Severe Fever with Thrombocytopenia Syndrome Virus RNA in Semen, Japan

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Severe fever with thrombocytopenia syndrome virus (SFTSV) can be transmitted between humans. We describe a case of severe fever with thrombocytopenia syndrome in which SFTSV RNA was detected in semen after its disappearance from serum. Our findings indicate possible sexual transmission of this emerging virus.

Severe fever with thrombocytopenia syndrome (SFTS) is a life-threatening emerging infectious disease caused by severe fever with thrombocytopenia syndrome virus (SFTSV), a tickborne virus (genus *Banyang virus*, family *Phenuiviridae*). Recently, the person-to-person transmission of SFTSV has been described (*1*,*2*), and the most common risk factor of the transmission is direct blood exposure (*2*). However, SFTSV RNA has been detected in nonblood samples, such as throat, urine, and fecal specimens, especially in fatal cases (*3*). Asymptomatic infections through personal contact without blood exposure have also been reported (*1*). We describe a case in which viral RNA was detected in semen after viral RNA clearance from blood.

During May 2018, a previously healthy 50-year-old man hunted boar in the Goto Islands in western Japan. Eight days after hunting, he experienced high fever, myalgia, and diarrhea. He did not have hematuria or bloody diarrhea. Disturbance of consciousness occurred 6 days after symptom onset; on that day, he visited a local hospital and was referred to and admitted to Nagasaki University Hospital (Nagasaki, Japan). Body temperature was 39.0°C, and he was disoriented; Glasgow coma scale score was 9. He had no jaundice, signs of meningeal irritation, or apparent tick bites. Laboratory tests at admission had the following results: leukocytes 2.4×10^3 cells/µL; platelets 35×10^3/µL; serum creatine 3.04 mg/dL; aspartate aminotransferase 508 U/L; lactate dehydrogenase 1,404 U/L; and creatine kinase 15,449 U/L.

Because of the patient's low platelet count and other suggestive signs and symptoms, we suspected SFTS. Serum SFTSV RNA level was 2.03×10^8 copies/mL by real-time reverse transcription PCR (RT-PCR) analysis (Appendix, https://wwwnc.cdc.gov/EID/article/25/11/1061-App1.pdf). We confirmed diagnosis of SFTS on the basis of these results; however, we did not detect viral RNA in a urine sample. We conducted RT-PCR tests of semen and urine using procedures developed for serum; all RT-PCR tests were performed in the Department of Virology, Institute of Tropical Medicine, Nagasaki University, Nagasaki.

We considered this case severe, with multiple poor prognosis factors, such as disturbance of consciousness, laboratory data, and high viral load in serum (*4*). We performed palliative therapy, including continuous hemodiafiltration, mechanical ventilation, and central venous nutrition. In addition, we treated the patient with recombinant human soluble thrombomodulin for disseminated intravascular coagulation (380 U/kg/d for 6 d) and granulocyte colony-stimulating factor (filgrastim) for neutropenia (300 µg on the third hospital day). We also administered intravenous immunoglobulin (5,000 mg/d for 3 d), because it has been reported effective for SFTS (*5*), and the patient received platelet transfusions for severe thrombocytopenia.

We observed restoration of platelet count 10 days after symptom onset. Other abnormal laboratory findings recovered 7–13 days after symptom onset. The viral load in serum began to decrease from day 8 after onset and became negative on day 30 after onset. Although the patient's general status was gradually improved and laboratory tests recovered to almost normal levels by day 30, we detected

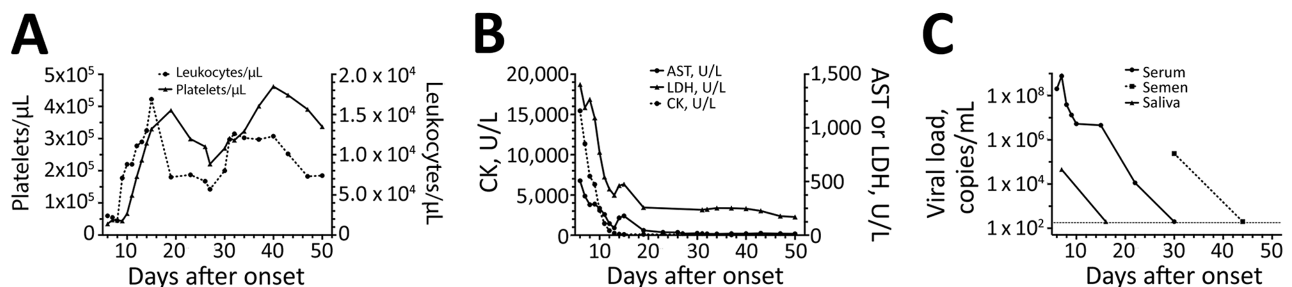

Figure. Laboratory data and viral loads during course of illness for patient with severe fever with thrombocytopenia syndrome, Japan. A) Leukocyte and platelet counts; B) AST, LDH, and CK levels; C) viral loads in serum, semen, and saliva. Dashed line in panel C indicates detection threshold (2×10^2 copies/mL). AST, aspartate aminotransferase; CK, creatine kinase; LDH, lactate dehydrogenase.

SFTSV RNA at 2.4×10^5 copies/mL in his semen that day. On day 44, we could no longer detect semen SFTSV RNA, and he was discharged on day 51 after onset (Figure 1).

In this study, SFTSV RNA was detected in semen, and SFTSV persisted longer in semen than in serum. It is well known that some viruses, such as Zika virus and Ebola virus, can be sexually transmitted; these viruses have been detected in semen for a prolonged period after symptom onset (*6*,*7*). Thus, we considered the potential risk for sexual transmission of SFTSV.

Compared with that of Zika and Ebola viruses, the clinical significance of potential sexual transmission of SFTSV is unknown. However, this possibility should be taken into consideration in sexually active patients with SFTSV. Our findings suggest the need for further studies of the genital fluid of SFTS patients, women as well as men, and counseling regarding sexual behavior for these patients.

About the Author

Dr. Koga is a member of the Respiratory and Infectious Diseases Departments at Nagasaki University. His research interests include viral and fungal infections.

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Canine Distemper Virus in Asiatic Lions of Gujarat State, India

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In September 2018, an epizootic infection caused by canine distemper virus emerged in an Asiatic lion population in India. We detected the virus in samples from 68 lions and 6 leopards by reverse transcription PCR. Whole-genome sequencing analysis demonstrated the virus strain is similar to the proposed India-1/Asia-5 strain.

Canine distemper virus (CDV; genus *Morbillivirus*) causes highly contagious disease in a wide range of carnivores. Epizootic disease in lions in a wildlife sanctuary in California, USA, in 1992 and Serengeti National Park, Tanzania, in 1994 underlined the potential of CDV to cause fatality in wild felids (*1*,*2*). The disease often manifests as respiratory and gastrointestinal signs that progress to neurologic disease (*2*).

A single isolated population of Asiatic lions (*Panthera leo persica*) resides in the Gir forests of Gujarat State, India, the last natural habitat for this species. Conservation efforts brought this lion population back from the brink of extinction and increased their numbers (*3*).

During 2 weeks in September 2018, the unusual death of 28 lions of all age groups was reported from Gir Wildlife Sanctuary. A detailed investigation revealed 18 additional lions exhibited dullness, dehydration, lacrimation, cough, diarrhea, and seizures. Necropsy of 2 carcasses showed edema and purulent exudates in the lungs. Histopathology of lungs from both lions showed mononuclear cell infiltration with mild thickening of interalveolar septa.

The Indian Council of Medical Research, National Institute of Virology (Pune, India), received ocular,

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Appendix

RNA Extraction

We completed the following for serum, saliva, and semen samples.

For each sample, we mixed a 250 µL volume with 750 µL of Isogen-LS (Nippon Gene, https://www.nippongene.com) and extracted RNA according to the manufacturer's protocol. To efficiently extract RNA, we used Ethachinmate (Nippon Gene) as a co-precipitating agent in RNA precipitation with isopropanol. We dissolved the extracted RNA with 50 µL of RNase-free water and stored at −80°C until use.

Real-time RT-PCR

We measured Viral copy numbers by real-time RT-PCR as previously described (*1*). We designed SFTSV-specific primers and a probe based on the RdRp region. The sequence of forward (SFTS_QPCR_965F) primer was 5′-GCRAGGAGCAACAARCAAACATC-3′ and of reverse primer (SFTS_QPCR_1069R) was 5′-GCCTGAGTCGGTCTTGATGTC-3′. The PrimeTime qPCR probe was FAM/5′-CTCCCRCCC-3′/ZEN/5′-TGGCTACCAAAGC-3′/IBFQ (Integrated DNA Technologies, https://www.idtdna.com). The RT-PCR reaction was performed using a One Step PrimeScript RT-PCR Kit (Takara Bio Inc., www.takara-bio.com) and a 7500 Real-time RT-PCR System (Applied Biosystems, https://www.thermofisher.com). We quantified

the copy numbers by a standard curve method. We prepared the standard RNA as previously described (*2*), and adjusted concentrations at 10^7, 10^6, and 10^5 copies/5 µL. We used 5 µL of the standard RNase-free water as negative control and extracted RNA samples for the quantification. We performed all measurements in duplicate.

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