Fig. A2


100
AB091394
AB222182
AB073912
AB369691
AP003430
100
AB481229
AB291963
AB246676
AB291962
AB630971
AY115488
AB222183
74
97
51
FJ527832
AB222184
100
99
FJ426403
100
83
JN837481
70
100
AB591734
FJ426404
74
AB630970
79
AB074918
89
AB074920
AB089824
100
AB481228
67
100
86
51
Genotype 3 AB290312 Sw MON 2006
Genotype 3c-like JQ953664 Sw FRA 2006
Genotype 3i FJ998008 Wb GER 2007
70
97
BBH JQ424437 Sw BOL 2006
BBH JQ424441 Sw BOL 2006
BBH JQ424440 Sw BOL 2006
100
BBH JQ424439 Sw BOL 2006
BBH JQ424442 Sw BOL 2006
98
AF336298
AF336297
BBH JQ929110 Hu NLD 2009
99
BBH JQ929104 Hu NLD 2008
55
BBH JQ929123 Hu NLD 2011
AF336290
BBH KF303501 Wb GER 2008
100
BBH AF336293 Sw NLD 2001
95
BBH EF194044 Hu FRA 2006
74
BBH EF113906 Hu FRA 2006
58
BBH JF730384 Hu FRA 2009
63
99
KJ742844
KJ742846
KJ742841
KJ742840
99
BBH JF730402 Hu FRA 2009
78
BBH JQ929111 Hu NLD 2009
BBH JQ929105 Hu NLD 2008
BBH JQ929121 Hu NLD 2011
80
BBH JQ929107 Hu NLD 2008
56
BBH JQ929108 Hu NLD 2009
BBH JQ929119 Hu NLD 2011
BBH Genotype 3i FJ705359 Wb GER 2006
BBH KC758129 Hu NLD 2012
93
BBH Genotype 3 KC618403 Hu GER 2013
BBH Genotype 3 KC618402 Hu GER 2013
BBH KC758127 Hu NLD 2012
BBH AB671132 Hu JAP 2010
BBH JQ929118 Hu NLD 2010
BBH JQ929122 Hu NLD 2011
BBH JQ929112 Hu NLD 2009
BBH JQ929117 Hu NLD 2010
78
Genotype 3g AF455784 Sw KYR 2004
100
71
57
Genotype 3e JQ953665 Sw FRA 2006
56
KJ742839
JQ013795
50
AB248522
88
98
60
AB290313
Genotype 3c EU360977 Sw SWE 2008
AB369687
100
EU723512
FJ956757
JQ953666
100
FJ653660
KJ742845
KJ742843
AB291961
EU375463
KJ742842
EU495148
99
93
JQ013791
68
AB573435
AB602441
84
100
JF443720
72
M74506
99
HM439284
100
JN998607
95
JX120573
99
100
JQ001749
100
EF206691
0.05

Figure A2. Phylogenetic tree based on a 231-nucleotide partial sequence of open reading frame 2 (ORF) 2 of the HEV genome (a fragment from the 343 nucleotide-long sequence analyzed in Figure 1 that corresponds to nucleotides 6,063-6,293 of genome GenBank accession no. FJ705359).

The HEV sequences obtained in our laboratory are indicated by a black frame. The 10 sequences with the highest BLAST scores (excluding those from our laboratory or with a query coverage <98%) recovered from the NCBI GenBank nucleotide sequence database (indicated in boldface, underlined, labeled with BBH (for best BLAST hit), GenBank accession number, host, country and year of sample collection or sequence submission) with the near full-length genome obtained in this study (GenBank accession no. KJ701409) have been incorporated into the phylogeny reconstruction in addition to a comprehensive set of 245 full-length genome sequences that were downloaded from the Virus Pathogen Resource database (1) (labeled, if they are clustered with sequences from the present study, with genotype and subtype, GenBank accession number, host, country and year of sample collection or sequence submission). To allow for the better legibility of the tree, branches were collapsed when they did not directly link to sequences from the present study and when the bootstrap value at node was >90%. Nucleotide alignments were performed using the MUSCLE software (http://www.ebi.ac.uk/Tools/msa/muscle/). The tree was constructed using the MEGA 5 software (http://www.megasoftware.net/) and the neighbor-joining method. Branches with bootstrap values were obtained from 1,000 resamplings of the data, and values >50% are labeled on the tree. The scale bar indicates the number of nucleotide substitutions per site.

BBH, best BLAST hit; BOL, Bolivia; GER, Germany; FRA, France; Hu, Human; JAP, Japan; KYR, Kyrgyzstan; MON, Mongolia; NLD, the Netherlands; Sw, Swine; SWE, Sweden; URU, Uruguay; Wb, wild boar.