Zoonotic and Foodborne Transmission of Hepatitis E Virus

Xiang-Jin Meng, MD, PhD

1 Department of Biomedical Sciences and Pathobiology, College of Veterinary Medicine, Virginia Polytechnic Institute and State University, Blacksburg, Virginia

Address for correspondence X. J. Meng, MD, PhD, Department of Biomedical Sciences and Pathobiology, Virginia Tech, CRC-Integrated Life Science Building, 1981 Kraft Drive, Blacksburg, VA 24061-0913 (e-mail: xjmeng@vt.edu).

Abstract

Hepatitis E is an important disease in many developing countries of Asia and Africa with large explosive outbreaks and is also endemic with sporadic or cluster cases of hepatitis in many industrialized countries. The causative agent, hepatitis E virus (HEV), is currently classified in the family Hepeviridae. Thus far, four putative genera of HEV representing mammalian, avian, and fish species have been identified and characterized worldwide. Within the mammalian HEV that infects humans, genotypes 1 and 2 are associated with epidemics and restricted to humans, whereas genotypes 3 and 4 are zoonotic and associated with sporadic and cluster cases of hepatitis E. As a fecal–orally transmitted disease, waterborne transmission is still an important route of HEV transmission especially for large outbreaks associated with genotypes 1 and 2. However, genetic identification of numerous animal strains of HEV and the demonstrated ability of cross-species infection by these animal strains have significantly broadened the host range and diversity of HEV and raised public health concerns for zoonosis and food safety associated with genotypes 3 and 4 HEV infection. Pigs and likely other animal species serve as reservoirs for HEV. Direct contact with infected pigs and other animals and consumption of contaminated animal meat and meat products pose risks for HEV infection. In this article, the current understanding of the zoonotic and foodborne transmissions of HEV as well as strategies to prevent zoonosis and ensure food safety is discussed.
The viruses within the genus Hepevirus all infect mammals and have been genetically identified from humans, pig, mongoose, deer, rat, rabbit, and ferret (► Fig. 1). However, the recent identification of genetically and phylogenetically distinct strains of HEV from several animal species such as fish and bat9,10 warrant reclassification of HEV in the near future.

The genus Hepevirus includes four recognized genotypes and at least two putative new genotypes.8 Genotype 1 HEV consists of Asian strains of human HEV that are responsible for large outbreaks in humans. Genotype 2 HEV consists of a single Mexican strain and some African strains of human HEV and is also associated with epidemics in humans. Genotype 3 HEV contains strains from sporadic, cluster, and chronic cases of hepatitis E in humans and from several animal species including pig, deer, rat, mongoose, and rabbit. Genotype 4 HEV includes strains from sporadic and cluster cases of hepatitis E in humans and animal HEV strains from pigs and possibly cattle and sheep.3 The two putative new genotypes of mammalian hepeviruses include strains of HEV from rat and ferret,11–13 and a novel strain of HEV from wild boars in Japan.14,15 A tentative genus Orthohepevirus is proposed here to include all these mammalian strains of HEV (►Table 1).

Avian HEV from chicken16 is currently classified as a floating species within the family Hepeviridae.8 However, avian HEV is genetically and phylogenetically distinct from the mammalian hepeviruses sharing only ~50% nucleotide sequence identity.17–19 Therefore, avian HEV should be classified as a separate genus,4,20 and the tentative genus Avihepevirus is proposed here to include all three genotypes of avian HEV worldwide: genotype 1 from chickens in Australia and Korea, genotype 2 from chickens in the United States, and genotype 3 from chickens in Europe and China.19,21,22

The novel strain of HEV, cutthroat trout virus (CTV)10 isolated from spawning adult trout in the United States, belongs to a new genus as well, and the tentative genus Piscihepevirus is proposed here for CTV. The novel strain of HEV recently identified from bats9 is also phylogenetically distinct from the known HEV strains, and thus is proposed to form a tentative genus Chiropteranhepevirus (►Table 1).

The novel strain of HEV, cutthroat trout virus (CTV)10 isolated from spawning adult trout in the United States, belongs to a new genus as well, and the tentative genus Piscihepevirus is proposed here for CTV. The novel strain of HEV recently identified from bats9 is also phylogenetically distinct from the known HEV strains, and thus is proposed to form a tentative genus Chiropteranhepevirus (►Table 1).

### The Ever-Expanding Host Range of HEV

Genetic identification of HEV strains from various animal hosts and the demonstration of cross-species infection by some animal strains of HEV have broadened the host range and genetic diversity of virus (►Table 1).3,5

### Table 1 Proposed nomenclature of the hepatitis E virus (HEV)

<table>
<thead>
<tr>
<th>Proposed genera</th>
<th>Natural hosts</th>
</tr>
</thead>
<tbody>
<tr>
<td>Orthohepevirus</td>
<td></td>
</tr>
<tr>
<td>Genotype 1</td>
<td>Man</td>
</tr>
<tr>
<td>Genotype 2</td>
<td>Man</td>
</tr>
<tr>
<td>Genotype 3</td>
<td>Man, domestic and wild pig, deer, mongoose, rabbit, rat</td>
</tr>
<tr>
<td>Genotype 4</td>
<td>Man, domestic and wild pig, cattle, sheep</td>
</tr>
<tr>
<td>Putative genotype 5</td>
<td>Rat, ferret</td>
</tr>
<tr>
<td>Putative genotype 6</td>
<td>Wild pig</td>
</tr>
<tr>
<td>Avihepevirus</td>
<td></td>
</tr>
<tr>
<td>Genotype 1</td>
<td>Chicken (Australia, Korea)</td>
</tr>
<tr>
<td>Genotype 2</td>
<td>Chicken (USA, Canada)</td>
</tr>
<tr>
<td>Genotype 3</td>
<td>Chicken (Europe, China)</td>
</tr>
<tr>
<td>Piscihepevirus</td>
<td></td>
</tr>
<tr>
<td>Cutthroat trout virus</td>
<td>Brown, Apache, and Gila trouts</td>
</tr>
<tr>
<td>Chiropteranhepevirus</td>
<td>Bat</td>
</tr>
</tbody>
</table>

Seminars in Liver Disease Vol. 33 No. 1/2013

Zoonotic and Foodborne Transmission of HEV Meng

This document was downloaded for personal use only. Unauthorized distribution is strictly prohibited.
Domestic Pig

The first animal strain of HEV, swine hepatitis E virus (swine HEV), was identified and characterized in 1997 from domestic pigs in the United States. Thus far, two genotypes of HEV, genotypes 3 and 4, have been identified from pigs worldwide. HEV infection is widespread in swine farms and generally infects pigs of 2 to 4 months of age. The infected pigs are subclinically and generally have a transient viremia lasting for 1 to 2 weeks, and fecal virus shedding lasting for approximately 3 to 7 weeks. Gross pathological lesions were absent in the liver, although microscopic lesions of hepatitis characterized by multifocal lymphoplasmacytic hepatitis and focal hepato-cellular necrosis were observed. The transmission route for HEV in pigs is fecal–oral and virus-containing feces are the main source of virus for transmission. However, under experimental conditions, infection of pigs with HEV via the oral route of inoculation has been difficult, even though pigs can be readily infected via the intravenous route of inoculation. How HEV maintains in swine herds remains unknown; both genotypes 3 and 4 HEV from pigs are zoonotic and infect humans.

Wild Boar

Free-living wild boars (Sus scrofa) that are indigenous in many countries are known to harbor HEV. Human habitation changes from rural to suburban areas, increased agricultural use of lands, deforestation, recreational hunting, and consumption of wild boar meats have increased the chances of contact exposure of wild boars to humans. The HEV strains identified in wild boars worldwide are mostly genotype 3, although strains belonging to genotype 4 as well as a putative new genotype have also been detected in wild boars. Like domestic pigs, the genotypes 3 and 4 HEV from wild boars infect humans.

Chicken

Avian hepatitis E virus (avian HEV) was genetically identified from chickens with hepatitis-splenomegalic syndrome (HSS) in the United States. Avian HEV shares approximately 80% nucleotide sequence identity with the big liver and spleen disease virus (BLSV) from chickens in Australia, suggesting that BLS and HSS in the United States are caused by variant strains of the same virus. Avian HEV shares 50 to 60% nucleotide sequence identities and common antigenic epitopes in the capsid protein with human HEVs. At least three genotypes of avian HEV have been identified from chickens worldwide. In the United States, HEV infection in chickens is enzootic, and approximately 71% of chicken flocks and 30% of chickens were seropositive for avian HEV antibodies. The morbidity and mortality of HSS or BLS associated with avian HEV infection are low, and avian HEV infection in chickens is mostly subclinical. Gross lesions including subcapsular hemorrhages and enlarged livers were present in some but not all infected chickens, and microscopic hepatitis lesions are characterized by lymphocytic periphlebitis and phlebitis in the livers. Evidence of avian HEV infection in humans is currently lacking.

Rat

Strains of HEV have now been genetically identified from various species of rats. The rat HEV shared only approximately 60% and 50% sequence identity with other mammalian HEV and avian HEV, respectively, and thus belongs to a putative new genotype within the proposed Orthohepevirus genus. It remains to be determined if this putative new genotype of rat HEV can infect humans. Most recently, strains of HEV belonging to the genotype 3 have also been identified from rats in the United States, suggesting that some strains of rat HEV are likely zoonotic and may infect humans.

Rabbit

A genetically distinct strain of HEV that is related to genotype 3 was identified from rabbits in China, and the United States, and France. The rabbit HEV shares approximately 74%, 73%, 78 to 79%, 74 to 75%, and 46 to 47% nucleotide sequence identity with genotypes 1, 2, 3, 4 HEV, and avian HEV, respectively. The capsid protein of the rabbit HEV cross-reacted with antibodies raised against avian, rat, swine, and human HEV. Since the rabbit HEV belongs to the zoonotic genotype 3, thus the rabbit HEV may infect humans. Under experimental conditions, the rabbit HEV was successfully transmitted to pigs further demonstrating the ability of cross-species infection by rabbit HEV.

Deer

Antibodies to HEV have been detected in sika deer, Yezo deer, and red deer. Strains of genotype 3 HEV have been genetically identified from sika deer in Japan and roe deer in Hungary. HEV transmission from deer to humans via the consumption of contaminated deer meat has been documented.

Mongoose

Approximately 8 to 21% of the mongooses in Japan were seropositive for HEV antibodies. Strains of genotype 3 HEV have been genetically identified from mongoose. Whether the mongoose HEV infects humans remains unknown, although genotype 3 HEV is known to be zoonotic.

Bat

Drexler et al tested 3,869 bat samples from 85 different bat species worldwide for HEV RNA. Novel strains of HEV were identified from African, Central American, and European bats. The bat HEV forms a novel phylogenetic clade belonging to a separate genus within the family Hepeviridae. Evidence of HEV transmission from bats to humans was absent.

Ferret

A unique strain of HEV was genetically identified from ferrets in the Netherlands. The ferret HEV shared the highest nucleotide sequence identity (72.3%) with the putative new genotype of rat HEV. Phylogenetic analysis revealed that the ferret HEV was distinct from the known genotype 1–4 mammalian HEV in the proposed Orthohepevirus genus and
clustered with the putative new genotype of rat HEV (►Table 1).

**Fish**

The CTV isolated from spawning adult trout in the United States shares only approximately 13 to 27% amino acid sequence identity with the proposed genera *Orthohepevirus* and *Avihepevirus*, and therefore likely belongs to another new proposed genus *Piscihepevirus* (►Table 1). Unlike other strains of HEV, CTV can be efficiently propagated in the Chinook salmon embryo (CHSE-214) cell line.

**Cattle**

Antibodies to HEV have been detected in cattle from different countries. A 189-bp sequence of HEV was reportedly amplified from the fecal samples of eight cows in China, and the bovine HEV appears to be a genotype 4.48

**Sheep**

Serological evidence of HEV infection in sheep has been reported in China and Spain. A short 189-bp sequence of HEV was amplified from six sheep fecal samples in China by the same laboratory that reported the sequence of bovine HEV, and the sheep HEV also appears to be a genotype 4. The genotype 4 HEV-like sequences reportedly amplified from sheep and cattle require further independent confirmation.

**Other Potential Animal Reservoirs**

In addition to the animal species described above from which strains of HEV have been genetically identified, serological evidence of HEV infection has been reported in several other animal species such as dog, cat, goat, and nonhuman primates, suggesting that these animals have been exposed to HEV as well. Identification of the source of seropositivity from these animal species will likely discover new HEV strains and further expand the host range and animal reservoirs of HEV.

**Zoonotic Transmission of HEV**

Zoonotic transmission is responsible for the sporadic and cluster cases of human hepatitis E caused by genotypes 3 and 4. Cases of persistent hepatitis E in immunocompromised individuals are also linked to the zoonotic genotype 3 HEV infection.4

**Cross-Species Infection by HEV**

Genotypes 1 and 2 HEV have a limited host range and are restricted to humans: Attempts to experimentally infect pig, rat, and goat with genotypes 1 and 2 human HEV were unsuccessful.52,53 In contrast, genotypes 3 and 4 HEV have a much broader host range and can infect across species barriers: genotypes 3 and 4 swine HEV infected nonhuman primates;54,55 and conversely genotypes 3 and 4 human HEV infected pigs.24,54,56,57 Cross-species HEV infection has also been reported in other animal species (►Fig. 1). Lambs and Wistar rats were reportedly infected by human HEV isolates of presumably genotype 1 origin, although others failed to infect goats or rat with genotypes 1 and 2 HEV. The avian HEV from a chicken successfully infected turkeys, but failed to infect two rhesus monkeys, suggesting that avian HEV is likely not zoonotic and may not infect humans. The strains of HEV from rabbits infected pigs and genotypes 1 and 4 human HEV also reportedly infected rabbits. The mechanisms and genetic determinant(s) of cross-species HEV infection remain unknown.

**Pigs as a Reservoir for Zoonotic HEV Transmission**

It has been demonstrated that pig handlers such as pig farmers and swine veterinarians are at increased risk of HEV infection. For example, swine veterinarians in the United States were 1.51 times more likely to be positive for HEV antibodies than age- and geography-matched normal blood donors. Individuals from traditionally major swine states such as Minnesota are more likely seropositive for HEV antibodies than those from traditionally nonswine States such as Alabama. In North Carolina, swine workers had a 4.5-fold higher HEV antibody prevalence rate than the control subjects. In Moldova, approximately 51% of swine farmers were seropositive for HEV antibodies, whereas only 25% of control subjects with no occupational exposure to swine were seropositive. Pig is now a recognized reservoir for zoonotic HEV infection, and direct human contact with infected pigs poses a risk for HEV infection.

**Other Animal Reservoirs for Zoonotic HEV Transmission**

In addition to pigs, other animal species such as deer and rabbit also serve as potential reservoirs for HEV. For example, zoonotic transmissions of hepatitis E from deer to humans and from a pet cat to human owner were reported. Workers from the Iowa Department of Natural Resources (DNR) who had contacts with wildlife animal species had a higher HEV antibody prevalence rate than normal blood donors (p < 0.05). Understanding the natural history and mechanisms of cross-species infection of HEV will be critical for effectively preventing zoonotic human infection by HEV.

**Zoonotic Source of Virus for Persistent Infection in Immunocompromised Individuals**

Recently, persistent HEV infection has become an emerging and significant clinical problem with considerable morbidity and mortality in immunocompromised individuals such as organ transplant recipients; patients with HIV infections; non-Hodgkin lymphoma, and lymphoblastic leukemia. Approximately 58 to 92% of the HEV-infected organ transplant recipients developed persistent infection. Thus far, cases of persistent infections are almost exclusively caused by strains of HEV belonging to the genotype 3, suggesting that the source of infection is likely zoonotic in nature. In immunocompetent individuals, a lower dose of virus exposure through direct contact with infected animals or consumption of undercooked animal meat may only result in subclinical or self-limiting acute infection because hepatitis E is known to be a dose-dependent disease: A high dose causes biochemical and clinical hepatitis whereas a low dose causes only subclinical infection.

This document was downloaded for personal use only. Unauthorized distribution is strictly prohibited.
However, in immunocompromised individuals that cannot effectively clear the virus even exposed at a low dose, the infection can progress into chronicity. Therefore, individuals with immunosuppressive conditions should avoid eating undercooked animal meat or contact with potentially HEV-infected animals.

**Foodborne Transmission of HEV**

**Animal Meat Products as the Sources for Foodborne Transmission**

Approximately 2% of the pig livers sold in local grocery stores in Japan,87 4% in Germany,88 6.5% in the Netherlands,89 and 11% in the United States90 tested positive for the zoonotic genotype 3 HEV RNA. The contaminating virus in the commercial pig livers remains fully infectious,90 and incubation of the contaminated meat at a temperature (56°C) equivalent to a medium-to-rare cooking condition did not inactivate the virus completely.91 Many sporadic and cluster cases of hepatitis E have been linked to the consumption of contaminated raw or undercooked animal meat and meat products.92–95 For example, severe hepatitis E developed in a Japanese man after consumption of contaminated wild boar meat; another man contracted fulminant hepatitis after eating the same wild boar meat.93,94 The zoonotic genotype 4 HEV was detected from the patient serum and wild boars with indistinguishable nucleotide sequences. A cluster case of hepatitis E patients was linked to the consumption of raw deer meats in Japan.44 Importantly, the HEV sequence amplified from the leftover frozen deer meat was nearly identical to the HEV sequence amplified from the patients. Additionally, consumption of game meat is also a risk factor for HEV infection.93

It appears that large pork production chains in some countries are contaminated by HEV, which raises a public health concern for potential foodborne HEV transmission because of the high-volume consumption of pork products worldwide. In the United Kingdom, HEV was detected in pig livers in a slaughterhouse, in surface samples from a processing plant, and in pork sausages and surface samples at the point of sale.96 In Czech Republic, Italy, and Spain, among the 337 fecal, liver, and meat samples from pigs at slaughterhouses tested, HEV RNA was detected in 41% (Italy) and 41% (Spain) fecal samples, 5% liver and 2.5% meat (Czech Republic).97 Approximately 6% of the sausages sampled at processing and at the point of sale in Spain were also positive for genotype 3 HEV RNA.97 In France, pig liver sausages (figatelli) were responsible for some sporadic cases of hepatitis E.98 Acute or recent HEV infection was observed in 7 of 13 individuals who ate figatelli, but in none of the 5 individuals who did not eat figatelli. The genotype 3 HEV sequences amplified from 7 of the 12 figatelli from supermarkets were genetically linked to the patients who ate figatelli. In Japan, foodborne HEV transmission has been demonstrated in Kiami and Abashiri via consumption of grilled pig entrails.99

The potential widespread dissemination of HEV through pork production chains and the hidden danger of potential subsequent foodborne transmission especially in immunocompromised individuals are of significant concerns.100 Taken together, these data clearly showed that foodborne transmission is an important route of HEV transmission that is responsible for the sporadic and cluster cases of hepatitis E worldwide.

**Contaminated Shellfish as the Source for Foodborne Transmission**

HEV replicates in the liver as well as in gastrointestinal tract,56,101 and infected humans and other animals excreted large amounts of HEV in feces,57,102 which poses a concern for environmental contamination and food safety. HEV has been detected in swine manure and wastewater associated with hog operations,73 and in concrete pits and lagoons of swine manure storage facilities in the United States.102 Genotype 3 HEV RNA was detected in swine manure collected from concrete holding pits and from lagoons on pig farms; importantly, the HEV detected in pig manure slurry remains infectious.102 In Korea, HEV RNA resembling the genotype 3 swine HEV was detected in oysters.103 Consumption of contaminated shellfish has been implicated in sporadic cases of acute hepatitis E.104–106 An outbreak of hepatitis E on a cruise ship was linked to the consumption of shellfish while on board.107 Therefore, contaminated shellfish is an emerging source of foodborne HEV transmission.

**Contaminated Water as the Source for Foodborne and Waterborne Transmission**

Contamination of water by HEV from human and other animal wastes can lead to subsequent contamination of food and produce, and thus leading to potential foodborne transmission.3,108,109 Historically, waterborne epidemics are the characteristic of hepatitis E outbreaks in humans in regions where sanitation conditions are poor.1 Untreated sewage water contamination of drinking water and contaminated well or river water used for washing and drinking purpose are the main sources of HEV transmission in developing countries.110 In India, a significantly higher prevalence of HEV antibodies was detected in sewage workers (57%) than in controls (19%), and sewage workers with ≥5 years of employment history had a much higher seropositivity rate.111 In HEV endemic regions, the use of river water for bathing, waste disposal, and drinking purposes is also a significant risk factor.112–115 In Turkey, individuals who used untreated waste water for irrigation purposes have a significantly higher HEV antibody prevalence rate (34.8%) than the control subjects with similar age and socioeconomic status.116

In industrialized countries with good sanitation conditions and water treatment measures, outbreaks of waterborne HEV transmission are rare. However, the existence of numerous zoonotic strains of HEV from various animal species implies that land application and runoffs of HEV-containing animal manure and feces could contaminate irrigation or coastal water with concomitant contamination of produce or shellfish.3,102,109 thus posing a risk of foodborne and waterborne HEV transmission. For example, in Canada, genotype 3 HEV of swine origin was detected on irrigated field-grown strawberries; irrigation water was suspected as the source of the strawberry contamination.117 Strains of
infectious HEV of both human and swine origins have been detected in sewage water in industrialized countries.\(^{118–122}\) Therefore, contaminated water could be a source of food contamination, thus leading to foodborne HEV transmission.

**Other Uncommon Routes of HEV Transmission**

**Vertical Transmission**

Vertical HEV transmissions from mother-to-fetus were reportedly associated with a high neonatal mortality, including premature birth, increased fetal loss and acute hepatitis in the newborns.\(^ {123–125}\) For example, vertical HEV transmission was detected in approximately 33% of HEV-infected pregnant women.\(^ {124}\) HEV RNA was reportedly detected in the colostrum of HEV-infected mothers, although breast-feeding appears to be safe for the infants.\(^ {126}\) Under experimental conditions, however, vertical HEV transmission in animal models has not been demonstrated. For example, infectious HEV was detected in egg whites from embryonated eggs hatched from chickens infected experimentally with an avian strain of HEV, but there was no evidence of complete vertical transmission.\(^ {127}\) Also, pregnant sows inoculated with a genotype 3 HEV became infected, but vertical transmission to the fetuses was not detected.\(^ {128}\) Similarly, pregnant rhesus macaques experimentally infected with HEV failed to transmit the virus to offspring.\(^ {129}\) Therefore, further in-depth studies are warranted to definitively understand the potential risk of vertical HEV transmission.

**Blood-Borne Transmission**

Blood-borne transmission of HEV through blood transfusions, although rare, has been documented.\(^ {95,130–138}\) For example, some blood donors have tested positive for HEV RNA. In Japan, HEV RNA was detected in 8 of the 41 blood donors with elevated ALT levels.\(^ {135–138}\) Screening donor blood for acute markers of HEV infection will reduce the risk of potential bloodborne transmission.

**Prevention of Foodborne and Zoonotic Transmission of HEV**

A vaccine against HEV in humans was recently licensed for use in China, but not in other countries.\(^ {139}\) In the absence of a vaccine in most parts of the world, preventive measures such as good hygiene practice and avoidance of drinking water of unknown purity are necessary to minimize the risk of HEV infection. Because swine and several other animal species are reservoirs for HEV, an important measure to prevent zoonotic infection is to wash hands thoroughly with soap and water after handling pigs and other infected animals. The majority of the sporadic and cluster cases of hepatitis E are associated with the consumption of raw or undercooked animal meat products; therefore, an important preventive measure for foodborne HEV transmission, especially in immunocompromised individuals, is to avoid eating undercooked animal meat. Even though HEV infection in pigs is nonpathogenic, it will still be advantageous for the swine industry to develop a vaccine against HEV infections in pigs because such an animal vaccine will minimize the risk of zoonotic transmission and increase pork safety.\(^ {3}\)

**References**


Huang FF, Sun ZF, Emerson SU, et al. Determination and analysis of the complete genomic sequence of avian hepatitis E virus (avian HEV) and attempts to infect rhesus monkeys with avian HEV. J Gen Virol 2004;85(Pt 6):1609–1618


Cossaboom CM, Córdoa L, Dryman BA, Meng XJ, Hepatitis E virus in rabbits, Virginia, USA. Emerg Infect Dis 2011;17(11):2047–2049


Takahashi K, Kitajima N, Abe N, Mishiro S. Complete or near-complete nucleotide sequences of hepatitis E virus genome recovered from a wild boar, a deer, and four patients who ate the deer. Virology 2004;330(2):501–505


72 Wedemeyer H, Pischke S, Manns MP. Pathogenesis and treatment of hepatitis e virus infection. Gastroenterology 2012;142(6):1388–1397, e1
87 Yazaki Y, Mizuo H, Takahashi M, et al. Sporadic acute or fulminating hepatitis E in Hokkaido, Japan, may be food-borne, as suggested by the presence of hepatitis E virus in pig liver as food. J Gen Virol 2003;84(Pt 9):2351–2357


Khuroo MS, Kamili S, Khuroo MS. Clinical course and duration of viremia in vertically transmitted hepatitis E virus (HEV) infection in babies born to HEV-infected mothers. J Viral Hepat 2009;16(7):519–523


