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Identification of a novel hepatitis E virus genotype in rats – a candidate for establishment of a rodent model for hepatitis E?

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Hepatitis E is a rare human disease in developed countries. It is caused by genotypes 1-4 of hepatitis E virus (HEV), which are most likely zoonotically transmitted to humans from domestic pigs and wild boars. Multiple reports on the detection of HEV-specific antibodies in rats suggested the presence of an HEV-related agent; however, infectious virus or a viral genome could not be demonstrated so far.

Using a newly developed nested broad-spectrum RT-PCR protocol capable of detecting different HEV types of humans, pigs and birds, HEV-like sequences were detected in samples of wild Norway rats (*Rattus norvegicus*) from Hamburg (Germany). Virus particles with morphology reminiscent of HEV were demonstrated in the samples. Comparison of the complete genome sequence of the novel virus (tentatively designated as rat HEV) to other human and animal HEV strains revealed sequence identities between 49.5 % and 55.9 % and a genome organization similar to other HEV strains. Using real-time RT-PCR, the highest virus amount was detected in the liver of the infected rats. In addition, HEV-specific antigen was demonstrated in hepatocytes by immunohistochemistry.

It could be concluded that rat HEV represents a novel genotype of HEV, which is only distantly related to human and pig HEV, but has similar biological properties. Experimental infection trials with laboratory rats are ongoing assessing the suitability of rat HEV infection as a rodent model for human hepatitis E, which is not available so far. In addition, further investigations should clarify the zoonotic potential of rat HEV.