

Andes Virus on a Cruise Ship, what it Tells us About the Global Pandemic Preparedness Agenda



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Summary

The outbreak of hantavirus disease caused by Andes virus aboard a cruise ship is a reminder of the challenges posed by emerging diseases in the modern era. While Andes virus-associated disease can be particularly severe, it is unlikely to spread extensively beyond the current number of cases or emerge as a large epidemic, especially if public health measures are followed. Nonetheless, the outbreak exemplifies the complexity of international outbreak response with differences in national preparedness frameworks and the rapid spread of mis-/disinformation. We discuss this outbreak in the context of global epidemic and pandemic preparedness and emphasize the importance of sustained, inclusive global collaborative One Health approaches to preparedness and response. We stress the urgent need for global coordination, discuss specific challenges, and provide recommendations for further strengthening of global preparedness.

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We are currently (May 2026) witnessing an outbreak of a rare but severe disease caused by Andes virus (*Orthohantavirus andesense*). Andes virus is a New World hantavirus that occasionally spills over from its rodent reservoir host to humans, with short human-to-human transmission chains—not reported for other hantaviruses. Hantaviruses are not new, but relatively unknown to the broader public as they typically cause zoonotic spillover in restricted areas, but not larger epidemics or pandemics. The *Hantaviridae* family is diverse, comprising 8 genera capable of infecting fish, reptiles and mammals. Zoonotic infections in humans have only been described for one of these, the genus *Orthohantavirus* with at least 38 recognized species.¹ Pathogenic orthohantaviruses, carried by different rodents, cause hundreds of cases of hantavirus cardiopulmonary syndrome (HCPS) annually in the Americas with case fatality rates for reported clusters ranging from 25 to 40%, and thousands of cases of hemorrhagic fever with renal syndrome (HFRS) with <0.1–15% fatality rate in Europe and Asia.² The hantavirus taxonomy reflects their ecological relationships, as each species of hantavirus primarily has its own reservoir host, reflecting long-term co-evolution of hantaviruses and their reservoir hosts across different geographic regions.³ The specific virus causing the current outbreak, Andes virus, has been identified predominantly in the long-tailed rat (*Oligoryzomys longicaudatus*) endemic in Argentina and Chile.⁴

Most human emerging viruses derive from an animal reservoir. Indeed, many human endemic viruses are believed to derive from past zoonotic spillover events. The emergence and spread of SARS coronaviruses 1 and 2, or mpox virus clades Ib and IIb, are examples of the consequence of the introduction of animal viruses into a relatively naive human population. In parallel, recurrent outbreaks of other spillovers such as MERS coronavirus, Ebola virus and Lassa fever virus remind us of the importance of sustained preparedness, surveillance, and rapid response capacity. There is consensus in the emerging infectious diseases

community that the frequency and geographic impact of such events are increasing, driven by a combination of ecological, environmental, and societal factors.⁵ Climate change, altered temperature and rainfall patterns, land-use change, deforestation, urbanisation, agricultural expansion, and extractive industries open ecosystems to human incursion. This results in new and longer human–animal interfaces, providing increased opportunities for pathogen spillover events.^{6,7} Once spillovers occur, increasing population density and global connectivity facilitate more rapid dissemination across regions and continents, accelerating outbreaks depending on where the spillovers occur. Importantly, epidemics amplify pre-existing weaknesses in society, and disproportionately impact vulnerable groups. In the current digital era, that vulnerability increasingly includes susceptibility for misinformation.⁵

The current Andes virus outbreak is another reminder of the challenges posed by zoonotic pathogens in an interconnected world. Andes virus is a rare cause of human disease, with a little over 100 cases in 2025 in Argentina and Chile.⁸ Andes virus is of immediate concern for those directly exposed and their close contacts, because it can cause severe disease with a high lethality rate, and unlike other hantaviruses can be transmitted to close contacts of infected individuals. Fortunately, this virus does not transmit efficiently in humans and it has mostly been limited to small household clusters that have been contained by public health measures. A larger cluster in 2018 in Argentina, involving 34 persons with different transmission cascades and an initial R_0 of 2.12, emphasizes the need for continued awareness.⁹ A major challenge for containment is the prolonged incubation period of hantavirus infection, ranging from approximately 7 days to 6–7 weeks.¹⁰ These estimates were derived largely from nosocomial and intrahousehold person-to-person transmission events, where the timing and nature of exposure could be readily defined. Hence, they may not fully capture the epidemiology of broader community

clusters,^{10,11} where exposure patterns, intensity of contact, and transmission chains may differ. This relatively long incubation period creates substantial operational challenges for contact tracing, clinical monitoring, and quarantine, often with significant impacts on the lives of those affected. As mentioned above Andes virus is unlikely to pose a major epidemic threat, however it highlights another reality of modern outbreak response: even relatively small outbreaks can rapidly become operationally complex in a highly connected world.

What makes this outbreak particularly notable is its setting: the introduction by one infected passenger, who travelled through South America, onto a long-distance transatlantic cruise. Cruise ships are known as places where virus transmission is facilitated due to a convergence of factors: boarding of passengers and staff from different places in the world into common spaces where groups of people converge for relatively long periods of time. These circumstances facilitate the spread of respiratory or gastrointestinal viruses. For example, during the COVID-19 outbreak aboard the Diamond Princess cruise ship, the reproductive number of SARS-CoV-2 was considerably higher than in the community.¹² Despite protocols in place for this specific travel sector, outbreaks are a relatively regular occurrence, often experienced as an inconvenience, although they pose complex dilemmas between public health and the tourism sector's interests for local authorities.¹³

This specific cruise ship hantavirus outbreak is a very low probability but complex event. First, the disease is very rare and not well known outside endemic countries, so it is not the first diagnosis being considered when investigating a patient with severe respiratory disease; secondly the incubation period is long, therefore having a second person with fever 2–3 weeks later may not raise a flag immediately. Finally, the involvement of passengers from 23 countries, and the respective health- and port authorities, elevated outbreak response into a daunting logistical challenge.

Outbreak response

How does outbreak response work? At its core, preparedness and response to emerging diseases relies on answering a series of critical questions in order to develop and enact disease control measures as rapidly and accurately as possible: what pathogen causes this disease; how can we diagnose and track it; what is the spectrum of disease symptoms and how can they be treated; what are the kinetics of shedding from infected individuals and how does it translate to risk of spreading and containment measures; what are the sources, modes of transmission, how is it best prevented or contained; what is the impact of those interventions on society as a whole and on specific communities who are most vulnerable? How can these communities best be reached and supported, and can those impacts be

mitigated? Answering these questions requires a combination of existing scientific knowledge from multiple disciplines beyond field epidemiology, laboratory investigation, and real-time outbreak research, which needs to be done in close collaboration between public health, academic, and societal partners, and leveraging the often valuable knowledge and experience gained in endemic countries. However, outbreaks do not wait for study results, and they often evolve more quickly than evidence can be generated, necessitating action on incomplete information, likely to be adapted with new insights. In addition, response to emerging diseases is highly contextual and cultural. What is regarded as a reason for full blown action in one part of the world may be met with a more hands-off approach in others. Providing an effective evidence-based emerging disease response that is actionable in the given context requires a well-prepared collaborative ecosystem in which answers to these questions can be generated fast and reliably. That is by no means an easy task to perform. Indeed, emerging disease outbreak response can rightfully be described as “building the ship while sailing.”

When looking at the current hantavirus outbreak, several important observations emerge. First, it took approximately a month between the initial cases of respiratory disease in the MV *Hondius* and their correct diagnosis. This delay was influenced, in part, by the complexity of the situation: one passenger died, a partner became ill after disembarking and was hospitalised in South Africa, another passenger disembarked for medical evaluation, and additional patients started to develop illness while the vessel was still at sea after the prolonged incubation period. The first indication of hantavirus as a possible cause came from diagnostic testing performed in South Africa. While the exact details of the outbreak are still being clarified, the broader lesson is that similar scenarios could happen in many parts of the world. Most hospitals do not routinely investigate causes of severe respiratory disease beyond routine diagnostics at their location, unless someone raises a specific epidemiological suspicion. As a result, cases caused by rare pathogens, which are not well known outside their endemic region, will inevitably be missed. Second, even for known pathogens like hantaviruses, for which there is an established diagnostic toolkit, outbreak management hinges on initial pathogen identification. Once hantavirus infection was detected, thanks to the work of the National Institute of Communicable Diseases in South Africa, essential molecular and serological assays were available for patient management and contact follow-up. For unknown pathogens, the delay in detecting the causative agent and the subsequent roll-out of diagnostic assays can be much longer.

When looking at other potential medical counter measures, despite longstanding recognition of hantaviruses as pathogens with severe clinical outcomes, and

evidence for human-to-human transmission for some lineages, therapeutic and vaccine development remains limited, and clinical evidence supporting available interventions is sparse. Human monoclonal antibody therapeutics and vaccines have been developed, but they have so far not reached wider clinical use.^{14,15}

Other important knowledge gaps also remain around hantavirus ecology, drivers of spillovers, the development of key model systems for rapid assessment of potential changes in virus traits, and pre-clinical studies on potential medical and non-medical interventions due to patchy sources of funding and the lack of a private sector incentive. These gaps reflect the broader challenges associated with sustaining fundamental research on relatively rare viruses. Yet, these investments could provide the foundation for preparedness and response efforts for relatively rare but high-consequence pathogens.

International coordination

This collaborative response is further hampered by the fact that international guidance may be implemented differently in different countries. On top of that, excessive media coverage, partly driven by the post-COVID-19 trauma but also by changing media dynamics with the algorithm-driven attention industry complicates communication about a severe but epidemiologically containable disease. The outbreak was relatively small in terms of number of cases, but quite challenging from a public health and logistical perspective. Because multiple WHO member states and regions were involved, information sharing and response activities must be coordinated through mechanisms established under the International Health Regulations (IHR), including communication between National IHR Focal Points. Protocols for case definitions, case ascertainment, testing, contact tracing, isolation, and quarantine require substantial coordination and, where possible, harmonization. The intersection of public health response, international travel, and maritime operations also requires engagement from multiple national authorities and ministries in each country. Coordination therefore extended across WHO headquarters, regional WHO offices, the European Centre for Disease Prevention and Control (ECDC), member states, and national public health agencies. As in other epidemics, it also included reference- and research laboratories, and international expert networks, including those in Andes virus-endemic countries. WHO works with a global network of collaborating centres and advisory groups to exchange information and technical support. The implementation of protocols and recommendations can vary substantially between countries, even when guided by broadly similar evidence as was also seen during the COVID-19 pandemic. Across the expanding landscape of global

preparedness initiatives, there is also increasing demand for rapid information sharing, technical consultation, assessment of research priorities, and evaluation of the availability of medical and non-medical countermeasures, diagnostics, and response capacities. While these efforts reflect growing engagement in preparedness activities, they also highlight the need for more sustainable, and interoperable global preparedness frameworks. While already extremely challenging, these efforts are further complicated by the current geopolitical climate, evolving national priorities, and pressures on multilateral systems supporting global preparedness and response.⁵

The infodemic

As concluded since the COVID-19 pandemic, modern-day epidemic response needs to manage information in an extremely pluralistic media landscape with online amplification of messages that increasingly start to spread offline in a race for the attention of readers or viewers. Inflamed by the COVID-19 pandemic, outbreak response no longer involves only viruses, hospitals, public health and research systems. It also involves navigating an information ecosystem that moves faster than most pathogens ever could. Public demand for information during outbreaks is understandable and important, particularly after the global trauma and disruption caused by COVID-19. But alongside legitimate questions and concerns, misinformation (false information, unintended), disinformation (fabricated messages), and malinformation (misused information with intent to damage) now spread rapidly across social and traditional media, often outpacing the ability of public health agencies and scientists to respond clearly and consistently.

The cruise ship Andes virus outbreak demonstrates this again. Almost immediately, online discussions began with inaccurate claims about the virus's origins, the modes of transmission, the intentions of scientists and public health officials, and the motivations behind response measures. Similar patterns emerged during COVID-19 and continue to shape public trust in vaccines, biomedical research, scientific institutions, and international health organisations. One of the uncomfortable realities of outbreak response is that scientific understanding evolves in real time and the need to keep an open mind towards incoming data and hypotheses may be at odds with the request for clarity from policy makers and society. Public health recommendations may change as more information becomes available, and different countries may implement different approaches depending on healthcare infrastructure, legal frameworks, operational capacity, and risk tolerance. From a public health perspective, that is often expected and rational. In the current media environment, however, these differences can easily be interpreted as confusion, disagreement, or incompetence, particularly

when simplified or emotionally charged narratives spread more quickly than nuanced scientific explanations. Preparedness and prevention, therefore, cannot focus only on diagnostics, surveillance systems, vaccines, or hospital capacity. It must also include sustained investment in public trust, scientific communication, and the ability to communicate uncertainty clearly during rapidly evolving outbreak situations.

Recommendations

The Andes virus outbreak on board of a cruise ship serves as another reminder that preparedness cannot remain a reactive exercise initiated only during crises. At a time when many research and public health institutes are facing significant financial constraints and infrastructure reductions, there is a risk that critical preparedness capacity may be lost. The current outbreak highlights the continued gap between pathogen risk recognition and the availability of deployable medical countermeasures. Preparing for them should take an “all of society” approach, involving stakeholders and societal groups beyond the public health field and at all steps of the preparedness and response cycle. We recommend the following steps.

Improvements in outbreak response:

1. **Invest in One Health early warning surveillance**, to provide essential information on potential epidemic threats before they evolve into outbreaks. Such surveillance can be targeted to areas with increased or increasing risk, and should increase understanding of pathogen diversity, reservoir hosts, their geographic range, and the infection dynamics in these hosts.
2. **Strengthen sustained investment in epidemic preparedness and response infrastructure**, with core capacity for case finding, contact tracing, testing, and the swift deployment of standard public health interventions.
3. **Expand integrated environmental surveillance approaches**, including wastewater, air, and surface sampling, in high-risk international travel and transport settings such as cruise ships, airports, ports, and other major transportation hubs. These approaches may provide earlier situational awareness and complement traditional clinical surveillance during emerging outbreak events.
4. **Strengthen development and access to field-deployable diagnostics, portable sequencing, real-time genomic analysis, and serology** capable of supporting outbreak detection and characterization outside centralized laboratory systems. Delays in identification remain one of the greatest operational vulnerabilities.
5. **Invest in building and sustain the specialist research infrastructure, high-containment laboratory capacity, and multidisciplinary scientific expertise** necessary

to investigate, characterise, and respond rapidly to emerging pathogens.

6. **Support and strengthen the research base** for development of scalable diagnostics, antivirals, vaccines, monoclonal antibodies, and adaptable platform technologies targeting pathogens with known epidemic potential.

Regarding international coordination:

7. **Develop and routinely implement multinational outbreak simulation exercises** focused on rare but high-consequence pathogens, including diseases with prolonged incubation periods and complex international contact tracing requirements.
8. **Continue strengthening of international preparedness frameworks**, including broad participation in WHO-led coordination mechanisms and implementation and ratification of pandemic agreement frameworks. This will continue to be essential for improving information sharing, outbreak coordination, equitable access to countermeasures, and international response capacity during future cross-border health emergencies.

Regarding the infodemic:

9. **Prepare for the growing challenge of misinformation and disinformation during outbreak response.** Rapidly evolving information environments can undermine public trust, complicate risk communication, and reduce confidence in evidence-based public health measures. Strengthening scientific communication capacity, trusted public engagement, and coordinated approaches to outbreak information management should therefore be considered integral components of epidemic and pandemic preparedness.

Final reflections

The ongoing Andes virus outbreak will not become the next pandemic. But this is also exactly why this outbreak matters. Smaller outbreaks are where preparedness gets tested. Real situations where multiple countries, laboratories, ministries, clinicians, and public health teams are all trying to make decisions quickly under time pressure with incomplete information. This event illustrates how even relatively small outbreaks can rapidly become operationally complex in a highly interconnected world, and the importance of WHO and the IHR.

The world has become incredibly efficient at moving people, animals, products, and information across continents at extraordinary speed. Public health systems, however, still struggle to move diagnostics, coordinate communication, enable countermeasures at

the same pace. A person can travel across half the planet faster than some laboratory systems can approve testing for a rare pathogen. This is not really a criticism of the people involved. It is simply the reality of how globalized modern life has become compared to how fragmented preparedness systems still are.

Importantly, this outbreak is still ongoing. Additional cases among contacts have emerged during the revision of this manuscript and more may yet emerge. Outbreaks rarely have a clear beginning and end. They unfold in waves of uncertainty, partial information, reassessment, and adaptation, usually while the public, media, and governments all expect immediate answers that science is not always capable of providing in real time. The MV *Hondius* outbreak should therefore not simply be a rare hantavirus event aboard a cruise ship. It should be viewed as a warning delivered at a manageable scale. Future spillover events are inevitable. Indeed, shortly after the original submission of this article, a major Ebola disease outbreak caused by Bundibugyo virus started in the Democratic Republic of Congo (DRC) and Uganda. On May 28, The Ministry of Health in DRC published updated figures reporting 125 confirmed cases, which included 17 deaths, and 906 suspected cases, which included 223 deaths. These were reported across Ituri, North Kivu, and South Kivu provinces. In Uganda 7 confirmed cases have been reported. This is of course a very concerning outbreak. All the reflections and suggestions made on the Andes virus outbreak apply also to this latest Ebola outbreak, which is even more complex to manage given the existing conflict in DRC.

Overall whether future outbreaks remain manageable or become much larger crises will depend largely on what happens in-between outbreaks. Strengthening rather than weakening international coordination mechanisms before crises occur will help reduce fragmentation, avoid inconsistent responses, ensure that public health decisions can be made rapidly across countries working under different legal, operational, and health-system contexts, and increase the changes of successful containment of outbreaks.

Contributors

MK drafted the outline, all authors reviewed and edited, MK, MP, and EK reviewed the draft and finalised the text. All authors have read, contributed to and agreed on the content, including the proposed revisions after review. MK is member of the coordination team of DURABLE, and responsible for liaising with expert networks relevant to emerging disease preparedness and response. DURABLE is co-funded by European Union's EU4Health programme (grant number 101102733).

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The authors are involved in all aspects of the preparedness and response cycle for emerging infectious diseases. This includes basic

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Declaration of interests

The authors declare no conflicts of interest.

References

- Bradford SB, Calisher CH, Klempa B, et al. ICTV virus taxonomy profile: hantaviridae 2024. *J Gen Virol*. 2024;105(4):001975. <https://doi.org/10.1099/jgv.0.001975>.
- Taylor SL, Schmaljohn CS, Williams EP, Jonsson CB. Pathogenicity and virulence of rodent-borne Orthohantaviruses. *Virulence*. 2025;16(1):2553784. <https://doi.org/10.1080/21505594.2025.2553784>.
- Bennett SN, Gu SH, Kang HJ, Arai S, Yanagihara R. Reconstructing the evolutionary origins and phylogeography of hantaviruses. *Trends Microbiol*. 2014;22(8):473–482. <https://doi.org/10.1016/j.tim.2014.04.008>.
- Medina RA, Torres-Perez F, Galeno H, et al. Ecology, genetic diversity, and phylogeographic structure of Andes virus in humans and rodents in Chile. *J Virol*. 2009;83(6):2446–2459. <https://doi.org/10.1128/JVI.01057-08>.
- WHO. Drawing light from the pandemic: a new strategy for health and sustainable development. <https://www.who.int/europe/publications/i/item/9789289051798>; 2021.
- Muylaert RL, Bovendorp RS, Sabino-Santos G Jr, et al. Hantavirus host assemblages and human disease in the Atlantic forest. *PLoS Negl Trop Dis*. 2019;13(8):e0007655. <https://doi.org/10.1371/journal.pntd.0007655>.
- Sikkema RS, Koopmans M. Viral emergence and pandemic preparedness in a One Health framework. *Nat Rev Microbiol*. 2026;24(1):29–44. <https://doi.org/10.1038/s41579-025-01243-1>.
- PAHO. Epidemiological alert Hantavirus pulmonary syndrome in Americas Region - 19 December 2025. <https://www.paho.org/en/documents/epidemiological-alert-hantavirus-pulmonary-syndrome-americas-region-19-december-2025>; 2025.
- Martínez VP, Di Paola N, Alonso DO, et al. "Super-spreaders" and person-to-person transmission of Andes virus in Argentina. *N Engl J Med*. 2020;383(23):2230–2241. <https://doi.org/10.1056/NEJMoa2009040>.
- Vial PA, Valdivieso F, Mertz G, et al. Incubation period of hantavirus cardiopulmonary syndrome. *Emerg Infect Dis*. 2006;12(8):1271–1273. <https://doi.org/10.3201/eid1208.051127>.
- Padula PJ, Edelstein A, Miguel SD, López NM, Rossi CM, Rabinovich RD. Hantavirus pulmonary syndrome outbreak in Argentina: molecular evidence for person-to-person transmission of Andes virus. *Virology*. 1998;241(2):323–330. <https://doi.org/10.1006/viro.1997.8976>.
- Lai CC, Hsu CY, Jen HH, Yen AM, Chan CC, Chen HH. The Bayesian susceptible-exposed-infected-recovered model for the outbreak of COVID-19 on the diamond princess cruise ship. *Stoch Environ Res Risk Assess*. 2021;35(7):1319–1333. <https://doi.org/10.1007/s00477-020-01968-w>.
- Neumann JA, Zimmermann J, Frese M, et al. Infectious diseases on passenger ships: port preparedness and response - a narrative systematic review. *Travel Med Infect Dis*. 2025;67:102886. <https://doi.org/10.1016/j.tmaid.2025.102886>.
- Paulsen GC, Frenck R Jr, Tomashek KM, et al. Safety and immunogenicity of an Andes virus DNA vaccine by needle-free injection: a randomized, controlled phase 1 study. *J Infect Dis*. 2024;229(1):30–38. <https://doi.org/10.1093/infdis/jiad235>.
- Mittler E, Wec AZ, Tynell J, et al. Human antibody recognizing a quaternary epitope in the Puumala virus glycoprotein provides broad protection against orthohantaviruses. *Sci Transl Med*. 2022;14(636):eabl5399. <https://doi.org/10.1126/scitranslmed.abl5399>.