

Figure. Close-up of liver granuloma with section through 3 *Schistosoma malayensis*-like ova embedded in dense fibrous tissue. The thin-walled, nonstriated helminth ova are not operculated and contain nonvital miracidial cells. Hematoxylin and eosin stain; original magnification  $\times 100$ .

because it was obtained from a relative, and possible unreported drug-related travel by the patient to neighboring countries cannot be fully excluded. *R. muelleri*, the jungle rat and definitive host for *S. malayensis*, is often seen at river banks (4), and rodent feces could have contaminated the water with schistosome eggs.

Future field studies are needed to identify focal hot spots of sylvatic transmission by snail examination and seroprevalence studies of persons living in rural areas, especially the Orang Asli population. Moreover, in light of growing ecotourism, which also encompasses stays at remote Orang Asli villages and canoeing on small streams (10), appropriate public health measures, such as rodent and snail control near tourist sites, should be implemented.

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## Asian Musk Shrew as a Reservoir of Rat Hepatitis E Virus, China

**To the Editor:** Rat hepatitis E virus (HEV), a member of genus *Hepevirus* in the family *Hepeviridae*, was first detected in Norway rats in Germany in 2010 (1, 2). Since then, this rat HEV has been detected in multiple wild rat species in the United States, Vietnam, Germany, and Indonesia (3-7). Studies have shown that rat HEV failed to infect rhesus monkeys and pigs,

suggesting that rat HEV is restricted to its natural host (6, 8). However, it is not known whether animals other than rats are susceptible to rat HEV.

The Asian musk shrew (*Suncus murinus*), also called the Asian house shrew, is a small mole-like mammal belonging to the family *Soricidae* (order *Soricomorpha*), and wild rats are classified in the family *Muridae* (order *Rodentia*). Musk shrews originated from the Indian subcontinent and are now found from southern Asia and Afghanistan to the Malay Archipelago and southern Japan. These shrews are commensal rodents, commonly found living in human households. We previously showed that rat HEV infection frequently occurs in wild rats in Zhanjiang City, Guangdong Province, China (9). Asian musk shrews share this same environment; thus, they can be exposed to rat HEV derived from wild rats.

To determine whether Asian musk shrews are a reservoir for rat HEV, we examined 260 shrews (112 males, 148 females) that were trapped in Zhanjiang City during December 2011–September 2012. Of the 260 trapped shrews, 147 were from Mazhang District (23 from a pig farm and 124 from the villages of Chiling, Chofa, Beigou, Huangwai, Houyang, and Nanpan) and 113 were from Chikan District.

Blood samples were collected from the shrews, and serum was separated by centrifugation (2,500 × *g* for 20 min at 4°C), and stored at –80°C until use. We tested the serum samples for the presence of HEV IgG and IgM antibodies by using an ELISA based on rat HEV-like particles, as described (3). Of the 260 samples, 27 (10.4%) were HEV IgG positive and 12 (4.6%) were HEV IgM positive. Of these, 3 IgG-positive and 1 IgM-positive samples were among the 113 samples (2.7% and 1.0%, respectively) collected from shrews in Chikan District, and 24 IgG-positive and 11 IgM-positive samples were among the 147 samples (16.3% and 7.5%, respectively) collected from shrews in 6 villages (124

total samples) and the pig farm (23 total samples) in Mazhang District. The IgG-positive rate was higher for shrews from Mazhang District than for those from Chikan District ( $p < 0.05$ ); the rates of IgM-positivity did not differ significantly. The IgG-positive rate among the 6 villages varied substantially (8.3%–71.4%) (online Technical Appendix Table 1, [wwwnc.cdc.gov/EID/article/19/8/13-0069-Techapp1.pdf](http://wwwnc.cdc.gov/EID/article/19/8/13-0069-Techapp1.pdf)). The IgG-positive rates were 11.6% (13/112) in male and 9.5% (14/148) in female shrews, respectively; the difference in rates between the sexes was not statistically significant.

A total of 12 IgM-positive serum samples were selected for HEV RNA testing by nested broad-spectrum reverse transcription PCR (2); results for 5 were positive (online Technical Appendix Table 2). The length of the nested reverse transcription PCR products was 334 nt. After the primer sequences were removed, we sequenced the remaining 281 nt corresponding to nt 4107–4387 in the C-terminal open reading frame 1 of the rat HEV genome (GU345042) (GenBank accession nos. KC473527–KC473531). Phylogenetic analysis indicated that the 5 HEV isolates were all classified into the same group as rat HEV and clearly separated into 2 clusters, A and C. Cluster A isolates were further divided into 2 subclusters, sub-A1 (CHZ-sRat-E-1107) and sub-A2 (CHZ-sRat-E-1133) (Figure). Strains CHZ-sRat-E-739, CHZ-sRat-E-1086, and CHZ-sRat-E-1129 belong to cluster C. These findings are of limited precision because of the short sequence that was analyzed, and, thus, they may not be predictive of results obtained with complete genomes.

Rat HEV isolated from the *S. murinus* shrews shared 77.4%–99.6% nt sequence identity with other rat HEV strains; the sequences were especially similar to those of HEV isolates from wild rats in this area (GenBank accession nos. KC465990–KC466001) (online Technical Appendix Table 3). In addition, nucleotide sequences from

subcluster A1 and A2 and cluster C rat and shrew strains shared 97.5%–99.6%, 96.8%–97.2%, and 94.0%–97.5% identity, respectively (online Technical Appendix Table 3). These results indicate that rat HEV infection occurs in *S. murinus* shrews and that these rodents are a reservoir for rat HEV.

Evidence indicates that rat HEV may be capable of inducing an immune response in humans; thus, this virus may be relevant to the epidemiology of HEV in humans (10). A key step in understanding this epidemiology is to know the reservoirs of rat HEV, especially reservoirs like *S. murinus* shrews, which live in close proximity to humans.

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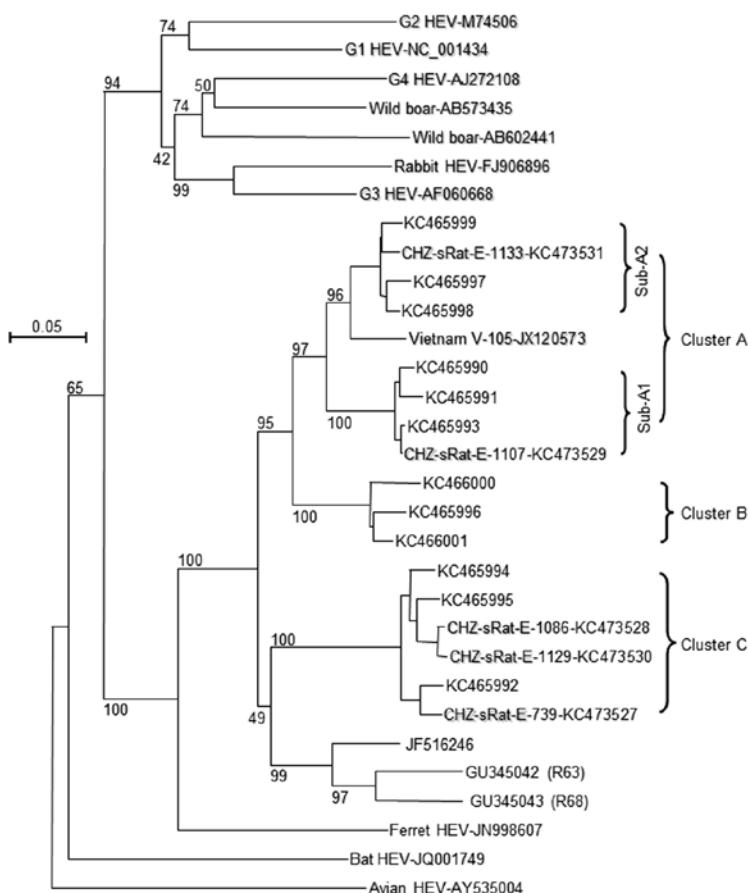


Figure. Phylogenetic analysis of rat hepatitis E virus (HEV) isolated from Asian musk shrews (*Suncus murinus*) in Zhanjiang City, China. Nucleic acid sequence alignment was performed by using ClustalX 1.81 ([www.clustal.org](http://www.clustal.org)). The genetic distance was calculated by using the Kimura 2-parameter method. The phylogenetic tree, with 1,000 bootstrap replicates, was generated by the neighbor-joining method based on the partial sequence (281 nt) of HEV open reading frame 1 of genotype 1–4, wild boar, rabbit, ferret, bat, avian, and rat HEV isolates. The scale bar indicates nucleotide substitutions per site.

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## No Evidence for Hepatitis E Virus Genotype 3 Susceptibility in Rats

**To the editor:** Hepatitis E virus (HEV) is a positive-sense single-stranded RNA virus (genus *Hepevirus*, family *Hepeviridae*) (1). In humans, acute hepatitis infection caused by HEV is a serious public health concern in developing countries. Four HEV genotypes, G1–4, have been isolated from humans (2). G3 and G4 HEV have also been isolated from swine, wild boars, wild deer, and mongooses; these animals are thought to be the reservoirs of HEV (3). Direct evidence has indicated that HEV is transmitted from pigs or wild boars to humans; therefore, hepatitis E caused by G3 and G4 HEV infection is recognized as a zoonosis (3).

Although rats have long been suspected to be a potential reservoir for human HEV, no direct evidence has been found. The susceptibility of rats to human HEV genotypes is