
Comparison of hepatitis E virus sequences from humans and swine, the Netherlands, 2008-2015.

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Until the beginning of this century, in the developed world, hepatitis E virus (HEV) was seen as a travellers disease and autochthonous HEV infection was rarely observed. Now a days HEV infections become common and recent studies showed that zoonotic hepatitis E virus genotype 3 infections occur frequently in industrialized countries. Pigs have been shown to be a major reservoir of hepatitis E genotype 3 virus, only the transmission route(s) from pigs to humans are ill-defined. Consumption of undercooked meat products is the likely transmission route however the virus could also spread via surface water or crops. Partly orf 1 and orf 2 sequences of HEV isolates were obtained from individual pigs and from blood donors and hepatitis patients. 372 human samples and at least 10 HEV positive caecum swine samples per year were collected in the Netherlands in 2000 and between 2008 and 2015 and sequenced. All generated HEV sequences from human and pig samples were aligned with a proposed reference set from the literature. In total, 91 HEV ORF1 sequences and 300 HEV ORF2 sequences from pigs, patients and blood donors were included in the analysis. Sequence comparison showed that all sequences were genotype 3 except for six patients (with travel history). HEV gt3c was the most common subgenotype. Whereas the proportion of gt3c significantly increased between 2000 and 2008 it remained constant between 2008 and 2015. Of the circulating HEV subgenotypes, there was no difference observed between the human and the pig isolates. This is compatible with the assumption that HEVs from swine are the major source of HEV infections in humans. Hepatitis E viruses in humans are very likely to originate from pigs, but it is unclear why HEV gt3c has become the predominant subtype in the Netherlands.