Hepatitis E virus (HEV) was first described in 1983 in Russia following investigation of a hepatitis outbreak in a Soviet military camp in Afghanistan (1), and the first genome sequence was described in 1991 (2, 3). Four genotypes and 24 subtypes were defined (4). Genotypes 1 and 2 are anthropoctic only and circulate in developing countries, whereas genotypes 3 and 4 circulate in humans and mammals, mostly swine (5, 6). HEV-3 is the majority genotype in Western developed countries, where hepatitis E was considered until recently as imported from areas of hyperendemicity, but it turned out that most cases are autochthonous (5, 6). Moreover, the existence of a porcine reservoir and foodborne transmission were demonstrated for genotypes 3 and 4 HEV (6–8). Southern France has been identified as an area of hyperendemicity (5). HEV RNA was detected there in pig liver sausages, which can transmit HEV when eaten uncooked (5, 6, 9–11). In our geographical area, southeastern France, HEV infection is of particular concern in kidney transplant recipients, among whom the estimated incidence was 1.2% or higher and the progression rate to chronic infection was 80% (12).

In 2009, HEV RNA of genotype 3e was obtained from a 46-year-old French kidney transplant recipient who had been in a minority of infections in France, including infections in solid organ transplant recipients (12–14). In our center, HEV-3e was mostly detected in other kidney transplant recipients (12, 15). The HEV genome described here is the first of subtype 3e, and the second overall, recovered from solid organ transplant recipients. The highest nucleotide similarity (89%) was found in sequences recovered in Germany and Japan from pigs (GenBank accession numbers FJ998015 and AB248520, respectively), while the closest HEV genome recovered from a human was from a Japanese patient (AB291958). Coding regions corresponding to ORFs 1, 2, and 3 were found to encode peptides of 1,696, 617, and 122 amino acids, respectively. Continuing HEV surveillance in human and animal reservoirs is critical to gain a better knowledge of the diversity and epidemiology of this virus.

**Nucleotide sequence accession number.** The sequence is available in GenBank under accession no. KF922359.

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**REFERENCES**


