Autochthonous Infections with Hepatitis E Virus Genotype 4, France

Technical Appendix

Technical Appendix Figure 1. Weekly monitoring of the numbers of serum samples tested for hepatitis E virus (HEV) and the number with positive anti-HEV IgM and HEV RNA test results during December 13, 2010–April 4, 2011. Data are entered into a Microsoft Excel file each week (1). EPIMIC, a biosurveillance program (1), automatically and instantly calculates the mean value and the standard deviation (SD) for all entered datasets. Any significant increase beyond the critical threshold, defined by the mean value +2 SDs, generates a red signal. Values that exceed the critical threshold are indicated in the figure by a black triangle and red font.
Technical Appendix Figure 2. Phylogenetic tree based on partial (204-nt) sequence of open reading frame 2 of the hepatitis E virus (HEV) genome (nt 6066–6269; GenBank accession no. AB291961). The phylogenetic analysis is as described in the Figure, except that avian (Av) HEV sequence AY043166 was used as an outgroup. Sequences obtained from humans in Marseille, France, during January–March 2011, are shown in boxes with gray background; black circles indicate patients who ate uncooked pig liver sausage. Genotype is indicated on the right. The scale bar indicates the number of nucleotide substitutions per site. HEV sequences are labeled with GenBank accession number, host, country where isolated, and collection or submission date. CHN, China; DEU, Germany; ESP, Spain; FRA, France; Hu, human; IND, India; JPN, Japan; MAR, Marseille; MEX, Mexico; NLD, the Netherlands; Sw, swine; SWE, Sweden; TWN, Taiwan; USA, United States; Wb, wild boar.
Technical Appendix Figure 3. Phylogenetic tree based on partial (537 nt) nucleotide sequence of the 3’-end of open reading frame 2 of the hepatitis E virus (HEV) genome (nt 6439–6975; GenBank accession no. AB291961). The phylogenetic analysis is as described in the Figure, except that avian (Av) HEV sequence AY043166 was used as an outgroup. Sequences obtained from humans in Marseille, France, during January–March 2011, are shown in boxes with gray background; black circles indicate patients who ate uncooked pig liver sausage. Genotype is indicated on the right. The scale bar indicates the number of nucleotide substitutions per site. HEV sequences are labeled with GenBank accession number, host, country where isolated, and collection or submission date. CHN, China; ESP, Spain; Hu, human; ITA, Italy; JPN, Japan; KOR, South Korea; MNG, Mongolia; Sw, swine; THA, Thailand; TWN, Taiwan; USA, United States.
Reference