reverse transcription-polymerase chain reaction (RT-PCR) analysis for HCV RNA was performed using a real-time LightCycler PCR (Roche Diagnostics, Basel, Switzerland) as described previously [21,27]. Experiments were done in triplicate.

Western Blot Analysis

The preparation of cell lysates, sodium dodecyl sulfate-polyacrylamide gel electrophoresis, and immunoblotting analysis with a PVDF membrane was performed as described previously [28]. The antibodies used to examine the expression levels of HCV proteins were those against NS4A (a generous gift from Dr. A. Takamizawa, Research Foundation for Microbial Diseases, Osaka University) and NS5B (a generous gift from Dr. M. Kohara, Tokyo Metropolitan Institute of Medical Science, Japan). Anti-β-actin antibody (AC-15; Sigma, St. Louis, MO) was also used to detect β-actin as an internal control. Immunocomplexes on the membranes were detected by enhanced chemiluminescence assay (Western Lightning Plus-ECL; Perkin-Elmer Life Sciences, Boston, MA).

RT-PCR and Sequencing

To amplify genome-length HCV RNA, RT-PCR was performed separately in two fragments as described previously [21,27]. Briefly, one fragment covered from the 5′-terminus to NS3, with a final product of approximately 5.1 kb, and the other fragment covered from NS2 to NS5B, with a final product of approximately 6.1 kb. These fragments overlapped at the NS2 and NS3 regions and were used for sequence analysis of the HCV open reading frame (ORF) after cloning into pBR322MC [28]. SuperScript II (Invitrogen, Carlsbad, CA) and KOD-plus DNA polymerase (Toyobo, Osaka, Japan) were used for RT and PCR, respectively. Plasmid inserts were sequenced in both the sense and antisense directions using Big Dye terminator cycle sequencing on an ABI PRISM 310 genetic analyzer (Applied Biosystems, Foster City, CA). The nucleotide sequences of each of 10 (OL cell series) or 3 (OL8, OL11, and OL14 cell series) independent clones obtained were determined.

Molecular Evolutionary Analysis

Nucleotide and deduced aa sequences of the clones obtained by RT-PCRs were analyzed by neighbor-joining analysis using the program GENETYX-MAC (Software Development, Tokyo, Japan).

Antiviral Assay

To monitor the anti-HCV activity of telaprevir, genome-length HCV RNA-replicating cells were plated onto 6-well plates (2×10^5 cells for OL(0Y) cells or 8×10^4 for OL(4Y), OL8(4Y), OL11(4Y), or OL14(4Y) cells per well). After 24 hrs in culture, the cells were treated with telaprevir (a generous gift from Dr. T. Furihata, Chiba University, Japan) at 0.2 μM or 0.4 μM for 3 days. After

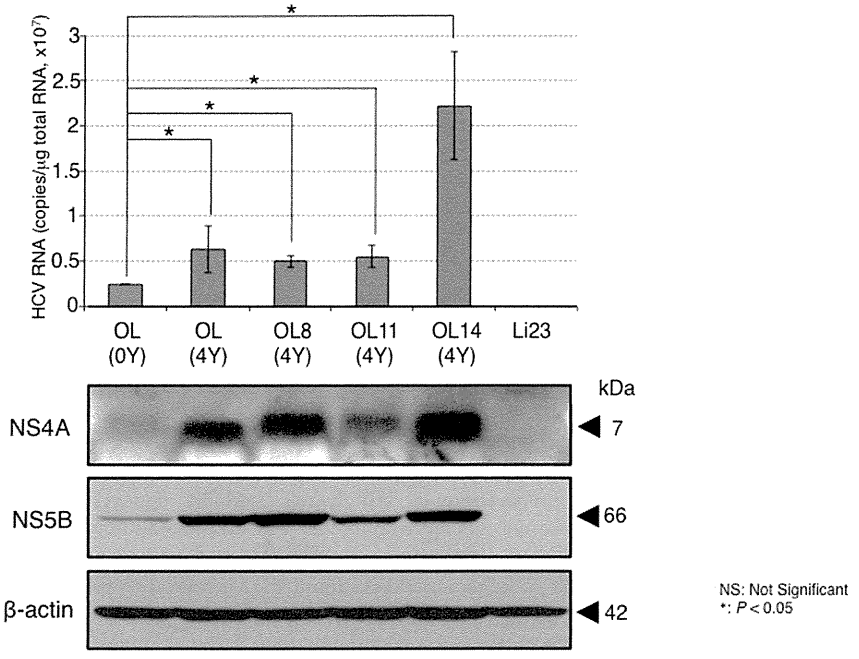

Figure 1. Characterization of genome-length HCV RNA-replicating cells after 4 years in culture. (A) Quantitative analysis of intracellular genome-length HCV RNA. The total RNAs from OL(4Y), OL8(4Y), OL11(4Y), and OL14(4Y) cells used were analyzed. The levels of intracellular genome-length HCV RNA were quantified by LightCycler PCR. OL(0Y) and Li23 cells were used as a positive and a negative control, respectively. (B) Western blot analysis. The cellular lysates from the cells used for RT-PCR analysis were also used for comparison. NS4A and NS5B were detected by Western blot analysis. β-actin was used as a control for the amount of protein loaded per lane.
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treatment, the cells were subjected to quantitative RT-PCR analysis for HCV RNA.

Statistical Analysis

The significance of differences among groups was assessed using Student's *t*-test. $P<0.05$ was considered significant.

Results

Efficient replication of genome-length HCV RNA is maintained in long-term cell culture

To prepare the specimens for the genetic analysis of HCV, genome-length HCV RNA-replicating OL(0Y), OL8(0Y), OL11(0Y), and OL14(0Y) cells were cultured for 4 years. Since we previously demonstrated that the levels of HCV RNAs increased in all cases after 2 years of constitutive HCV RNA replication [26], in the present study we examined the levels of intracellular HCV RNAs after the cell culture of 4 years by quantitative RT-PCR. The results revealed that the levels of HCV RNAs in all cases were significantly higher than that of OL(0Y) cells (Fig. 1). Western blot analysis for HCV NS4A and NS5B also showed that the expression levels in all cases were higher than that of OL(0Y) cells. However, the present results were matched with previous findings regarding a 2 year-culture [26], revealing that the levels of HCV RNAs of OL8(4Y) and OL11(4Y) cells become lower than those of OL8(0Y) or (2Y) and OL11(0Y) or (2Y) cells, respectively. Unlike the results for the OL8 or OL11 series, the levels of HCV RNAs of OL(4Y) or OL14(4Y) cells were each maintained throughout cultures of 2 years and 4 years. Overall, we showed that the HCV RNA levels in all cases were more than 5×10^6 copies/μg of total RNA, indicating that efficient HCV RNA replication occurred during those 4 years.

We next examined whether infectious HCV particles are produced from genome-length HCV RNA-replicating cells after 4 years of culture, although it has been reported that infectious particles were not produced in genome-length HCV RNA-replicating cell systems [6,8]. To clarify this point, we performed infection experiments to HCV (JFH-1) susceptible HuH-7-derived RSc and Li23-derived ORL8 cells [21] using the supernatant of OL(0Y), OL(4Y), OL8(4Y), OL11(4Y), or OL14(4Y) cells as an inoculum. At 7 days and 8 days post-infection, we quantified the Core in the supernatants by enzyme-linked immunosorbent assay and HCV RNA in the cells by quantitative RT-PCR. The results (Fig. S1) showed that both Core and HCV RNA were not detected in our long-term cultured cells, suggesting that the cells produced no infectious virus particles over time.

Genetic variations of genome-length HCV RNAs during long-term cell culture

To clarify the genetic variations of HCVs during the period of cell culture, we carried out sequence analysis of genome-length HCV RNAs obtained from OL(2Y), OL(4Y), OL8(2Y), OL8(4Y), OL11(2Y), OL11(4Y), OL14(2Y), and OL14(4Y) cells. The determined nucleotide sequences of genome-length HCV RNAs were compared with those of the original ON/C-5B/QR,KE,SR RNA [21] used for the establishment of the OL(0Y), OL8(0Y), OL11(0Y), and OL14(0Y) cell lines. To compare the nucleotide sequences, the data on genome-length HCV RNAs from OL(0Y), OL8(0Y), OL11(0Y), and OL14(0Y) cells were also used [21]. Most of the sequence analysis was performed in two separate parts: one part covers from the 5′-terminus to NS2, which is mostly nonessential for RNA replication, and the other part covers from NS3 to NS5B, which is essential for RNA replication. The results revealed that the numbers of base substitutions in both regions

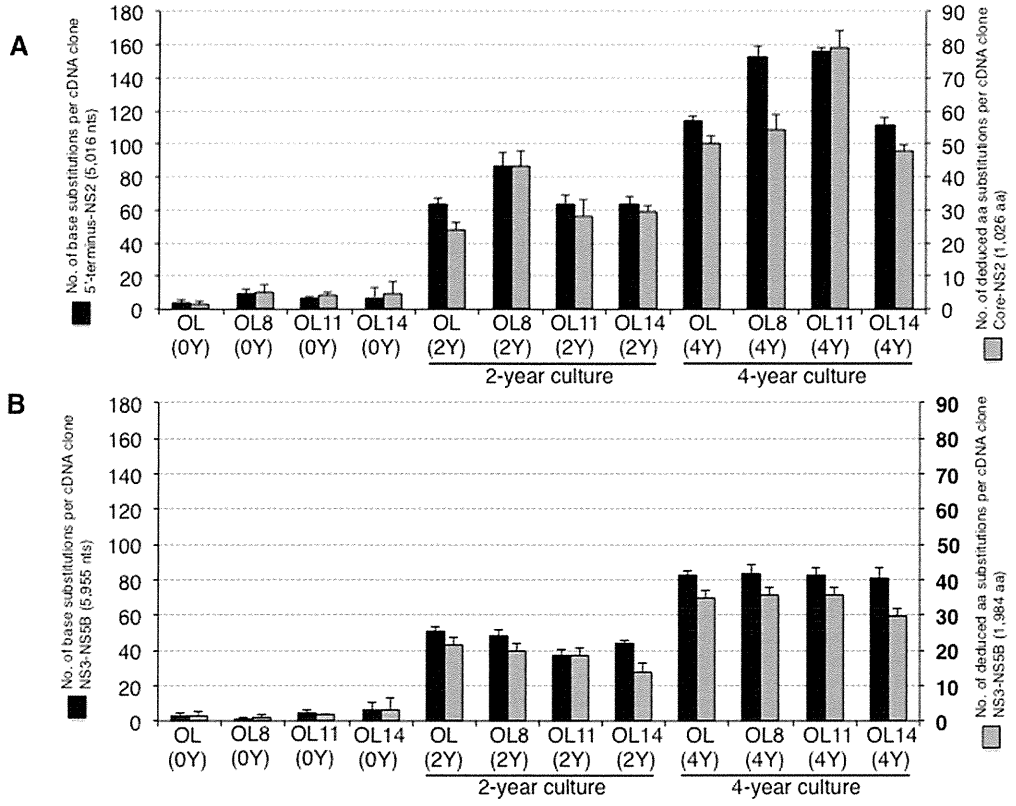

Figure 2. Genetic variations occurring in long-term replication of genome-length HCV RNAs. (A) Genetic variations in the 5′-terminus-NS2 regions. The left vertical line indicates the mean numbers of base substitutions detected per cDNA clone, by comparison with ON/C-5B/QR,KE,SR RNA [21]. The right vertical line indicates the mean numbers of aa substitutions in the Core-NS2 regions deduced per cDNA clone, by comparison with the original aa sequences deduced from ON/C-5B/QR, KE, SR RNA [21]. (B) Genetic variations in the NS3-NS5B regions. The mean numbers of base substitutions and aa substitutions are indicated as shown in (A).
doi:10.1371/journal.pone.0091156.g002

increased in a time-dependent manner (Fig. 2A and 2B). The numbers of deduced aa substitutions in HCV ORFs correlated well with the numbers of base substitutions of genome-length HCV RNAs (Fig. 2A and 2B). These base substitutions were considered mutations that occurred during the intracellular replication of genome-length HCV RNA. Based on the results after 2 or 4 years in culture, we calculated the apparent mutation rates of genome-length HCV RNAs in these cell lines. For this analysis, genome-length HCV RNA was divided into three parts: the 5′-terminus-EMCV IRES regions (partly essential for RNA replication), the Core-NS2 regions (nonessential for RNA replication), and the NS3-NS5B regions (essential for RNA replication). The results revealed that the mutation rates (base substitutions/site/year) in the three distinct regions calculated from the data of the 2-year culture were about the same as the mutation rates calculated from the data of the 4-year culture (Fig. 3). These results suggest that genetic variations of HCV have occurred at the same speed for four years in Li23-derived genome-length HCV RNA replicating cells. Furthermore, we noticed that the mutation rates in the NS3-NS5B regions ($2.7–4.0\times10^{-3}$) were lower than those in the 5′-terminus-EMCV IRES regions ($4.1–6.9\times10^{-3}$) and the Core-NS2 regions ($5.3–9.1\times10^{-3}$) (Fig. 3). Moreover, we examined the numbers of synonymous (dS) and nonsynonymous (dN) mutations with transition (Ts) or transversion (Tv) in two divided regions (Core-NS2 and NS3-NS5B). The results are summarized in Table 1. The dN/dS ratio in the Core-NS2 and NS3-NS5B regions were 1.55 to 3.00 and 0.45 to 1.06, respectively. These values imply the positive selection in Core-NS2 regions and the purifying (stabilizing) selection in NS3-NS5B regions except OL11(2Y) and OL8(4Y) cells. Since the dN/dS ratios in NS3-NS5B regions of OL11(2Y) and OL8(4Y) cells were 1.06 and 1.03, respectively, we can estimate that neutral selection acted in these cells. In addition, the Ts/Tv ratios in the Core-NS2 and NS3-5B regions were 3.50 to 7.21 and 3.58 to 10.08, respectively. These results showed a tendency similar to that found in a previous study [20] using HuH-7-derived genome-length HCV RNA-replicating cells, suggesting that the NS3-NS5B regions, which are essential for RNA replication, are evolutionally limited. Together these results indicate that HCV can mutate at the same level in both HuH-7-derived cells and Li23-derived cells.

Characterization of aa substitutions in HCV ORFs during long-term cell culture

We next characterized aa substitutions in HCV ORFs that occurred during 4 years in culture of OL(0Y), OL8(0Y), OL11(0Y), and OL14(0Y) cells. The conserved aa substitutions (mutated in all 10 clones sequenced in the cases of OL(2Y) or OL(4Y) cells and mutated in all 3 clones sequenced in the cases of OL8(2Y), OL8(4Y), OL11(2Y), OL11(4Y), OL14(2Y), or OL14(4Y) cells) are summarized in Table 2 (Core-p7 regions) and Table 3 (NS2-NS5B regions). Among the many aa substitutions, only 19 were the same as those detected in the 2-year culture of one of five kinds of HuH-7-derived genome-length HCV RNA (O strain of genotype 1b)-replicating cell lines [20] (Tables 2 and 3). In addition, 17 aa were substituted to the type of

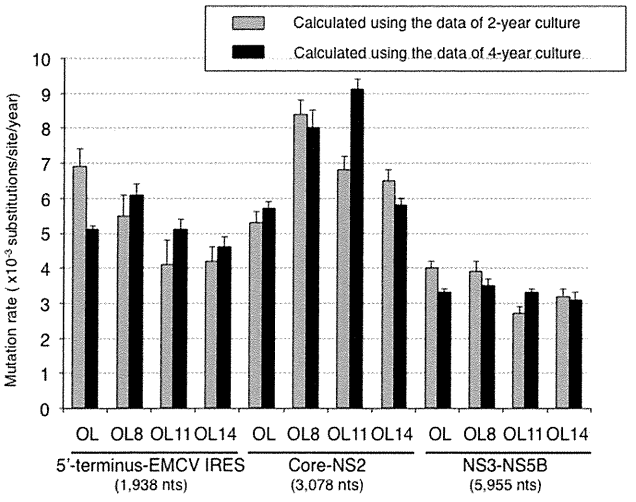

Figure 3. Mutation rates of genome-length HCV RNAs in long-term cell culture. The mutation rates of three regions (5′-terminus-EMCV-IRES, Core-NS2, and NS3-NS5B) of genome-length HCV RNAs (OL, OL8, OL11, and OL14) were calculated using the sequence data obtained from 2- or 4-year cell culture. The vertical line indicates the means of the mutation rates calculated using the nucleotide sequences of 10 clones (OL) or 3 clones (OL8, OL11, or OL14) of genome-length HCV RNAs, by comparison with the original sequence (ON/C-5B/QR,KE,SR RNA) [21].
doi:10.1371/journal.pone.0091156.g003

JFH-1 strain (genotype 2a: accession number AB237837) (Tables 2 and 3). We noticed that 12 aa substitutions were commonly detected in at least two different cell lines (Tables 2 and 3). The remaining 338 conserved aa substitutions were independently caused in each of the Li23-derived genome-length HCV RNA-replicating cell lines (Tables 2 and 3). However, from these results, we cannot conclude it whether genetic variations of HCV occur in a cell-line-specific manner or in a random manner.

Genetic deletions were characterized in the first half of genome-length HCV RNAs during long-term cell culture

Recently, Pacini et al. demonstrated that naturally occurring HCV subgenomic RNAs, mostly lacking the E1 or E2 region, were capable of autonomous replication and could be packaged and secreted in viral particles [29]. In the present cell-based study also, we detected several conserved deletions within genome-length HCV RNAs, although a previous study using HuH-7-derived cell lines did not reveal any conserved deletions [20]. As shown in Figure 4, all deletions were located in the first half of genome-length HCV RNA. In OL8(2Y) and OL8(4Y) cells, a conserved 51 nucleotides (nts) deletion in frame was detected, resulting in a 17 aa deletion (aa 686–702 in the E2). In OL14(2Y) and OL14(4Y) cells also, two kinds of conserved 3 nts deletion in frame were detected, resulting in a 1 aa deletion in each (aa 414 in the E2 and aa 847 in the NS2). Furthermore, a conserved 105 nts deletion in frame was observed in OL14(4Y) cells, resulting in a 35 aa deletion (aa 725–746 in the E2 and aa 747–759 in the NS2). In addition, 26 nts (nt 1248–1273) located between the Neo^R gene and IRES was conservatively deleted in OL11(2Y) and OL11(4Y) cells. These results suggest that nonessential regions for RNA replication are deleted during long-term culture of Li23-derived cells. However, such deletion was not caused in the OL cell series.

Genetic diversity of genome-length HCV RNA arising during long-term cell culture

Based on the sequence data of all clones obtained after 0-year, 2-year, and 4-year culture, we examined the genetic diversities of genome-length HCV RNAs by the construction of phylogenetic trees. The results revealed that the genetic diversities of genome-length HCV RNAs were clearly expanded at both the nucleotide (Fig. 5) and aa (Fig. S2) sequence levels in the 5′-terminus-NS2 regions and the NS3-NS5B regions, and that the 10 clones derived from OL cell series and 3 clones derived from each other cell series were clustered and located at similar genetic distances from the origin (ON/C-2 or O/3-5B/QR,KE,SR for the nucleotide sequence level and O/C-2 or O/3-5B/QR,KE,SR for the aa sequence level [21]) (Fig. 5 and Fig. S2).

We next compared the nucleotide sequences among 10 independent OL(4Y) clones obtained after 4-year cell culture. In

Table 1. Base substitutions occurring in genome-length HCV RNAs during long-term cell culture.

Full-length HCV RNA series	Ts				Tv				dN/dS		Ts/Tv	
	dN		dS		dN		dS					
	C-NS2	NS3-5B	C-NS2	NS3-5B	C-NS2	NS3-5B	C-NS2	NS3-5B	C-NS2	NS3-5B	C-NS2	NS3-5B
OL(2Y)	21.2±1.4	11.5±1.4	9.1±1.5	29.3±2.0	3.1±1.4	9.0±1.5	1.1±0.3	0.5±0.5	2.38	0.69	7.21	4.29
OL8(2Y)	34.3±4.9	14.3±1.2	12.3±2.1	23.7±.25	7.7±0.6	5.7±1.2	1.7±0.6	4.3±0.6	3.00	0.71	5.00	3.80
OL11(2Y)	23.3±4.0	13.0±1.0	17.0±3.6	16.0±4.0	6.0±3.6	6.0±1.7	0.7±0.6	2.0±0	1.66	1.06	6.05	3.63
OL14(2Y)	18.7±1.5	11.0±1.0	16.3±2.1	29.3±4.7	8.7±0.6	2.7±2.9	1.3±0.6	1.3±1.5	1.55	0.45	3.50	10.08
OL(4Y)	47.4±3.2	22.1±1.7	16.4±2.0	45.1±2.5	5.1±0.9	13.1±1.2	4.0±0.5	2.3±0.5	2.57	0.74	7.01	4.36
OL8(4Y)	56.7±4.2	35.7±1.2	29.7±2.5	38.3±2.3	14.3±0.6	12.3±0.6	1.3±0.6	8.3±0.6	2.29	1.03	5.51	3.58
OL11(4Y)	66.7±4.9	26.3±0.6	30.0±5.6	42.0±3.6	16.3±2.9	6.7±1.5	4.3±0.6	6.7±3.2	2.42	0.68	4.68	5.13
OL14(4Y)	34.3±1.5	23.7±1.2	27.3±3.5	47.3±2.9	10.3±1.2	5.0±0	1.3±0.6	3.7±1.5	1.56	0.56	5.29	8.19

Base substitutions were counted by comparison with the sequence of genome-length HCV RNA (ON/C-5B/QR,KE,SE [20]).
Average numbers of base substitutions per cDNA clone are shown.
Ts: Transition; Tv: Transversion; dN: Nonsynonymous; dS: Synonymous.
doi:10.1371/journal.pone.0091156.t001

Table 2. Conservative aa substitutions occurring during long-term replication of genome-length HCV RNAs (I).

	OL		OL8		OL11		OL14	
Region								
Core	V46A	**T52A**	K10R[a,b]	T11S	(I30T)	**S53P**	K10R[a,b]	**K12N**[b]
(1~191)	L133F[b]	**G146R**	**Q20R**	V31A	T125S	**L133S**	**K23M**	E54G
	N163D	**L185S**	W76R	E89V[b]	M134T	**L139P**[b]	**S56P**	I65V
			L91P	N118I	A150T	N163T[a,b]	A180V	
			E159V	N163T[a,b]				
			P170A					
E1	**Y201H**	Y214C	C207Y	**V230A**	D206G	V240L	V203I	**C226R**[b]
(192~383)	D218T	**L246P**	C281Y	**V284A**	A241T	S251G[a]	S251G[a]	**Y276H**
	F271S	I287N	**L286P**	F293L	S283P	**V284G**	L308S	**A343V**[c]
	Y298H[c]	C306S	S294L	**V313A**[b]	C304R	**M318V**[a]	**A380S**	
	W320R	**L332P**	(M318V)[a]	M323L	V365A	L377F		
	L359F		**T329A**	**L338F**				
			Q342R	V344G				
			A351P	**S363P**				
			W368R	F378L				
E2	R386C	I414T	**R386H**	N395D	S408P	R424G	I411V	**I414Δ**
(384~746)	S450P	M456T	K410E	**N417D**	**L427P**	(G436E)	**S419R**	I422T
	E464A[c]	N532G	**N428D**	(I462V)	F447L	(S449P)	R483G	D520G
	N556S	K596E	I462A	**D481E**	S449L	**F465L**	K562E	T563M
	R614G	**M631T**	**Y507H**[b]	**G523S**	(Q467H)	V514G	C564W	**T680S**[c]
	E650G	L692P	L537P[b]	**N548S**[c]	E533G	C569R	**D698G**	V699A
	V710A	L721P[a]	**T561S**	E591G	N577T[c]	(L603M)	Δ725–746	
			S668P	I674T[b]	V609I	D610G		
			Δ686–702	**V709A**	Y611C	W616R		
			W736R		N623S	S663G		
					F679L	V710I		
					V712A	L721P[a]		
					V731A			
p7	E749K	**G764S**	**S767P**	(L797I)	N750D	L766F	(L748P)	Δ747–759
(747~809)	**L769P**				L799P		**F771L**	**I778V**

[a]Conservative aa substitutions detected in at least two of four cell line series.
[b]Conservative aa substitutions detected in HuH-7-derived cell line series (O, OA, OB, OD, or OE) used in the previous study [20].
[c]Conservative aa substitutions that became the same aa as the JFH-1 strain.
Conservative aa substitutions detected after 2-year and 4-year cultures are shown by bold letters.
Conservative aa substitutions detected only after 2-year culture are shown within parentheses.
doi:10.1371/journal.pone.0091156.t002

the 5′-terminus-NS2 regions and the NS3-NS5B regions derived from OL(4Y) cells, 0.38–1.28% and 0.22–0.56% differences in nucleotide sequences were observed, respectively. These results suggest that the quasispecies nature of genome-length HCV RNA was acquired steadily over long-term intracellular RNA replication.

Classification of mutations occurred in genome-length HCV RNAs during long-term cell culture

We next examined the mutation patterns occurring in genome-length HCV RNAs. The results revealed that U to C and A to G transition mutations were the most and second-most frequent mutations in total, although three cases (OL8(2Y), OL8(4Y), and OL14(4Y)) showed the opposite result (Table 4). High frequencies of U to C and A to G mutations were also observed in a previous study using HuH-7-derived HCV replicon- or genome-length HCV RNA-replicating cell lines [19,20]. The rarest mutation was C to G transversion in 2-year and 4-year cultures (Table 4). This result was the same as in a previous report using HuH-7-derived cell systems [20]. Since the frequency of U to C and A to G mutations was two or three times higher than that of C to U and G to A mutations, the GC content of HCV RNA increased significantly in a time-dependent manner in both the 5′-terminus-NS2 regions (Fig. 6A) and the NS3-NS5B regions (Fig. 6B). The increase in GC content of HCV RNA was observed in all Li23-derived cells after 2-year or 4-year culture. In the 5′-terminus-NS2 regions of HCV RNA, a remarkable (more than 1%) increase in GC content was found after the 4-year culture of all the cells except OL14(0Y) cells (Fig. 6A).

The time-dependent increase in the GC content of the HCV RNA may gradually change to an energetically stable form during

Table 3. Conservative aa substitutions occurring during long-term replication of genome-length HCV RNAs (II).

	OL		OL8		OL11		OL14	
Region								
NS2	Y835H	F886L[b]	**M814I**	**I824V**	W845R	**V853A**	F823S	**W844R**
(810~1026)	**L892S**		L849F	**R852G**	D871G	**T877A**	**Q847H**	**Y848Δ**
			A855T	**Q903R**[a,c]	I885T	(P898L)	Q903R[a,c]	I983T
			K927R	E1019G	Q903R[a,c]	V913A		
					L924S			
NS3	V1081A	**E1202A**	**P1122S**	V1415I	**S1173L**	M1205V	M1268V	P1290H
(1027~1657)					**T1280A**	(I1412V)	D1581G	R1596K
					F1501Y[c]	Q1606R	A1647T[c]	
					F1644L			
NS4A	Q1703R							
(1658~1711)								
NS4B	**S1827T**[c]	**V1880A**[b]			I1769V	**Q1804R**	A1743V	S1827A
(1712~1972)	**P1908L**	L1956M			Q1955R		V1906A	
NS5A	**L2003F**	H2057R	**R1978K**	D1979E	K2050R	**F2099Y**[c]	L2125V[c]	**D2220G**[a]
(1973~2419)	S2246P	I2252S	K1998R	S2079Y	**T2217I**	I2274V	F2281L[a,c]	**D2292E**[a,b]
	T2278A	**F2281L**[a,c]	K2212R[c]	**D2220G**[a]	K2277R	S2283P[a]	F2352L	S2355T
	S2283P[a]	**D2292E**[a,b]	**E2263G**	**E2265V**	K2320R[a]	**T2336S**[c]	S2373P	D2374N
	K2320R[a]	S2338P	V2270A	K2280D	T2351A	**F2352S**	A2382V	G2396R
	S2355P	P2369H	**Y2293H**	D2305N	**W2405R**[a,b]		**S2401N**	W2405R[a,b]
	S2384P	**M2388T**	S2342P[b]	L2347R			**C2418R**[b]	
	G2403R	**S2409R**	F2352V	T2364A				
			D2377G[b]	**S2380T**				
			D2381G	S2387P[b]				
			W2405R[a,b]	S2406A				
			E2410K					
NS5B	K2470R	**D2771N**[c]	S2975G[c]	**I3004V**	K2493R	T2549A	**A2444T**	**H2539R**
(2420~3010)	L2853I	Q2933R			K2689R	Q2728R	V2918I	
	V3000A							

[a]Conservative aa substitutions detected in at least two of four cell line series.
[b]Conservative aa substitutions detected in HuH-7-derived cell line series (O, OA, OB, OD, or OE) used in the previous study [20].
[c]Conservative aa substitutions that became the same aa as JFH-1strain.
Conservative aa substitutions detected after 2-year and 4-year cultures are shown by bold letters.
Conservative aa substitutions detected only after 2-year culture are shown in parentheses.
doi:10.1371/journal.pone.0091156.t003

RNA replication. We assumed that the increase in GC content is due to an increase in G- and C-ending codons, except for AGG and UUG codons, for efficient expression in human cells, so-called codon optimization [30], and we examined this possibility. The results in the NS3-NS5B regions revealed the time-dependent increase of G- and C-ending codons, except for AGG and UUG codons, in all four cell series (Table 5). However, this phenomenon was not remarkable in the Core-NS2 regions (Table 5). These results suggest that codon usage in the NS3-NS5B regions adapts to efficient translation in the human cells in a time-dependent manner. Further long-term cell cultures will clarify this point.

Usefulness of long-term cultured genome-length HCV RNA-replicating cells as a source of resistant HCV for anti-HCV agents

As described above, we demonstrated that genetic mutations and the diversity of HCV RNA expanded during long-term culture of genome-length HCV RNA-replicating cells. From these results, we assumed that these HCV populations that mimic the state of long-term persistent infection become the source of resistant HCV for anti-HCV agents. To clarify this point, we examined the effect of telaprevir, an inhibitor of HCV NS3-4A protease, which is the first directly acting antiviral reagent to be used for the treatment of HCV genotype 1, using 4-year cultured cell lines [31]. To know the effective concentration area, we first evaluated the anti-HCV activity of telaprevir using our previously developed HCV reporter assay systems (HuH-7-derived OR6 [27] and Li23-derived ORL8 [21]). The results revealed that 50% effective concentration (EC_{50}) values were 0.17 μM and 0.14 μM in the OR6 and ORL8 assay systems, respectively, indicating that telaprevir exhibited strong anti-HCV activities in our HCV cell culture systems (data not shown). In reference to these EC_{50} values, we next examined the anti-HCV activity of telaprevir at 0.2 and 0.4 μM for 3 days on OL(4Y), OL8(4Y), OL11(4Y), and OL14(4Y) cells. OL(0Y) cells were also used as a control. Telaprevir at 0.2 and 0.4 μM inhibited approximately 60% and

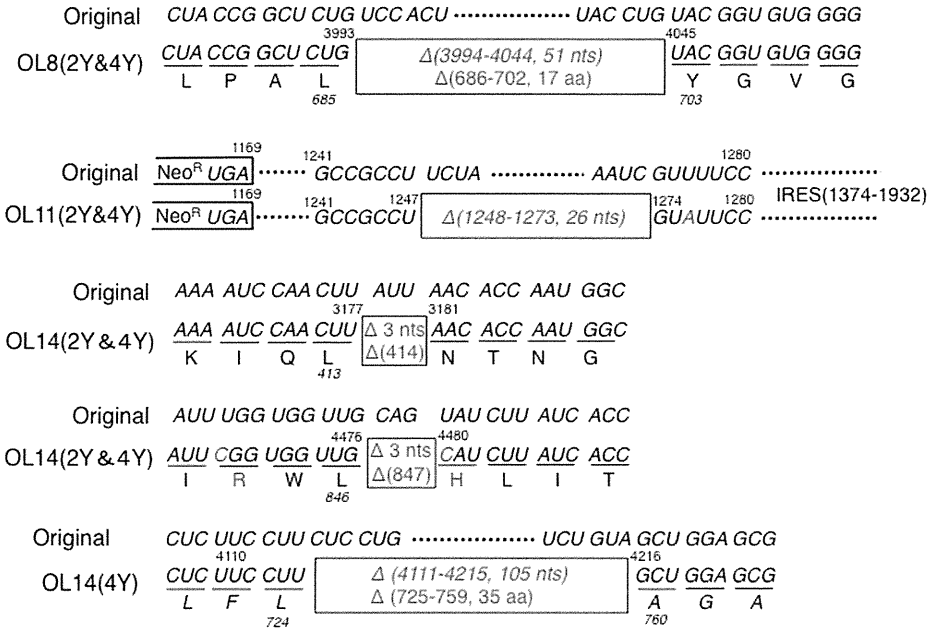

Figure 4. Genetic deletions occurred in the first half of genome-length HCV RNAs during the long-term cell culture. The conservative deleted portions in the genome-length HCV RNAs derived from OL8(2Y), OL8(4Y), OL11(2Y), OL11(4Y), OL14(2Y), or OL14(4Y) cells were shown by boxes. The original sequence was from ON/C-5B/QR,KE,SR RNA [21].
doi:10.1371/journal.pone.0091156.g004

80%, respectively, of HCV RNA replication on OL(0Y) cells, as expected from the results of the reporter assay, and that the anti-HCV activities of telaprevir on OL(4Y), OL11(4Y), and OL14(4Y) cells were similar to that on OL(0Y) cells (Fig. 7A). Unexpectedly, however, HCV RNA replication on OL8(4Y) cells was highly sensitive to telaprevir. Approximately 97% of HCV RNA replication was inhibited by 0.2 μM of telaprevir (Fig. 7A). These results suggest that HCV mutations that occur during long-term cell culture do not control the anti-HCV activity of telaprevir. Next we examined the possibility that long-term cultured cells can become the source of telaprevir-resistant HCV. First, OL(0Y) and OL(4Y) cells were treated with or without 0.4 μM of telaprevir (3 times at 6-day intervals) and 0.8 μM of telaprevir (3 times at 6-day intervals) in the presence of G418. The growth of the cells treated with telaprevir first slowed but then recovered. In this stage, we checked the anti-HCV activity of telaprevir at 0.2 μM for 3 days on telaprevir-treated OL(0Y) and OL(4Y) cells (designated OL(0Y)T and OL(4Y)T cells, respectively) with untreated OL(0Y) and OL(4Y) cells. The results clearly indicated that OL(0Y)T and OL(4Y)T cells completely converted telaprevir-sensitive phenotypes into telaprevir-resistant phenotypes (Fig. 7B). It is noteworthy that telaprevir-resistant OL(4Y)T cells were provided without a decrease in the level of HCV RNA replication. These results suggest that long-term cultured OL(4Y) cells may easily convert the phenotypes against anti-HCV drugs such as telaprevir.

Discussion

In the present study, using Li23-derived cells unlike HuH-7, we characterized the genetic evolution and dynamics of HCV in the long-term culture of four kinds of genome-length HCV RNA-replicating cells, and demonstrated that genetic mutations of HCV accumulated and the genetic diversity of HCV expanded in a time-dependent manner. The GC content of HCV RNA was also significantly increased in a time-dependent manner. These phenomena, including the increased mutation rates, were consistent with those observed in the previous study using HuH-7-derived cell culture systems [19,20]. However, we detected several in-frame deletions in the structural regions, suggesting that the environment maintaining RNA genomic stability differs between Li23 and HuH-7 cells. Furthermore, we observed for the first time that GC content in nonstructural regions increased for codon optimization in human cells. Moreover, we demonstrated that the long-term cultured genome-length HCV RNA-replicating cells were useful as a library source for the isolation or characterization of resistant HCVs against anti-HCV agents.

Using Li23-derived cell culture systems, we observed that the mutation rates of HCV RNAs were $4.0–9.0\times10^{-3}$ and $2.7–4.0\times10^{-3}$ base substitutions/site/year in 5′-terminus-NS2 regions and NS3-NS5B regions, respectively. These values were 2.1–6.4 times and 1.4–2.9 times higher than those ($1.4–1.9\times10^{-3}$ base substitutions/site/year) previously obtained in chimpanzees [15,16] and in a patient [14] with chronic hepatitis C. Since we previously found that the mutation rates of genome-length HCV RNAs were $4.4–7.4\times10^{-3}$ and $2.5–3.7\times10^{-3}$ base/substitutions/site/year in 5′-terminus-NS2 regions and NS3-NS5B regions, respectively, using HuH-7-derived cell culture systems [21], most of the mutation rates were proved not to change, regardless of the cell type. Since the selective pressures of the humoral immune responses [17] targeting the envelope proteins and cellular immune responses [18] targeting all HCV proteins function *in vivo*, the mutation rates obtained using the cell culture systems without the immunological pressure would be reasonable values as a potential mutation rate of HCV in RNA replication.

Thus far, many studies using the HCV replicon system, including the whole-virus system of JFH-1 strain HCV, have clarified the aa positions that are essential for the efficient HCV reproduction [32–34]. On the basis of those reports, we made lists of functional aas in HCV genotype 1 (partly genotype 2a) (Tables S1 and S2) and then checked whether the position of each

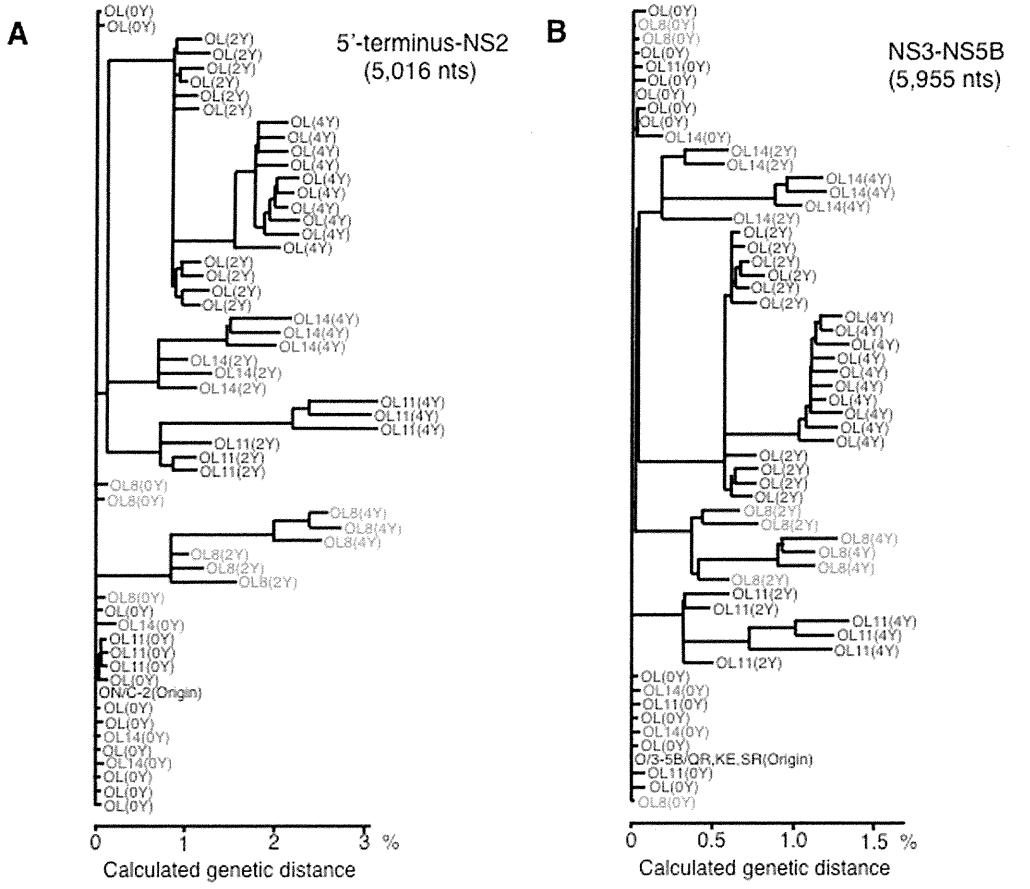

Figure 5. Phylogenetic trees of genome-length HCV RNA populations obtained in long-term cell culture. The phylogenetic trees are depicted on the basis of nucleotide sequences of all cDNA clones obtained by 0-year, 2-year, and 4-year cultures of OL, OL8, OL11, and OL14 cells. (A) The 5′-terminus-NS2 regions of genome-length HCV RNA. ON/C-2 indicates the original sequences of the 5′-terminus-NS2 regions of ON/C-5B/QR,KE,SR RNA [21]. (B) The NS3-NS5B regions of genome-length HCV RNA. O/3-5B/QR,KE,SR indicates the original sequences of the NS3-NS5B regions of ON/C-5B/QR,KE,SR RNA [21].
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functional aa was the same as the position of the aa substitution detected in this study. This investigation revealed that most of the functional aas were conserved during the 4-year culture of genome-length HCV RNA-replicating cells, suggesting that the basic HCV RNA replication mechanism does not change during long-term cell culture. However, as we observed several aa substitutions in the Core from OL11 series, the function of the Core may be lost in long-term-cultured OL11 cells, although the Core is not essential for RNA replication.

Although our report is the only one to conduct genetic variation and diversity analyses of HCV during the long-term HCV RNA replication of genotype 1b in cell culture, several similar reports use long-term HCV RNA (JFH-1 strain of genotype 2a)-replicating HuH-7-derived cells [35–41]. In those studies, many adaptive mutations were found as the result of long-term persistent HCV reproduction. Although it is a bit complicated to decide the corresponding aa positions exactly, as the O strain and JFH-1 strain belong to different genotypes, we examined whether the substituted aas detected in this study were found in those adaptive mutations obtained from reports using the JFH-1 strain. We noticed that only I414T substituted between 2- and 4-year cultures of OL cells was the same aa substitution as the JFH-1 strain (Table S3). It is unlikely that this substitution functions as an adaptive mutation for RNA replication because the HCV RNA level decreased between 2- and 4-year cultures (Fig. 1 and [26]). It is also unlikely that this substitution increases virus production because virus particles were not produced from the cells cultured for 2 or 4 years (Fig. S1). However, we can exclude the possibility that other aa substitutions detected at the corresponding positions to the JFH-1 strain are adaptive mutations.

In our previous study using HuH-7-derived cell culture systems, we noticed that none of the aa substitutions were detected in the N-terminal half (242 aa of aa 1976 to 2217) of the NS5A after 2-year cultures, suggesting that this region would be the most critical for maintaining RNA replication. However, we detected many aa substitutions in this region in all Li23-derived cell lines after 2-year or 4-year cultures (Table 3). These were the following aa substitutions: L2003F and H2057R in OL series; R1978K, D1979E, K1998R, S2079Y, and K2212R in OL8 series; K2050R, F2099Y, and T2217I in OL11 series; L2125V in OL14 series. These results suggest that the N-terminal half of NS5A also possesses further variability to allow a better environment for HCV RNA reproduction. Another interesting feature we noticed is that several aa substitutions were spontaneously detected in the interferon (IFN) sensitivity determining region (ISDR) [42] (aa 2209–2248) and in the IFN/Ribavirin (RBV) resistance-determining region (IRRDR) [43] (aa 2334–2379) of NS5A in the cells without IFN or RBV treatment. In

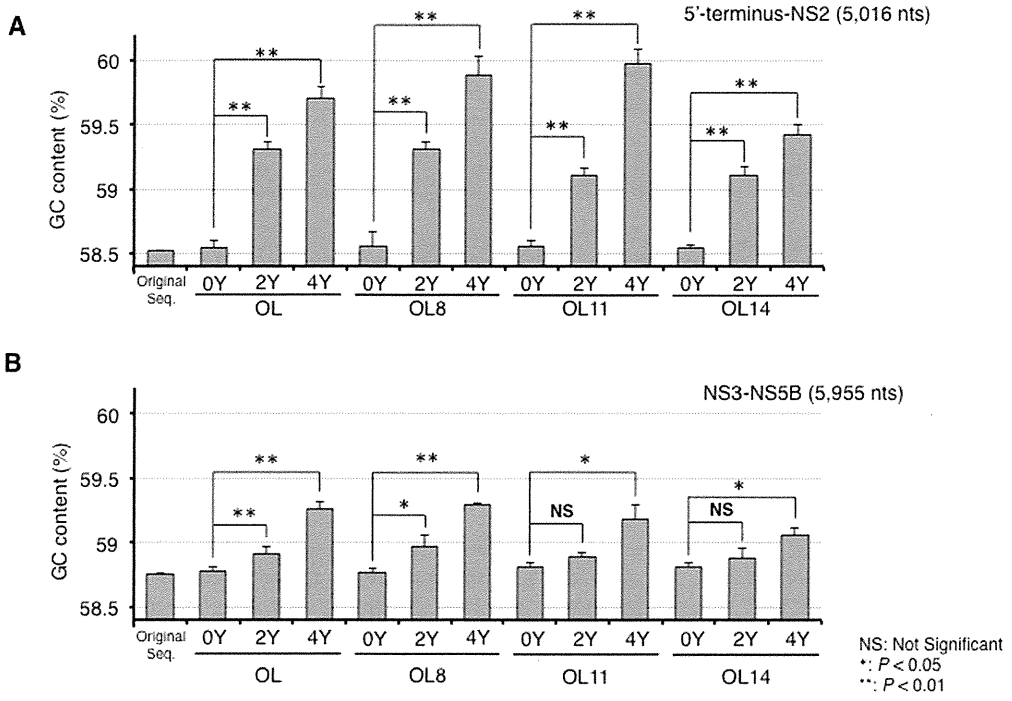

Figure 6. Increased GC content of genome-length HCV RNAs occurring in long-term RNA replication. The GC content of cDNA clones obtained by 0-year, 2-year, and 4-year culture of OL, OL8, OL11, and OL14 cells was calculated. The values indicate the means of 10 clones (OL) or 3 clones (OL8, OL11, or OL14). (A) The 5′-terminus-NS2 regions. (B) The NS3-NS5B regions.
doi:10.1371/journal.pone.0091156.g006

Table 4. Base substitution patterns occurred in genome-length HCV RNAs during the long-term cell culture.

	Average numbers of base substitutions per cDNA clone										
Base									**Sum**		**HuH-7-derived**
substitution	OL	OL	OL8	OL8	OL11	OL11	OL14	OL14	OL~OL14	OL~OL14	O, OA, OB, OD&OE
pattern	(2Y)	(4Y)	(2Y)	(4Y)	(2Y)	(4Y)	(2Y)	(4Y)	(2Y)	(4Y)	(2Y)*
Transition											
U →C	46.0	79.9	38.7	69.3	31.0	74.7	32.7	51.0	37.1±6.8	68.7±12.6	32.1±3.5
A →G	25.0	39.4	39.3	77.0	26.0	71.3	29.3	57.7	29.9±6.5	61.4±16.7	30.5±6.2
C →U	13.3	22.7	14.7	27.0	15.3	32.7	16.3	29.7	14.9±1.3	28.0±4.2	11.3±2.2
G →A	8.7	15.5	10.7	20.0	10.3	19.0	11.7	24.3	10.4±1.3	19.7±3.6	10.5±4.0
Transversion											
C →A	6.1	9.1	9.0	9.7	1.3	6.3	4.0	3.3	5.1±3.3	7.1±2.9	1.7±1.1
U →G	2.2	6.5	1.0	6.0	2.7	7.0	1.0	6.7	1.7±0.9	6.6±0.4	2.5±1.3
A →U	1.4	1.8	4.7	13.0	2.3	8.0	2.7	2.7	2.8±1.4	6.4±5.2	2.2±1.4
U →A	1.8	3.5	3.3	4.3	5.7	10.0	1.7	5.7	3.1±1.9	5.9±2.9	2.8±1.3
A →C	3.9	5.7	3.0	3.7	1.0	4.7	3.0	4.3	2.7±1.2	4.6±0.8	3.9±0.8
G →U	1.2	2.2	1.3	2.3	1.3	4.3	3.3	3.3	1.8±1.0	3.0±1.0	1.9±0.6
G →C	3.3	4.1	1.0	1.7	1.3	2.3	1.0	1.0	1.7±1.1	2.3±1.3	2.4±1.6
C →G	0.2	3.4	1.0	1.3	1.0	0.0	0.7	2.0	0.7±0.4	1.7±1.4	1.5±1.3

Base substitutions were counted by the comparison with the sequence of genome-length HCV RNA (ON/C-5B/QR,KE,SR [20]).
*Data from the previous study [20].
doi:10.1371/journal.pone.0091156.t004

Table 5. Contribution degrees of the G- and C-ending codons except AGG and UUG codons in the GC content increase during 2-year or 4-year cell cultures.

C-NS2				
	OL	**OL8**	**OL11**	**OL14**
2Y culture	9.3*/24.0** (39%)	7.3/27.7 (26%)	4.3/20.6 (21%)	3.0/17.4 (17%)
4Y culture	9.8/38.1 (26%)	6.7/49.8 (13%)	17.7/54.7 (32%)	5.0/24.3 (21%)
NS3-5B				
	OL	**OL8**	**OL11**	**OL14**
2Y culture	2.1/9.0 (23%)	4.0/12.7 (31%)	0/7.9 (0%)	3.3/6.7 (49%)
4Y culture	12.5/29.9 (42%)	13.7/32.0 (43%)	6.7/25.8 (24%)	16.0/18.0 (89%)

*The increased numbers of G- and C-ending codons except AGG and UUG codons per cDNA clone.
**The increased numbers of G and C per cDNA clone.
doi:10.1371/journal.pone.0091156.t005

ISDR, K2212R (OL8 series), T2217I (OL11 series), D2220G (OL8 and OL14 series), and S2246P (OL series) were detected. Furthermore, in IRRDR, T2336S (OL11 series), S2338P (OL series), S2342P (OL8 series), L2347R (OL8 series), T2351A (OL11 series), F2352V (OL8 series), F2352S (OL11 series), F2352L (OL14 series), S2355P (OL series), S2355T (OL14 series), T2364A (OL8 series), P2369H (OL series), S2373P (OL14 series), D2374N (OL14 series), and D2377G (OL8 series) were detected (Table 3). These aa substitutions except for D2220G also appeared in a seemingly random manner, although aa 2352 and 2355 were hot spots for aa substitutions in the Li23-derived cell culture system but not in the HuH-7-derived cell culture system [20]. These results suggest that the sensitivity to IFN or RBV might change during long-term cell culture, although it has not yet been proved that variations in ISDR or IRRDR may change the sensitivity to IFN or RBV.

When we explored this possibility, we newly noticed that L2003F (L31F in NS5A) was detected as a conservative aa in

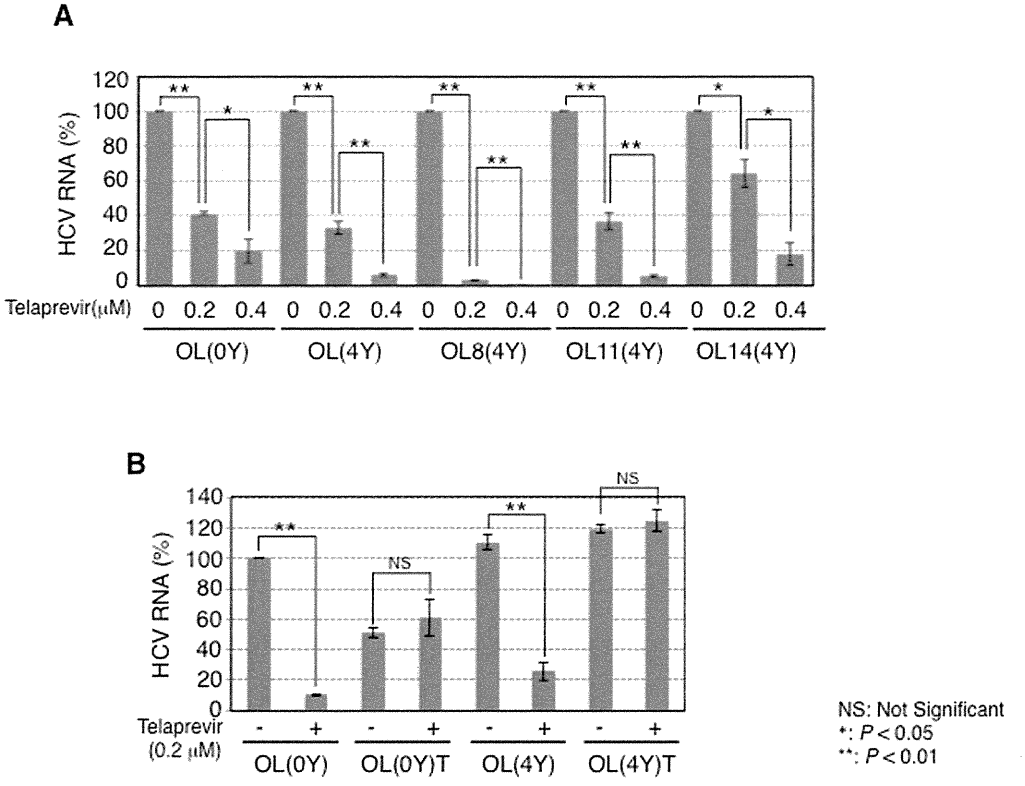

Figure 7. Sensitivity to telaprevir of the 4-year cultured genome-length HCV RNA-replicating cells. (A) Telaprevir sensitivities on genome-length HCV RNA replication in OL(4Y), OL8(4Y), OL11(4Y), and OL14(4Y) cells. OL(0Y) cells were used as a control. The cells were treated with telaprevir for 72 h, and then the levels of intracellular genome-length HCV RNA were quantified by LightCycler PCR. (B) Telaprevir-treated OL(0Y) and OL(4Y) cells (designated as OL(0Y)T and OL(4Y)T, respectively) became telaprevir-resistant easily. Telaprevir treatment and quantitative RT-PCR were preformed as shown in (A).
doi:10.1371/journal.pone.0091156.g007

OL(2Y) and OL(4Y) cells. F in aa 2003 has been reported as an aa showing low-level resistance to daclatasvir (BMS-790052), an NS5A inhibitor that will soon serve as a clinical cure [44]. Furthermore, V1081A (V55A in NS3) was also detected as a conservative aa in OL(4Y) cells. A in aa 1081 has been reported as an aa showing low-level resistance to boceprevir, an NS3-4A serine protease inhibitor that was approved as a new direct-acting antiviral drug [45]. These facts indicate that clones resistant to anti-HCV agents emerge naturally without treatment. Since V1081A and L2003F were detected in all HCV clones derived from OL(4Y) cells, these aa substitutions may possess some advantage for cell proliferation. Furthermore, as a minor population, a larger number of resistant HCV clones may emerge from such a long-term cell culture. Although neither daclatasvir nor boceprevir was available in this study, we demonstrated that telaprevir-treated OL(4Y) cells completely and easily converted a telaprevir-sensitive phenotype into a telaprevir-resistant phenotype without a decrease in the level of HCV RNA replication, suggesting that telaprevir-resistant HCV clones rapidly became dominant populations in the telaprevir-treated OL(4Y) cells.

As well as V1081A and L2003F, we noticed for the first time that D2292E (D320E in NS5A) appeared in OL(2Y), OL(4Y), OL14(2Y), and OL14(4Y) cells as a conservative aa substitution, although our previous study using HuH-7-derived cells detected D2292E as a conservative aa substitution after 2-year cultures of genome-length HCV RNA-replicating OB and OE cells [20]. It has been reported that D2292E is an aa substitution that causes resistance to cyclosporine (CsA) and other cyclophilin inhibitors, including NIM811 and DEB025 [46,47]. These facts also indicate that the HCV species possessing D2292E substitution can become the main species naturally in cultured cells without CsA or other treatments.

This study demonstrated that a single genome-length HCV RNA could exhibit a remarkable diversity after 4 years in cell culture with RNA replication. Our results, together with previous results, suggest that such diversity of HCV obtained by long-term cell culture may be useful not only for understanding the genetic variations and diversity of HCV but also for the examination of the resistant spectrum of anti-HCV agents.

Supporting Information

Figure S1 No infectious virus production from long-term cultured genome-length HCV RNA-replicating cells. HCV infection to RSc (1×10^4) and ORL8c (5×10^3) cells was performed using the supernatant (each 1 ml after filtering through a 0.20-μm filter [Kurabo, Osaka, Japan]) of OL(0Y), OL(4Y), OL8(4Y), OL11(4Y), or OL14(4Y) cells as an inoculum, as described previously [23]. As a positive control, HCV JFH-1 virus was used for the infection at a multiplicity of infection of 0.1 or 1.0. At 7 days and 8 days, (A) the levels of Core in the supernatant after filtering through a 0.20-μm filter were quantified by enzyme-linked immunosorbent assay (Mitsubishi Kagaku Bio-Clinical Laboratories, Tokyo, Japan) and (B) the levels of intracellular HCV RNA were quantified by LightCycler PCR, as described previously [21,27].
(TIF)

Figure S2 Phylogenetic trees of deduced aa in ORF of genome-length HCV RNA populations obtained in long-term cell culture. The phylogenetic trees are depicted on the basis of aa sequences deduced from all cDNA clones obtained by 0-year, 2-year, and 4-year cultures of OL, OL8, OL11, and OL14 cells. (A) The Core-NS2 regions in ORF of genome-length HCV RNA. O/C-2 indicates the original aa sequences of the Core-NS2 regions in ORF of ON/C-5B/QR,KE,SR RNA [21]. (B) The NS3-NS5B regions in ORF of genome-length HCV RNA. O/3-5B/QR,KE,SR indicates the original aa sequences of the NS3-NS5B regions in ORF of ON/C-5B/QR,KE,SR RNA [21].
(TIF)

Table S1 Comparative list of functional aas in HCV genotype 1 and aa substitutions detected in this study (I).
(DOC)

Table S2 Comparative list of functional aas in HCV genotype 1 and aa substitutions detected in this study (II).
(DOC)

Table S3 Hereditary aa substitutions detected in persistent HCV JFH-1 (genotype 2a) infection; comparison with aa substitutions detected in this study.
(DOC)

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Author Contributions

Conceived and designed the experiments: NK. Performed the experiments: NK HS YU HD. Analyzed the data: NK HS YU HD. Contributed reagents/materials/analysis tools: KM SS HD MI. Wrote the paper: NK.

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Adenosine Kinase Is a Key Determinant for the Anti-HCV Activity of Ribavirin

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Ribavirin (RBV) is often used in conjunction with interferon-based therapy for patients with chronic hepatitis C. There is a drastic difference in the anti–hepatitis C virus (HCV) activity of RBV between the HuH-7-derived assay system, OR6, possessing the RBV-resistant phenotype (50% effective concentration [EC_{50}]: >100 μM) and the recently discovered Li23-derived assay system, ORL8, possessing the RBV-sensitive phenotype (EC_{50}: 8 μM; clinically achievable concentration). This is because the anti-HCV activity of RBV was mediated by the inhibition of inosine monophosphate dehydrogenase in RBV-sensitive ORL8 cells harboring HCV RNA. By means of comparative analyses using RBV-resistant OR6 cells and RBV-sensitive ORL8 cells, we tried to identify host factor(s) determining the anti-HCV activity of RBV. We found that the expression of adenosine kinase (ADK) in ORL8 cells was significantly higher than that in RBV-resistant OR6 cells harboring HCV RNA. Ectopic ADK expression in OR6 cells converted them from an RBV-resistant to an RBV-sensitive phenotype, and inhibition of ADK abolished the activity of RBV. We showed that the differential ADK expression between ORL8 and OR6 cells was not the result of genetic polymorphisms in the ADK gene promoter region and was not mediated by a microRNA control mechanism. We found that the 5' untranslated region (UTR) of ADK messenger RNA in ORL8 cells was longer than that in OR6 cells, and that only a long 5' UTR possessed internal ribosome entry site (IRES) activity. Finally, we demonstrated that the long 5' UTR functioned as an IRES in primary human hepatocytes. *Conclusion*: These results indicate that ADK acts as a determinant for the activity of RBV and provide new insight into the molecular mechanism underlying differential drug sensitivity. (HEPATOLOGY 2013;58:1236-1244)

See Editorial on Page 1203

Hepatitis C virus (HCV) is an enveloped RNA virus, the genome of which consists of a positive-stranded 9.6-kilobase (kb) RNA encoding 10 structural and nonstructural (NS) proteins.[1] The combination of pegylated-interferon (Peg-IFN) and ribavirin (RBV) was the standard treatment for patients with chronic hepatitis C (CHC) until last year, when a new triple-agent combination therapy using an inhibitor of HCV NS3-4A protease (i.e., either telaprevir or boceprevir), in combination with Peg-IFN and RBV, was started.[2] The sustained virologic response (SVR) rate of genotype 1 using this new therapy is expected to increase from 55% to more than 70%.[3] However, there has also been an increase in side effects by RBV in the triple therapy, including several severe side effects, such as skin rash by telaprevir, ageusia by boceprevir, and advanced anemia by telaprevir/boceprevir.[3,4]

Abbreviations: Abs, antibodies; ADK, adenosine kinase; 5azaC, 5-azacytidine; CC_{50}, 50% cytotoxic concentration; cDNA, complementary DNA; CHC, chronic hepatitis C; EC_{50}, 50% effective concentration; GTP, guanosine triphosphate; HCV, hepatitis C virus; HPLC, high-performance liquid chromatography; IMPDH, inosine monophosphate dehydrogenase; IMP, inosine-5'-monophosphate; IRES, internal ribosome entry site; kb, kilobase; mRNA, messenger RNA; NS, nonstructural protein; nt, nucleotide; ORF, open reading frame; 4-PBA, 4-phenylbutyric acid; Peg-IFN, pegylated-interferon; PHHs, primary human hepatocytes; RACE, rapid amplification of cDNA ends; RBV, ribavirin; RL, renilla luciferase; RMP, RBV 5'-monophosphate; RT-PCR, reverse transcription-polymerase chain reaction; siRNA, small interfering RNA; miRNAs, microRNAs; SNP, single-nucleotide polymorphism; SVR, sustained virologic response; UTR, untranslated region.

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The main hurdle to resolving the side-effect profile is that the anti-HCV mechanism of RBV is not well understood, although several possible mechanisms have been proposed.[5,6] To date, there has been no cell-culture system enabling analysis of the anti-HCV mechanism of RBV at clinically achievable concentrations (5-14 μM), because the human hepatoma cell line, HuH-7, which has been the only cell line available for robust HCV replication, is not sensitive to RBV.[5,7,8] Indeed, we also observed that the 50% effective concentration (EC_{50}) of RBV against HCV RNA replication in our developed HuH-7-derived assay system (OR6), in which the genome-length HCV RNA (O strain of genotype 1b) encoding renilla luciferase (RL) replicates efficiently, was more than 100 μM, and 50% cytotoxic concentration (CC_{50}) was also more than 100 μM.[9,10]

On the other hand, we recently found that a new human hepatoma cell line, Li23, whose gene expression profile was distinct from that of HuH-7, enabling efficient HCV RNA replication and persistent HCV production, was sensitive to RBV.[10-12] Indeed, the EC_{50} value of RBV against HCV RNA replication in our developed Li23-derived assay system (ORL8), which is comparable to the OR6 assay system, was 8.7 μM, and the CC_{50} value was more than 100 μM.[10] It was noteworthy that this EC_{50} value was equivalent to the clinically achievable concentrations of RBV. Therefore, this finding led us to analyze the anti-HCV mechanism of RBV, and, consequently, we found that the anti-HCV activity of RBV was mediated by the inhibition of inosine monophosphate dehydrogenase (IMPDH), and that IMPDH was required for HCV RNA replication.[10]

From these findings, we anticipated that the comparative analysis of RBV-sensitive ORL8 cells and RBV-resistant OR6 cells would lead to the identification of host factor(s) determining the anti-HCV activity of RBV. Here, we report the finding that adenosine kinase (ADK) is an essential determinant of the anti-HCV activity of RBV.

Materials and Methods

Cell Cultures. HuH-7- and Li23-derived cells and PH5CH8 cells were maintained as described previously.[11] HT17 cells were cultured in Dulbecco's modified Eagle's medium supplemented with 10% fetal bovine serum. Primary human hepatocytes (PHHs; PhoenixBio, Higashihiroshima, Japan) were also maintained in the medium for the Li23-derived cells.

Reagents. RBV was kindly provided by Yamasa (Chiba, Japan).

Inosine-5'-monophosphate (IMP) and nucleoside triphosphates (cytidine triphosphate, uridine triphosphate, adenosine triphosphate, and guanosine triphosphate [GTP]) were also purchased from Yamasa. ABT-702 was purchased from Calbiochem (San Diego, CA). 5-azacytidine (5azaC) and 4-phenylbutyric acid (4-PBA) were purchased from Sigma-Aldrich (St. Louis, MO).

Western Blotting Analysis. Preparation of cell lysates, sodium dodecyl sulfate polyacrylamide gel electrophoresis, and immunoblotting analysis were performed as previously described.[13] Polyclonal-ADK (ab54818; Abcam, Cambridge, MA), monoclonal-ADK (F-5; Santa Cruz Biotechnology, Santa Cruz, CA), and β-actin (AC-15; Sigma-Aldrich) antibodies (Abs) were used.

Reverse-Transcription Polymerase Chain Reaction. Reverse-transcription polymerase chain reaction (RT-PCR) was performed to detect ADK messenger RNA (mRNA), as described previously,[14] using the primer sets (ADKF and ADKR; ADK-5'-untranslated region [UTR]-187nts and ADK-5'-UTR checkR) listed in Supporting Table 1.

Quantitative RT-PCR. Quantitative RT-PCR analysis for ADK mRNA was performed using a real-time LightCycler PCR (Roche Diagnostics, Indianapolis, IN), as described previously,[11] with the primer sets (ADKF and ADKR; ADK-5'UTR-384nts and ADK-5'UTR checkR; ADK-5'UTR-318nts and ADK-5'UTR checkR; ADK-5'UTR-187nts and ADK-5'UTR checkR; ADK-5'UTR-125nts and ADK-5'UTR checkR) listed in Supporting Table 1.

RL Assay. RL assay was performed as described previously.[9] Experiments were performed at least in triplicate.

High-Performance Liquid Chromatography Analysis. Quantitative high-performance liquid chromatography (HPLC) analysis was performed using the

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