

Evidence shows human transmission in deadly outbreak of mysterious disease in Bolivia

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Researchers have discovered that a deadly virus found in Bolivia can spread from person to person in healthcare settings, raising potential

concerns of additional outbreaks in the future, according to new findings presented today at the annual meeting of the American Society of Tropical Medicine and Hygiene (ASTMH). The research also provides preliminary evidence regarding the species of rodent that carries the virus and may spread it to people or to other animals that can infect humans.

Researchers from the U.S. Centers for Disease Control and Prevention (CDC) laid out new clues to the many mysteries surrounding the Chapare virus, which caused at least five infections near Bolivia's capital city, La Paz, in 2019—three of them fatal. Prior to that, the only record of the [disease](#) was a small cluster and a single confirmed case in 2004 in Bolivia's Chapare Province, about 370 miles east of La Paz. The recent outbreak surprised health authorities, since initially all they knew was that it was a hemorrhagic fever that produced symptoms similar to diseases such as Ebola. It sparked a rapid mobilization of infectious disease experts from Bolivia's Ministry of Health, the CDC and the Pan-American Health Organization (PAHO) to explore the origins of the disease, including securing samples from patients and developing a new diagnostic test.

"Our work confirmed that a young medical resident, an ambulance medic and a gastroenterologist all contracted the virus after encounters with infected patients—and two of these healthcare workers later died," said Caitlin Cossaboom, DVM, Ph.D., MPH, an epidemiologist with the CDC's Division of High-Consequence Pathogens and Pathology. "We now believe many bodily fluids can potentially carry the virus."

Cossaboom said the confirmation of human-to-human transmission shows healthcare providers and anyone else dealing with suspected cases must take extreme care to avoid contact with items that may be contaminated with blood, urine, saliva or semen. For example, there is evidence that the medical resident who died from the disease may have

been infected while suctioning saliva from a patient. The ambulance medic who was infected, but survived, was likely infected when he resuscitated the same medical resident as she was being transported to the hospital after she fell ill. Researchers also detected viral RNA in the semen of one survivor 168 days after infection, which also raises the possibility of sexual transmission. Further investigation is necessary to learn about other potential routes of transmission.

Chapare belongs to a group of viruses called arenaviruses. They include dangerous pathogens such as Lassa virus, which causes thousands of deaths annually in West Africa, and Machupo virus, which has caused deadly outbreaks in Bolivia. Like those pathogens, Chapare virus can cause hemorrhagic fevers—a condition also seen in Ebola patients that can produce severe problems across multiple organs, leaving patients struggling to survive. Cossaboom noted that patients in the 2019 Chapare outbreak suffered fevers, abdominal pain, vomiting, bleeding gums, skin rash and pain behind the eyes. There is no specific treatment, so patients are treated mainly with intravenous fluids and other supportive care.

There is still much that remains unknown about Chapare virus, chiefly where it originated, how it infects humans, and the likelihood of larger outbreaks in Bolivia and elsewhere in South America. Cossaboom presented new evidence of Chapare viral RNA detected in rodents collected from an area around the home and nearby farmlands of the first patient identified in the 2019 outbreak—an agriculture worker who also died. She cautioned that the evidence stops well short of proving the rodents were the source of his infection—viral RNA is not proof that the rodents were infectious—though it offers an important clue.

"The genome sequence of the RNA we isolated in rodent specimens matches quite well with what we have seen in human cases," she said.

The rodent species that tested positive for viral RNA, commonly known

as the pigmy rice rat and the small-eared pigmy rice rat, are found across Bolivia and several neighboring countries. Rodents are a key source or reservoir of similar viruses, including Lassa virus.

Scientists believe the Chapare virus could have been circulating in Bolivia for several years, but infected patients may have been wrongly diagnosed as suffering from dengue, a disease that is common in the region and can produce similar symptoms.

All-hands on deck to solve a deadly mystery

Cossaboom's colleague at the CDC, Maria Morales-Betoulle, Ph.D., described an intensive effort involving Bolivian health officials in La Paz, scientists from the Bolivian Center for Tropical Diseases (CENETROP) in Santa Cruz de la Sierra, colleagues at PAHO and infectious disease experts at CDC headquarters in Atlanta to get a handle on the 2019 outbreak. She said that when it became clear the illness was not caused by dengue, patient samples collected by Bolivian authorities were quickly dispatched to a highly secure biosafety level 4 (BSL-4) CDC laboratory. Once there, they were subjected to analysis with advanced next generation genome sequencing technology. CDC experts were able to identify the virus as Chapare because it matched sequence data derived from the patient involved in the original 2004 infection.

"We isolated the virus, and we were expecting to find a more common disease, but the sequence data pointed to Chapare virus," Morales-Betoulle said. "We were really surprised because the 2019 outbreak in La Paz occurred long after the first case was identified in 2004."

Morales-Betoulle said that the availability of new sequencing tools allowed CDC experts to rapidly develop an RT-PCR test for detecting Chapare—the same type of test often used to diagnose COVID-19, which is considered the gold standard for diagnostics. The investigation

then moved back to CENETROP in Santa Cruz de la Sierra, where there is a BSL-3 lab and team capable of securing and analyzing patient samples.

She said several collaborators on the team involved in the Chapare response already were in South America investigating other viral hemorrhagic fevers when the 2019 outbreak occurred.

"That allowed us to mobilize and move really quickly," she said.

Morales-Betoulle and Cossaboom said future work will focus on using the diagnostic tests to conduct surveillance to identify additional human infections and field work to determine whether rodents are involved in spreading the disease. Since the outbreak, CENETROP identified three additional suspected cases, including one involving a child. All are believed to have survived. Additional testing at CDC is anticipated.

"While there is still much that remains unknown about Chapare virus, it's commendable how quickly this team was able to develop a diagnostic test, confirm human-to-human transmission and uncover preliminary evidence of the [virus](#) in rodents," said ASTMH President Joel Breman, MD, DTPH, FASTMH. "It's a valuable lesson that international scientific teams, equipped with the latest tools and freely sharing their insights, are our best front-line defense against the disruptive threats of deadly infectious diseases."

Provided by American Society of Tropical Medicine & Hygiene

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