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Cruise-linked Andes virus and severe hantavirus lung disease: A narrative review

Amogh Verma [a,b,1,2], Sreshta Akkineni [c,3], Lavanya Yaidikar [d,4], Balakrishnan Madhavan [e,5], Channagiri Srinivas Bhargavram [f,1], Sourav Sudan [g,1], Ranjana Sah [h], Rahul Singla [i,j,1,6], Tweheyo Ronald [k,7,*], Sanjit Sah [l,m,n]

[a] Rama Medical College Hospital & Research Centre, Pilkhuwa, Hapur, Uttar Pradesh 245304, India
[b] Medicos In Research, Nautanwa, Maharajganj, Uttar Pradesh 273164, India
[c] Kakatiya Medical College, Warangal, Telangana 506007, India
[d] Department of Pharmacology, Krishna Teja Pharmacy College, Tirupati, Andhra Pradesh 517506, India
[e] Department of Opthalmology, Sree Balaji Medical College & Hospital, Bharath Institute of Higher Education & Research, Chennai, Tamil Nadu 600044, India
[f] Department of Internal Medicine, Bassett Medical Center, Cooperstown, New York 13326, United States
[g] Department of Internal Medicine, Saint Vincent Hospital, Worcester, MA 01608, United States
[h] Saveetha Medical College and Hospital, Saveetha Institute of Medical and Technical Sciences, Saveetha University, Chennai, Tamil Nadu 602105, India
[i] Guru Gobind Singh Medical College and Hospital, Faridkot, Punjab 151203, India
[j] University of Iowa Family Medicine Center, Sioux City, Iowa 51104, United States
[k] Faculty of Health Sciences, Busitema University, Mbale City, Eastern Region, Uganda
[l] Dr. D. Y. Patil Medical College Hospital and Research Centre, Dr. D. Y. Patil Vidyapeeth (Deemed-to-be-University), Pimpri, Pune 411018, Maharashtra, India
[m] Dr. D. Y. Patil Dental College and Hospital, Dr. D. Y. Patil Vidyapeeth (Deemed-to-be-University), Pimpri, Pune 411018, Maharashtra, India
[n] Department of Medicine, Korea University, Seoul 02481, South Korea

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ABSTRACT

The 2026 cruise-linked Andes virus (ANDV) outbreak represents a rare but high-consequence travel-associated zoonotic event, combining likely land-based acquisition before embarkation, limited onboard human-to-human transmission, delayed clinical recognition, and multinational public health coordination. This narrative review synthesizes current evidence on the outbreak, ANDV biology, transmission dynamics, clinical presentation, diagnostics, management, and implications for maritime and expedition travel medicine. As of 2 July 2026, the World Health Organization (WHO) had reported 13 cases linked to the motor vessel (M/V) Hondius outbreak, including 12 laboratory-confirmed infections, one probable case, and three deaths. Following completion of the 42-day follow-up period for all identified contacts without additional secondary cases, WHO considered transmission interrupted and the outbreak contained. Available evidence supports likely land-based acquisition before embarkation followed by limited onboard human-to-human transmission, without sustained spread. Severe hantavirus cardiopulmonary syndrome may begin with nonspecific fever, malaise, myalgia, gastrointestinal symptoms, or respiratory complaints, then progress abruptly to pulmonary oedema, shock, and fatal cardiopulmonary collapse. Because no licensed antiviral therapy or vaccine is available, early recognition, cautious fluid management, intensive supportive care, ventilatory support, and timely transfer to intensive care or extracorporeal membrane oxygenation-capable centres remain central. The outbreak highlights critical preparedness gaps in shipboard triage, contact tracing, specimen transport, genomic surveillance, risk communication, and cross-border follow-up. Strengthening One Health-informed pre-travel counseling, post-travel

* Corresponding author.
E-mail address: tweheyo.publish@gmail.com (T. Ronald).
[1] Co-first authors.
[2] ORCID: 0000–0003–2499-4874
[3] ORCID: 0009–0007–1369-4274
[4] ORCID: 0000–0002-3059-970X
[5] ORCID: 0009–0000–5612-8490
[6] ORCID: 0009–0005–4510-2910
[7] ORCID: 0009–0001–4529-9574

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symptom surveillance, and maritime outbreak protocols is essential for future expedition-associated zoonotic threats.

Introduction

The cruise-linked hantavirus outbreak first reported in May 2026 is important not simply because it occurred on a ship (World Health Organization, 2026a; World Health Organization, 2026b; World Health Organization, 2026c; World Health Organization, 2026d) (Fig. 1). Its significance lies in the collision of two epidemiological systems that are usually managed separately: zoonotic exposure in endemic landscapes and person-to-person risk management within an enclosed international conveyance. International investigation, laboratory testing, and contact tracing progressively clarified the outbreak, and the World Health Organization (WHO) ultimately concluded that transmission had been interrupted after completion of follow-up for all identified contacts (World Health Organization, 2026e). The event therefore provides a rare opportunity to examine how a severe zoonotic infection capable of limited human-to-human transmission can challenge clinical recognition, contact management, medical evacuation, and international coordination in a mobile multinational population.

Hantaviruses are zoonotic viruses maintained primarily in rodent reservoirs (Sagadevan et al., 2023). In the Americas, infection may lead to hantavirus cardiopulmonary syndrome (HCPS), also called hantavirus pulmonary syndrome (HPS), a severe disease characterized by fever, myalgia, gastrointestinal symptoms, abrupt respiratory compromise, pulmonary oedema, hypotension, and shock (Hjelle and Torres-Pérez, 2010). WHO identifies ANDV as currently the only known hantavirus with documented limited human-to-human transmission, mainly among close and prolonged contacts (World Health Organization, 2026a; World Health Organization, 2026b; World Health Organization, 2026c; World Health Organization, 2026d; World Health Organization, 2026e; Martinez et al., 2005; Watson et al., 2014; World Health Organization, 2026f; Public Health Agency of Canada, 2026). The 2026 event therefore extends beyond classical cruise-associated infectious disease narratives, which often focus on norovirus, influenza, coronavirus disease, or Legionella (Neumann et al., 2025). ANDV introduces a different risk model: an infection usually acquired from contaminated rodent excreta, but capable of secondary spread under restricted interpersonal conditions. That feature makes the outbreak a test of shipboard triage, international notification, laboratory coordination, clinical evacuation, and post-disembarkation surveillance. This review examines the 2026 cruise-linked Andes virus outbreak, focusing on its zoonotic origin, limited onboard human-to-human transmission, clinical severity, and maritime public health implications. It also outlines key gaps in early recognition, contact monitoring, diagnostics, and evacuation preparedness.

Methods

This review was developed through a targeted literature search from database inception to 2 July 2026, with greater emphasis on evidence published during the last 5 to 10 years because of its relevance to contemporary outbreak investigation, genomic epidemiology, intensive care management, infection prevention, and maritime public health. Earlier landmark studies were included when they provided foundational evidence on ANDV, hantavirus HCPS, or documented person-to-person transmission. PubMed/MEDLINE, Embase, Scopus, Web of Science, and Google Scholar were searched, supplemented by authoritative public health sources from the WHO, Pan American Health Organization (PAHO), European Centre for Disease Prevention and Control (ECDC),

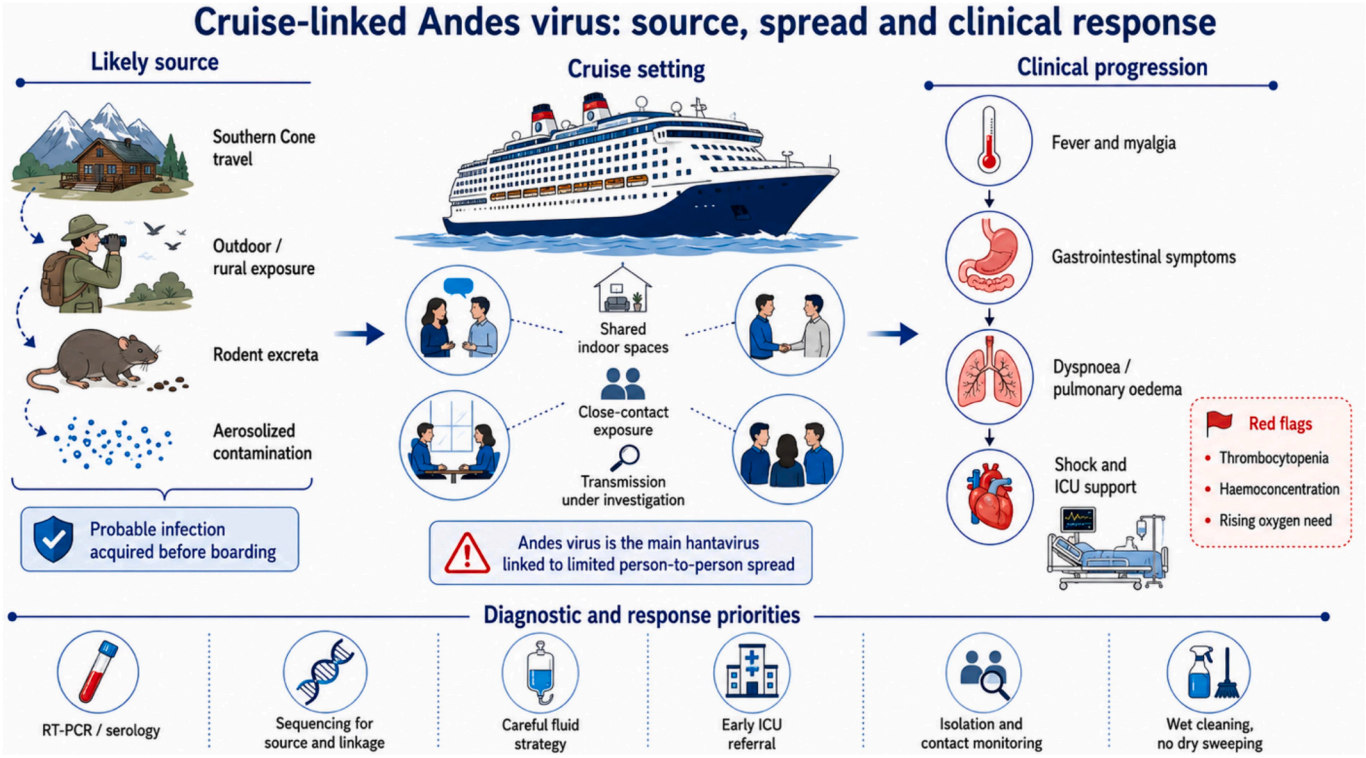

Fig. 1. Cruise-linked Andes virus outbreak: likely land-based acquisition, limited onboard human-to-human transmission, clinical progression, and response priorities. *Illustration was prepared using an author-designed layout and vector elements adapted from Flaticon, SVG Repo, Pixabay, PublicDomainVectors, Wikimedia Commons and author-drawn components according to their respective licensing terms.*

United States Centers for Disease Control and Prevention (CDC), and United Kingdom Health Security Agency (UKHSA). The WHO Disease Outbreak News updates of 4 May, 8 May, 13 May, 28 May, and 2 July 2026, together with the WHO rapid risk assessment version 2.0 dated 15 May 2026, were used to reconstruct the evolving epidemiology and final status of the cruise-linked outbreak. These were supplemented by ECDC daily surveillance updates through 17 May 2026, Public Health Agency of Canada (PHAC) communication on the Canadian confirmed case, and ECDC rapid scientific advice on laboratory testing and infection prevention and control for ANDV. Search terms included combinations of "hantavirus," "Andes virus," "Orthohantavirus andesense," "hantavirus cardiopulmonary syndrome," "hantavirus pulmonary syndrome," "human-to-human transmission," "person-to-person transmission," "Argentina," "Chile," "Patagonia," "cruise ship," "maritime outbreak," "travel-associated infection," "ecotourism," "rodent-borne disease," "infection prevention and control," "medical evacuation," "intensive care," and "extracorporeal membrane oxygenation." Relevant clinical reviews, outbreak investigations, epidemiological studies, surveillance reports, and technical guidance documents were included. Non-authoritative media reports and sources without clear epidemiological or clinical relevance were excluded. Evidence was synthesized narratively across outbreak chronology, transmission plausibility, clinical course, diagnostics, case management, infection prevention, international coordination, and maritime preparedness. No quantitative pooling was performed because the aim was to provide an interpretive narrative review of a rapidly evolving outbreak and its subsequent containment rather than a systematic review or meta-analysis.

Discussion

The outbreak as a maritime spillover event

The affected voyage departed Ushuaia, Argentina, on 1 April 2026 and traveled through remote South Atlantic and Antarctic-associated locations. WHO reported that the probable index case had traveled for more than three months in Argentina, Chile, and Uruguay before boarding, developed symptoms on 6 April, and died onboard on 11 April without microbiological testing (World Health Organization, 2026b). Subsequent cases emerged among passengers and crew from late April onward. The latest epidemiological assessment supports likely acquisition of the initial infection or infections on land before embarkation, followed by limited human-to-human transmission aboard the vessel (World Health Organization, 2026e). The exact source and route of the initial exposure remain unresolved, although WHO has stated that exposure in Chile can be excluded on the basis of the interval between travel and symptom onset (World Health Organization, 2026d; World Health Organization, 2026e).

The consequences of the outbreak extended beyond the vessel as passengers and crew disembarked, were medically evacuated, or returned home through multiple jurisdictions. Follow-up therefore encompassed individuals managed or disembarked through Tristan da Cunha, Saint Helena, Ascension, Praia, Tenerife, and the Netherlands, as well as contacts associated with subsequent international flights (World Health Organization, 2026a; World Health Organization, 2026b; World Health Organization, 2026c; World Health Organization, 2026d; World Health Organization, 2026e). Tristan da Cunha is particularly important in the outbreak chronology: a passenger who developed symptoms after disembarkation was initially classified as a probable case and was later laboratory confirmed after a specimen was shipped to and tested in the United Kingdom (World Health Organization, 2026e). The delay illustrates how restricted diagnostic capacity in remote settings can prolong case classification even when clinical recognition and isolation occur promptly.

By 2 July 2026, the total remained 13 cases, but the laboratory classification had changed to 12 confirmed ANDV infections and one probable case; three patients had died, corresponding to a case fatality ratio of 23% (World Health Organization, 2026e). Among ten patients admitted to hospital, eight had recovered and been discharged, while two remained under medical treatment (World Health Organization, 2026e). Contact tracing and follow-up had extended across 33 countries and overseas territories, with 317 high-risk contacts completing quarantine and active monitoring and 336 low-risk contacts completing self-monitoring (World Health Organization, 2026e). No additional secondary cases were detected during the completed 42-day follow-up period. WHO therefore concluded that transmission had been effectively interrupted, that the outbreak was contained, and that no further related transmission was expected (World Health Organization, 2026e).

The outbreak is therefore best understood not as an ongoing international transmission threat, but as a contained maritime amplification event whose importance lies in how a rare zoonosis interacted with close-contact networks, diagnostic delay, remote medical infrastructure, and rapid international dispersal (**Fig. 2**).

Andes virus biology and the human-to-human exception

The genus *Orthohantavirus* contains multiple rodent-associated viruses, but their clinical syndromes differ by geography (Song et al., 2025; Gourjault et al., 2023). Hantaviruses in Europe and Asia are typically linked to haemorrhagic fever with renal syndrome, whereas New World hantaviruses in the Americas are associated with HCPS (Brügger and Chuard, 2022). Human-to-human transmission has not been documented for Europe and Asia-associated hantaviruses, while ANDV in South America has been linked to uncommon secondary transmission among close contacts (Ferrés et al., 2024; Martinez-Valdebenito et al., 2014). ANDV is maintained in South American rodent reservoirs, particularly the long-tailed pygmy rice rat (*Oligoryzomys longicaudatus*) (Torres-Pérez et al., 2025; Campbell et al., 2015). Endemic risk is concentrated in Argentina and Chile, with cases associated with rural, peri-rural, forested, and outdoor exposure contexts (Astorga et al., 2018; Alonso et al., 2019). Human infection can occur through inhalation of aerosolized rodent excreta, direct contamination of mucous membranes, and less commonly bites (Schöffel et al., 2018). The human-to-human component of ANDV is epidemiologically unusual but not speculative (Alonso et al., 2020).

The biological basis for ANDV person-to-person transmission remains incompletely defined, but available evidence supports a narrow transmission phenotype rather than efficient respiratory spread. Earlier outbreak investigations suggested transmission during the prodromal phase or shortly after it ended (Martinez et al., 2005; Toro et al., 1998; Yates et al., 2002; Enría et al., 1996), while more recent work has examined viraemia and viral shedding in body fluids during acute infection (Fabbri and Maslow, 2001; Stephenson, 1997). These findings are important because they move the discussion beyond whether secondary transmission can occur toward when and under what biological conditions it is most plausible. For the cruise outbreak, this supports careful attention to symptom timing, close-contact intensity, and exposure to body fluids or respiratory secretions, rather than assuming uniform risk across all passengers and crew. The 2018 to 2019 Epuyén outbreak in Chubut Province, Argentina, included 34 confirmed cases and 11 deaths, with transmission driven by symptomatic individuals in social settings (Elias et al., 2021). The transmission was a single zoonotic introduction, followed by spread linked to social gatherings and close-contact networks (Martínez et al., 2020). The cruise event is different from household or community outbreaks because the exposure environment is mobile, confined, and multinational. The ship setting compresses contact networks and then redistributes them through disembarkation, flights, medical evacuation, and repatriation. This creates a surveillance problem rather than a pandemic problem: the virus does not appear readily transmissible at population scale, but missed symptomatic cases can generate difficult contact tracing across jurisdictions. Preliminary genomic analysis adds weight to this interpretation: available sequences from outbreak-associated cases showed

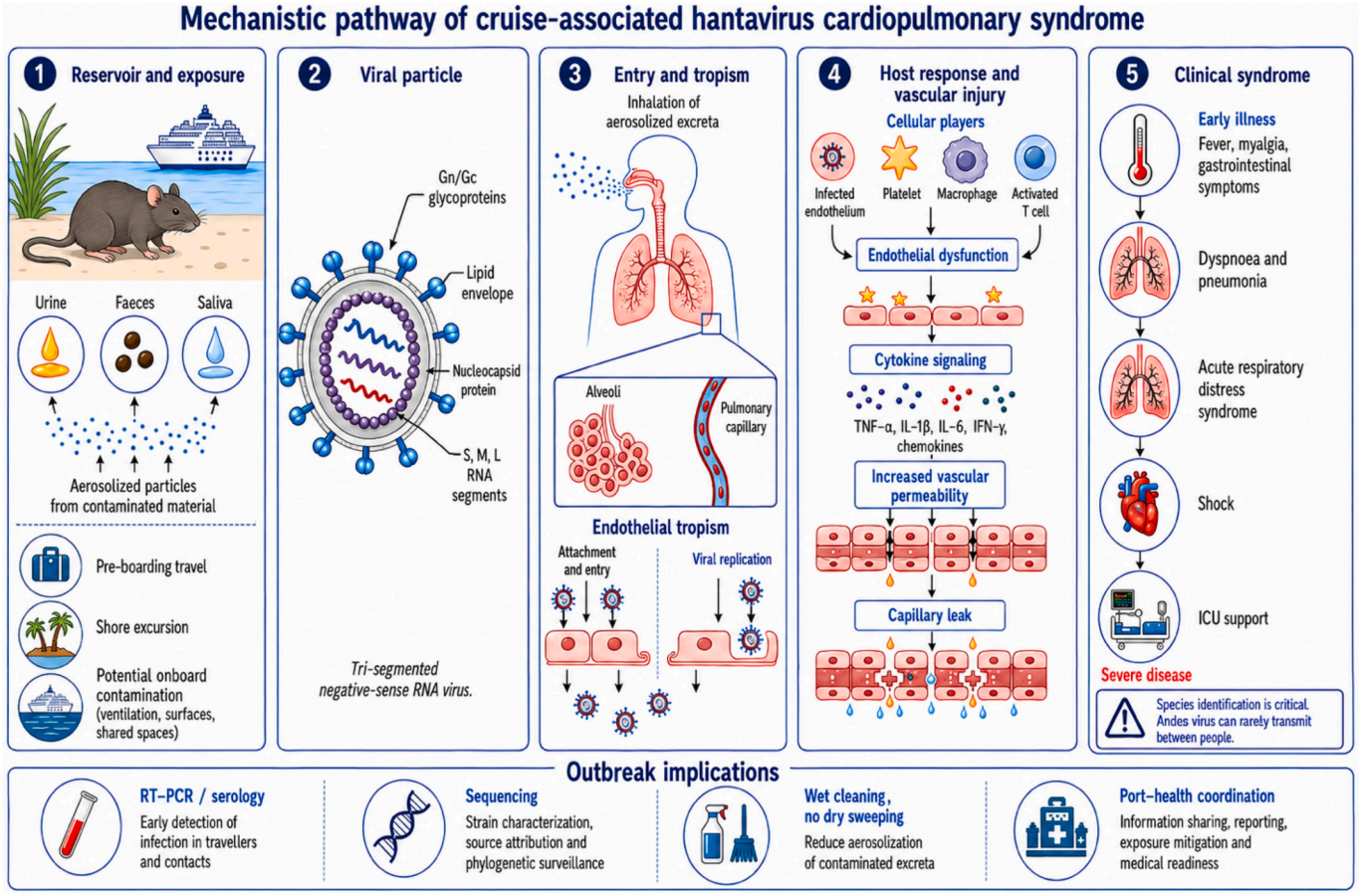

Fig. 2. Mechanistic pathway and outbreak implications of Andes virus-associated hantavirus cardiopulmonary syndrome in a cruise-linked setting. *Illustration was prepared using an author-designed layout and elements adapted from Flaticon, OpenClipart, FreeSVG, Wikimedia Commons, Servier Medical Art vector and author-drawn components according to their respective licensing terms.*

very high similarity, with no more than one single nucleotide polymorphism difference per individual, supporting either a single zoonotic spillover event or a very small number of closely related spillovers followed by limited human-to-human spread (Palacios, 2026).

WHO's final outbreak assessment retained a precautionary transmission framework, recognizing possible spread through contact with infected individuals or contaminated surfaces, direct deposition of infectious respiratory particles onto exposed mucosal surfaces, and/or inhalation of infectious respiratory particles. However, the observed transmission pattern and absence of additional secondary cases were not consistent with the dynamics of a highly transmissible airborne pathogen (World Health Organization, 2026e). This distinction supports layered infection prevention measures without implying sustained airborne or pandemic-level transmission.

Viral pathogenesis and endothelial barrier dysfunction

Unlike many viral pneumonias, severe HCPS is not best understood as direct destructive infection of the alveolar epithelium. ANDV disease is strongly linked to endothelial dysfunction, immune activation, platelet involvement, and increased vascular permeability (Gorbunova et al., 2011). Hantaviruses infect endothelial cells without producing widespread endothelial necrosis, which helps explain the abrupt transition from a nonspecific febrile illness to capillary leak, pulmonary oedema, hypotension, and shock (Gavrilovskaya et al., 2012; Koster and Mackow, 2012). Studies suggest that altered endothelial barrier integrity, including changes in vascular endothelial growth factor signaling and adherens junction regulation, contributes to the cardiopulmonary phenotype (Hepojoki et al., 2014; Mackow et al., 2013; Mackow and Gavrilovskaya, 2009). This pathobiology is clinically relevant because aggressive fluid administration may worsen pulmonary oedema, whereas early haemodynamic monitoring, cautious volume strategy, and timely escalation to ventilatory or extracorporeal support directly address the dominant physiological failure (López et al., 2021; Arauco Brown et al., 2014).

Clinical course and management priorities

HCPS begins with a nonspecific prodrome that can resemble influenza, coronavirus disease, viral gastroenteritis, dengue, leptospirosis, sepsis, or community-acquired pneumonia (Ramos et al., 2000). Several early clinical and laboratory features can help distinguish HCPS from routine travel-associated respiratory or gastrointestinal illness. A compatible exposure history followed by fever, prominent gastrointestinal symptoms, thrombocytopenia, haemoconcentration, leukocytosis, pulmonary infiltrates, hypotension, or rapidly increasing oxygen requirement should prompt early consideration of hantavirus infection (Van Hook, 2018). This is particularly important because the cardiopulmonary phase may evolve quickly, and waiting for advanced respiratory failure can delay transfer to an intensive care-capable facility (Ulloa-Morrison et al., 2024; Dobrica et al., 2023). In returned travelers from endemic regions, HCPS should therefore remain in the differential diagnosis alongside dengue, leptospirosis, rickettsial infection, severe bacterial sepsis, influenza, coronavirus disease, and atypical pneumonia. The early symptom profile in the 2026 cluster, including fever, malaise, gastrointestinal symptoms, pneumonia, acute respiratory distress, and shock, is consistent with severe ANDV disease. Symptom onset after hantavirus exposure typically occurs within one to six weeks, and WHO's

updated outbreak assessment supports 42 days of monitoring or quarantine for high-risk contacts after last exposure. Clinical deterioration can be sudden (Dobrica et al., 2023; de Lemos et al., 2022). The age profile of the affected travel cohort also matters. WHO reported a median passenger age of 65 years among cases (World Health Organization, 2026c), making rapid recognition and early escalation especially important because severe HCPS can be more consequential in older individuals and those with comorbidities (Dobrica et al., 2023; Chang et al., 2007). Careful fluid administration, oxygen support, intubation and ventilation when needed, and cardiac monitoring are essential for disease monitoring and management (Ulloa-Morrison et al., 2024; Essex et al., 2023). Most fatal HCPS cases die within 24 to 48 h after onset of the cardiopulmonary phase, which makes early recognition more consequential than later diagnostic certainty (Campos et al., 2009; Chertcoff and Quadrelli, 2002). No licensed antiviral treatment or vaccine is available for ANDV or HCPS. Ribavirin has been evaluated for hantavirus pulmonary syndrome but has not shown effectiveness in that syndrome, while supportive intensive care remains the core intervention (Mertz et al., 2004). Early extracorporeal membrane oxygenation (ECMO) at signs of decompensation has been associated with high survival despite cardiopulmonary collapse, although this requires highly specialized centres and rapid transfer pathways (Arauco Brown et al., 2014; Wernly et al., 2011). The maritime context sharpens the clinical challenge. A cruise ship may have medical personnel and stabilizing capacity, but it cannot substitute for an intensive care unit (ICU), advanced ventilatory support, invasive haemodynamic monitoring, blood gas and lactate surveillance, or ECMO readiness. Rapid transfer to mainland healthcare facilities may be difficult in remote maritime settings, making early evacuation planning essential.

Diagnostics and genomic epidemiology

Laboratory confirmation relies on reverse transcription polymerase chain reaction (RT-PCR), serology for hantavirus-specific immunoglobulin M (IgM), rising immunoglobulin G (IgG) titres, and sequencing when available (Lundkvist et al., 2013; Iheukwumere et al., 2023). For clinicians and microbiologists, the timing of testing is central to interpretation. RT-PCR is most useful during acute symptomatic disease, particularly before or during early cardiopulmonary involvement, whereas serology supports diagnosis through hantavirus-specific IgM or a rising IgG titer (Nunes et al., 2019). Anti-hantavirus antibodies may be negative early in the febrile prodrome, so a negative early serological result should not override a compatible exposure history and evolving clinical syndrome (Ksiazek et al., 1995; Vial et al., 2023). Conversely, routine testing of asymptomatic contacts has limited value because a negative result does not exclude later disease within the incubation period (Schöffel et al., 2018). In the cruise-linked setting, this distinction supports monitoring-led, risk-stratified testing rather than indiscriminate screening of low-risk contacts; testing may be symptom-triggered or applied serially to high-risk contacts according to public health policy. Testing strategy should remain linked to symptoms, exposure intensity, and timing. ECDC's rapid advice specifically addresses laboratory testing for asymptomatic high-risk contacts, while WHO notes that routine testing of contacts is not supported for outbreak control and that low-risk contacts should undertake passive self-monitoring. WHO also described coordinated testing across South Africa, Switzerland, the Netherlands, Senegal, the United Kingdom, and Argentina. Genomic analysis is especially important in this outbreak because it can help distinguish a single introduction followed by secondary transmission from multiple independent exposures. Ongoing sequencing analyses of surveillance samples from Chile and Argentina may help compare the outbreak-associated strain with regional ANDV diversity and further clarify the circumstances of the initial introduction (World Health Organization, 2026e; Medina et al., 2009). For outbreak interpretation, genomic data should not be treated as an accessory. In this setting, sequencing informs attribution of source geography, reconstruction of transmission chains, and assessment of whether cases represent linked human-to-human spread. It also protects against premature ecological blame by differentiating likely pre-boarding acquisition from port-associated or ship-associated exposure.

Why shipboard settings alter risk without creating pandemic potential

The significance of the shipboard setting lies in contact structure rather than in evidence of efficient population-level transmissibility. A vessel creates a relatively stable network in which repeated close interactions may occur before an unusual infection is recognized; subsequent disembarkation and repatriation can then disperse that network rapidly across multiple jurisdictions (Huang and Bashford, 2025; Chew Ng et al., 2025). In the motor vessel (M/V) Hondius outbreak, this combination complicated case finding, exposure reconstruction, contact tracing, and continuity of follow-up without producing sustained transmission beyond the outbreak-associated network. The completed investigation now strengthens this distinction. Human-to-human transmission occurred aboard the vessel, but no additional secondary cases were detected after all identified contacts completed the 42-day follow-up period (World Health Organization, 2026e). The confined maritime environment therefore appears to have facilitated limited transmission without creating the transmission dynamics of a highly transmissible airborne pathogen. The operational problem was not uncontrolled community spread, but delayed recognition of a severe infection within a mobile population whose members subsequently entered multiple healthcare and public health systems.

Public health response and international coordination

The 2026 response illustrates the function of the International Health Regulations (2005) in managing a mobile outbreak (Pan American Health Organization, 2026). International coordination encompassed case isolation and clinical management, laboratory testing, medical evacuation, passenger and crew repatriation, cross-border information exchange, and contact follow-up across 33 countries and overseas territories (World Health Organization, 2026e). By 2 July, 317 high-risk contacts had completed quarantine and active monitoring, and 336 low-risk contacts had completed self-monitoring, with no additional secondary cases detected during the full 42-day follow-up period (World Health Organization, 2026e). The successful completion of this process converted a complex multinational outbreak into a demonstrable endpoint of transmission interruption. Contact management requires a precautionary but proportionate approach. WHO recommends active monitoring and home or facility quarantine of high-risk contacts for 42 days after the last exposure, while low-risk contacts should undertake passive self-monitoring and seek medical evaluation if symptoms occur. The updated incubation analysis estimated a mean incubation period of 22 days and reaffirmed 42 days as the appropriate quarantine period for high-risk contacts (World Health Organization, 2026d). This distinction is central to proportional outbreak control because it separates close or prolonged exposure from casual travel association. WHO also stated that routine laboratory testing of contacts is not supported for outbreak control and that low-risk contacts do not require quarantine; however, asymptomatic high-risk contacts should still undergo active monitoring and home or facility quarantine for 42 days after last exposure.

Infection prevention and control should reflect the severity of ANDV disease and uncertainty regarding transmission routes. ECDC recommends standard precautions for all patients and placement of suspected or confirmed cases in negative-pressure isolation rooms where available, or otherwise in well-ventilated single rooms. Healthcare workers should wear a filtering facepiece class 2 or 3 (FFP2/3) respirator, eye protection, a fluid-resistant long-sleeved gown, and gloves when providing care, including during aerosol-generating procedures. When patients must leave the isolation room, they should wear a type IIR medical/surgical mask or a non-valved FFP2/3 respirator if tolerated and

compatible with clinical care (European Centre for Disease Prevention and Control, 2026).

The critical operational lesson is that rare zoonoses need pre-planned conveyance protocols. Expedition cruises often travel through remote ecological zones where rodent-borne, avian, marine, and environmental pathogens intersect with limited evacuation infrastructure (Andersen-Ranberg et al., 2024). Vessel operators, port states, and public health authorities require protocols that begin before the diagnosis is confirmed, because confirmatory testing may lag behind clinical deterioration.

Research priorities raised by the event

The outbreak creates an opportunity to modernize how travel-associated zoonoses are studied. Traditional outbreak reports often reconstruct who became ill, when symptoms began, and where patients traveled. For ANDV on a ship, that is necessary but insufficient. Transmission assessment requires integration of cabin networks, dining exposure, medical contacts, shore activity logs, pre-boarding itineraries, flight manifests, clinical viral kinetics, serology timing, and viral genomic relatedness. The response has already generated a coordinated prospective natural-history study across 21 participating countries, designed to examine transmission dynamics, incubation periods, immune responses, viral kinetics, and determinants of severe disease through harmonized longitudinal follow-up (World Health Organization, 2026e). Such a platform could provide the person-level temporal data needed to resolve several of the uncertainties outlined in Tables 1 and Table 2.

Although the operational framework and clinical investigation dataset are structured around ANDV, we propose that their underlying operational architecture can be adapted to other high-consequence infections encountered in maritime or expedition settings. Early syndromic triage, exposure mapping, risk-stratified contact management, advance evacuation planning, cross-border notification, and integration of clinical, microbiological, and movement data are broadly transferable; pathogen-specific incubation periods, diagnostic assays, isolation precautions, and post-exposure monitoring windows should be modified accordingly.

Implications for ecotourism and maritime medicine

Expedition tourism is expanding into remote ecologies where travelers may encounter pathogens outside routine pre-travel counseling frameworks. Most routine tourism does not carry meaningful hantavirus

Table 1
Operational framework for outbreak response to cruise-linked Andes virus infection.

Decision node	Minimum operational trigger	Action threshold	Failure mode prevented	Output for authorities
Pre-disembarkation triage	Any compatible febrile, gastrointestinal, or respiratory illness in a person linked to a known or probable ANDV case or in a recently repatriated passenger within the incubation window	Separate clinical assessment pathway before general passenger processing, with immediate isolation of suspected cases	Mixing symptomatic and asymptomatic travelers during port arrival	Cleared, suspect, probable, confirmed, or non-case categorization
Cabin-level risk mapping	Shared cabin or repeated enclosed-space exposure to a symptomatic case	Active monitoring for the full maximum incubation window and home or facility quarantine for high-risk contacts for 42 days after last exposure	Under-identification of high-intensity exposure pairs and delayed recognition of secondary cases	High-risk contact registry with exposure category, last exposure date, and quarantine end date
Medical-room exposure audit	Unprotected examination, aerosol-generating procedure, specimen handling, body-fluid exposure, or close care of a symptomatic case without appropriate personal protective equipment	Occupational health follow-up and symptom-triggered testing, with risk-stratified quarantine when exposure is high risk	Missed healthcare-associated transmission	Healthcare worker exposure log with personal protective equipment breach status
Flight and transfer reconstruction	Passenger seated near or traveling with a symptomatic case during deterioration or during repatriation after onboard exposure	Manifest-based notification and receiving-country alert, including seating proximity, transfer route, and receiving public health authority	Loss of contacts after international travel	Cross-border contact tracing file linked to repatriation pathway
Early evacuation planning	Compatible febrile, gastrointestinal, or respiratory illness in a high-risk contact, particularly with thrombocytopenia, haemoconcentration, persistent tachycardia, increasing respiratory rate, new oxygen requirement, or evolving chest imaging abnormalities	Notify the receiving centre and transport team, assess transfer route and weather constraints, and prepare evacuation before haemodynamic or respiratory instability develops	Loss of the safe evacuation window during rapid cardiopulmonary deterioration	Provisional evacuation status and receiving-centre plan
Urgent critical-care transfer	Worsening hypoxaemia, escalating oxygen requirement, hypotension, rising lactate, pulmonary oedema, or rapid clinical progression	Immediate transfer to an ICU-capable facility; early discussion with an ECMO-capable centre when cardiopulmonary deterioration is evolving	Transfer only after established shock or refractory respiratory failure	Highest-priority evacuation tier
Environmental source inquiry	Pre-boarding rural travel, rodent-contaminated accommodation, birdwatching, camping, fieldwork, or poorly ventilated cleaning exposure	Backward exposure investigation with local public health teams	Misattribution of source to shipboard contamination alone	Exposure reconstruction dossier
Genomic linkage assessment	Two or more confirmed cases with overlapping exposure windows	Whole-genome or near-complete sequencing where feasible, including comparison of single nucleotide polymorphism differences across cases	False assumption of single-chain transmission or missed recognition of a single zoonotic introduction followed by limited secondary spread	Phylogenetic linkage report
Asymptomatic high-risk contact testing decision	High-risk exposure to a confirmed or probable ANDV case, especially cabin, intimate, healthcare, or prolonged indoor exposure	Testing strategy guided by symptom status, timing from exposure, national policy, and repeat testing if early or inconclusive results occur	False reassurance from early negative testing or unnecessary testing of low-risk contacts	Testing decision record with exposure category, specimen date, result status, and retesting plan
Public communication release	Confirmed ANDV diagnosis or credible suspected transmission cluster	Risk communication that separates severity from transmissibility, clarifies quarantine only for high-risk contacts, and avoids implying routine tourism risk	Panic, stigma, false reassurance, or inappropriate travel and trade concerns	Public-facing risk statement

Table 2
Integrated clinical, microbiological, epidemiological, and operational dataset for investigation of cruise-linked Andes virus transmission.

Domain	Variable to collect	Preferred resolution	Analytical purpose	Endpoint
Specimen strategy	Whole blood, serum, plasma, respiratory sample, saliva, urine, and post-mortem tissue where applicable	Specimen type linked to date of collection and symptom day	Define which specimen types are most informative across disease stages	Stage-specific diagnostic yield
Molecular detection	Reverse transcription polymerase chain reaction result, assay target, cycle threshold value, and repeat testing status	Days from symptom onset and days from last exposure	Assess viraemia kinetics and reduce misclassification from early or late testing	Viral load proxy curve
Serological profile	Hantavirus-specific immunoglobulin M, immunoglobulin G, paired serology, and neutralization where available	Acute and convalescent samples	Distinguish acute infection, delayed seroconversion, and past exposure	Seroconversion pattern
Genomic characterization	Consensus sequence, genome segment coverage, intrahost variants, lineage assignment, and single nucleotide polymorphism distance between cases	Near-complete genome where feasible	Differentiate single introduction with onward spread from multiple environmental exposures	Phylogenetic linkage inference
Clinical-laboratory phenotype	Platelet count, hematocrit, leukocyte count, creatinine, lactate, liver enzymes, inflammatory markers, and arterial blood gas parameters	Serial measurements from prodrome to cardiopulmonary phase	Identify early biological markers of progression to severe HCPS	Severity prediction profile
Endothelial and vascular dysfunction	Pulmonary oedema, capillary leak indicators, hypotension, vasopressor need, fluid balance, and echocardiographic findings	Time-stamped clinical and imaging data	Link viral infection to the dominant pathophysiological mechanism of HCPS	Cardiopulmonary deterioration model
Exposure-linked diagnostic timing	Date of suspected rodent exposure, date of first contact with symptomatic case, symptom onset, first test, repeat test, and date of last high-risk exposure	Person-level exposure and testing timeline	Interpret negative results within the incubation window and define optimal retesting points	Exposure-to-diagnosis interval
Transmission-pair assessment	Symptom overlap, contact intensity, shared cabin or enclosed-space exposure, body-fluid exposure, genomic similarity, and timing of infectious-phase contact	Dyad-level comparison	Estimate biological plausibility of person-to-person transmission	Probable transmission-pair classification
Differential diagnosis panel	Dengue, leptospirosis, rickettsial infection, influenza, coronavirus disease, bacterial sepsis, atypical pneumonia, and other regional pathogens	Initial and repeat testing where clinically indicated	Prevent diagnostic anchoring on hantavirus alone during early illness	Exclusion-supported case classification
Treatment-response markers	Oxygen requirement, ventilatory support, vasopressor dose, fluid balance, extracorporeal membrane oxygenation referral, renal replacement therapy, and survival status	Serial clinical trajectory	Correlate early laboratory and physiological markers with escalation needs	Management-response trajectory
Quarantine and monitoring dataset	Exposure category, last exposure date, quarantine start and end date, daily symptom diary, daily temperature, respiratory symptoms, gastrointestinal symptoms, and breach or non-adherence events	Daily person-level monitoring for 42 days after last high-risk exposure	Detect secondary cases early and evaluate whether monitoring intensity matched exposure risk	Contact monitoring completion profile
Repatriation pathway	Disembarkation port, transfer date, flight or transport route, seating proximity to cases, medical escort status, transit country, and receiving public health authority	Individual travel timeline linked to case or contact status	Prevent loss of exposed passengers after international movement and support cross-border contact tracing	Repatriation-linked exposure map
Risk communication and adherence	Advice received, quarantine instructions, public health contact date, misinformation exposure, adherence barriers, and healthcare-seeking behavior after symptoms	Contact-level and country-level documentation	Assess whether guidance was understood and whether public communication reduced panic without minimizing risk	Risk communication effectiveness profile

risk, but rural lodging, field activities, poorly ventilated cabins, rodent-contaminated spaces, and cleaning of contaminated areas remain relevant exposure contexts. WHO and CDC prevention guidance emphasize rodent avoidance, safe cleaning, ventilation, wet-cleaning methods, secure food storage, and avoidance of dry sweeping or vacuuming contaminated material. Cruise medicine must therefore move beyond syndromic management of common gastrointestinal and respiratory outbreaks. Rare high-fatality zoonoses require rapid escalation triggers, off-ship laboratory pathways, safe specimen transport, and pre-identified receiving centres. In ANDV-compatible illness, the most dangerous interval is not after confirmatory testing; it is the period when patients have nonspecific symptoms and remain socially active. The event also argues for better integration between pre-travel counseling and post-travel surveillance. Passengers returning from expedition itineraries should be given symptom windows, exposure prompts, and clear instructions for informing clinicians about travel and contact history. Without that linkage, ANDV can enter a diagnostic blind spot where early fever and diarrhea are treated as routine travel illness until cardiopulmonary deterioration occurs. Public communication should distinguish expedition-linked, close-contact risk from routine tourism.

Conclusion

The 2026 M/V Hondius-associated ANDV outbreak should be understood as a contained maritime amplification event rather than a signal of pandemic emergence. It demonstrates how likely land-based acquisition, limited onboard human-to-human transmission, delayed recognition, remote evacuation constraints, and multinational repatriation can transform a rare zoonotic event into a complex international response. The principal lessons are the need for early clinical suspicion, risk-stratified contact management, clear infection prevention measures, and pre-planned evacuation pathways for expedition and maritime settings.

Declaration of Financial Interests

The authors declare no financial interests relevant to this study.

Declaration of Non-Financial Interests

Except for the editorial role of Dr. Amogh Verma, who is currently an Associate Editor/Editorial Board Member, the authors declare no non-financial interests relevant to this study.

Ethical Approval

Not required.

Ethical approval statement

Ethical approval was not required for this study, as it is a narrative review based exclusively on previously published liter ature and publicly available data. No human participants were recruited, no patient-identifiable information was used, and no primary clinical or experimental data were collected. The work was conducted in good faith and in accordance with standard principles of academic integrity and responsible scholarly reporting.

Human Ethics and Consent to Participate

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Clinical Trial Registration Details/Number

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Research Registry Number

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Generative AI Use Statement

Generative AI tools, including Paperpal and ChatGPT, were utilized solely for language refinement, grammar enhancement, and stylistic refinement. These tools had no role in the conceptualization, data analysis, interpretation of results, or substantive content development of this manuscript. All intellectual contributions, data analysis, and scientific interpretations remain the sole work of the authors. The final content was critically reviewed and edited to ensure accuracy and originality. The authors take full responsibility for the accuracy, originality, and integrity of the work presented.

Declaration of competing interest

Dr. Amogh Verma serves as an Associate Editor/Editorial Board Member for Clinical Infection in Practice. He was not involved in the editorial handling, peer review, or decision-making process of this study. The remaining authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this study.

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