Intensive Care Admissions for Severe Chikungunya Virus Infection, French Polynesia

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During the 2014–2015 chikungunya outbreak in French Polynesia, 64 patients with confirmed chikungunya virus infection were admitted into intensive care. Sixty-three were nonpregnant adults; 11 had an atypical form, 21 had severe sepsis or septic shock, and 18 died. These findings indicate that critical illness frequently complicates the course of chikungunya virus infection.

The first case of chikungunya virus (CHIKV) infection in French Polynesia (Tahiti) was diagnosed in May 2014; it was imported from Guadeloupe Island in the Caribbean (*1*). During the outbreak that developed during October 2014–March 2015, ≈25% of the local population (272,000 residents) became infected with CHIKV (*2*). French Polynesia has 2 potential mosquito vectors for CHIKV: *Aedes aegypti* and *A. polynesiensis.* Phylogenic analysis showed that the French Polynesia strain of CHIKV belongs to the Asian lineage and is closely related to the strain collected in Guadeloupe and the British Virgin Islands in 2014, showing 99.9% homology with that strain (*3*). To describe patient characteristics and clinical courses of chikungunya patients in French Polynesia during 2014–2015, we retrospectively reviewed the medical files of all patients with documented CHIKV infection.

CHIKV infection was defined by the association of compatible symptoms of fever and arthralgia and positive IgM serology or positive blood reverse transcription PCR (RT-PCR). We defined types of CHIKV infection as follows: 1) common form (i.e., only fever or arthralgia); 2) atypical form (i.e., involvement of ≥1 organ systems); and 3) severe form (i.e., failure of ≥1 organ systems or admission to an intensive care unit [ICU]).

We used standard definitions for organ system failures and severe sepsis shock (*4*). Organ failures were defined by a Sequential Organ Failure Assessment score ≥3 for each organ. Encephalitis was defined in accordance with Position Consensus Statement of the International Encephalitis Consortium criteria (*5*) and myocarditis in accordance with Consensus Statement of the European Society of Cardiology criteria (*6*).

During the outbreak, CHIKV was confirmed in 63 adults and one 11-year-old girl (Table). Forty-two patients had positive results for blood RT-PCR, and 22 had positive results for IgM serology. Virus load in serum was high; median load was 7.52 $\log_{10}$ copies/mL (interquartile range 3.47–9.39 $\log_{10}$ copies/mL). Of 5 patients with encephalitis symptoms, 3 had positive results for cerebrospinal fluid RT-PCR.

Forty-nine (76%) patients had a preexisting disease, 33 (51%) required invasive mechanical ventilation, 40 (62%) were in shock and needed vasoactive drugs, and 30 (46%) required renal replacement therapy. The ICU death rate for chikungunya was 28%, slightly higher than the usual 22% ICU death rate (A. Koeltz, unpub. data). Five patients had encephalitis, 2 had myocarditis, and 4 had Guillain-Barré syndrome (GBS). Fifty-five patients had a severe form of chikungunya, and 21 had illness consistent with the case definition for severe sepsis; for 2 patients, no other cause for GBS than CHIKV was identified. Two patients had CHIKV–leptospirosis co-infection, and 1 had CHIKV–dengue virus co-infection. Among the 55 patients who had the severe form of chikungunya, 17 had exacerbations of a chronic condition.

Chikungunya can be complicated by severe multiple organ failure and lead to death either from exacerbation of a preexisting disease or by severe atypical infection. Severe septic shock directly attributable to CHIKV was reported during the 2014 outbreak (*7*,*8*), and these reports seem consistent with our study (2 cases). This finding could be explained by the fact that chikungunya induces lymphopenia.

Neurologic complications of arbovirus infections are well documented, as illustrated by the high incidence of GBS reported during French Polynesia's outbreak of Zika virus (42 cases) (*9*). In our study, we observed 4 severe cases of GBS, and 10 GBS cases were managed in the hospital during the outbreak; GBS incidence was 4 times higher than usually observed in this hospital.

The most severe atypical complication in our study was myocarditis (2 cases), which had a 100% case-fatality rate. These deaths included an 11-year-old child and a 56-year-old woman without preexisting disease.

Our findings indicate that critical illness frequently complicates the course of CHIKV infection. Hospitals in chikungunya-endemic areas should be aware of the potential for increases in the number of ICU admissions during outbreaks.

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About the Author

Dr. Koeltz is a cardiac anesthesiologist at Bichat Claude-Bernard University Hospital in Paris. His research interests include infectious diseases in tropical areas.

Table. Clinical and laboratory characteristics of 64 patients with chikungunya virus infection admitted into the intensive care department, French Polynesia, 2014–2015*

Characteristic	Result
Baseline	
Median age, y (IQR)	62 (49–71)
Sex, no. (%)	
M	37 (58)
F	27 (42)
Preexisting disease, no. (%)	
Hypertension	37 (58)
Diabetes mellitus	22 (34)
Chronic renal failure	15 (23)
Chronic heart failure	12 (19)
Chronic liver disease	3 (5)
None	15 (23)
Simplified Acute Physiology Score (IQR)	48 (28.5–68.5)
Chikungunya diagnosis, no. (%)	
By reverse transcription PCR	42 (66)
By IgM	26 (41)
By reverse transcription PCR and IgM	4 (6)
Finding at admission	
Organ failure,† no. (%)	
Hemodynamic	40 (63)
Renal	30 (47)
Neurologic	20 (31)
Respiratory	33 (52)
Hepatic	16 (25)
Hematologic	9 (14)
Laboratory‡	
Leukocyte count, cells/m^3, median (IQR)	11,600 (7,200–15,200)
Lymphocyte count, cells/m^3, median (IQR)	1,000 (600–1,500)
Lymphopenia, <1,000 cells/m^3 (% of patients)	36 (56)
Platelet count, cells/m^3, median (IQR)	155,000 (79–208)
Platelet count, <150,000 cells/m^3 (% of patients)	34,000 (53)
Creatinine, μmol/L, median (IQR)	132 (79–184)
Creatine phosphokinase, mmol/L, median (IQR)	222 (124–1,160)
Alanine aminotransferase, UI/L, median (IQR)	35 (19–76)
C-reactive protein, mg/L, median (IQR)	10.6 (2.8–18.3)
Procalcitonin, μg/L, median (IQR)	1.72 (0.42–18.3)
Lactate, mmol/L, median (IQR)	2.6 (1.1–5.4)
Chikungunya reverse transcription PCR‡	
Viral load in serum, log_{10} copies/mL (IQR)	7.52 (3.47–9.39)
Viral load in cerebrospinal fluid,§ log_{10} copies/mL (IQR)	4.18 (3.86–4.26)
Outcome variable	
ICU length of stay, d, median (IQR)	3 (2–7)
Crude intensive care unit deaths, no (%)	18 (28)

*IQR, interquartile range.
†Organ failure is defined according to a Sequential Organ Failure Assessment score ≥3 for each organ.
‡Blood samples during the first 24 h. Reference values are as follows: leukocytes, 4.0–10.0 × 10^3 cells/mm^3; lymphocytes, 1.5–3.4 × 10^3 cells/mm^3; platelets, 150–400 × 10^3/mm^3; creatinine, 0.56–1.0 mg/dL; creatine phosphokinase, 0–130 U/L; alanine aminotransferase, 0–35 U/L; C-reactive protein, <5 mg/L; procalcitonin, <0.5 ng/mL; lactate, 5–15 mg/dL.
§Virus load was positive for 5 of the 9 cerebrospinal fluid samples.

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African Swine Fever Virus, Siberia, Russia, 2017

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African swine fever (ASF) is arguably the most dangerous and emerging swine disease worldwide. ASF is a serious problem for the swine industry. The first case of ASF in Russia was reported in 2007. We report an outbreak of ASF in Siberia, Russia, in 2017.

African swine fever (ASF) is arguably the most dangerous swine disease worldwide. ASF virus (ASFV) is highly virulent for domestic swine and remains a global threat because no effective vaccine is available to eradicate the disease. The emergent potential of ASF has been demonstrated by its spread into Russia. In the 10 years since ASF was first diagnosed in the Caucasian region of Russia (*1*), the disease has reached Palearctic regions and is spreading into western Europe (*2*,*3*).

In 2017, the Federal Service for Veterinary and Phytosanitary Surveillance (Rosselkhoznadzor) reported that, during 2007–2017, >1,000 ASF outbreaks resulted in deaths of ≈800,000 pigs in 46 regions across Russia (*4*). Production of backyard swine industry decreased by almost half, from 1,119 tons of pork in 2007 to 608 tons of pork in 2017 (*5*). However, highly industrialized pig farms showed increased production every year during this same period, despite the ASF epidemic.

ASF has seriously affected and is actively spread by wild boar populations in Russia, but accurate numbers of boar killed by ASF or culling attempts are difficult to estimate. In June 2017, ASF was detected in the Czech Republic in 2 wild boar (*6*), demonstrating disease spread toward western Europe. In 2017, ASFV cases among backyard domestic pigs were detected in July in Romania (*7*), and later in October 2017 in Moldova (*8*). We report an outbreak of ASF in Far Eastern Russia.

Early in March 2017, an ASF outbreak was reported on 1 backyard farm in the Irkutsk region near the border with Mongolia (Figure) (*5*). All pigs had clinical signs typical of acute ASF, and 40 pigs died within 6 days of the appearance of the first clinical signs. In a 5-km risk zone established around the affected farm, 1,327 pigs were slaughtered within 3 days. Epidemiologic analysis showed that the farmer used table leftovers to feed pigs.

ASFV DNA was identified by real-time PCR in the frozen pork products found on the farm. The origin of contaminated pork products is still under investigation. It is likely that ASFV-contaminated pork products provided a source of infection because these products are the most common source of ASF infection on backyard farms (*9*). ASF outbreaks nearest to the outbreak in Irkutsk occurred >4,000 km away in European Russia. Such a long geographic distance between ASF outbreaks within the country demonstrates that ASFV has a tremendous capacity for transboundary and transcontinental spread.

We identified the ASFV isolate from Irkutsk (ASFV/Irkutsk/dom/2017) by using nucleotide sequencing and molecular analysis. This isolate has capsid protein P72 genotype II and central variable region I and is an intergenic region (IGR) I variant (GenBank accession nos. KY963545, KY938010, and KY982843, respectively) according to the nomenclature of Gallardo et al. (*10*). The intergenic region between the *I73R* and *I329L* genes at the right end of the ASFV/Irkutsk/dom/2017 genome contains no additional tandem-repeat sequences. The ASFV IGRI variant is identical to the ASFV/Georgia/wb/2007 index isolate of the epidemic in Georgia in 2007 but represents an ASFV variant that is rare among recent ASFV isolates in Russia. In comparison, all recent ASF outbreaks in European Russia and eastern Europe have been caused by ASFV of the IGRII variant, which has an insertion of a tandem-repeat sequence in the intergenic region between the I173R and the I329L protein genes.