Characterization of full-length hepatitis C virus sequences for subtypes 1e, 1h and 1l, and a novel variant revealed Cameroon as an area in origin for genotype 1

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In this study, we characterized the full-length genome sequences of seven hepatitis C virus (HCV) isolates belonging to genotype 1. These represent the first complete genomes for HCV subtypes 1e, 1h, 1l, plus one novel variant that qualifies for a new but unassigned subtype. The genomes were characterized using 19–22 overlapping fragments. Each was 9400–9439 nt long and contained a single ORF encoding 3019–3020 amino acids. All viruses were isolated in the sera of seven patients residing in, or originating from, Cameroon. Predicted amino acid sequences were inspected and unique patterns of variation were noted. Phylogenetic analysis using full-length sequences provided evidence for nine genotype 1 subtypes, four of which are described for the first time here. Subsequent phylogenetic analysis of 141 partial NS5B sequences further differentiated 13 subtypes (1a–1m) and six additional unclassified lineages within genotype 1. As a result of this study, there are now seven HCV genotype 1 subtypes (1a–1c, 1e, 1g, 1h, 1l) and two unclassified genotype 1 lineages with full-length genomes characterized. Further analysis of 228 genotype 1 sequences from the HCV database with known countries is consistent with an African origin for genotype 1, and with the hypothesis of subsequent dissemination of some subtypes to Asia, Europe and the Americas.

INTRODUCTION

Hepatitis C virus (HCV) is one of the major causative agents for chronic hepatitis, cirrhosis and hepatocellular carcinoma (Farci et al., 1991; Liang & Heller, 2004; Nishioka, 1991). As reported by the WHO, HCV infects about 2.2% of the world’s population, with over a million new cases occurring each year. Furthermore, 27% of these infected individuals eventually progress to liver cirrhosis among whom 25% finally develop hepatocellular carcinomas (Alter, 2007). HCV is a positive-sense RNA virus that exhibits extensive genetic heterogeneity and a high level of resistance to antiviral drugs \textit{in vivo} and \textit{in vitro}. As such, HCV genetic variation poses a huge problem for global public health (Robinson \textit{et al.}, 2011).

To standardize HCV genetic diversity, consensus proposals for a unified system of HCV nomenclature were published after the 11th International Meeting for HCV and Its Related Viruses (Simmonds \textit{et al.}, 2005). It has been recommended that HCV isolates be classified into six major genotypes defined by phylogenetic analysis. Each genotype contains a variable number of subtypes that are related but genetically and epidemiologically distinct.
subtypes are defined as confirmed or provisional, depending on the availability of complete or partial genetic sequences, or defined as unassigned if less than three examples of a new subtype have been reported. Recently, panels of complete HCV genome sequences have been provided for HCV genotypes 2, 3, 4 and 6 in a series of our previous studies (Li et al., 2006, 2009a, b, 2012; Lu et al., 2006, 2007a, b, 2008, 2013; Wang et al., 2009; Xia et al., 2008). However, similar information is still in short supply for genotype 1. As noted in the HCV nomenclature guidelines (Simmonds et al., 2005), three subtypes (1a, 1b and 1c) of HCV-1 have been confirmed with full-length genomic sequences, while nine subtypes (1d–1l) remained provisionally assigned due to the availability of only partial sequences. Although since then a complete genomic sequence has been reported for subtype 1g (Bracho et al., 2008), the other eight subtypes remain to be sequenced in their entirety.

Evolutionary studies have shown that different HCV genotypes originated in specific geographical regions, such as genotypes 3 and 6 in South and South East Asia (Fu et al., 2012; Pybus et al., 2009), genotype 2 in West Africa (Markov et al., 2009), and genotypes 1 and 4 in Central Africa (Njouom et al., 2007, 2012). Cameroon is located in Central Africa and a diverse range of subtypes of HCV-1, HCV-2 and HCV-4 have been reported from the country. Previous studies have reported Cameroonian isolates of subtypes 1b, 1e, 1h and 1l (Ndjomou et al., 2003; Njouom et al., 2003a, b, 2007; Pasquier et al., 2005); three samples from these studies remained and were used here to generate full genome sequences. In addition, during routine diagnostic HCV screening and genotyping services provided by a company in the UK, four unique HCV-1 isolates were found among patients originating from Cameroon; these represent subtypes 1e and 1l, and a novel HCV-1 variant. The full-length sequences of these four isolates are also provided here. It is hoped that this valuable genomic data will add to our current understanding of HCV classification and nomenclature, and facilitate future studies of HCV molecular epidemiology, evolution and genetics.

RESULTS

Genome sequences and organization

Full-length genome sequences were characterized for seven HCV genotype 1 isolates: 136142, 148636, 160526, 166212, EBW9, EBW424 and EBW443, each with 19–22 overlapping fragments (Fig. S1, available in JGV Online). These genomes were 9420–9439 nt in length, starting from the extreme 5’UTR end through to the variable region of the 3’UTR (Table 1). Each had a single ORF of length 9039–9063 nt. The 5’UTRs were 340–342 nt long, while the 3’UTR lengths varied from 32 to 40 nt. The sizes of the other eight protein genes were consistent with those of Table 1.

<table>
<thead>
<tr>
<th>Sequence name</th>
<th>Age</th>
<th>Sex</th>
<th>Origin</th>
<th>Full</th>
<th>ORF 5’UTR</th>
<th>Core</th>
<th>E1</th>
<th>E2</th>
<th>P7</th>
<th>NS2</th>
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<td>–</td>
<td>–</td>
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<td>341</td>
<td>573/191</td>
<td>576/192</td>
<td>1089/367</td>
<td>189/63</td>
<td>651/217</td>
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<td>F</td>
<td>Ebolowa</td>
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<td>9039/3013</td>
<td>341</td>
<td>573/191</td>
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<td>783/261</td>
<td>1344/448</td>
<td>1776/591</td>
</tr>
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*The H77 genome (GenBank accession no. NC_004102) is included for comparison.

Table 1: Patient and sequence length (nucleotides/amino acids) information for the seven genotype 1 isolates

Bold entries indicate regions of variable length.
the H77 strain (Table 1) with the exception of the E2 (364–371 aa) and NS5A (448–449 aa) genes.

**Phylogeny of full-length genome sequences**

A maximum-likelihood (ML) tree was estimated using 52 full-length HCV genome sequences (Fig. 1). The phylogeny exhibited seven major branches, representing HCV genotypes 1–7, each supported by a maximum bootstrap support of 100%. The most recent HCV classification types 1–7, each supported by a maximum bootstrap.

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**Phylogeny of partial NS5B region sequences**

A segment of the NS5B region corresponding to nucleotides 8276–8615 of the H77 reference genome, has been found reliably to differentiate HCV genotypes and subtypes in most cases (Murphy et al., 2007). To investigate the full genetic diversity of HCV genotype 1, 141 HCV-1 sequences of this genome region were analysed, each representing an individual isolate and including the seven from this study. The resulting ML tree shows 19 major lineages within HCV genotype 1 (new genomes indicated by black circles in Fig. 1). Isolates EBW9 and EBW443 formed a cluster of two taxa, designated subtype 1h, and isolate 160526 was placed as a single branch corresponding to a new subtype equivalent. Adjacent to the latter lineage, a tight cluster was formed by the isolates EBW424, 136142 and 166212, designated subtype 1l. The isolate 148636, which represents subtype 1e, was also represented in this tree by a single branch. Thus, the three subtypes, 1e, 1h and 1l, were confirmed for the first time in this study by full-length genome sequencing. Similarly, the 160526 sequence should be considered to be a new but currently unclassified subtype equivalent.

**HCV genotype 1 distribution globally and in Cameroon**

At the time of study, the Los Alamos HCV database provided 228 sequences that were classified as subtypes 1c to 1m and for which the country of sampling was stated. Using this information, we summarized the geographical distribution of HCV-1 strains (after excluding subtypes 1a and 1b, which are found worldwide). As shown in Table 2, subtypes 1c and 1g were the most widely distributed subtypes; they have been identified in seven and eight countries, respectively. This was followed by subtypes 1d, 1e and 1h, which have been reported from four, three and three countries, respectively. In contrast, the other six subtypes appeared to be restricted; they have only been found in one or two countries. The greatest number of subtypes was found in Canada followed by France and Cameroon. On a continental scale, North America showed the largest genetic diversity of HCV-1 isolates, representing eight subtypes (Table 3). This was followed by Africa, which showed seven subtypes, and by Europe, which showed six subtypes. Only one or two subtypes were reported from other continents. The continent for which the largest number of HCV-1 isolates has been reported was Africa (47.4%), followed by Asia (37.3%) and America (8.33%). Although these results may be interpreted as suggesting that HCV-1 originated in North America, it is much more likely that this genotype originated in Africa. Many of the recently reported divergent HCV isolates sampled in Canada are known to be from recent African immigrants to that country (Li et al., 2012).

Because six isolates from this study were classified into subtypes 1e, 1h and 1l, all available sequences belonging to these three subtypes were analysed separately. As shown in Fig. 3(a), these sequences originated most frequently in Cameroon (87/96), while only a few (9/96) were sampled from other countries (e.g. France, Canada and Vietnam; all these locations are linked to colonial-era France). The phylogeny in Fig. 2 suggests that isolates from these three countries were interspersed among those from Cameroon, implying that subtypes 1e, 1h and 1l had origins in Cameroon and were later brought to other continents, most likely by French colonial travellers. This may be also the case for subtype 1d, although no isolates were entirely sequenced in the present study. As summarized in Table 2...
Fig. 1. An ML phylogenetic tree estimated using full-length genomic sequences of HCV. Reference sequences from confirmed subtypes of genotypes 1, 2, 3, 4, 5, 6 and 7 are included, together with the seven new isolates from this study (black circles). Each genotype is denoted at the right-hand side of the tree. Within genotype 1, all subtypes and equivalents are also indicated. Isolates are named using the following format: subtype _ sampling country _ sampling date (if available) _ isolate name _ accession number. The symbol ‘?’ indicates that a subtype has not been assigned. Bootstrap supports are shown at internal branches and the scale bar represents 0.10 nt substitutions per site. Country codes: CA, Canada; CM, Cameroon; EG, Egypt; ES, Spain; HEC, <?>; HK, <?>; ID, Indonesia; IN, India; JP, <?>; MD, <?>; TH, <?>; UK, US, USA; VN, Vietnam.
and Fig. 2, 1d isolates have been isolated not only in Tunisia, a former French colonial country in Africa, but also in France and The Netherlands in Europe.

We also investigated all available HCV-1 sequences from Cameroon. Among these, 15 (representing 13 individual isolates) had no subtype designations. Analysis of the NS5B region sequences from Cameroon (solid diamonds in Fig. 2) revealed that one of them was classified into subtype 1e, two into 1l and three into 1b; the remaining seven formed four independent clusters labelled as subtype 1(I), subtype 1(II), subtype 1(III), subtype 1(IV) and subtype 1(V), respectively. Similarly, sequences that had subtype designations were also classified. Except for 1e, 1h and 1l, only one isolate of 1a (Njouom et al., 2003b) and five isolates of 1b were from Cameroon. However, after reanalysis, the isolate classified as subtype 1a was found to group into subtype 1e (represented by a solid square in Fig. 2). Thus to date no subtype 1a isolate has been identified in Cameroon. In summary, HCV-1 isolates sampled in Cameroon (102 in total) represented four of the 13 assigned subtypes and five of the six unassigned lineages (Figs 2 and 3).

Specific variations in the E2 and NS5A regions

The number of amino acids in the E2 and NS5A regions varied from 364 to 371 and from 448 to 449, respectively, among the seven isolates determined in this study (Table 1). Within these two regions, many genetic differences were observed when compared with the H77 strain.

E2 region. Generally, the E2 protein of HCV has 11 potential glycosylation sites (Slater-Handshy et al., 2004). Compared with the H77 strain, the seven sequences from this study only showed six (N2, N4, N6, N7, N10 and N11) of these 11 sites conserved, while the other five sites (N1, N3, N5, N8 and N9) were variable. The N5 site is sited between two conserved amino acids (P471 and R483 according to N5, N8 and N9) were variable. The N5 site is sited between two conserved amino acids (P471 and R483 according to N5, N8 and N9) were variable. The N5 site is sited between two conserved amino acids (P471 and R483 according to N5, N8 and N9) were variable. The N5 site is sited between two conserved amino acids (P471 and R483 according to N5, N8 and N9) were variable. The N5 site is sited between two conserved amino acids (P471 and R483 according to N5, N8 and N9) were variable. The N5 site is sited between two conserved amino acids (P471 and R483 according to N5, N8 and N9) were variable. The N5 site is sited between two conserved amino acids (P471 and R483).
A variety of insertions and deletions were observed in the NS5A region among the new HCV-1 sequences reported in this study (Fig. 4). They were located in the subgenomic region of protein kinase region (PKR)-BD and Domain III. The PKR-BD of the 160526 isolate had an insertion of one amino acid at position 2262–2263; the Domain III of subtype 1h (EBW9 and EBW443) had one insertion at position 2328–2329 and one deletion at position 2414.

**Similarity plotting**

To exclude the possibility of viral recombination, pairwise nucleotide similarity curves were plotted along HCV genomes using the RDP3 software. Upon comparison of the seven isolates from this study with each other, and with the 45 reference sequences shown in Fig. 1 that represent various HCV genotypes and subtypes, no such evidence was detected (data not shown). Similarity plotting also showed that three hypervariable regions (HVR1, HVR2 and V3) were positioned as previously described (Simmonds, 2004).

**DISCUSSION**

In this study, full-length genome sequences of seven genotype 1 isolates of HCV were characterized (isolates EBW9, EBW424, EBW443, 136142, 148636, 160526 and 166212). Based on the consensus criteria for HCV classification and nomenclature (Simmonds *et al.*, 2005), isolate 148636 should be classified as subtype 1e, both EBW9 and EBW443 as subtype 1h, EBW424, 136142 and 166212 as subtype 1l, while isolate 160526 may represent a novel as yet unassigned subtype. These classifications are supported not only by analysis of full-length genome sequences but also by analysis of partial Core, E1 and NS5B regions (Figs 1, 2 and S2). Previous nomenclature guide-
Fig. 3. Distribution of genotype 1 isolates in different countries and in Cameroon. (a) Histogram showing the frequencies of subtype 1e, 1h and 1l in four countries (CM, Cameroon; CA, Canada; FR, France; VN, Vietnam; ?, unknown country). The number of isolates is shown above each column while the country of origin is indicated below. (b) Histogram showing the frequencies of genotype 1 subtypes sampled in Cameroon. The number of isolates is shown above each column.

Fig. 4. Analysis of amino acid sequences in the E2 and NS5A regions. Amino acids are shown using standard IUPAC codes and bars indicate indels. Isolate names are listed to the left of the alignment while amino acid positions (relative to the H77 reference genome) are indicated above.
lines (Simmonds et al., 2005) regarded subtypes 1e, 1h and 1l as being provisional subtypes. With the seven full-length genome sequences characterized here, the definition of these three subtypes is now confirmed. However, a formal designation cannot currently be made for the potential new subtype represented by isolate 160526, because no other closely related isolates have been identified; isolate 160526 therefore remains an unassigned subtype equivalent. Within genotype 1, full-length genome sequences are still missing for subtypes 1d, 1f, 1i, 1j, 1k and 1m; this situation should be rectified in future studies in order to further develop HCV nomenclature, which provides important background information for effective HCV prevention and treatment.

Previously, a total of 13 subtypes (1a–1m) of HCV genotype 1 have been proposed (Simmonds et al., 2005). Of these, subtypes 1a and 1b are distributed worldwide and for this reason were not analysed in this study. In addition to subtypes 1a–1m, this study proposes the existence of six genotype 1 lineages that are equivalent to new but unassigned subtypes. Each of these lacks a sufficient number of closely related isolates to meet the criteria for proposing new subtypes, although they showed sufficient genetic distances from other subtypes to qualify. Excluding subtypes 1a and 1b, we also summarized the genetic diversity and geographical distribution of the remaining 11 assigned subtypes and the six unassigned lineages. Genotype 1 isolates most often originated in Cameroon. It has been previously noted that HCV-1 has been historically endemic in Africa, particularly in Central-West Africa (Simmonds et al., 2005). Of the 108 isolates classified into subtypes 1c–1m that were reported as being African in origin, we found isolates of subtypes 1e, 1h and 1l from Cameroon accounted for more than 80% (87/108) (Fig. 3a) (Ndjomou et al., 2003; Njoum et al., 2003b; Pasquier et al., 2005). This could be taken as evidence suggesting that these three subtypes originated in Cameroon and that from Cameroon they subsequently disseminated to other areas. These subtypes were possibly amplified in Cameroon by unsafe medical interventions, such as the use of intravenous antimalarial drugs and contaminated blood transfusions that are considered to be major historical risk factors for HCV infection among people in Cameroon (Pépin & Labbé, 2008; Pépin et al., 2010). Remarkably, among these three subtypes, four isolates have been detected in Quebec, Canada (Murphy et al., 2005), three in Vietnam (GenBank numbers AB306393, AB306376 and AB301765), and one in France (Laperche et al., 2005). Historically, these three countries/regions were linked to the former French colonial empire. Similar links among geographical regions for various strains of HCV genotype 2 have been proposed to result from the actions of former European colonial powers (Li et al., 2012; Markov et al., 2012). Such scenarios could have also occurred for a variety of HCV-1 lineages and the currently observed worldwide circulation of subtypes 1a and 1b may thus reflect such consequences. Among the six unassigned lineages of genotype 1, five have also been discovered in Cameroon, namely lineages 1(II), 1(III), 1(IV), 1(V) and 1(VI). This may further suggest Cameroon as the area where HCV-1 originated, although more comprehensive sampling of HCV from other countries of West and Central Africa will be necessary before this hypothesis can be confirmed.

METHODS

Subjects and specimens. Three serum samples, EBW9, EBW443 and EBW424, were collected during 2000–2003 among patients living in Cameroon (Pasquier et al., 2005). Detailed information of the age and gender of these three patients and dates of sampling are shown in Table 1. In addition, four samples (148636, 136142, 166212 and 160526) were provided by Micropathology Ltd in the UK, who identified them as atypical HCV genotype 1 sequences during routine service provision to a range of primary healthcare providers. These samples were obtained from patients who were believed to have acquired their infections in Cameroon.

PCR amplification and sequencing. Full-length HCV genome sequences were each determined from 140 μl of serum sample using the approaches we have recently described (Li et al., 2012). Briefly, RNA extraction (Qiagen Viral RNA extraction kit, Qiagen) and cDNA synthesis (RevertAid First Strand cDNA Synthesis kit, Fermentas) were performed following the manufacturer’s guidelines; overlapping fragments spanning the full HCV genome were amplified using conventional nested or semi-nested PCR with the primers listed in Table S1 (only degenerate primers are shown). Standard procedures were adopted to avoid possible carryover contamination (Kwok & Higuchi, 1989). At least one negative control, one positive control, and a blank composed of water were included in each of the following steps: RNA extraction, reverse transcription, and the first and second rounds of PCR. After PCR, the amplicons were purified using QIAquick PCR purification kit (Qiagen) according to the manufacturer’s protocol. To obtain consensus sequences that reflected the possible heterogeneity of the viral population within each individual, purified amplicons were sequenced directly in both directions. Some fragments amplified using degenerate primers failed to yield clear sequencing chromatograms. These fragments were cloned into the pGEM-T Easy Vector (Promega), of which four clones each were picked and sequenced. All sequencing reactions were conducted using ABI Prism BigDye 3.0 Terminators with an appropriate primer and resolved on an ABI Prism 3500 genetic analyser (PE Applied Biosystems). Any errors in base calling were corrected using the SeqMan program and the edited sequences inspected for functional regions of the genome (DNASTAR). Finally, the obtained sequences were aligned using BioEdit (Hall, 1999), in which any further manual adjustments and corrections were made.

In the Los Alamos HCV database (Kuiken et al., 2005), full-length HCV genome sequences are available for four HCV-1 subtypes: 1a, 1b, 1c and 1g. An alignment was constructed that comprised nine genome sequences were each determined from 140 μl of serum sample using the approaches we have recently described (Li et al., 2012). Briefly, RNA extraction (Qiagen Viral RNA extraction kit, Qiagen) and cDNA synthesis (RevertAid First Strand cDNA Synthesis kit, Fermentas) were performed following the manufacturer’s guidelines; overlapping fragments spanning the full HCV genome were amplified using conventional nested or semi-nested PCR with the primers listed in Table S1 (only degenerate primers are shown). Standard procedures were adopted to avoid possible carryover contamination (Kwok & Higuchi, 1989). At least one negative control, one positive control, and a blank composed of water were included in each of the following steps: RNA extraction, reverse transcription, and the first and second rounds of PCR. After PCR, the amplicons were purified using QIAquick PCR purification kit (Qiagen) according to the manufacturer’s protocol. To obtain consensus sequences that reflected the possible heterogeneity of the viral population within each individual, purified amplicons were sequenced directly in both directions. Some fragments amplified using degenerate primers failed to yield clear sequencing chromatograms. These fragments were cloned into the pGEM-T Easy Vector (Promega), of which four clones each were picked and sequenced. All sequencing reactions were conducted using ABI Prism BigDye 3.0 Terminators with an appropriate primer and resolved on an ABI Prism 3500 genetic analyser (PE Applied Biosystems). Any errors in base calling were corrected using the SeqMan program and the edited sequences inspected for functional regions of the genome (DNASTAR). Finally, the obtained sequences were aligned using BioEdit (Hall, 1999), in which any further manual adjustments and corrections were made.

To amplify the extreme 5’ ends in a semi-nested PCR, the upstream primer used was H77-3end (30 bp), while the downstream primers were 4-367R or 4-342R (Table S1). This strategy was used for all seven HCV-1 isolates since the extreme 5’ ends of their 3’ UTRs are highly

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conserved. To amplify the 3’ ends, a semi-nested PCR or nested RACE PCR was utilized in which the upstream primers were specific to the 3’ end of the N5S region, while the downstream primers used were poly(A), NUP or 1-9411R (see Table S1). The primer 1-9411R was designed based on the conserved 3’UTR region upstream to the poly(A) tail.

All PCRs were conducted with an initial denaturation at 95 °C for 3 min, followed by 35 cycles each consisting of 95 °C for 30 s, 55 °C for 30 s and 72 °C for a variable time according to the fragment sizes (about 1 min/kb). The final cycle of extension was at 72 °C for 7–10 min. All PCRs utilized the Taq DNA polymerase system (Roche).

Phylogenetic analyses and inspection of genome sequences. The seven full-length HCV genomic sequences obtained were annotated according to the standard nucleotide numbering scheme of the H77 genome, from the extreme 5’ end to the 3’X tail (Kuiken & Simmonds, 2009). To classify subtypes more clearly we retrieved all HCV-1 sequences available in the Los Alamos HCV database that have lengths of greater than 9000 nt. We identified 543 such sequences for subtype 1a, 478 for 1b, three for 1c, one for 1g, and 14 representing unclassified genotype 1 isolates (database accessed on June 25, 2012). From these, two each belonging to subtypes 1a and 1b, all those belonging to subtypes 1c and 1g, as well as the 14 unclassified sequences (13 of which were found to belong to subtype 1a) were retained; these were subjected to phylogenetic analysis together with reference genomes representing genotypes 2, 3, 4, 5, 6 (Simmonds et al., 2005) and 7 (Murphy et al., 2007). Together with the seven sequences obtained in this study, a total of 52 sequences were considered.

These 52 full-length HCV genomic sequences were aligned using BioEdit and investigated with the MEGA5 sequence editor (Tamura et al., 2011). Particular interest was paid to amino acid variation in the interferon-sensitivity determining region (ISDR) (Enomoto & Sato, 1995), the RNA-activated protein kinase region (PKR), and some other domains in the E2 and NS5A regions (Gale & Katze, 1998; Gale et al., 1998; Taylor et al., 1999).

To explore genetic variation and subtype classifications within HCV genotype 1, an NS5B region dataset was assembled that represented all assigned subtypes and unassigned variants. Only two sequences were selected as representatives of subtypes 1a, 1b and 1c, as these subtypes are well known to be prevalent worldwide and are represented by thousands of sequences in the Los Alamos HCV database. However, for all other subtypes (such as 1d–1m) all available partial NS5B sequences were retrieved from the database. To understand the diversity of HCV-1 strains in Cameroon, all HCV-1 isolates sampled in Cameroon were retrieved regardless of whether they had a subtype assigned or not. In total, the NS5B dataset contained 141 HCV-1 sequences, each approximately 340 nt long and corresponding to nucleotide positions 8276–8615 in the H77 genome.

ML phylogenetic trees were reconstructed for the two sequence datasets using MEGA5 (Tamura et al., 2011). The most appropriate nucleotide substitution model for phylogenetic analysis was determined using the model selection procedure implemented in the program Modeltest (Posada & Crandall, 1998). For the full-length and partial NS5B alignments, the GTR+1+Γ model was found to be the best. To assess the statistical robustness of phylogenetic groupings, bootstrap analyses were conducted with 500 replicates. The sequence name, sampling country, subtype and accession number were indicated at the tips of the resulting phylogenies.

To exclude recent virus recombination events (Colina et al., 2004; Kalinina et al., 2002, 2004; Lee et al., 2010; Legrand-Abraannel et al., 2007; Noppornpanth et al., 2006), the rVPH software (Martin et al., 2010) was run with settings as previously described (Lu et al., 2007a). This analysis was only performed for the full-length alignment.

Geographical distribution of HCV-1 sequences. In the Los Alamos HCV database a total of 76 912 sequences were classified as HCV-1 (including five recombinants; accessed on 25 June 2012). Among these, subtype 1a had 33 086 sequences; subtype 1b had 40 752; subtypes 1c–1m had 385; and 2689 sequences had no subtype designations. To analyse the geographical distribution of HCV-1 sequences, only subtypes 1c–1m were included (because subtypes 1a and 1b are distributed worldwide). When the cloning status of these 385 sequences was examined we were able to distinguish 228 individual isolates. Because the seven new genomes in this study all had origins in Cameroon and all (excluding one) belong to subtypes 1e, 1h and 1l, the 228 individual isolates were further analysed to see if they were sampled in Cameroon, or were classified as subtypes 1e, 1h and 1l.

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