

were almost identical to those of the Japanese broad tapeworm available in the GenBank database (sequence similarities of 99% [GenBank accession no. KY000483] and 100% [KY000484], respectively), thus providing unequivocal support that this plerocercoid was a larva of the *D. nihonkaiense* tapeworm reported from North America.

This report provides additional evidence that salmon from the Pacific coast of North America may represent a source of human infection. Because Pacific salmon are frequently exported unfrozen, on ice, plerocercoids may survive transport and cause human infections in areas where they are not endemic, such as China, Europe, New Zealand, and middle and eastern United States (1). It is probable that most diphyllbothriosis cases originally attributed to *D. latum* may have been caused by *D. nihonkaiense* tapeworms. For more effective control of this human foodborne parasite, detection of the sources of human infection (i.e., host associations), and critical revision of the current knowledge of the distribution and transmission patterns of individual human-infecting tapeworms are needed.

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Dr. Kuchta is a researcher at the Institute of Parasitology, Czech Academy of Sciences. His research interests include biology, phylogeny, and molecular diagnosis of parasitic helminths, mainly those that cause diphyllbothriosis and sparganosis.

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Address for correspondence: Roman Kuchta, Biology Centre of the Academy of Sciences, Institute of Parasitology, Branišovská 31 České Budějovice 370 05, Czech Republic; email: krtek@paru.cas.cz

## Hepatitis E Virus Infection in Solid Organ Transplant Recipients, France

Sebastien Lhomme, Laurent Bardiaux, Florence Abravanel, Pierre Gallian, Nassim Kamar, Jacques Izopet

Author affiliations: Institut National de la Santé et de la Recherche Médicale, Toulouse, France (S. Lhomme, F. Abravanel, N. Kamar, J. Izopet); Centre Hospitalier Universitaire de Purpan, Toulouse (S. Lhomme, F. Abravanel, J. Izopet); Université Paul Sabatier, Toulouse (S. Lhomme, F. Abravanel, N. Kamar, J. Izopet); Etablissement Français du Sang Pyrénées Méditerranée, Toulouse (L. Bardiaux); Etablissement Français du Sang Alpes Méditerranée, Marseille, France (P. Gallian); Ecole des Hautes Études en Santé Publique, Marseille (P. Gallian); Centre Hospitalier Universitaire de Rangueil, Toulouse (N. Kamar)

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The rate of transfusion-transmitted hepatitis E virus (HEV) in transplant recipients is unknown. We identified 60 HEV-positive solid organ transplant patients and retrospectively assessed their blood transfusions for HEV. Seven of 60 patients received transfusions; 3 received HEV-positive blood products. Transfusion is not the major route of infection in this population.

Hepatitis E virus (HEV; family *Hepeviridae*, genus *Orthohepevirus*) is a single-stranded, positive-sense RNA virus of  $\approx 7.2$  kb. At least 4 genotypes are responsible for hepatitis E in humans (HEV-1–4). HEV-1 and HEV-2 infect only humans, while HEV-3 and HEV-4 have animal reservoirs (1). In developed countries, the main source of HEV transmission is the consumption of raw or undercooked, infected meat or direct contact with infected animals. Cases of bloodborne transmission have also been reported (1–3).

Transfusion-transmitted infections in solid organ transplant (SOT) patients remains a major concern; the frequency at which these infections occur is unknown (4). SOT patients receiving transfusions are at risk of contracting HEV because systematic screening for the virus is rare. For SOT patients exposed to HEV, infection can become chronic, with rapidly progressing liver disease (1). Because of the high incidence of HEV infection in the Midi-Pyrénées area (1), SOT patients are regularly screened for HEV RNA, and diagnosis of HEV infection is made at the time of alanine aminotransferase elevation.

We investigated retrospectively the extent to which transfusion-transmitted HEV infections occurred in a cohort of 60 SOT patients infected with HEV from January 1, 2009, through June 30, 2014. We found that 7 (11.7%) of these SOT patients were potentially infected through transfused blood products because they were given transfusions in the 6 months preceding the diagnosis (online Technical Appendix Table 1, <https://wwwnc.cdc.gov/EID/article/23/2/16-1094-Techapp1.pdf>); the remaining 53 HEV-positive patients were infected by other modes. The median HEV RNA concentration in recipient blood was 5.4 log copies/mL (range 3.6–6.8 log copies/mL) or 5.2 log IU/mL (range 3.4–6.6 log IU/mL). The median interval between transfusion and diagnosis was 4 months (range 0.2–5.0 months). HEV infections developed in 4 patients (R1, R3, R4, and R5) 6 months after transplantation. Transmission of HEV by the graft was excluded in these patients by examining the samples from the organ donors at the time of donation. None of them tested positive for HEV RNA.

We collected the 231 blood samples corresponding to the 7 patients' donors (stored by the French Blood Agency) and tested them individually for HEV RNA and HEV IgM/IgG (online Technical Appendix). Of these samples, 7 (3.0%) tested positive for HEV RNA (online Technical Appendix Table 2). This analysis revealed that 3 patients (recipients R1, R2, and R3) received  $\geq 1$  blood components derived from the 7 HEV RNA-positive donations; 4 patients were not given viremic donations.

The median HEV RNA dose given to the recipients was 5.1 log copies (range 3.8–8.4 log copies) or 4.9 log IU (range 3.6–8.2 log IU). Recipient R1 received blood components from 1 viremic donor (D1), while R2 and R3 received blood

components from 3 HEV RNA-positive donors (D2.1–D2.3 and D3.1–D3.3, respectively). Phylogenetic analyses of the 348-nt partial sequences of the open reading frame (ORF) 2 region (online Technical Appendix) showed that R1/D1 and R3/D3.1 sequences clustered together (Figure); nucleotides were  $>99.0\%$  identical in both cases, confirming transfusion-transmitted HEV infection. Phylogenetic analysis of R2/D2.3 showed they clustered together but had a lower sequence identity (84.2%), suggesting transmission could have been mediated by another mechanism.

Another study conducted from January 2004 through June 2009 in France found that the risk factors associated with HEV transmission in SOT patients were eating pork meat, game, and mussels (5). Thus, the risk for transfusion-transmitted HEV infection is lower than the risk for acquiring an HEV infection from other sources in the environment in this population. Our study supports these results; we identified viremic donors as the source of infection in 2 (or possibly 3) of 60 HEV-positive SOT patients using phylogenetic analyses.

In France, HEV-positive samples were found in 1/2,218 blood donations, with HEV RNA concentrations of  $<60$  to 29,796 IU/mL (6). In the Netherlands, 1/2,671 donations was viremic, with HEV RNA concentrations from  $<25$  to 470,000 IU/mL (7). Published data indicate that the minimum infectious dose in donations is 7,056 IU (3.85 log IU) (8). A recent study found that donations associated with HEV-transmission had higher HEV RNA concentrations than did those that were not associated with HEV transmission (9). In our study, the 3 blood donations implicated in HEV transmission had HEV RNA doses  $>5.7$  log copies (i.e., 5.5 log IU). Another parameter that must be considered is the presence of HEV antibodies in the donor or in the recipient, although the concentration needed to protect against an HEV infection is still unclear.

We conclude that, although transfusion-transmitted HEV infection can occur in SOT patients, blood transfusion is not the main source of transmission in these patients in France. Optimal policies for screening blood donations for HEV must be defined according to epidemiologic data.

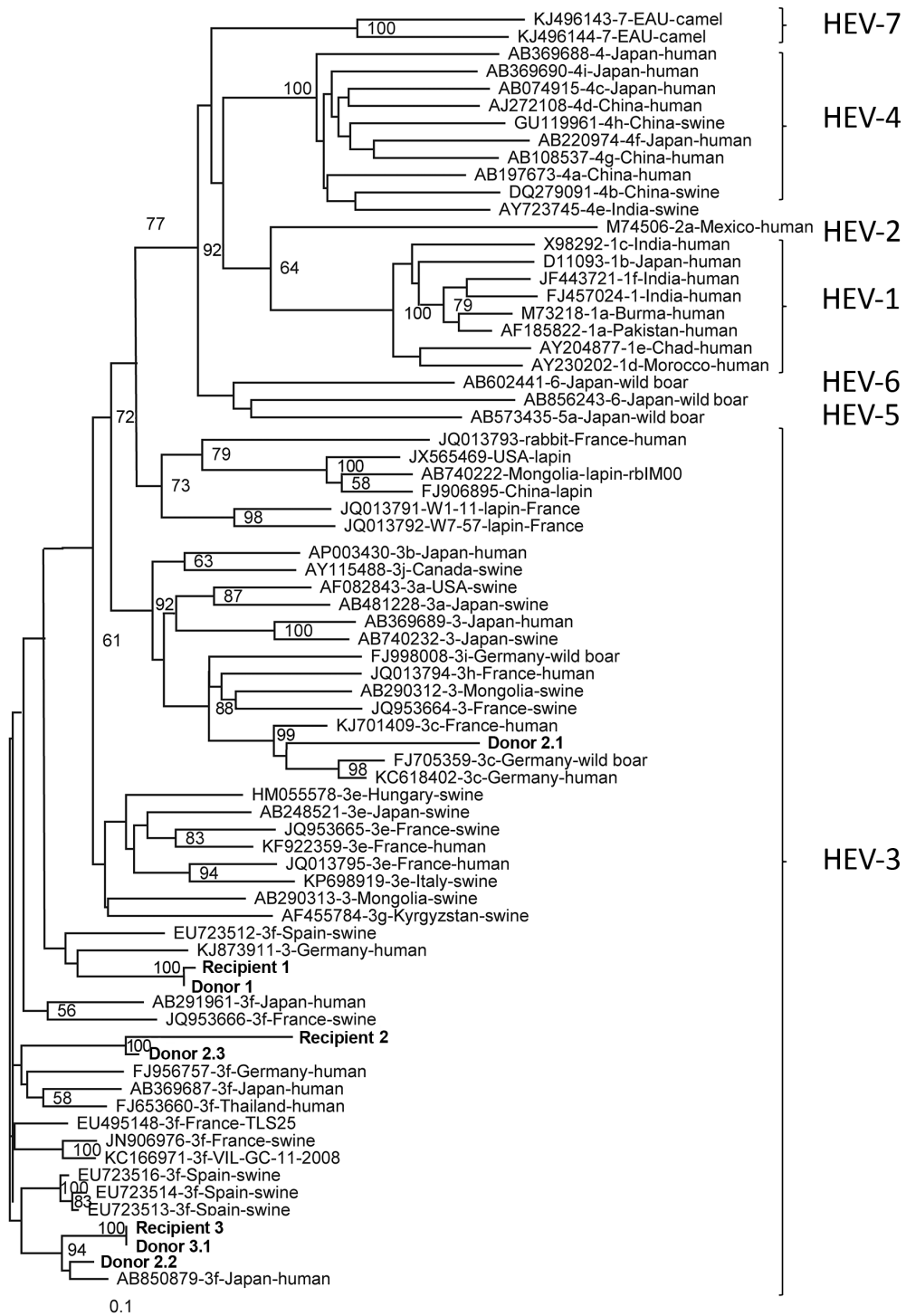
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Dr. Lhomme is a researcher in the Virology Department at Toulouse University Hospital. His main research interest is in the genetic variability of hepatitis E virus.



**Figure.** Phylogenetic tree of hepatitis E virus (HEV) isolates from 3 HEV-positive blood donors and 3 solid organ transplant recipients (shown in bold), France, compared with reference isolates. The tree was constructed by using partial open reading frame 2 sequences (348 nt). HEV genotypes are indicated at right. A confirmed case of transfusion-transmitted HEV infection requires evidence of infection in the recipient and donor and that the nucleotide sequences of these isolates be identical. The isolates from France were deposited in GenBank under accession nos. KX452928–KX452935; accession numbers, sources, and location of isolation for other isolates are indicated. Scale bar indicates nucleotide substitutions per site.

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Address for correspondence: Jacques Izopet, Laboratory of Virology–Toulouse University Hospital, National Reference Center for Hepatitis E Virus, INSERM UMR 1043 & CNRS UMR 5282, 31059 Toulouse CEDEX, France; email: [izopet.j@chu-toulouse.fr](mailto:izopet.j@chu-toulouse.fr)

## Emergence of *bla*<sub>NDM-7</sub>–Producing *Enterobacteriaceae* in Gabon, 2016

Mesmin Moussounda, Seydina M. Diene, Sandra Dos Santos, Alain Goudeau, Patrice François, Nathalie van der Mee-Marquet

Author affiliations: Hôpital d’Instruction des Armées Omar Bongo Ondimba, Libreville, Gabon (M. Moussounda); Centre Hospitalier Régional Universitaire, Tours, France (M. Moussounda, S. Dos Santos, A. Goudeau, N. van der Mee-Marquet); University of Geneva Hospitals, Geneva, Switzerland (S.M. Diene, P. François)

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Reports of carbapenemase-producing *Enterobacteriaceae* in Africa remain rare and assess mostly *bla*<sub>OXA-48</sub>–producing isolates from Mediterranean countries and South Africa. We identified *bla*<sub>NDM-7</sub>–producing *Enterobacteriaceae* in Gabon in 2016. The isolates contained *bla*<sub>NDM-7</sub> *IncX3* plasmids that were unusual and similar to the one described in a colistin-resistant *Klebsiella pneumoniae* SZ04 isolate from China.

Carbapenems are used as last-line antimicrobial drugs for treating infections caused by multidrug-resistant gram-negative bacilli. Their effectiveness is challenged by the emergence of carbapenemase-producing *Enterobacteriaceae* (CPE). A new type of  $\beta$ -lactamase, *bla*<sub>NDM?</sub> was reported from a patient in Sweden in 2007 (1). Since then, *bla*<sub>NDM</sub> CPE have been identified worldwide and described as endemic to the Indian subcontinent and the Balkans (2). In countries to which they are nonendemic, CPE are reported mainly from patients with a history of hospitalization in a CPE-endemic area and, more rarely, in patients without history of travel (3). Reports on CPE in Africa are scarce, likely because monitoring of antimicrobial resistance remains uncommon. *bla*<sub>OXA-48</sub> and *bla*<sub>NDM-1</sub> CPE have been reported from the Maghreb area, Nigeria, Kenya, and South Africa, and single cases of *bla*<sub>NDM-4</sub> and *bla*<sub>NDM-5</sub> *Escherichia coli* have been reported in Cameroon, Algeria, and Uganda (2,4,5).

In January 2016, we conducted a point-prevalence study in all patients at the military general hospital of Libreville, Gabon. We collected demographic and clinical data and screened patients by rectal swabbing with Amies medium transport swabs (Copan Italia SPA, Brescia, Italy). The swabs were placed in 0.5 mL sterile water; 0.1 mL of the resulting suspension was streaked onto a selective agar plate provided for the identification of bacteria resistant to third-generation cephalosporins (CHRO-Magar, Paris, France). The plates were incubated for 48 h at 35°C. We used matrix-assisted laser desorption/ionization time-of-flight mass spectrometry technology (Bruker, Bremen, Germany) to confirm each isolate thought to be *Enterobacteriaceae*.

We performed antimicrobial drug susceptibility testing by the agar disk diffusion method (<http://www.eucast.org/>). Isolates resistant to second- and third-generation cephalosporins were investigated for MIC of ertapenem using Etest (bioMérieux, Marcy-L’Étoile, France) and for carbapenemase production by the CarbaNP test (bioMérieux). For molecular characterization, we performed Sanger sequencing of PCR amplicons of the gene. Purified genomic DNA of the *bla*<sub>NDM</sub>–producing isolates was subjected to whole-genome sequencing on a HiSeq system (Illumina, San Diego, CA, USA). Reads were filtered for quality with fastq-mcf (Ea-utils: <http://code.google.com/p/ea-utils/>).

# Hepatitis E Virus Infection in Solid Organ Transplant Recipients, France

## Technical Appendix

### Methods

#### Detection of Hepatitis E Virus (HEV) Antibodies

Anti-HEV IgM/IgG were detected by enzyme-linked immunosorbent assay (Wantai, Beijing, China).

#### Plasma HEV RNA Concentrations

HEV RNA in donor blood was detected and quantified by using a validated real-time PCR protocol with a detection limit of 100 copies/mL (i.e., 60 IU/mL) (1).

#### HEV Genotype Determination

HEV was genotyped by sequencing a 348-nt fragment within the open reading frame (ORF) 2 gene (2). The sequences were compared with reference HEV sequences (3). A confirmed case of transfusion-transmitted HEV infection requires evidence of infection in the recipient and a component of the blood from the donor testing positive for HEV RNA. It also requires that the nucleotide sequences of the 2 isolates be identical.

**Technical Appendix Table 1.** Characteristics of the 7 transplant recipients potentially infected with HEV through blood transfusion, France

Recipient	Sex	Organ transplanted	Age at ALT elevation	HEV antibody titer before transfusion,*		Interval between event and ALT elevation, mo		HEV RNA concentration at ALT elevation,	
				IgG	IgM	Transfusion	Transplantation	log copies/mL	Genotype
R1	F	Liver	34	–	–	4	3	5.9	3
R2	M	Kidney	41	–	–	1	42	3.6	3f
R3	F	Liver	42	–	–	4	4	6.6	3f
R4	F	Liver	57	+, 0.25	–	4	4	5.4	3f
R5	F	Kidney	65	–	–	4	4	4.1	3f
R6	M	Heart	44	–	–	5	7	6.8	3f
R7	F	Liver	55	+, 10.97	–	0.2	82	5.1	3c

ALT, alanine aminotransferase; HEV, hepatitis E virus.

**Technical Appendix Table 2.** Characteristics of the 7 blood donors with HEV RNA–positive, archived blood samples, France

Donor/ recipient	HEV RNA concentration, log copies/mL	Geno type	Anti-HEV IgG titer, U/mL	Anti-HEV IgM	HEV-positive blood component	Estimated transmitted volume, mL	Transfused dose of HEV RNA, log copies
D1/R1	4.7	3	+	+	Red blood cell unit	10	5.7
D2.1/R2	2.8	3c	–	–	Red blood cell unit	10	3.8
D2.2/R2	3.3	3f	+, 0.37	+	Pooled platelet concentrate	67	5.1
D2.3/R2	6.6	3f	not determined	not determined	Pooled platelet concentrate	63	8.4
D3.1/R3	4.3	3f	–	–	Amotosalen-treated plasma	209	6.6
D3.2/R3	3.0	Na	+, 2.97	+	Pooled platelet concentrate	69	4.8
D3.3/R3	2.6	Na	–	–	Pooled platelet concentrate	67	4.4

HEV, hepatitis E virus; Na, not available due to low HEV RNA concentration.

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