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Two studies reveal how Andes Virus spread aboard a cruise ship and trace its genetic history to Patagonia

Investigators faced two urgent questions when an outbreak of Andes virus emerged aboard a cruise ship travelling across the South Atlantic in April 2026: how the virus spread among passengers and crew, and where the infection originated. Two complementary studies, published November 12 in *Science*, provide new insights into this rare public health event.

Thirteen people were sickened by the virus, three of whom ultimately died. What began as an outbreak aboard a single vessel soon became an international scientific investigation that brought together laboratories, researchers, and public health institutions across multiple countries to reconstruct an unusual global health concern and response.

Combining epidemiological evidence with viral genome sequencing, the international team found strong evidence that Andes virus spread from person to person during the voyage. The genomic investigation also uncovered a connection between the outbreak virus and cases previously identified in northern Patagonia, Argentina. At the time, viruses detected near Villa Meliquina in 2018 were among its closest known genetic relatives. That finding prompted a second study to examine historical cases, regional epidemiological evidence, and the circulation of related viral lineage over time.

Together, these studies reveal how a virus with a long history in South America is linked to the 2026 outbreak. The findings also tell a broader story about scientific preparedness, in which knowledge is accumulated over decades, expertise is distributed across countries, and longstanding research relationships are essential to understanding a rapidly unfolding global health event.

Reconstructing an outbreak at sea

The MV Hondius departed Ushuaia, Argentina, on April 1, 2026, for a voyage across the South Atlantic. During the journey, passengers and crew developed severe respiratory illnesses. Laboratory investigations at South Africa's National Institute for Communicable Diseases (NICD) helped identify hantavirus infection in the outbreak.

By the end of the investigation, 12 infections had been laboratory-confirmed and one additional case was considered probable. Further testing identified Andes virus, a pathogen that circulates naturally in parts of Argentina and Chile.

Unlike most hantaviruses, which primarily infect humans through exposure to infected rodents, Andes virus can also spread between people under certain circumstances. Understanding which route of transmission occurred aboard the MV Hondius was central to the investigation, and therefore, researchers needed to determine whether passengers and crew experienced separate exposures before departure, or the virus spread among individuals during the voyage. The team combined the timing of illnesses, documented contacts between individuals, and viral genome sequencing, a technique that allows scientists to compare the genetic material of viruses recovered from different patients.

Laboratories in Canada, France, the Netherlands, Senegal, South Africa, Spain, and Switzerland generated viral genome sequences from outbreak cases. These data were then compared alongside epidemiological findings to reconstruct probable transmission patterns. The results revealed striking genetic similarities among the outbreak viruses. Considered together with the timing of symptoms and known contacts, the genomic evidence strongly supported person-to-person transmission aboard the vessel.

In one case, a patient developed symptoms on May 31, approximately 60 days after the ship departed Argentina and following prolonged close contact with another infected individual. This interval exceeded the 45-day incubation window used to evaluate possible infections acquired before boarding and provided especially compelling evidence of transmission during the voyage.

Importantly, the findings did not establish an entirely new or unusually transmissible viral strain. Rather, the outbreak involved a virus already known to have the capacity for human-to-human transmission.

Tracing the virus's history to Patagonia

In a second study, investigators compared viral sequences from the cruise ship cases with historical samples and surveillance data collected in Argentina to learn whether the virus was circulating before the MV Hondius set sail. A close genetic relationship emerged between the outbreak virus and Andes viruses previously detected near Villa Meliquina, where two brothers had hantavirus pulmonary syndrome in 2018. The second investigation also examined historical cases, regional epidemiological evidence, and additional viral sequences from Neuquén Province. Further analyses identified related viruses among cases recorded between 2018 and 2025, revealing a lineage documented in northern Patagonia years before the cruise ship outbreak.

Researchers reconstructed the journey of the first two cases, a couple who had travelled extensively through Argentina and Chile in a motor home before boarding the vessel, to investigate the possible origin of the initial infections. Since both individuals died before providing detailed accounts of their possible exposures, investigators used other sources of evidence, including border-crossing records, visits to birdwatching sites, information from regional authorities, and the known geographic distribution of rodents that carry Andes virus, to help piece together the couple's movements. The couple entered Argentina through the Icalma Pass on January 31, about 62 days before symptoms first appeared on April 3. That interval exceeded the 45-day window used to assess possible exposures, making their documented passage through the region too early to readily explain the infection.

The investigators concluded that the closest genetic match could help reveal the virus 's evolutionary history without identifying where the initial infection had occurred.

Years of research and surveillance in Argentina, including work by researchers at the Administración Nacional de Laboratorios e Institutos de Salud Dr Carlos G Malbrán (ANLIS-Malbrán), provided historical evidence that made it possible to connect the 2026 outbreak to a lineage documented years earlier. What appeared to be an unexpected outbreak at sea was linked to a much longer history of viral circulation on land, even as the exact pathway connecting the two remains uncertain.

Why international collaboration made the difference

When viruses spread between people over a relatively short period, their genomes may differ by only a handful of nucleotides, the individual building blocks of genetic material. In some transmission investigations, differences of just one to five nucleotides can be relevant to interpreting how closely infections are related.

At that level of similarity, even a small technical difference in sequencing or data analysis can matter. An apparent genetic variation might reflect a genuine change in the virus, or it might arise from the methods used to generate and interpret the sequence.

Researchers in seven countries generated viral sequences using different technologies and analytical approaches for the MV Hondius investigations. Rather than relying solely on their independently produced results, participating teams shared underlying sequencing data, compared analytical methods, and reviewed genetic differences together. This cross-institutional verification helped researchers distinguish meaningful viral variation from potential technical artifacts, strengthening confidence in the genomic evidence used to investigate transmission.

"No single laboratory could have told this story on its own," said Gustavo Palacios, PhD, Professor of Microbiology at the Icahn School of Medicine at Mount Sinai. "Some

teams understood the virus's history in South America, while others brought expertise in outbreak investigation, diagnostics, or genomic analysis. What made the difference was our ability to bring that knowledge together, challenge our own assumptions, and independently verify the evidence. That's what allowed us to build a stronger and more reliable picture of what happened."

The World Health Organization (WHO) helped coordinate information-sharing and public health investigations across affected countries following notification of the official outbreak.

In Switzerland, laboratories at Geneva University Hospitals, the University of Geneva, and the University of Zurich generated the first complete outbreak-associated Andes virus genome made publicly available on May 7, providing an early foundation for comparative genomic analysis.

This was followed by the release of additional viral sequences and a preliminary analysis by the broader scientific team, including data from the earliest identified outbreak cases. "Our contribution demonstrates the importance of sustained investment in scientific expertise and genomic capabilities across regions. The ability of institutions in Africa to contribute directly to investigations of emerging infectious threats anywhere in the world is an essential component of a truly interconnected and resilient global health security system," said Moussa Moïse Diagne, PhD, Head of the Genomic Sequencing Lab and Deputy Head of the WHO Collaborating Centre for Arboviruses and Viral Hemorrhagic Fevers at Institut Pasteur de Dakar.

Meanwhile, researchers in Argentina and Chile brought longstanding experience studying Andes virus in South America. From Chile, teams at Pontificia Universidad Católica de Chile, together with researchers at Universidad San Sebastián and Fundación Ciencia & Vida, contributed throughout the investigation, bringing longstanding expertise in Andes virus, including its clinical and epidemiological characteristics and genetic diversity.

Historical samples and genetic information collected through years of research in Argentina were essential to interpreting the outbreak's evolutionary history.

The two international investigations were a collaboration by the Icahn School of Medicine at Mount Sinai in the United States; ANLIS-Malbrán in Argentina; Erasmus University Medical Center in the Netherlands; Geneva University Hospitals and the University of Geneva in Switzerland; Institut Pasteur in Paris; Institut Pasteur de Dakar in Senegal; the National Institute for Communicable Diseases in South Africa; the Instituto de Salud Carlos III in Spain; and the Public Health Agency of Canada, alongside other academic and public health partners. Researchers and public health experts from

Chile, the World Health Organization, the University of Zurich, and additional institutions also contributed to the studies.

"These studies demonstrate the power of international collaboration. The rapid sharing of epidemiological and genomic data across borders, and the close collaboration of Member States and academic, technical and operational partners, were essential throughout. The International Health Regulations and coordination by the World Health Organisation were vital in facilitating the timely exchange of information between Africa, South America, Europe, and the wider world. Infectious diseases do not respect borders, and controlling them requires strong partnerships, transparent information-sharing, and sustained investment in preparedness, surveillance, laboratory networks, and emergency response," said Maria Van Kerkhove, Director of the WHO's Department of Epidemic and Pandemic Management.

"This was an extraordinary international effort and a demonstration of what we can achieve by working together across institutions and borders. The experience reinforces why investing in national capacities and international scientific networks before a crisis is so essential," said Isabella Eckerle, Director of the joint Centre for Emerging Viral Diseases at Geneva University Hospitals and the University of Geneva.

At the heart of this effort was a principle that extends well beyond Andes virus: international scientific networks cannot be assembled overnight. Their effectiveness during an emergency depends on relationships, expertise, and capabilities developed and maintained long before they are needed.

For public health teams, the studies reinforce the value of sustained surveillance, preserved historical samples, and the ability to interpret genomic evidence alongside travel histories and epidemiological information.

For researchers, they demonstrate why careful genomic analysis and international cooperation go hand in hand. Preparedness begins long before an outbreak: the scientific expertise, data, technical capacities, and relationships needed during an emergency must already be in place.

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For enquiries and interview requests, please contact: Media@nicd.ac.za.

Vuyo Sabani: Senior Communications Manager

National Institute for Communicable Diseases