

PUBLIC HEALTH ALERTS | IN PARTNERSHIP WITH CIDRAP

Andes Hantavirus Outbreak on a Cruise Ship, 2026

Andes Virus Outbreak Working Group*

On April 27, 2026, a man (later classified as Patient 3 in the outbreak) was medically evacuated to Ascension Island from the Dutch-flagged expedition cruise ship *MV Hondius*; he had severe acute respiratory infection (SARI) and reported shortness of breath and fever that had begun on April 21. He had signs of pneumonia, although findings on chest radiography were unremarkable. While he was on Ascension Island, his condition worsened, and he was transferred to Johannesburg, South Africa, for ventilator support and intensive care.¹ He was in shock and had acute respiratory distress syndrome; findings on chest radiography were consistent with atypical pneumonia. The differential diagnosis in this clinical context is very broad and includes atypical pneumonias, bacterial or fungal sepsis, and vectorborne diseases such as malaria or dengue. The diagnostic evaluation, including respiratory pathogen panels, malaria smear and antigen, fungal biomarkers, blood cultures, and legionella urinary antigen, was unrevealing. Further details are provided in the Supplementary Appendix, available with the full text of this article at evidence.nejm.org.

A virtual consultation was held on May 2 with medical specialists from South Africa, the United Kingdom, and Holland to discuss the potential link to two recent fatalities associated with the same ship. On May 2, the United Kingdom officially reported a cluster of cases of severe acute respiratory illness of unknown cause, resulting in two deaths and one critical illness in a passenger aboard the cruise ship, to the World Health Organization through the International Health Regulations of 2005. The Netherlands also reported the illnesses through the restricted Early Warning and Response System (EWRS).

The cruise ship had departed Ushuaia, Argentina, on April 1 and followed an itinerary across the South Atlantic. In the first person who died (Patient 1), respiratory symptoms developed on April 6, and he died on board the ship on April 11 with SARI and respiratory failure. No microbiological tests were performed. He had a 3-month history of travel to Argentina, Chile, and Uruguay before his departure on the cruise.² His body was taken off the ship at the scheduled stop at Saint Helena on April 24. His partner (Patient 2), who also went ashore that day, began to have similar symptoms and started a return journey to the Netherlands by way of Johannesburg on April 25. She was too ill to complete her connecting flight and died in the emergency department at a Johannesburg hospital.

Given the travel history, the negative respiratory results, and the rapid progression of illness in Patients 1, 2, and 3, the differential diagnosis was expanded to include hantavirus cardiopulmonary syndrome, and samples from Patient 3 were sent to the National Institute for Communicable Diseases (NICD) in South Africa, where the diagnosis was confirmed

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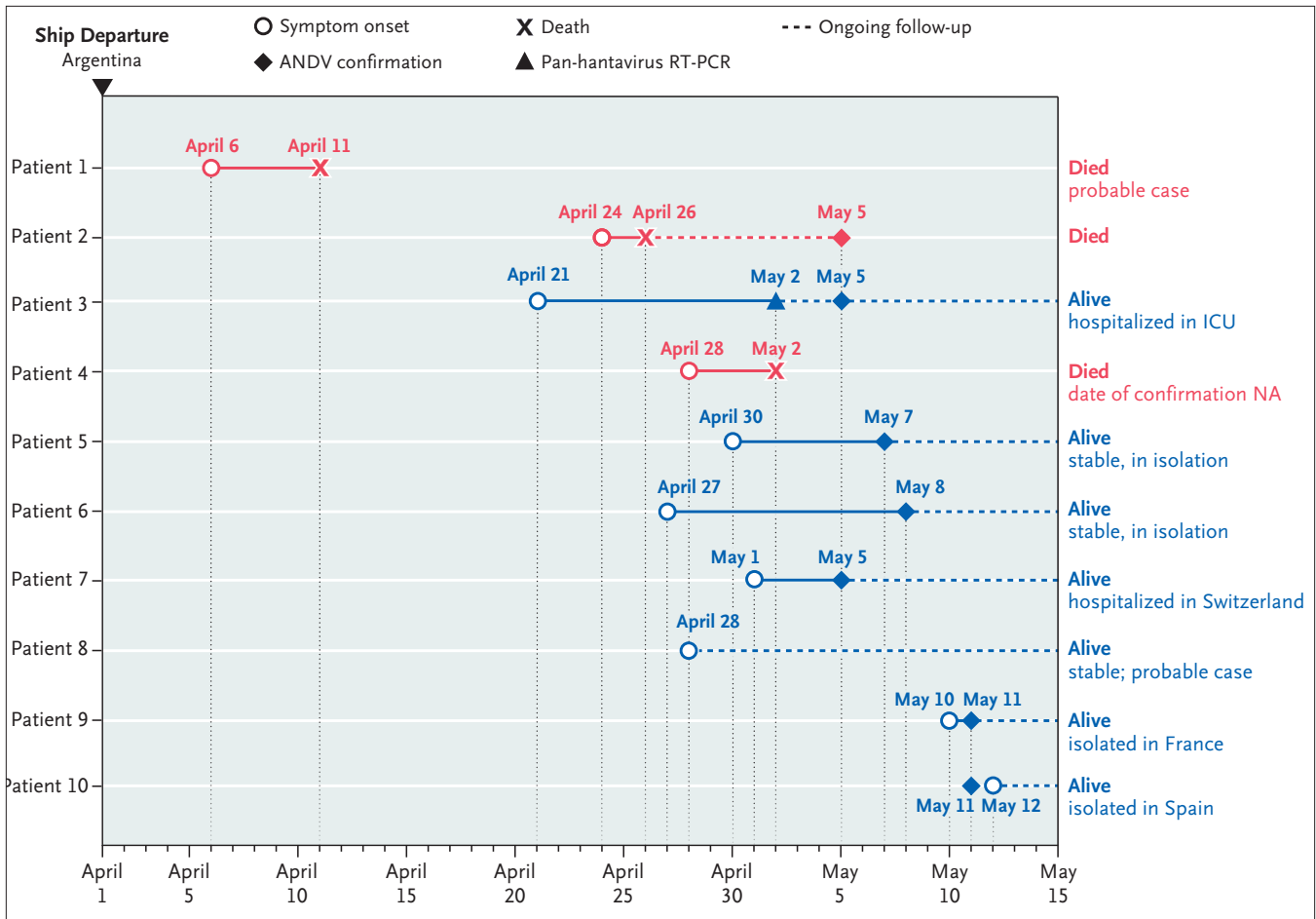


Figure 1. Timeline of the First 10 Cases Associated with the *MV Hondius*.²

ANDV denotes Andes virus, ICU intensive care unit, NA not available, and RT-PCR reverse-transcriptase polymerase chain reaction.

on May 2 by pan-hantavirus reverse-transcriptase–polymerase-chain-reaction (RT-PCR) assay (details are provided in the Supplementary Appendix). An antemortem sample from Patient 2 was retrieved, and sequencing of the L segment from Patients 2 and 3 at the NICD confirmed the presence of Andes virus (ANDV) on May 5 (see the Supplementary Appendix).³

On May 2, the cruise ship had a total of 147 persons on board, including 88 passengers and 59 crew members, from 23 countries. As of May 13, 2026,⁴ a total of 10 cases had been identified (an 11th was subsequently reclassified as not a case), including 3 resulting in death (Fig. 1). However, because not everyone on board was tested, 3 deaths among 10 cases may represent an overestimation of the case fatality ratio. All cases to date have been among passengers or crew on board the ship. Beyond the first 3 cases, 7 addi-

tional confirmed or probable cases have been identified. A German national (Patient 4) died from a SARI on May 2, and later testing in the Netherlands confirmed ANDV. Two crew members — the doctor on the ship (Patient 5) and an expedition guide (Patient 6) — were medically evacuated to the Netherlands, tested positive by PCR and sequencing for ANDV on May 7 and 8, respectively, and were in stable condition at the time of this report.

On April 22, Patient 7 disembarked on the island of Saint Helena mid-voyage, while still asymptomatic, before the hantavirus outbreak had been declared, and returned to Switzerland. After receiving the notification from the ship operator, the patient presented to a Zurich hospital, was isolated, and underwent testing; a PCR assay was positive for ANDV. Patient 8, a passenger who disembarked in Tristan da Cunha, began to have symptoms on April

28 and is currently receiving medical care; the illness in this patient is considered a probable case because of limited access to testing. Two additional confirmed cases (in France and Spain) were detected among persons evacuated from the ship in Tenerife, Spain; symptoms developed in these patients after they had disembarked from the ship — one on May 10 (Patient 9) and the other on May 12 (Patient 10). PCR testing in the patients in this outbreak has been performed in different laboratories with the use of locally validated assays in the respective countries.

Early sequencing of ANDV from the patients showed a high degree of similarity to previously reported sequences from Argentina. An initial zoonotic introduction before the departure of the ship from Argentina on April 1 is likely, because symptoms developed in Patient 1 on April 6, and he had a 3-month travel history to regions with known enzootic circulation of ANDV. No samples were available from this patient. Sequencing of samples from the subsequent patients showed a high level of genetic similarity, with a maximum of one detected single-nucleotide polymorphism per patient.³ Further epidemiologic analysis is needed to determine whether this outbreak resulted from one or more zoonotic spillover events or from human-to-human transmission, as was seen in the 2018 outbreak, which showed similar clustering and absence of viral genetic diversity.⁵

The situation is evolving, and the World Health Organization and European Center for Disease Prevention and Control assess the global risk as low. The primary source of the outbreak is under active investigation, and experts who have experience with ANDV are collaborating to focus on

exposures to South American rodents that occurred before the departure of the ship.

Disclosures

Author disclosures are available at evidence.nejm.org.

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