Evidence for Novel Hepaciviruses in Rodents

To cite this version:

HAL Id: hal-02395310
https://hal.umontpellier.fr/hal-02395310
Submitted on 5 Dec 2019

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L’archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Distributed under a Creative Commons Attribution 4.0 International License
Evidence for Novel Hepaciviruses in Rodents

Jan Felix Drexler1, Victor Max Corman1, Marcel Alexander Müller1, Alexander N. Lukashev2, Anatoly Gmyl2,3, Bruno Coutard4, Alexander Adam5, Daniel Ritz1, Lonneke M. Leijten6, Debby van Riel6, Rene Kallies1, Stefan M. Klose7, Florian Gloza-Rausch1,8, Tabea Binger1, Augustina Annan9, Yaw Adu-Sarkodie10, Samuel Oppong10, Mathieu Bourgarel11, Daniel Rippa12, Bernd Hoffmann13, Mathias Schlegel14, Beate M. Kümmerer1, Detlev H. Krüger15, Jonas Schmidt-Chanasit16, Alvaro Aguilar Setién17, Veronika M. Cottontail17, Thiravat Hemachudha18, Supaporn Wacharapluesadee18, Klaus Osterrieder19, Ralf Bartenschlager12, Sonja Matthee20, Martin Beer13, Thijs Kuiken6, Chantal Reusken21, Eric M. Leroy22,23, Rainer G. Ulrich14, Christian Drosten1

1 Institute of Virology, University of Bonn Medical Centre, Bonn, Germany, 2 Chumakov Institute of Poliomyelitis and Viral Encephalitides, Moscow, Russia, 3 Lomonosov Moscow State University, Moscow, Russia, 4 Architectures et Fonctions des Macromolécules Biologiques, UMR 7257 CNRS and Aix-Marseille University, Marseille, France, 5 Institute of Pathology, University of Cologne Medical Centre, Cologne, Germany, 6 Erasmus MC, Department of Viroscience, Rotterdam, The Netherlands, 7 Institute of Experimental Ecology, University of Ulm, Ulm, Germany, 8 Noctalis, Centre for Bat Protection and Information, Bad Segeberg, Germany, 9 Kumasi Centre for Collaborative Research in Tropical Medicine (KCCR), Kumasi, Ghana, 10 Kwanje Nkhumu University of Science and Technology, Kumasi, Ghana, 11 Centre de Cooperation Internationale de Recherche en Agronomie pour le Développement, UPR AGIRs, Montpellier, France, 12 Department of Infectious Diseases, Molecular Virology, Medical Faculty, Heidelberg University, Heidelberg, Germany, 13 Friedrich-Loeffler-Institut, Institute for Virus Diagnostics, Greifswald–Insel Riems, Germany, 14 Friedrich-Loeffler-Institut, Institute for Novel and Emerging Infectious Diseases, Greifswald–Insel Riems, Germany, 15 Institute of Medical Virology (Helmut Ruska Haus), Charité Medical School, Berlin, Germany, 16 Bernhard Nocht Institute for Tropical Medicine, Department of Virology, Hamburg, Germany, 17 Unidad de Investigación Médica en Inmunología, Hospital de Pediatría, México DF, Mexico, 18 Chulalongkorn University, Faculty of Medicine, Neuroscience Center for Research and Development, Bangkok, Thailand, 19 Institute of Virology, Free University of Berlin, Department of Veterinary Medicine, Berlin, Germany, 20 Department of Conservation Ecology and Entomology, Stellenbosch University, Stellenbosch, South Africa, 21 Netherlands Center for Infectious Disease Control, Bilthoven, The Netherlands, 22 Centre International de Recherches Médicales de Franceville, Franceville, Gabon, 23 Institut de Recherche pour le Développement, UMR 224 (MIVEGEC), IRD/CNRS/UM1, Montpellier, France

Abstract

Hepatitis C virus (HCV) is among the most relevant causes of liver cirrhosis and hepatocellular carcinoma. Research is complicated by a lack of accessible small animal models. The systematic investigation of viruses of small mammals could guide efforts to establish such models, while providing insight into viral evolutionary biology. We have assembled the so-far largest collection of small-mammal samples from around the world, qualified to be screened for bloodborne viruses, including sera and organs from 4,770 rodents (41 species); and sera from 2,939 bats (51 species). Three highly divergent rodent hepacivirus clades were detected in 27 (1.8%) of 1,465 European bank voles (Myodes glareolus) and 10 (1.9%) of 518 South African four-striped mice (Rhabdomys pumilio). Bats showed anti-HCV immunoblot reactivities but no virus detection, although the genetic relatedness suggested by the serologic results should have enabled RNA detection using the broadly reactive PCR assays developed for this study. 210 horses and 858 cats and dogs were tested, yielding further horse-associated hepaciviruses but none in dogs or cats. The rodent viruses were equidistant to HCV, exceeding by far the diversity of HCV and the canine/equine hepaciviruses taken together. Five full genomes were sequenced, representing all associated hepaciviruses but none in dogs or cats. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.


Editor: David Wang, Washington University, United States of America

Received February 19, 2013; Accepted April 22, 2013; Published June 20, 2013

Copyright: © 2013 Drexler et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Funding: This study was funded by the European Union FP7 projects EMPERIE (Grant agreement number 223498), EVA (Grant agreement number 228292) and ANTIGONE (Grant agreement number 278976) and the German Research Foundation (DFG grant DR 772/3-1, KA1241/18-1) to CD; the German Federal Ministry of Education and Research (BMBF) through the National Research Platform for Zoonoses (project code 01KI1018), the Umweltbundesamt (FKZ 370941401), and the Robert Koch-Institut (FKZ 1362/1-924) to RGU; and the Thailand Research Fund (grant RDGS420089) to TH and SW. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing Interests: The authors have declared that no competing interests exist.

* E-mail: drosten@virology-bonn.de
Author Summary

The hepatitis C virus (HCV) is one of the most relevant causes of liver disease and cancer in humans. The lack of a small animal model represents an important hurdle on our way to understanding, treating, and preventing hepatitis C. The investigation of small mammals could identify virus infections similar to hepatitis C in animals that can be kept in laboratories, such as rodents, and can also yield insights into the evolution of those ancient virus lineages out of which HCV developed. Here, we investigated a worldwide sample of 4,770 rodents, 2,939 bats, 210 horses and 858 cats and dogs for HCV-related viruses. New viruses were discovered in European bank voles (Myodes glareolus) and South African four-striped mice (Rhabdomys pumilio). The disease in bank voles was studied in more detail, suggesting that infection of the liver occurs with similar symptoms to those caused by HCV in humans. These rodents might thus enable the development of new laboratory models of hepatitis C. Moreover, the phylogenetic history of those viruses provides fascinating new ideas regarding the evolution of HCV ancestors.

Introduction

Hepatitis C virus is one of the leading causes of human morbidity and mortality due to hepatitis, liver cirrhosis, and hepatocellular carcinoma [1,2,3]. It has become the main reason for liver transplantation in developed countries and represents an economic burden exceeding 1 billion US$ of direct health costs [4,5]. New estimates of the burden of disease suggest at least 185 million individuals worldwide have been seropositive in 2005, with a tendency to increase [6]. Treatment has considerably improved due to the optimization of antiviral regimens and the advent of new antiviral drugs [7,8,9]. However, treatment in resource-limited settings is hardly accessible [10]. The most effective instrument to prevent new infections with HCV would be a prophylactic vaccine. Unfortunately, chimpanzees are the only known animal species to adequately reflect human HCV infection [11]. Vaccine development is hampered by the lack of a small animal model accessible at early stages of vaccine development [12,13]. Mice cannot be infected with HCV [14], but rats and mice engrafted with human hepatoma cells or transgenic for human CD81 and other co-receptor molecules have been proposed [12,15,16,17]. Mouse-adapted HCV has also been generated [16,18]. Still, these models are highly demanding from a technical point of view and reflect only parts of the pathogenesis and lifecycle of HCV, precluding their wide application [12,19].

A HCV-related hepacivirus of unknown origin, termed GBV-B, has been used as a surrogate model for HCV infection involving New World monkeys, where it causes hepatitis upon experimental inoculation [20,21]. The use of a surrogate model based on a related virus indicates a way to study HCV pathogens and immunity, even though neither monkeys nor apes are acceptable laboratory models in terms of accessibility and ethics [12,13,22]. Non-Primate hepacviruses related to HCV have also been detected in dogs and horses [23,24]. While horses cannot be considered as laboratory models, dogs at least have compatible body sizes. However, additional to ethical controversies, infected dogs showed grossly deviating pathology in that they appeared to have higher virus concentrations in respiratory specimens than in the liver [23]. So far there is no evidence of antibodies against the virus in dogs, limiting their utility as a vaccination challenge model [23,24]. No hepacviruses have been detected in other animals that could be kept in laboratories with reasonable effort, and under ethically acceptable conditions.

The targeted identification of animal hepacviruses might help elucidating the obscure origins of HCV and yield more accessible HCV surrogate models. We have recently demonstrated that the systematic investigation of small mammal reservoirs can yield novel viruses that are genetically closely related to human pathogenic viruses, such as the paramyxoviruses mumps and Nipah virus [25]. Biological and ecological considerations direct research interests to animals with properties supportive of virus maintenance. The close social interaction of certain bat species forming large and dense social groups favors virus maintenance [25,26]. Virus spreading by bats may be facilitated by their migratory lifestyle, but also by human activities such as hunting of bats as bushmeat and human invasion of remote habitats [27,28,29]. Several rodent species are also in focus as potential virus reservoirs, as they constitute habitat generalists and follow human civilization, providing opportunities for virus transmission [30,31]. Even though rodents form smaller social groups than bats, some rodent species have a high population turnover, which should enable efficient maintenance of viruses through the continuous replenishment of susceptible individuals [26,32]. Among terrestrial mammals, rodents and bats together constitute about two thirds of the 5,487 known mammalian species [33]. Screening of wild mammals with a view on laboratory models should be oriented by criteria such as small body size and the ability to adapt to laboratory conditions, which applies to rodents, but not bats [12,34]. Here we have investigated 7,709 bats and rodents pertaining to 92 species sampled globally in ten tropical and temperate countries. The investigation was complemented by a comparison of virus diversity in 1,068 horses, cats and dogs.

Materials and Methods

Ethics statement

All animals were handled according to national and European legislation, namely the EU council directive 86/609/EEC for the protection of animals. For all individual sampling sites, study protocols including trapping, sampling and testing of animals were approved by the responsible animal ethics committees as detailed below. All efforts were made leave animals unharmed or to minimize suffering of animals. Any surgical procedure was performed under sodium pentobarbital/ketamine anesthesia. Trapping of rodents in Germany was conducted in the framework of hantavirus monitoring activities and was coordinated by the Friedrich-Loeffler-Institut, the Federal Research Institute for Animal Health. Rodent monitoring in the federal states Mecklenburg-Western Pomerania, Thuringia, Baden-Wuerttemberg and North Rhine Westphalia was coordinated by the Julius Kuhn Institute (permit numbers LALLF M-V/TSD/7221.3-2.1-030/09, TH 15-107/09, BW 35-9185.82/0261 and NW 20.09.210). Additional animals were provided by forest institutions and pest management institutions in Mecklenburg-Western Pomerania, Thuringia, Brandenburg, Lower Saxony, Baden-Wuerttemberg, Berlin and Budapest which caught and sacrificed the animals during their official duties without necessity of further permits. Rodents and other small mammals trapped by cats were included in the investigations. Rodent sampling in South Africa was licensed by Cape Nature under permit numbers 317/2003 and 360/2003. Rodent sampling in The Netherlands was licensed by the Dutch animal ethic committee (DEC) under permit numbers 200700119, 200800113 and 200800055. Rodent sampling in Thailand was granted by the Agricultural Zoology Research Group, Department of Agriculture, Thailand (permit no. K.U./14-182). Rodent
sampling in Gabon was licensed by the Ministry of Water and Forest, statement 003/MEF/SG/DGFEF/DFC from 2011. Rodent sampling in Mexico was licensed by Secretaría del Medio Ambiente del gobierno de México (SEMARNAT) under permit number SGPA/DGVS/06203/12. Horse, dog and cat samples were collected from regular diagnostic specimens sent to the OIE Reference Laboratory for Equine Influenza and Herpesviruses at the Freie Universität Berlin. Sampling and capture of bats as well as sample transfers were done under wildlife permits and ethics clearances: Panama (Research-Permit STRI: STRI2563 (PI VC) - IACUC 100316-1001-18/Research-Permit ANAME: SE/A-68-11/Ethics-Permit: IACUC 100316-1001-18/Export Permits: SEX/A-30-11, SEX/A-55-11, SEX/A-91-10, SEX-A-26-10); Ghana (Research Permit: 2008–2010 (A04957)/Ethics-Permit: CHRP/49/09/Export-Permit: State Agreement between Ghana and Hamburg (BNI)); Australia (Research Permit: S11828 and S11762/Ethics-Permit: TRIM 01/1118(2), TRIM 06/3569, and University of Queensland/Animal Ethics Committee SIB600/05/ DEST/Export-Permit: DE201-12); Papua-New Guinea (Ethics-Permit: PNG/NatMus/2002/Export-Permit: Conducted by Papua New Guinea National Museum); Gabon (Ethics-Permit: 0002/1 MEFPA/SG/DGFEF/DFC); Germany (Ethics-Permit: LANU 314/5/3277.41.6).

Sampling and RNA purification
For all sampling and exportation of specimens, permission was obtained from the respective authorities (see Acknowledgement for individual permits). Animals were caught with mist nets, live or snap traps, identified by trained field biologists on site or prior to dissection (where applicable), euthanized and dissected in the respective laboratories. Canine, feline and equine samples were routine diagnostic specimens. Between 10–140 mL of blood were extracted using the Qiagen Viral RNA Mini kit (Qiagen, Hilden, Germany). Approximately 30 mg of solid organ tissue were homogenized in a TissueLyser (Qiagen) and purified using the Qiagen Viral RNA Mini kit (Qiagen, Hilden, Germany). Approximately 30 mg of solid organ tissue were homogenized in a TissueLyser (Qiagen) and purified using the Qiagen Viral RNA Mini kit (Qiagen, Hilden, Germany). The 5' terminus of the core gene. 454 junior next generation sequencing was used for confirmation of 5'-UTR sequences. For determination of the 3'-genome end, viral RNA was adenylated using a poly-A-polymerase (Clontech, Paris, France) followed by 3'RACE using the Invitrogen GeneRacer Kit (Invitrogen).

Phylogeny
Bayesian tree topologies were assessed with MrBayes V3.1 [36] using the WAG amino acid substitution matrix and BEAST V1.7.4 [37] using the GTR model for nucleotide sequences and the FLU model for amino acid sequences. For MrBayes, two million MCMC iterations were sampled every 100 steps, resulting in 20,000 trees. For BEAST, 10,000,000 generations run under a strict clock were sampled every 1,000 steps, resulting in 10,000 trees. Burn-in was generally 25% of tree replicates. A human pegivirus (previously termed GBV-C1; GenBank, U36390) was used as an outgroup. Maximum Likelihood analyses were used to confirm Bayesian tree topologies using the WAG amino acid substitution model and 1,000 bootstrap replicates in PhyML [38]. Trees were visualized in FigTree from the BEAST package and DensiTree [39].

Folding
RNA secondary structures in viral 5' and 3' genome ends were inferred manually basing on covariant base pairing and thermodynamic predictions using mfold [40] in an alignment of rodent, primate and canine/equine hepaciviruses generated with MAFFT [41].

Prediction of signal peptidase cleavage and N-/O-glycosylation sites
Putative cellular signal peptidase (SP) cleavage sites were predicted based on artificial neural networks (NN) and hidden Markov models (HMM) using the SignalP 3.0 Server [42]. N- and O-glycosylation sites were determined using the online tools NetNGlyc 1.0 Server and NetOglyc Server [43,44].

Genome comparison
Putative genes were annotated based on predicted signal peptide (SP) cleavage sites (where applicable) and sequence homology to HCV, GBV-B and canine/equine hepaciviruses. Alignments were generated using MAFFT [41]. Amino acid percentage identity matrices were calculated using MEGA5 [45] with the pairwise deletion option.

Statistics
Comparison of mean virus concentrations was done using an ANOVA analysis with Scheffé post-hoc tests in the SPSS V20 software package (IBM, Ehningen, Germany). Cross-tables were done using Epinfo7 (www.cdc.gov/epiinfo).

Serology
HCV Western blot. Western blot (WB) analysis was performed with commercially available HCV strips (recomBlot HCV IgG 2.0 and recomLine HCV IgG, Microgen, Neuried, Germany). Bat and rodent sera were diluted 1:100 for screening. Horseradish peroxidase-labelled goat anti-bat immunoglobulin (Ig) conjugate (Bethyl, Montgomery, AL, USA) or goat-anti mouse Ig (Dianova, Hamburg, Germany) were used as secondary antibodies (dilution, 1:500). For rodent WB, a tertiary horseradish
peroxidase-labelled donkey-anti goat Ig (Santa Cruz Biotechnology, Santa Cruz, CA, USA) was used for signal amplification. Blots were evaluated following the manufacturer’s instructions.

**HCV immunofluorescence assay.** An indirect immunofluorescence assay (IFA) was done using HCV-infected HuH7-cells (strain JCl) or replicon JFH1-transfected cells. Cells were fixed with paraformaldehyde (4%), permeabilized with 0.5% Triton X-100 in 1×PBS for 5 minutes and processed as described previously [46]. Bat sera were diluted 1:50. Reactions were detected with goat-anti-bat Ig (Bethyl, 1:1000) and cyanine 2 (Cy2)–labelled goat-anti-goat Ig (Dianova, 1:100). For control reactions, a polyconal rabbit NS3-Ig raised against the NS3 helicase domain (Invitrogen, 1:1000) were used.

**Rodent hepacivirus immunofluorescence assay.** VerOFM cells were transfected in suspension using FuGENE HD (Promega, Mannheim, Germany) with 0.75 µg plasmid expressing the complete His-tagged NS3 proteins of the rodent hepaciviruses RMU10-3382 (rNS3RMU10-3382) and NLR-AP70 (rNS3AP70) and fixed 24 hours later with acetone/methanol (80%/20%). *Myodes glareolus* sera were screened at dilutions of 1:10 and 1:40. For secondary detection, a goat-anti-mouse Ig (Dianova, 1:2000) and a donkey-anti-goat cyanine 3-labelled Ig (Dianova, 1:200) were applied. Recombinant rNS3RMU10-3382 protein including a cleavable Thioredoxin/His tag was expressed in bacteria and purified under non-denaturing conditions following a standard protocol [47]. The untagged purified protein was used to produce specific rabbit polyclonal antiserum at Thermo Scientific Pierce custom antibody service. Rabbit antiserum against rNS3RMU10-3382 (1:2000) was used in parallel to an rNS3RMU10-3382-reactive rodent serum (1:50) for a co-localization study by confocal laser scanning microscopy. Here, secondary detection was performed using a cyanine 2-labelled goat-anti rabbit Ig (Dianova, 1:200) and a cyanin 3-conjugated goat-anti-mouse Ig (Invitrogen, 1:200).

**In-situ hybridization**

RNAscope RNA probes targeting a 978 nucleotide NS3 gene fragment of the *M. glareolus* clade 1 hepacivirus detected in specimens RMU10-3379 were custom designed by Advanced Cell Diagnostics (Hayward, CA, USA). RMU10-3379 was selected due to the reported respiratoryandalso positive for the interpretation of western blot results applicable in human diagnostics. Figure 2B provides examples of typical reaction patterns. The three IFA-positive sera were also positive in WB. For rodents, Table 1 shows that two (Helicase and NS4) to six (NS5B) sera reacted with individual antigens. Another 43 sera showed borderline reactivities comparable to the intensity of the WB cut-off control (examples of reactivities in Figure 2C). No rodent sera fulfilled the criteria for positive interpretation applicable in human diagnostics.

**Hepacivirus detection**

For the molecular analysis of bats, 2,939 sera from Gabon, Ghana, Papua-New Guinea, Australia, Thailand, Panama and Germany were tested for Hepacivirus RNA using several broadly reactive and highly sensitive RT-PCR assays, as detailed in Supplementary Table 2. Despite the apparent relatedness of putative bat hepaciviruses with HCV suggested by the serologic analyses, no hepacivirus RNA was detected in any of the specimens, whereas several PCR fragments from the NS3 gene were obtained which upon sequencing were identified as pegiviruses related to GBV-D [48].

Tested rodent specimens originated from Thailand, Gabon, South Africa, Germany, the Netherlands and Mexico (Supplementary Table 1). HCV-related sequences from the NS3 gene were detected in 37 out of 4,770 specimens (0.8%). Ten of these findings were from South African four-striped grass mice (*Rhadinonyx pumillus*, 10 of 518 individual animals, 1.9%). For these and all other positive specimens, a 978 nucleotide NS3 fragment was generated using additional primer pairs (Supplementary Table 2). The derived sequences pertained to one clade, and were different from each other by 21.1% on nucleotide, or 3.4% on translated amino acid level. Twenty-seven (1.8%) of 1,465 individual bank voles (*Myodes glareolus*) from Germany and The Netherlands yielded HCV-related NS3 sequences. The derived sequences fell into two separate clades. Clade 1 contained 23 sequences different from each other by up to 15.8% of nucleotides and 2.8% of translated amino acids. Clade 2 contained four sequences different by 1.6% nucleotides and 0.6% translated amino acids.

A Bayesian phylogeny of the partial NS3 gene shown in Figure 3A suggested that the *M. glareolus* hepacivirus clade 1 was monophyletic with HCV and the canine/equine hepaciviruses. *M. glareolus* hepacivirus clade 2 was most closely related to GBV-B while the *R. pumilio*-associated clade formed a sister taxon to all other hepaciviruses. An analysis of all replicate trees indicated that the deep phylogenetic nodes were not resolved (Figure 3A). The monophyly of HCV and the *M. glareolus* clade 1 hepaciviruses was maintained in 68.6% of tree replicates (3,430 of 5,000). In another 28.9% of trees (1,446/5,000), the two *M. glareolus* hepacivirus clades clustered together. Monophyly of all three rodent
hepacivirus clades and GBV-B was indicated in only 15 of 5,000 tree replicates (0.3%).

**Full genome characterization**

The near full genomes of five representative hepaciviruses from all rodent clades were determined, including two viruses from *R. pumilio*, two from *M. glareolus* clade 1 and one from *M. glareolus* clade 2 (identified by red squares in Figure 3A). The polyprotein genes were of different sizes including 2,781; 2,887; and 3,007 amino acid residues, respectively, compared to 3,008–3,033 in HCV. All genomes shared the typical hepacivirus polyprotein organization, encoding putative proteins in the sequence C-E1-E2-p7-NS2-NS3-NS4A/4B-NS5A-NS5B (Figure 3B). The putative structural C, E1, E2 and p7 proteins were predicted by signal peptidase cleavage site analysis (Supplementary Table S3) to be comparable in their sizes to that of known hepacivirus proteins.

![Figure 1. Sampling sites, years, species and families.](image-url)

A. Sampling sites yielding novel hepaciviruses are indicated in red, others in yellow. B. Placentalia (Eutheria) evolutionary lineages according to [76]. Major mammalian clades are identified at basal nodes of the Placentalia phylogeny: Afrotheria (e.g., elephants), Xenarthra, (e.g., anteaters) and Boreoeutheria, divided into the two superorders Euarchontoglires, (e.g., primates, rodents) and Laurasiatheria (e.g., dogs, bats). Sampled mammalian orders are shown in boldface type. Orders containing novel hepaciviruses identified in this study are shown in red and boldface. Orders with known hepaciviruses (perissodactyla, primates, carnivora) are given in red. Numbers of extant families and species per order adapted from [33] are indicated.

doi:10.1371/journal.ppat.1003438.g001
All rodent viruses had considerably fewer predicted glycosylation sites in their structural proteins, in particular their putative E2 proteins, as opposed to HCV. A detailed genome analysis is provided in Supplementary Figure 3B. In HCV, a very similar sequence (AAAAAAAAACAAA), located at nearly the same positions (codons 8–12) of the core gene induces production of a protein termed F in vitro due to ribosomal frameshift event [49]. Depending on the HCV genotype, the size of the F protein ranges from 126 to 162 amino acid residues which vary considerably in sequence composition [50]. The size of a putative F protein in SAR46 would be 65 amino acid residues and no homology to the HCV F proteins was observed.

The high degree of sequence homology of the RNA-dependent RNA polymerase (RdRp) genes between all members of the family Flaviviridae enabled a more comprehensive comparison of the novel viruses. In a Bayesian phylogeny of these genes across the flavivirus family, the rodent viruses formed a monophyletic sister-clade to HCV (Figure 4A). Topological robustness was assessed by the fixation, in parallel Bayesian phylogenies, of two alternative topological hypotheses, the first involving monophyly of HCV with the canine/equine viruses and M. glareolus clade 1, and the second assuming a separation of HCV and the canine/equine viruses from all rodent viruses and GBV-B. A Bayes factor test comparing the total model likelihood traces of these analyses indicated borderline-significant preference of the second hypothesis over the first (Log10 Bayes factor = 2.94). Figure 4B provides a comparison of RdRp-based amino acid distances within and between Flaviviridae genera.

In a Bayesian phylogeny of the full polyprotein, the rodent hepaciviruses and GBV-B were monophyletic, forming a sister
clade to the canine/equine hepaciviruses and HCV (Figure 5).
The rodent-associated clade had very long intermediary branches
and originated close to the root of all viruses. The full genome tree
had a better phylogenetic resolution compared to the partial NS3
phylogeny, but still contained topological uncertainties in some
deep nodes leading to rodent-associated taxa (Supplementary
Figure S1).
The genome ends of representatives of all three rodent viruses
were determined, including virus RMU10-3382 belonging to M.
glareolus clade 1, NLR-AP-70 belonging to M. glareolus clade 2, and
virus SAR-46 belonging to the R. pumilio hepacivirus clade.
Figure 5 and Supplementary Figure S2A show that the 5’
genome terminus of RMU10-3382 contained structural elements
typical of both pegiv- and HCV-like internal ribosomal entry sites
(IREs). Predicted structural similarities with the HCV-like IRES
included the first stem-loop element (termed Ia and highlighted in
orange in Figure 5) and one of two sites involved in miRNA122
binding [51], while most of the remaining stem-loop elements
(termed 3, 4 and 5 and highlighted in blue in Figure 5) were more
closely related to a pegivirus-like IRES. The 5’-end of AP-70 was
identical in structure to RMU10-3382 and contained only a few
nucleotide exchanges. SAR-46 contained the typical HCV-like
IREs structures including the characteristic stem-loop III
(Supplementary Figure S2B). The observed structural similarity between the first stem-loop of all rodent viruses described here and the prototype hepatitis C virus and GBV-B consisted of a hairpin with a six-nucleotide stem and four-five nucleotide loop. The equine/canine hepatitis viruses contained a similar structural element located as their second predicted IRES domain, instead of the most 5’-position this domain occupied in all other hepaciviruses. The RMU10-3382 and NLR-365 translation initiation sites contained a cytosine immediately following the putative start codon at position +4, which is suboptimal in the original Kozak sequence context (ACCATGG) but should not block initiation [52]. The 3’-ends of RMU10-3382 and SAR-46 contained three highly ordered stem-loop elements. In RMU10-3382, these RNA elements did not resemble any known 3’
-noncoding sequence RNA structure. In SAR-46, the 3’-terminal stem-loop structure, but not the preceding structures, resembled that of the HCV X-tail (Supplementary Figure S3). A similar 3’-terminal structure could be predicted for GBV-B, but not for the genetically related pegiviruses (Figure 5 and
Supplementary Figure S4). The 3’-end of NLR-AP-70 could not be determined. Contrary to HCV and GBV-B, no poly-uracil stretch was observed in the rodent hepaciviruses.

Natural history of hepacivirus infection in bank voles

Strain-specific real-time RT-PCR assays were used to determine viral RNA concentrations in tissues of 22 bank vole infected with clade 1 and 2 hepaciviruses. Mean RNA concentrations were highest in liver tissue (1.8×10^9 copies/gram), range, 1.5×10^8–
4.4×10^9). These concentrations were significantly higher than those in other organs or serum (ANOVA, F = 7.592, p < 0.0001; Figure 6A and Supplementary Figure S5). Figure 6B shows M. glareolus clade 1 hepatitis C virus RNA stained by in-situ hybridization (ISH) in liver tissue. Foci of viral RNA were located in the cytoplasm of M. glareolus hepatocytes, while no staining was observed in RT-PCR-negative M. glareolus liver specimens (Supplementary Figure S6 shows additional ISH details). Spleen, kidney, heart and lung tissues yielded no evidence of virus infection by ISH. Histopathological examination of eight RNA-positive animals (ANOVA, F = 7.592, p < 0.0001; Figure 6A and Supplementary Figure S5). Figure 6B shows M. glareolus clade 1 hepatitis C virus RNA stained by in-situ hybridization (ISH) in liver tissue. Foci of viral RNA were located in the cytoplasm of M. glareolus hepatocytes, while no staining was observed in RT-PCR-negative M. glareolus liver specimens (Supplementary Figure S6 shows additional ISH details). Spleen, kidney, heart and lung tissues yielded no evidence of virus infection by ISH. Histopathological examination of eight RNA-positive animals revealed low-grade focal lymphocytic invasion compatible with liver inflammation, such as shown in Figure 6C for two exemplary RNA-positive animals. Serological investigations in wild rodents were complicated by the fact that the vast majority of animals from virus-positive species were not live-trapped, therefore yielding no blood samples. Only post mortem peritoneal lavage fluids were collected from carcasses, but these were not qualified for serology. However, a subset of 97 live-trapped M. glareolus with appropriate blood samples were

Table 1. Western blot reactivity patterns.

<table>
<thead>
<tr>
<th>Western Blot</th>
<th>Interpretation*</th>
<th>Reactivities by individual antigens</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Bat species</td>
<td>NS5</td>
</tr>
<tr>
<td>Eulélion helvum</td>
<td>89</td>
<td>7</td>
</tr>
<tr>
<td>Rousettus aegyptiacus</td>
<td>5</td>
<td>3</td>
</tr>
<tr>
<td>Total (percent)</td>
<td>94</td>
<td>10</td>
</tr>
</tbody>
</table>

*Blot analysis criteria for human diagnostics provided by the manufacturer (Microgen, Neuried, Germany): A positive band was assigned the following point values: NS3, 3; Helicase, 3; NS5-12, 2; NS4, 4; Core, 8. Only weakly positive bands (visible, but weaker than the core antigen of the weak positive HCV control) were considered negative with the exception of the core antigen, which was then assigned 5 points. Blots were considered positive if the sum of points was equal to or greater than 10, borderline if the sum was between 6 and 9 points, and negative if the sum was equal to or below 5 points. Eight bat sera showing strongest Western Blot reactivity were end-point diluted to evaluate specificity of the reaction. Bands remained visible up to a dilution of 1:400. Some analyses were done using a follow-up version of the Microgen assay (recomline) with two separate core antigens and different interpretation criteria. Blots were then considered borderline if any two antigens showed higher intensity than a cut-off control, the helicase alone, the helicase and any NS antigen or any core epitope. Blots were considered positive in this assay version if both core antigens were positive, one core plus any other antigen or if three antigens showed higher intensities than the cut-off control. Reactivity of the secondary goat anti-mouse and tertiary donkey anti-goat antibodies used for rodent testing were controlled by using mouse anti-core and anti-NS3 monoclonal antibodies for primary reaction with blot antigens.

doi:10.1371/journal.ppat.1003438.s001

Rodent Hepaciviruses

PLOS Pathogens | www.plospathogens.org 7 June 2013 | Volume 9 | Issue 6 | e1003438
available. These were analyzed for antibodies against the *Myodes* hepacivirus clades 1 and 2 in an IFA using cells expressing the NS3 antigens of these viruses. Antibodies against the *Myodes* hepacivirus clade 1 NS3 antigen were found in eight animals (8.3%) at a median end-point titer of 1:2000 (range, 1:100–1:1600). Antibodies against the *Myodes* hepacivirus clade 2 NS3 antigen were detected in 12 animals (12.4%) at a median end-point titer of 1:6000 (range, 1:100–1:12800). The difference in antibody detection rates against clades 1 and 2 was not statistically significant (X² = 0.5, p = 0.5).

*Myodes* hepacivirus clade 1 antigen specificity was proven by counterstaining with a high-titered rabbit serum raised against the same recombinant NS3 antigen down to dilutions of >1:20,000. *Myodes* hepacivirus clade 2 antigen did not cross-react with this rabbit control serum even at high concentrations of 1:100, compatible with low NS3 amino acid sequence identity between the NS3 proteins of the two *Myodes* hepacivirus clades (42.4%, Supplementary Table S4). Neither hepacivirus clade 1, nor clade 2 antibody-positive sera cross-reacted with HCV by immunofluorescence and by immunoblot, indicating specific immune reactions against the viruses studied (exemplary results in Figure 6D). This was compatible with low NS3 amino acid sequence identities between both *Myodes* hepacivirus clades and HCV, ranging from 37.9–42.2% (Supplementary Table S4). Only one of the eight sera positive against *M. glareolus* clade 1 hepaciviruses also contained antibodies against *M. glareolus* clade 2 hepaciviruses (titers against clade 1 and clade 2 hepaciviruses were 1:200 and 1:3200, respectively).

Additional highly sensitive real-time RT-PCR assays were designed specifically for the *M. glareolus* clade 1 and 2 hepaciviruses and used to analyze the association of viral RNA and antibody status in the 97 *M. glareolus* sera. No hepacivirus RNA was detected in any of the IFA-positive sera, neither with the broadly reactive screening assays, nor with the additional real-time RT-PCR assay. Therefore, another 239 RNA eluates still containing sufficient volumes to permit screening for *M. glareolus* clade 1 and 2 hepaciviruses were re-tested with the strain-specific real time RT-PCR assays. Another 57 specimens positive for clade 1 hepaciviruses (23.9%), but no additional clade 2 hepaciviruses were detected. Sera from these PCR-positive animals were obtained and tested for antibodies. Three of the 57 clade 1 RNA-positive sera contained antibodies against clade 1 hepaciviruses (5.3%).

Because of previous reports of canine/equine hepaciviruses, all RT-PCR assays used in this study were also applied on specimens from horses, cats and dogs. No HCV-related sequences were found in any of the 858 canine or feline specimens. In seven of 210 horse sera (3.3%), sequences closely related to those equine hepaciviruses described previously from the US and New Zealand [24] were detected (9.5–13.0% exchanges in the 978 nucleotide NS3 gene fragment). Most of those nucleotide differences represented synonymous mutations, resulting in low amino acid distances of 0–1.2%. The novel hepaciviruses from German horses clustered phylogenetically with the previously described equine hepaciviruses (Figure 3A).

Discussion

Here we found molecular evidence for viruses related to HCV in rodents. Rodent hepaciviruses were detected in four-striped grass mice from South Africa, as well as in bank voles from Central Europe. The latter have already been successfully bred under laboratory conditions, indicating an approach to establish surrogate models for hepacivirus infection [53,54,55,56]. All discovered viruses originated from deep nodes close to the bifurcations separating genera within the flavivirus tree. In phylogenies on whole genome and individual gene alignments, the novel viruses clustered in a monophyletic clade with previously known hepaciviruses and GBV-B. The clade is highly diversified with NS5b amino acid sequence distances between taxa ranging up to 66.1%, exceeding that in the well-studied genus *Flavivirus* (55.8%). Maximal distances within the genera *Pegivirus* (52.9%) and *Pestivirus* (42.0%) are even lower, suggesting a particularly high diversity to exist in a tentative genus defined by the novel clade. Whereas this indicates that some or all of the novel rodent viruses together with GBV-B might alternatively form an independent genus, recent descriptions of novel pegi- and pestiviruses in bats and swine suggest the diversity also within these genera to be understudied [48,57,58]. Including the novel rodent viruses congenic with HCV and canine/equine viruses, the minimal distance between the genera *Hepacivirus* and *Pegivirus* would be 73.5%. While this is lower than the 85–88% between other pairs of genera, it is consistent with a separation threshold of 72.2% between all members of the genus *Flavivirus* and Tamana bat virus, for which a separate genus has been proposed [59]. This also corresponds to inter-generic distances within other well-studied families of plus-strand RNA viruses such as the *Picornaviridae*, whose twelve genera are mostly separated by 70–80% in the RdRp-encoding 3D gene [60].

**Figure 3.** Genomic characterization of the novel rodent hepaciviruses. A. Partial NS3 gene phylogeny. The analysis comprised a 978 nucleotide fragment of the HCV NS3 gene corresponding to positions 3,912–4,889 in HCV 1a H77 (GenBank, NC_00102). GenBank accession numbers of sequence hepaciviruses are indicated to the right of taxon names. Tree topology was inferred using BEAST with a GTR nucleotide substitution model as described in the methods section. Rodent hepaciviruses from this study are shown in red and boldface, equine hepaciviruses from this study are shown in blue and boldface. Red squares indicate those viruses whose near full-length genomes were generated. Statistical support of grouping is shown as posterior probabilities at deep nodes. Scale bar corresponds to genetic distance. To the right, 5,000 tree replicates of the same analysis are rendered using Densitree (initial 5,000 trees discarded as burn-in). Green line color indicates low probability of all trees, line thickness corresponds to concordant topologies across tree replicates. B. Genome organization of the novel rodent hepaciviruses. Genes were annotated as described in the methods section. Black arrows on the top indicate predicted signal peptidase cleavage sites. Red arrows below indicate N- and C-termini of G glycosylation sites. Putative gene starts and ends are numbered below polyprotein plots. HCV 1a strain H77 is depicted on top as a reference. RMU10-3382 (KC411777) also represents the highly similar virus NLR-365 (KC411796) in *M. glareolus* hepacivirus clade 1. SAR-46 (KC411807) also represents SAR-3 (KC411806), both from the *R. pumilio* hepacivirus clade. GenBank accession number of NLR-AP70 representing *M. glareolus* hepacivirus clade 2 is KC411784. The structural genome region included Core (C), Envelope 1 and 2 (E1 and E2) and p7 genes. The boxes in the HCV and SAR-46 Core gene indicate a putative F protein open reading frame. The putative Core gene at the N’-terminus of the rodent hepacivirus polyproteins included a high number of strongly basic lysine and arginine residues (*M. glareolus* clade 1, 29 of 163 residues (17.8%); *M. glareolus* clade 2, 23 of 149 (15.4%); *R. pumilio* clade, 28 of 172 (16.3%); compared to 31 of 191 (16.2%) in HCV-1a and 11 of the N’-terminal 200 residues (5.5%) in the pegivirus GBV-C1 not encoding a Core protein. Non-structural genes included an NS3 protease/helicase gene, the phosphoprotein NS5a and the NS5b gene encoding the RNA-dependent RNA polymerase. Within the NS4 gene, only the NS4b portion could be clearly identified for all viruses. An NS4a homologue could only be detected in virus SAR-46. IRES types and structural elements in the 3’-genome ends are depicted adjacent to the polyprotein plots for viruses NLR-3382 and SAR-46. Of NLR-AP70, only the 5’-end could be partially determined. This sequence was almost identical to RMU10-3382/NLR-365. The 3’-terminus of NLR-AP70 could not be determined.

doi:10.1371/journal.ppat.1003438.g003
Figure 4. Comparison of the novel rodent hepaciviruses with other Flaviviridae. A. Bayesian phylogeny of the Flaviviridae NS5B gene. The analysis was done in MrBayes and included representatives of all Flaviviridae genera and those five novel rodent viruses whose full polyprotein could be determined. The WAG amino acid substitution model was used. Statistical support of grouping from Bayesian posterior probabilities and 1,000 parallel Maximum Likelihood bootstrap replicates is indicated at deep node points. Scale bar corresponds to genetic distance. A tombusvirus (Lisianthus necrosis virus, GenBank accession number NC_007983) was chosen as an outgroup. B. Amino acid distance of the complete NS5B gene between genera.
within Flaviviridae clades. Maximum amino acid sequence distance was calculated with MEGAS using the pairwise deletion option and all Flaviviridae members contained in panel A. The dotted line indicates 70% distance for clarity of graphical presentation only.

doi:10.1371/journal.ppat.1003438.g004

**Figure 5. Complete polyprotein gene phylogeny and comparison of the genome termini between the novel rodent and prototype hepacviruses.** For the Bayesian phylogeny shown to the left, the WAG amino acid substitution model was used in MrBayes as indicated in the methods section. Statistical support of grouping from Bayesian posterior probabilities is indicated at node points. Scale bar corresponds to genetic distance. The Pestivirus BVDV (NC_001461) was chosen as an outgroup and truncated for graphical reasons. Branches leading to the novel hepacviruses from this study are in orange. GenBank accession numbers of analyzed hepacviruses correspond to those indicated in Figure 3A. The 5’- and 3’-genome termini were re-drawn from published foldings for equine hepacviruses [24], HCV [63,77] and GBV-B [78] and de novo for this study for the 5’- and 3’-ends of GBV-C1 and the 3’-end of GBV-B (see Supplementary Figure 4). Despite earlier attempts to fold the 3’-ncr of GBV-B [21] only the 3’-terminal stem-loop structure of GBV-B could be reliably folded due to the single sequence available. The folding of the 3’-end of RMU10-3382 remained tentative for the same reason. No sequence information was available for the 3’-ends of the canine/equine hepacivirus clade and *M. glareolus* hepacivirus clade 2 (indicated as “n.a.”). Typical pegivirus domains are highlighted in blue and ordered by arabian numbers. Typical hepacivirus domains are highlighted in orange and numbered by roman numbers.

doi:10.1371/journal.ppat.1003438.g005
Figure 6. Presentation of hepacivirus infection in bank voles. A. Hepacivirus RNA concentrations in Myodes glareolus. Bars represent means and standard deviation of hepacivirus clade 1- and 2-positive organs and serum. The number of biological replicates is indicated below bars. B. In situ hybridization of rodent hepacivirus clade 1 RNA in M. glareolus. Viral RNA was stained in liver tissue of M. glareolus specimen RMU10-3379 (viral RNA concentration, 9.4×10^8 copies per gram, GenBank accession no. KC411778). The RNA-negative specimen RMU10-3187 from the same species was processed identically and is shown below as a control. Positive staining is visible as distinct red granules in the cytoplasm of hepatocytes. Magnification was 100×, the inserts shows details of single hepatocytes in 10× higher magnification. Scale bars are shown to the lower right. C. Histopathology of M. glareolus liver specimens. Liver sections were stained by Hematoxylin and Eosin (H&E) and Epson van Giesson (EvG) stains. In H&E stains, black arrows point to inflammatory lymphocytic infiltrate. In EvG stains, black arrows highlight potential signs of fibrosis. Specimen 3180 shows intermediate portal inflammatory activity with potential low-grade fibrosis in a case with high hepacivirus RNA concentrations (1.5×10^8 copies/gram). Specimen 1602 shows low-grade portal inflammatory activity and low-grade fibrosis in a case with high hepacivirus RNA concentrations.
concentrations (3.4×10⁶ copies/gram). Specimen 3187 shows no significantly increased inflammatory activity and no signs of fibrosis in a case with no detectable hepatitis RNA. Due to highest tissue quality, a terminal hepatic venule instead of a portal triad is shown. D. Recognition of rodent hepatitis clade 1 antigens by M. glareolus serum. VeroFM cells expressing complete NS3 from M. glareolus hepatitis RMU10-3382 (GenBank, KC411777) were incubated with 1:2000-diluted rabbit-anti-NS3 3382 antiserum (control) or 1:50-diluted rodent serum (picture shows exemplary results for animal NLR 3/C12), followed by goat-anti-rabbit-Cy2 (green) and goat-anti-mouse-Cy3 (red) secondary immunoglobulins. For co-localization analysis of fluorescence signals, the 6th of 12 1-µM Z-stages is shown for every channel. Cross-reactivity with HCV antigens was analyzed by incubation of HuH7 cells, transfected with HCV replicon JFH1, with a rabbit-anti-human-HCV-NS3-49 serum, diluted 1:400 (control) or rodent serum NLR 3/C12 diluted 1:50, followed by goat-anti-rabbit-Cy2 (green) and goat-anti-mouse-Cy3 (red) secondary antibodies. Counterstaining was performed using DAPI. Bar, 25 µm.

doI:10.1371/journal.ppat.1003438.g006

The genetic elements potentially homologous to HCV detected in rodent viruses also included microRNA-122 binding sites in the 5’-ncr, an X-tail-like element in the 3’-terminus and a putative F gene in an alternative open reading frame (ORF) of the R. fulminis-associated virus. The F protein appears to be unessential for HCV replication, but the evolutionary conservation of its ORF suggests that it may play a critical regulatory role in virus propagation and survival [50]. In this regard, the F protein may be considered a counter-defense security protein that evolved to overcome mechanisms of host resistance [66]. The absence of paramount features typical of other genera and the presence of hepacivirus-like features suggest a tentative classification of the novel rodent viruses within the genus Hepacivirus, rather than a novel genus.

Within the genus, phylogeny suggests early divergence of ancestral rodent viruses from a lineage leading up to HCV and canine/equine hepaciviruses. Weakness of resolution in deep bifurcations of the NS3 gene phylogeny and lack of any highly significant preference for deep topological hypotheses in the NS5B gene phylogeny underlie the ancestral origin of these viruses. Within the current dataset we can consider them equidistant from each other by 48–60% AA distance. The divergence of these viruses is evidenced by the absence of detectable NS3 gene sequences. Within the genus Hepacivirus, their role in the evolution of HCV precursors, if any, remains to be determined.

Our serological evidence for hepaciviruses in bats is noteworthy even in absence of direct virus findings. Viruses from all Flaviviridae genera including Pegivirus, Pestivirus and Flavivirus have already been found in bats [48,70,71]. We could not exclude that the antibodies in bat sera reacting with HCV antigens were directed against viruses from other Flaviviridae genera, rather than bat hepaciviruses. However, there was no cross-reactivity between the NS3 proteins of the more closely related canine/equine hepaciviruses and HCV [24]. Similarly, the two bank vole hepacivirus clades from our study showed no serologic cross-reactivity. These data can therefore serve as very initial suggestions for the existence of bat hepaciviruses only. It should be noted that the degree of genomic similarity necessary for serologic cross-reactivity should have permitted RNA detection by the broadly reactive PCR assays used in this study. Whether bat hepaciviruses indeed exist will therefore require further evidence. A first step to this direction may be an analysis of an expanded bat sample by using the methods presented here.

Additional to phylogeny and genomic properties, the novel viruses resemble HCV in important traits of the natural history of infection. The detection of non-identical virus sequences in natural groups of animals, in combination with specific antiviral antibodies, proves continuous transmission of virus among animals. Induction of controlled infections in housed animals would thus be feasible. We found clear in-vivo evidence for hepatic tropism by demonstrating histopathological signs of liver inflammation,
excessive viral RNA concentrations in the liver, as well as in-situ hybridizations demonstrating intracellular genome replication in liver cells of bank voles. A somewhat lower degree of hepatic inflammation compared to that in some HCV-infected humans might be due to the shorter life span of bank voles rarely exceeding 1–2 years in the wild, or due to a higher capacity of tissue regeneration [72,73]. Interestingly, our serological investigations suggested bank voles might be able to clear hepacivirus infections, as antibodies did not co-occur with RNA in most, but not all animals [1]. Bank voles may therefore be more capable of clearing hepacivirus infection than humans. This would be compatible with infection patterns also observed in other Flaviviridae members, exemplified by the flavivirus West Nile virus in rhesus macaques, the pestivirus BVDV1 in cattle and the hepacivirus GBV-B in experimentally infected tamarins [61,74,75]. However, it would differ from equine hepaciviruses, in which RNA and antibodies co-occurred [24]. Controlled infection experiments in bank voles might yield relevant scenarios for the study of HCV persistence. Bank voles can be kept in the laboratory with comparatively little effort and have been used for virus infection studies, e.g., with herpesviruses, bornaviruses, hantaviruses, and flaviviruses [35,54,55,56]. Efforts to establish bank vole infection models may benefit from the discovery of two highly divergent clades in European and African rodent hepaciviruses.

**Supporting Information**

**Figure S1** BEAST polyprotein phylogeny including the novel rodent hepaciviruses. The complete polyprotein sequence of all hepaciviruses was analyzed in BEAST [37] using the FLU amino acid substitution matrix and a strict clock over 10,000,000 trees sampled every 1,000 generations. After exclusion of 2,500 trees as burn-in, all trees are depicted using Densitree [39]. Blue color corresponds to most probable topologies, red to second-best, green to third-best and dark green to remaining topologies. 6,950 of 7,500 trees replicates (92.7%) yielded a second-best, green to third-best and dark green to remaining topologies. The Ia loop is very similar in length and shape to HCV and other pegiviruses are marked in red, paired compensatory structures in both foldings are numbered according to [39]. Blue color corresponds to most probable topologies, red to second-best, green to third-best and dark green to remaining topologies.

**Figure S2** 5′-non-coding genome region (5′-ncr) of Hepaciviruses. A. 5′-end of RMU10-3382 (GenBank, KC411177). This structure was mostly related to the Pegasivirus type 4 IRES. Nucleotides conserved with other pegiviruses are marked in red, paired compensatory substitutions in NLR-365 (KC411796) and the partially available NLR-AP70 5′-UTR (KC411784) that support the structure are in green. The Ia loop is very similar in length and shape to HCV and GBV-B. The start codon is boxed in red, additional non-functional start codons between the poly-pyrimidine stretch typical for pegiviruses and the true start codon are boxed in blue. The binding site for microRNA-122 is underlined. B. 5′-end of SAR-46 (KC411807). This structure was mostly related to a Hepacivirus type 3 IRES. Nucleotides conserved with HCV are marked in red. The slippery site is underlined. The start codon is boxed. Stem-loop structures in both foldings are numbered according to Pegiviruses reference strains.

**Figure S3** 3′-non-coding genome region (3′-ncr) of Hepaciviruses. A. RMU10-3382 (GenBank, KC411177) 3′-end secondary structure. B. SAR-46 (KC411807) 3′-end secondary structure. For comparison, stem-loop (SL) SL3 of HCV1a strain H77 (NC_001655) is depicted to the right and structural similarities are highlighted in grey. PK = Pseudoknot.

**Figure S4** 5′- and 3′-non-coding genome region (5′-3′-ncr) of GBV-C1 and 3′-ncr of GBV-B. A. 5′-end secondary structure of GBV-C1/HPgV, GenBank accession no. U36380. Nucleotides conserved with other pegiviruses are marked in red, paired compensatory substitutions that support the structure are in green. Stem-loop structures are numbered by order of appearance. B. 3′-end secondary structure of GBV-C1/HPgV, GenBank accession no. U36380. C. Secondary structure of the third HCV-like domain of GBV-B, GenBank accession no. AF179612. Due to the single available sequence, the remaining 3′-ncr could not be reliably folded despite repeated attempts. The nucleotide sequence immediately following the polyprotein stop codon and directly before the stem-loop structure towards the 3′-end of GBV-B is shown.

**Figure S5** Hepacivirus RNA concentrations in individual solid organ specimens and blood. A. Hepacivirus-positive Myodes glareolus sampled 2008–2010 in The Netherlands and Germany. Virus concentrations are given in Log10 RNA copies per gram of tissue scaled on the y-axis for each rodent organ tested (x-axis). Horizontal bars represent mean virus concentrations per organ category. The number of available specimens per organ category is indicated below. Colors represent viruses from individual rodents as identified in the legend. B. Viral load in Log10 RNA copies per mL of blood in the same 21 animals. For one animal, no blood was available.

**Figure S6** In-situ hybridisation of M. glareolus hepacivirus clade 1 RNA in liver tissue. A. RNA-negative M.
glareolus specimen RMU10-3187 and B. RNA-positive M. glareolus specimen RMU10-3379 (viral RNA concentration, 9.4×10^6 copies per gram, GenBank accession no. KC411778) were stained at identical conditions. Power of magnification is indicated on the left. Scale bars are depicted to the lower right corner of every panel.

**Table S1** Sample characteristics. *GAB* = Gabon, GER = - Germany, NAM = Namibia, NEL = The Netherlands, RSA = Republic of South Africa, THA = Thailand, MEX = Mexico.

**Table S2** Oligonucleotides used for *Hepacivirus* RT-PCR screening, genome sequencing and virus quantification. *ID* = identity, *numbered after CHV polyprotein (GenBank # JF744991); *numbered after HCV genotype 1a polyprotein (GenBank # NC_004102); *numbered after CHV genome (GenBank # JF744991); *R = G/A, Y = C/T, S = G/C, W = A/T, M = A/C, K = G/T, H = A/C/T, B = C/G/T, I = inosine, FAM = 6-Carboxy-Fluorescein, JOE = 2,7-Dimethoxy-4,5-dichloro-6-carboxyfluorescein, VIC = proprietary dye (Life Technologies, Darmstadt, Germany), BHQ = Black hole quencher, MGBNFQ = Minor groove binder Non fluorescent quencher; *+/+* = Locked nucleic acids (LNA) First round RT-PCR used the SuperScript III (SSIII) one-step RT-PCR kit (Invitrogen, Karlsruhe, Germany). Amplification involved 15 min at 55°C; 3 min at 95°C, 45 cycles of 15 sec at 94°C, 20 sec at 60°C with a decrease of 1°C per cycle, and extension at 72°C for 45 seconds. Second round RT-PCR reactions used a touchdown protocol with reverse transcription at 48°C for 30 minutes, denaturation at 95°C for 3 minutes, followed by PCR 10 cycles of 15 sec at 94°C, 20 sec at 60°C with a decrease of 1°C per cycle, and extension at 72°C for 45 seconds, followed by another 40 cycles at 50°C annealing temperature. Second round reactions used the same cycling protocol without the RT step.

RNA quantification was performed in 25 μL reaction volumes using the SSIII One-Step RT-PCR system (Invitrogen) as described above with 300 nmol/L of respective forward and reverse primers and 200 nmol/L of respective probes. Amplification involved 15 min at 55°C; 3 min at 95°C; 45 cycles of 15 sec at 94°C, and 25 sec at 58°C. Fluorescence was measured at the 58°C annealing/extension step. Published assays from which oligonucleotide primers were used in this study included [35,79,80,81,82].

**Table S3** Putative cleavage sites for cellular signal peptides within the N-terminal half of hepacivirus polyproteins. NN: neural networks; HMM: hidden Markov models (the values represent probabilities for putative SP cleavage sites). Only SP cleavage sites predicted by both NN and HMM models (the values represent probabilities for putative SP cleavage sites) were supported by uncorrected S-correct scores (not shown). Hepaciviruses included were SAR46 (KC411807) and SAR3 (KC411806) from *Rhabdomyos papillimi*, RMU10-3382 (KC411777), NLR-365 (KC411796) and NLR-AP70 (KC411784) from *Myodes glareolus*, HCV-1a (NC_004102) and GBV-B (NC_001653).

**Acknowledgments**

We would like to thank Sebastian Brünink, Monika Eschbach-Bludau, Tobias Bleicker and Daniela Niemeyer at the Institute of Virology, Bonn for technical assistance. We are grateful to Gabor Horvath from the Institute of Innate Immunity, University of Bonn for confocal microscopy analyses, to Anna-Marie Corman for GIS image processing, and to Stephanie Kallis (Department of Infectious Diseases, Molecular Virology Heidelberg) for help in preparing reagents for serological assays. We are grateful to Wolfgang Preiner (Stellenbosch), Thomas Jäkel (Bangkok), Thomas Kruppa (BNI Hamburg), Jörg Thiel (Gotha), Margrit Bemmern (Schwierin), Daniela Reil, Christian Imhoff, Jens Jacob, Katarina Kühn, Engellert Kampling, Mechthild Budde, Dagmar Funck (JKI, Münster), Jona Freise, Brita Ottmann (LAVES, Oldenburg), Sebastian Guenther, Brigitte Bannert (Berlin), Henrik Greger (Stuttgart), Johannes Lang (Lüch), Anita Plenge-Böing (Hamburg), Nicole Schauerte (Frankfurt/Main), Susanne Modrow (Regensburg), Gerhard Maluck (Bergatreute), Richard Kruczewski (Borchsen), Julie Liéchère (Marseille), Maria Nermeth (Budapest), Sabrina Schmidt, Ulrike M. Rosenfeld, Anne Ballkema-Buschmann, Susanne Jäckel, Horst Schirrmeier, Hanan Sheikh Ali, Christian Kretzschmar, Konrad Wanka, Ute Wessels, Theres Wolny, Kathrin Baumann, Grit Moewert, Franziska Thomas, Mertens, Paul Dremsek, Katja Pfliève, Kerstin Tauscher, Angele Breithaupt, Nadja Lorenz, Christian Korthase, André Schütte, Julie Elkins and Sylvia Ferguson (FLI, Greifswald-Insel Riems) for field work and technical assistance.

**Author Contributions**


**References**


