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# Hantavirus exposure during expedition cruise travel: emerging challenges in maritime zoonotic preparedness

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***ABSTRACT:***

The hantavirus cluster reported in May 2026, associated with expedition cruise travel in the South Atlantic, highlights a rarely examined dimension of maritime infectious-disease preparedness: the movement of international travelers between semi-confined vessels and wildlife-associated settings. This narrative review examines hantavirus infection as a travel-associated zoonotic risk rather than a conventional shipboard outbreak. It summarizes hantavirus microbiology and transmission, with particular attention to rodent-associated environmental exposure, early clinical recognition, and the exceptional concern posed by Andes virus. The review also evaluates how shore landings, wildlife-associated excursions, delayed symptom onset, and post-disembarkation passenger dispersal may complicate exposure reconstruction and public-health response. Molecular diagnostics, genomic investigation, environmental assessment, and One Health surveillance are discussed as key tools for distinguishing shared shore-associated exposure from possible secondary transmission. In conclusion, this review identifies a preparedness gap at the interface of maritime travel, zoonotic ecology, and international surveillance. However, delayed diagnosis, severe disease progression, and geographically dispersed exposure can still complicate early recognition and response.

***Keywords:*** Hantavirus, Zoonosis, Cruise travel, One health, Maritime health, Andes virus, Rodent-borne viruses, Global preparedness.

## INTRODUCTION

As reported in the World Health Organization (WHO) Disease Outbreak News and the European Center for Disease Prevention and Control (ECDC)[1,2] updates issued in May 2026, a hantavirus cluster associated with expedition cruise travel in the South Atlantic has drawn attention to a relatively underexplored dimension of maritime infectious-disease preparedness. According to outbreak updates, suspected and confirmed cases, including fatal infections, were identified among passengers and crew members from several countries after travel aboard an expedition cruise vessel[1,2]. Although the assessed risk to the wider population has remained low, the event remains microbiologically important because it involves a rodent-borne zoonotic virus not traditionally associated with maritime outbreaks[1,2]. Unlike the gastrointestinal and respiratory pathogens more commonly reported on cruise ships, hantaviruses are rodent-borne negative-sense RNA viruses transmitted mainly through inhalation of aerosolized excreta in contaminated environments[3]. The suspected involvement of Andes virus has received particular attention because, unlike most hantaviruses, limited person-to-person transmission has previously been documented under close-contact conditions[3,4]. Expedition-style tourism may therefore create distinctive exposure scenarios, particularly during shore excursions to remote islands, polar routes, and wildlife-associated environments where rodent-reservoir surveillance and environmental monitoring are not routinely integrated into maritime preparedness systems[1,3].



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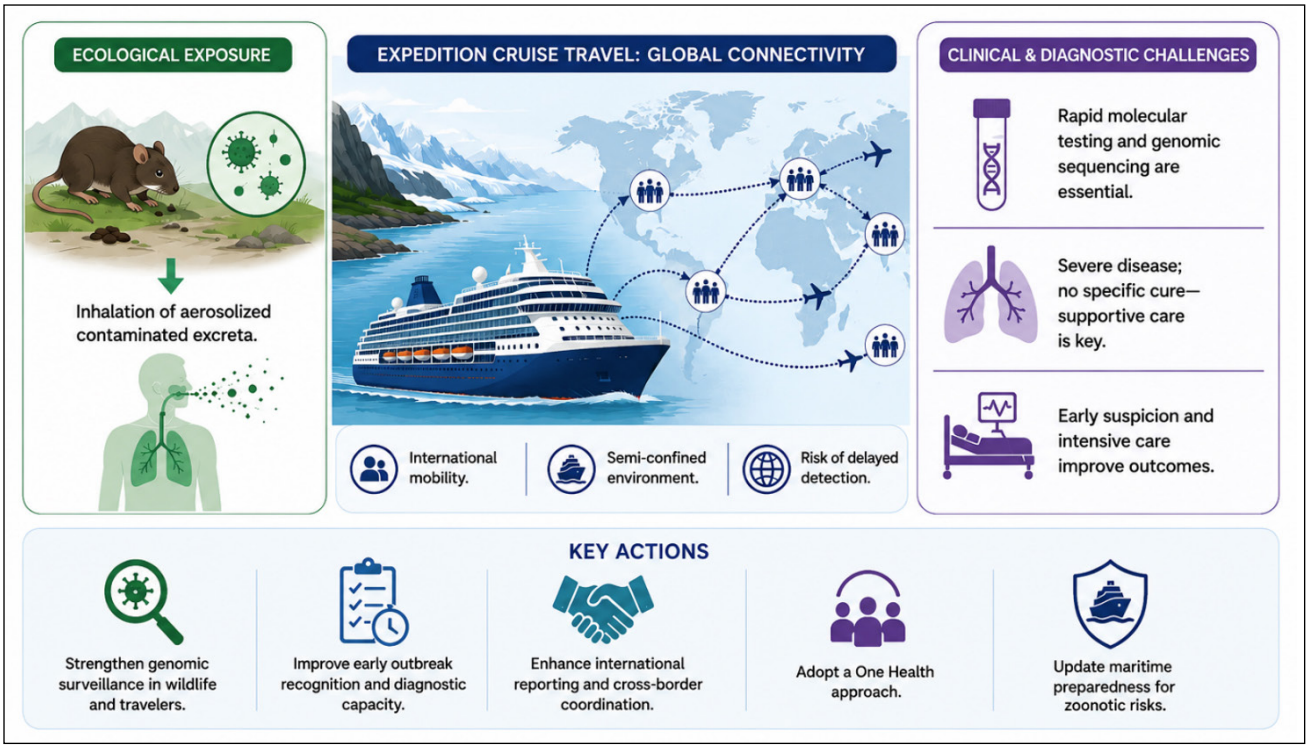


**Graphical Abstract.** Expedition cruise travel may expose passengers and crew to rodent-borne hantaviruses in remote ecosystems. The figure summarizes the exposure route, diagnostic and clinical challenges, and key preparedness actions, including genomic surveillance, early outbreak recognition, cross-border reporting, One Health coordination, and updated maritime protocols for zoonotic risks.

In expedition-cruise settings, hantavirus risk extends beyond onboard transmission. Exposure may occur during shore excursions or small-vessel landings in environments where rodent activity, contaminated dust, and ecological surveillance are not routinely assessed. This creates a preparedness challenge that connects microbiological risk with field exposure assessment, early clinical suspicion, molecular confirmation, genomic investigation, and coordinated zoonotic monitoring[5]. This gap is particularly relevant because most maritime preparedness frameworks were developed for onboard transmissible outbreaks rather than shore-acquired zoonotic spillover events. Current systems, therefore, remain largely oriented toward high-frequency threats such as norovirus, influenza, and coronavirus-associated respiratory infections[6]. However, expedition cruise travel may introduce additional risks, as passengers and crew can enter ecologically sensitive environments where rodent-borne or other zoonotic pathogens are not routinely considered in maritime outbreak algorithms. This narrative review uses the May 2026 hantavirus cluster as a timely example to examine preparedness gaps related to rodent-exposure assessment, diagnostic recognition, passenger tracing, genomic investigation, reporting obligations, and cross-border coordination in expedition cruise settings[1,2,6].

The May 2026 outbreak reports highlight how expedition cruise travel can create exposure conditions that differ substantially from conventional maritime tourism. Shore landings, wildlife-associated environments, and travel through remote regions may increase opportunities for contact with contaminated environments that are not routinely considered in standard shipboard outbreak preparedness[7]. At the same time, most maritime infectious-disease frameworks remain focused on common respiratory and gastrointestinal infections, whereas uncommon zoonotic pathogens may not immediately trigger clinical suspicion or targeted laboratory investigation[8]. Once passengers disembark and return to multiple countries, outbreak management may become operationally complex, requiring coordinated testing, traveler notification, quarantine decisions, and cross-border public-health communication[9].

Accordingly, this narrative review examines the microbiology and transmission of hantaviruses in the context of expedition cruise travel, with emphasis on reservoir-linked exposure pathways, the potential transmission concern associated with Andes virus, and the preparedness challenges posed by rare maritime zoonotic events. It further discusses diagnostic and genomic surveillance, integrated monitoring of rodent reservoirs and environmental exposure, passenger tracing, human outbreak investigation, and cross-border coordination as key components of future preparedness for ecologically-linked infectious threats. Because outbreak investigations and laboratory confirmation status may evolve over time, all outbreak-related information discussed in this review reflects publicly available WHO, ECDC, and CDC reports accessed in May 2026.

## HANTAVIRUS MICROBIOLOGY AND TRANSMISSION

Hantaviruses are enveloped, tri-segmented, negative-sense RNA viruses belonging to the family Hantaviridae and the genus Orthohantavirus. Their genome consists of small (S), medium (M), and large (L) RNA segments encoding the nucleocapsid protein, surface glycoproteins, and RNA-dependent RNA polymerase, respectively[10]. Complementary terminal non-coding regions form panhandle structures essential for viral transcription and replication, and the M segment encodes a glycoprotein precursor that is cleaved into Gn and Gc envelope glycoproteins[11]. Figure 1 summarizes these key structural and genomic features. Unlike many acute zoonotic viruses, orthohantaviruses are maintained through persistent infection in specific mammalian reservoir hosts, particularly rodents, although genetically related viruses have also been identified in shrews, moles, and bats[12,13]. The geographic distribution of human hantavirus disease, therefore, closely follows the ecology and distribution of infected reservoir populations.

Human infection occurs mainly through inhalation of aerosolized virus-contaminated urine, feces, or saliva released from infected rodents in enclosed or environmentally contaminated settings[14]. Less commonly, transmission may occur through direct contact with contaminated materials or rodent bites. The major transmission pathway and clinical outcomes associated with hantavirus infection are summarized in Figure 2. Hantaviruses are traditionally classified into Old World and New World groups according to their geographic distribution and associated clinical syndromes. Old World hantaviruses, including Hantaan, Puumala, Dobrava-Belgrade, and Seoul viruses, are mainly associated with hemorrhagic fever with renal syndrome (HFRS) in Europe and Asia, whereas New World hantaviruses such as Sin Nombre virus and Andes virus are linked to hantavirus cardiopulmonary syndrome (HCPS) in the Americas[3]. Clinical severity varies according to viral species, host factors, and access to supportive care, but HCPS may still exceed 30-40% mortality in severe cases[15].

From a microbiological perspective, hantaviruses are notable for their strong host specificity and ecological dependence. Viral maintenance within rodent populations is influenced by environmental conditions, rodent density, food availability, and human encroachment into wildlife-associated habitats[16]. Consequently, human infection is often associated with environmental exposure rather than sustained human transmission. Andes virus remains an important exception because limited person-to-person transmission has been documented during close-contact exposure, particularly in household and healthcare-associated settings[17].

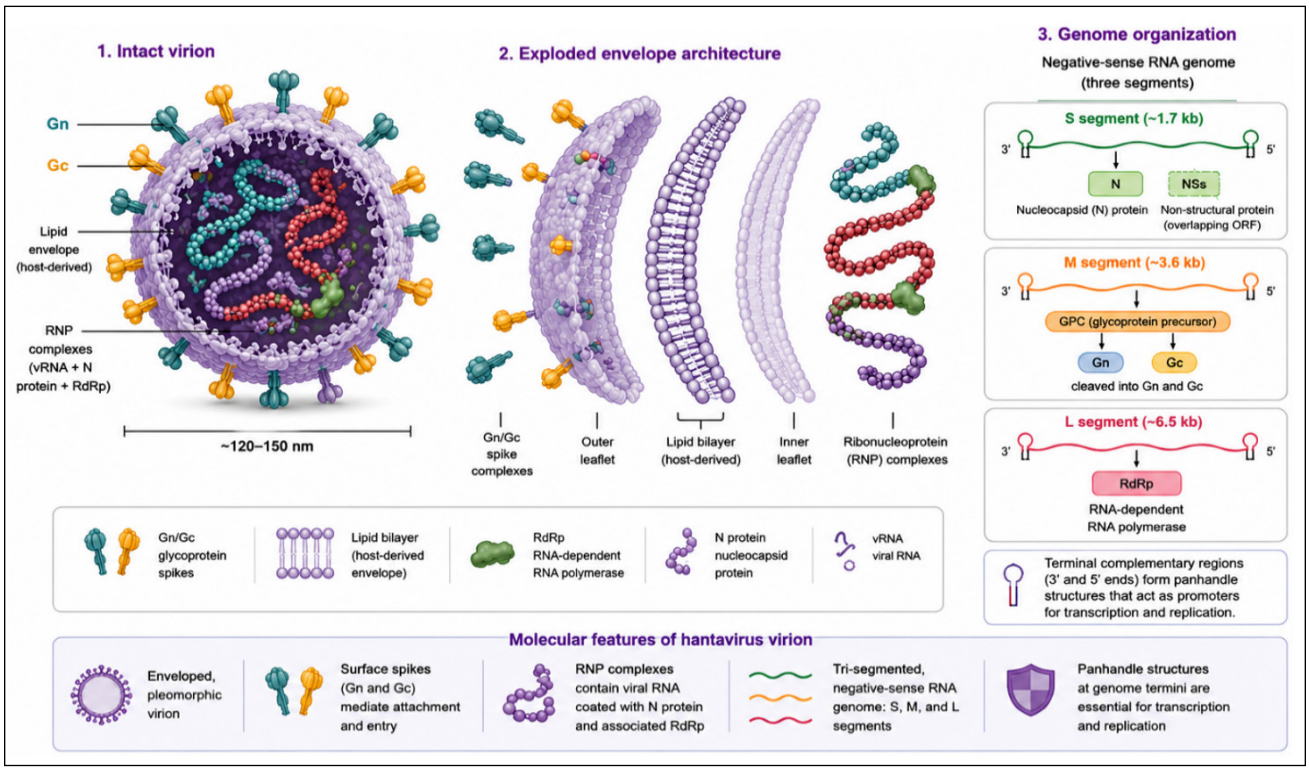


**Figure 1.** Structural organization and genome architecture of hantavirus. Hantaviruses are enveloped, pleomorphic, negative-sense RNA viruses with three genome segments: S, M, and L. These encode the nucleocapsid protein, Gn/Gc glycoproteins, and RNA-dependent RNA polymerase, respectively. The viral RNA forms ribonucleoprotein (RNP) complexes with nucleocapsid protein and RNA dependent RNA polymerase (RdRp), while complementary terminal regions form panhandle structures required for transcription and replication[11].

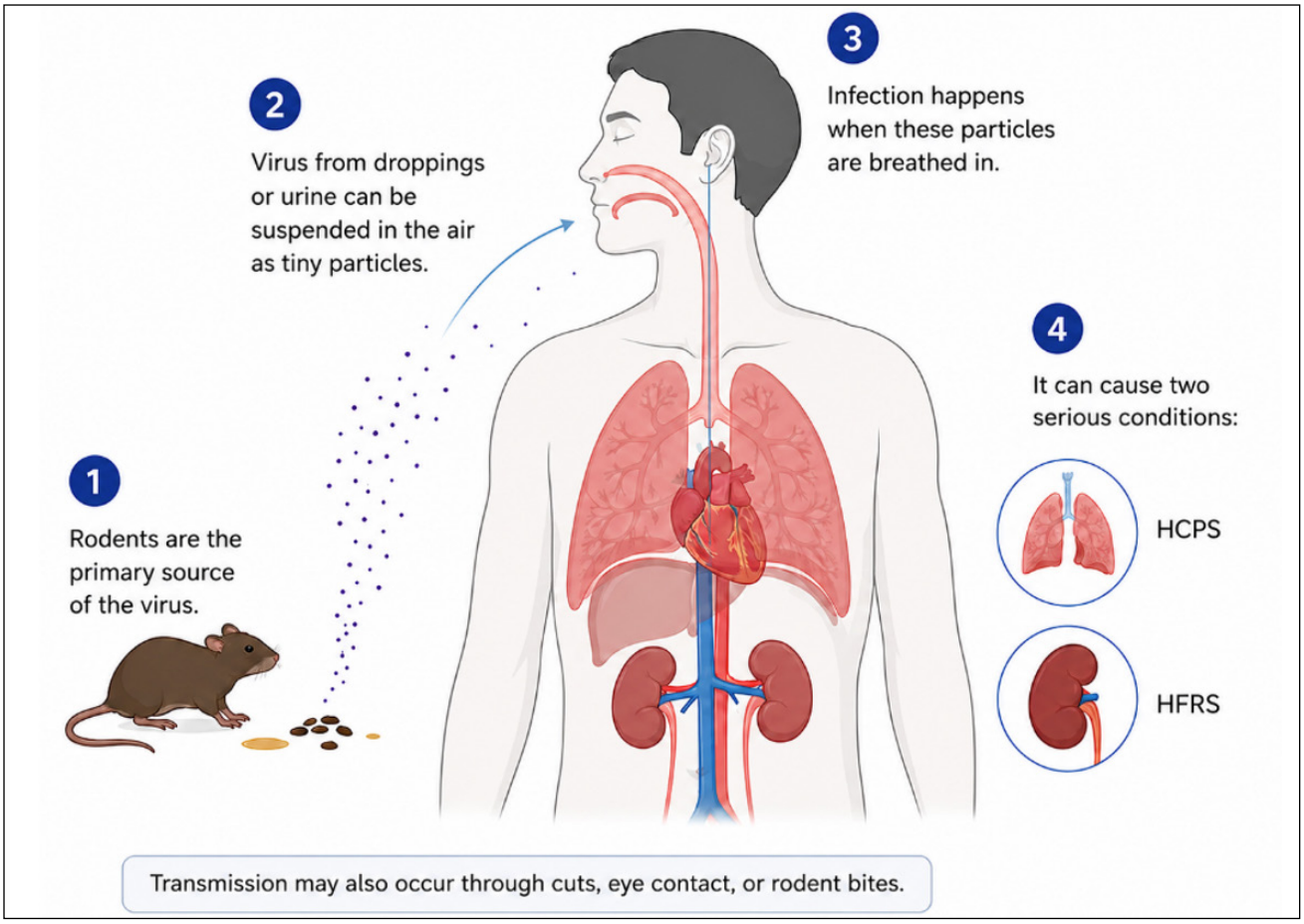


**Figure 2.** Simplified overview of hantavirus transmission and major clinical syndromes. Hantaviruses are maintained in rodent reservoirs and transmitted mainly through inhalation of aerosolized virus-contaminated excreta. Human infection may result in hantavirus cardiopulmonary syndrome (HCPS) or hemorrhagic fever with renal syndrome (HFRS), depending on the viral species involved. Additional transmission may occur through direct contact with contaminated materials or rodent bites.

This characteristic has important implications for outbreak investigation and infection-control preparedness in semi-confined travel environments such as expedition cruise vessels.

Recent advances in molecular epidemiology and genomic surveillance have improved understanding of hantavirus diversity, host adaptation, and transmission dynamics. Metagenomic sequencing and phylogenetic analysis are increasingly used to identify emerging orthohantaviruses, characterize transmission pathways, and differentiate imported infections from local exposure events[18]. These approaches are becoming particularly relevant in travel-associated outbreaks, where ecological exposure, delayed diagnosis, and international passenger movement may complicate early outbreak recognition and epidemiological investigation.

## CRUISE TRAVEL AS ENVIRONMENTAL EXPOSURE

Unlike conventional cruise tourism, expedition cruise travel should be viewed as a mobile ecological interface rather than only a shipboard public-health setting. Its microbiological relevance lies in the fact that passengers and crew may move between semi-confined maritime environments and remote terrestrial ecosystems where zoonotic pathogens circulate in wildlife reservoirs with limited routine surveillance. Polar and expedition ship-based tourism has expanded into fragile environments where governance, environmental monitoring, and operational biosecurity remain uneven, creating exposure contexts that differ from standard cruise outbreaks dominated by gastrointestinal and respiratory pathogens[7,19]. For hantaviruses, the primary exposure pathway is not usually person-to-person transmission but rather contact with contaminated environments. Human infection commonly follows inhalation of aerosolized rodent urine, feces, or saliva, particularly in enclosed, dusty, or poorly ventilated spaces contaminated by infected rodents[16,20]. In expedition cruise settings, such exposure may occur during shore landings, wildlife-associated excursions, visits to shelters or storage structures, or movement through disturbed natural environments. Therefore, a hantavirus cluster linked to cruise travel should not be interpreted simply as an onboard outbreak; it may instead represent a travel-associated spillover event acquired at the human–rodent–environment interface.

This distinction exposes a major preparedness gap. Maritime infectious-disease planning has historically focused on pathogens that spread efficiently within ships, such as norovirus, influenza viruses, and coronaviruses. However, scoping and systematic reviews[6,8] of passenger-ship preparedness show that existing literature and guidance remain concentrated mainly on respiratory and gastrointestinal infections, while less attention is given to vector-borne, environmental, or zoonotic threats linked to shore-based exposure. Consequently, expedition cruise medicine may fail to capture the environmental exposure history needed to suspect hantavirus infection early, especially when the initial presentation resembles non-specific influenza-like illness. The operational problem becomes greater after disembarkation. Hantavirus incubation can extend beyond the voyage period, so symptomatic disease may appear only after passengers have dispersed to multiple countries[3]. This weakens the epidemiological signal, separates cases across healthcare systems, and delays identification of a shared exposure source. From a microbiological standpoint, exposure reconstruction becomes as important as onboard infection control. Passenger itineraries, landing sites, environmental conditions, rodent activity, and shared excursion histories should therefore be treated as essential epidemiological data, not secondary travel details[16].

Expedition travel also intersects with broader ecological change. Hantavirus transmission is strongly influenced by rodent ecology, including reservoir density, food availability, climatic variation, and environmental disturbance[16]. Climate-related changes may influence hantavirus epidemiology indirectly by affecting reservoir-host populations, although the direction and magnitude of this effect vary by region and host species[21]. Although it would be inappropriate to claim that cruise travel itself increases hantavirus risk, expedition tourism can connect highly mobile international populations with ecological settings where rodent-borne viruses may be present but poorly monitored[22]. Thus, the key lesson is not that cruise ships are inherently high-risk environments for hantavirus transmission. Rather, expedition cruise travel can act as a bridge between remote zoonotic reservoirs and global human mobility.

This event also links maritime zoonotic exposure to the wider urban-health problem. Modern cities can act as reservoirs and amplifiers of infectious diseases because dense populations, mobility, ecological disruption, poor sanitation, sewerage systems, and rodent infestation create conditions for pathogen persistence and spread. Thus, travelers exposed to hantavirus in remote ecosystems may later enter urban health systems where diagnosis, surveillance, wastewater management, and rodent control become essential parts of preparedness[23]. Future preparedness should therefore move beyond ship-centered outbreak algorithms and incorporate zoonotic exposure assessment, rodent-risk awareness, excursion-site evaluation, molecular diagnostics, and international case tracing. This shift would make maritime preparedness more suitable for rare but consequential zoonotic events arising from modern travel into remote ecosystems. The main ecological and operational factors that may shape hantavirus-related preparedness during expedition cruise travel are summarized in Table 1.

## PREPAREDNESS GAPS FOR MARITIME ZOONOSES

Maritime zoonotic preparedness remains structurally underdeveloped because most shipboard public health systems are designed to detect illness after it appears on board, rather than to anticipate environmental exposures before embarkation, shore landing, or passenger dispersal. The International Health Regulations provide a framework for public-health capacities at points of entry, including ports, but their operational tools are still more effective for visible onboard illness, sanitation hazards, and conventional outbreak reporting than for reconstructing short-lived environmental exposures acquired during remote excursions[23,25,26]. This creates a critical blind spot for zoonoses such as hantavirus infection, where the decisive exposure may occur outside the vessel, while clinical disease may emerge only after the voyage has ended.

A first gap concerns pre-excursion ecological risk assessment. Expedition cruises frequently move passengers from a controlled ship environment into remote landscapes where rodent reservoirs, contaminated dust, abandoned shelters, storage areas, or poorly ventilated enclosed structures may be present. Yet maritime health procedures rarely require systematic documentation of shore-site ecology, evidence of rodent activity, local zoonotic alerts, or environmental contamination before passenger landing. This is important because ship sanitation inspections and certificates can identify onboard public-health risks, but they are not designed to evaluate dynamic zoonotic hazards at temporary excursion sites[25,26]. For rare rodent-borne infections, the risk unit is therefore not only the ship, but the combined itinerary-landing site-passenger pathway. A second gap is the limited sensitivity of routine maritime reporting tools for rare zoonoses. The Maritime Declaration of Health[27] is valuable for detecting illness during a voyage, but it depends heavily on symptoms already recognized onboard and does not capture detailed ecological exposures among apparently healthy passengers. This limitation is particularly relevant for hantavirus because fever, myalgia, headache, and early respiratory symptoms are nonspecific and may be mistaken for influenza-like illness, COVID-19, or other travel-associated viral infections. In such cases, the absence of an early zoonotic exposure history may delay molecular testing, isolation advice, contact classifi-

**Table 1.** Operational preparedness gaps, consequences, and response priorities for hantavirus-associated expedition cruise travel*.

| Expedition-cruise factor | Microbiological relevance | Preparedness gap | Consequence | Proposed action | Ref. |
|---|---|---|---|---|---|
| Remote shore landings | Exposure to ecologically sensitive and poorly monitored environments | Weak ecological risk assessment before passenger landing | Reduced early detection of zoonotic exposure | Pre-landing ecological risk assessment and rodent surveillance | Liggett et al[7] |
| Wildlife-oriented excursions | Increased human–animal–environment interaction | Exposure history may not be systematically documented | Missed epidemiological linkage between cases | Structured documentation of excursion activities and environmental exposures | Lamers et al[19] |
| Rodent-contaminated shelters and storage areas | Aerosolized exposure to rodent excreta containing hantaviruses | Limited hazard screening before shore activities | Unrecognized environmental exposure risk | Environmental screening and rodent-risk mitigation before shore activities | Jonsson et al[16] |
| Climate-sensitive rodent ecology | Reservoir density and viral circulation may vary seasonally | Static ecological risk maps may not reflect dynamic environmental conditions | Underestimation of regional zoonotic risk | Dynamic ecological surveillance integrating climate and rodent-monitoring data | Klempa[21] |
| Non-specific febrile illness after travel | Early hantavirus symptoms mimic common viral infections | Delayed zoonotic clinical suspicion | Delayed molecular diagnosis and supportive care | Early reverse transcription-polymerase chain reaction (RT-PCR) referral for febrile post-travel illness with ecological exposure history | Centers for Disease Control and Prevention[3] |
| Traditional passenger-ship outbreak models | Maritime preparedness still mainly targets gastrointestinal and respiratory pathogens | Rare zoonotic threats are under-represented in outbreak algorithms | Incomplete early outbreak characterization | Expand maritime outbreak protocols to include zoonotic exposure assessment | Neumann et al[6] |
| Fragmented port and ship coordination | Cross-border zoonotic events require a multi-agency response | Weak integration between maritime, laboratory, and public-health systems | Fragmented multinational outbreak response | Cross-border data sharing and itinerary-linked surveillance coordination | Anagnostopoulos et al[8] |
| Post-disembarkation illness | Cases may emerge after international passenger dispersal | Difficult exposure reconstruction across countries | Delayed contact tracing and public-health communication | Preservation of passenger itineraries, excursion records, and landing-site data | Sulleiro et al[22] |
| International passenger dispersal | Multi-country movement complicates epidemiological tracing | Weak interjurisdictional coordination during rare zoonotic events | Fragmented international case tracing | Rapid multinational communication and interoperable surveillance systems | Sulleiro et al[22], World Health Organization[24] |

*The table links expedition-specific exposure factors with microbiological relevance, preparedness weaknesses, likely public-health consequences, and practical response actions.

cation, and targeted public-health communication. A third gap involves contact tracing after passenger dispersal. Conventional cruise outbreak control often assumes a defined onboard population and a relatively traceable exposure window, but expedition-associated zoonoses are different because exposure may be environmental, the incubation period may extend beyond the voyage, and passengers may return to multiple countries before a cluster is recognized[22,24]. Under these conditions, preparedness depends on preserving high-resolution itinerary data, cabin allocation, excursion participation lists, landing-site records, and close-contact histories to support exposure reconstruction and multinational public-health communication. Generic digital proximity tracing alone is insufficient because rare high-consequence zoonoses require precise reconstruction of shared environmental exposure and close interpersonal contact, rather than broad proximity alerts. A fourth gap is the separation between maritime health, wildlife surveillance, and environmental health systems. One Health frameworks emphasize coordination across human, animal, and environmental sectors, but such integration remains limited within cruise itineraries, port-health operations, and expedition tourism planning[28,29]. For maritime zoonoses, One Health should extend beyond a conceptual framework and translate into operational measures, including pre-travel consultation with local public-health authorities, environmental risk assessment of landing sites, rodent-exposure warnings, crew training, safe environmental cleaning protocols, and rapid linkage between clinical laboratories and ecological surveillance teams. A fifth gap concerns diagnostic readiness at the ship-shore interface. Many vessels can manage acute medical emergencies, but rare zoonotic infections require access to specialized testing, reference laboratories, and cross-border result sharing[5,24]. A febrile traveler returning from a shore-based expedition itinerary should prompt a structured diagnostic pathway that includes travel geography, rodent exposure, excursion history, and possible risk of close-contact transmission when Andes virus is suspected. Without this pathway, cases may be investigated only after severe cardiopulmonary disease develops, reducing the value of early supportive care and delaying public-health intervention[3]. As illustrated in Figure 3, preparedness gaps for maritime zoonoses arise from the interaction among shore-associated exposure during expedition cruise travel, operational blind spots within maritime health systems, and downstream challenges that complicate outbreak recognition and international public health response.

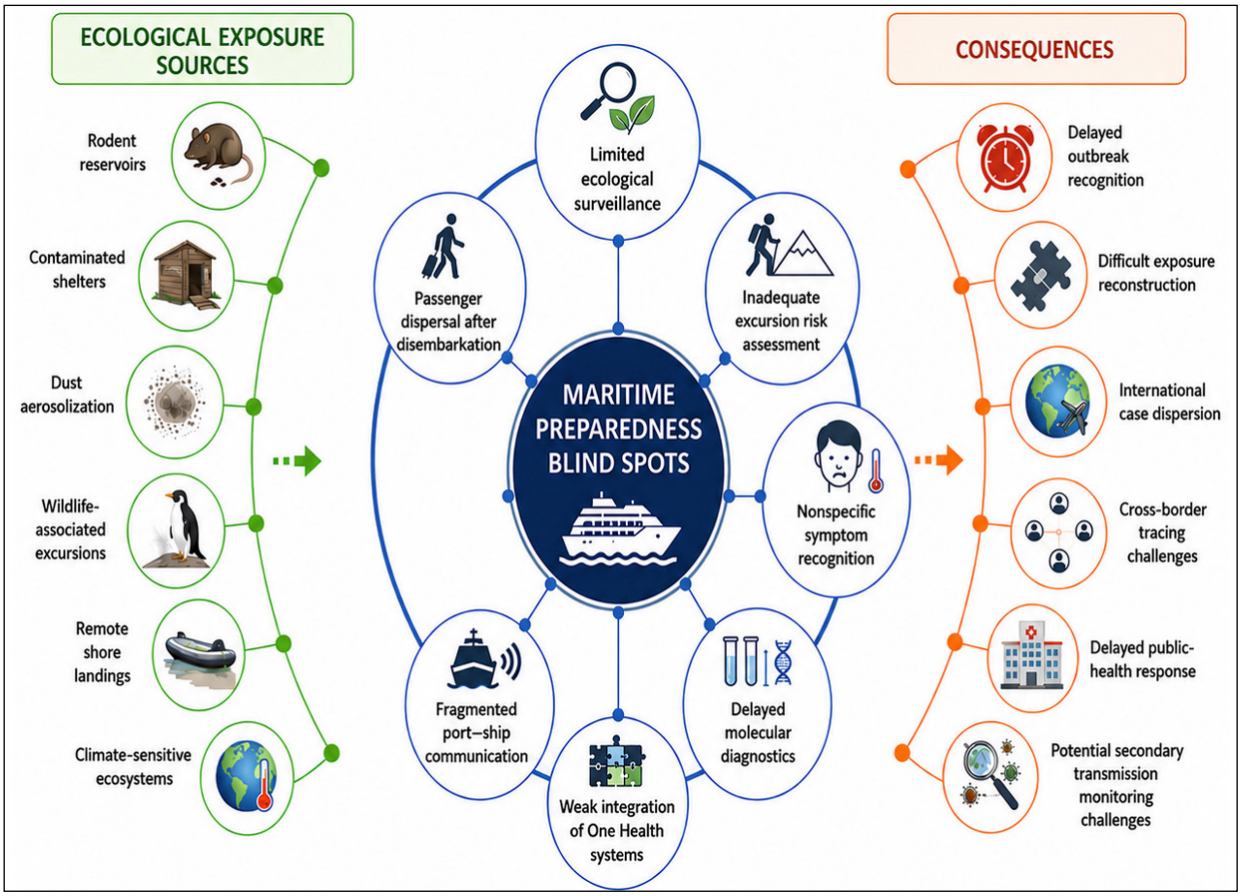


**Figure 3.** Preparedness gaps for maritime zoonotic threats during expedition cruise travel. The figure illustrates how environmental exposures during expedition cruise travel may interact with preparedness blind spots in maritime health systems, contributing to diagnostic delays, difficult exposure reconstruction, multi-country tracing challenges, and delayed public health response during rare zoonotic events.

Finally, preparedness is weakened by risk communication that is either too narrow or too alarmist. The Andes virus deserves attention because limited human-to-human transmission has been documented only under prolonged close-contact conditions; however, it should not be framed as efficiently transmissible as influenza or SARS-CoV-2. WHO and ECDC outbreak assessments published in May 2026 support proportionate response measures, including contact tracing, monitoring of exposed individuals, and assessment of close-contact transmission risk when Andes virus infection is confirmed[1,30]. The appropriate preparedness message is therefore balanced: expedition cruise travel does not make ships inherently high-risk for hantavirus, but it can connect international travelers with poorly monitored zoonotic reservoirs. Maritime preparedness must evolve from ship-centered outbreak response toward itinerary-centered ecological risk management.

## DIAGNOSTIC, GENOMIC, AND ONE HEALTH SURVEILLANCE

Diagnostic preparedness for expedition-cruise-associated hantavirus exposure should begin before laboratory testing, with systematic reconstruction of the ecological exposure. In this setting, the decisive event may not be an onboard contact, but a short shore-based encounter with contaminated dust, rodent excreta, abandoned structures, storage shelters, or wildlife-associated environments. Therefore, clinical triage should treat itinerary data, landing-site participation, rodent exposure, cabin proximity, and post-disembarkation illness as core diagnostic variables rather than secondary travel details. This is especially important because early hantavirus disease is clinically indistinct from many febrile respiratory or travel-associated illnesses and missed exposure history can delay appropriate molecular testing. The proposed integrated surveillance framework is summarized in Figure 4, highlighting how environmental exposure assessment, laboratory diagnostics, genomic investigation, environmental monitoring, and cross-sector One Health coordination may strengthen preparedness and reduce diagnostic delay during expedition cruise travel.

A practical diagnostic pathway should integrate molecular and serological testing according to disease stage. RT-PCR is most valuable during early or severe acute illness, when viral RNA may still be detectable, whereas IgM and IgG assays become more informative as the antibody response develops. For outbreak investigation, however, diagnostic confirmation alone is not sufficient. In a cruise-linked cluster, sequencing should be added whenever feasible to determine whether cases are epidemiologically linked to a shared reservoir-linked exposure or reflect possible onward transmission[31,32].

Genomic surveillance is particularly valuable in this scenario because hantavirus outbreaks can involve geographically dispersed cases after passengers return to different countries. Amplicon-based or tar-

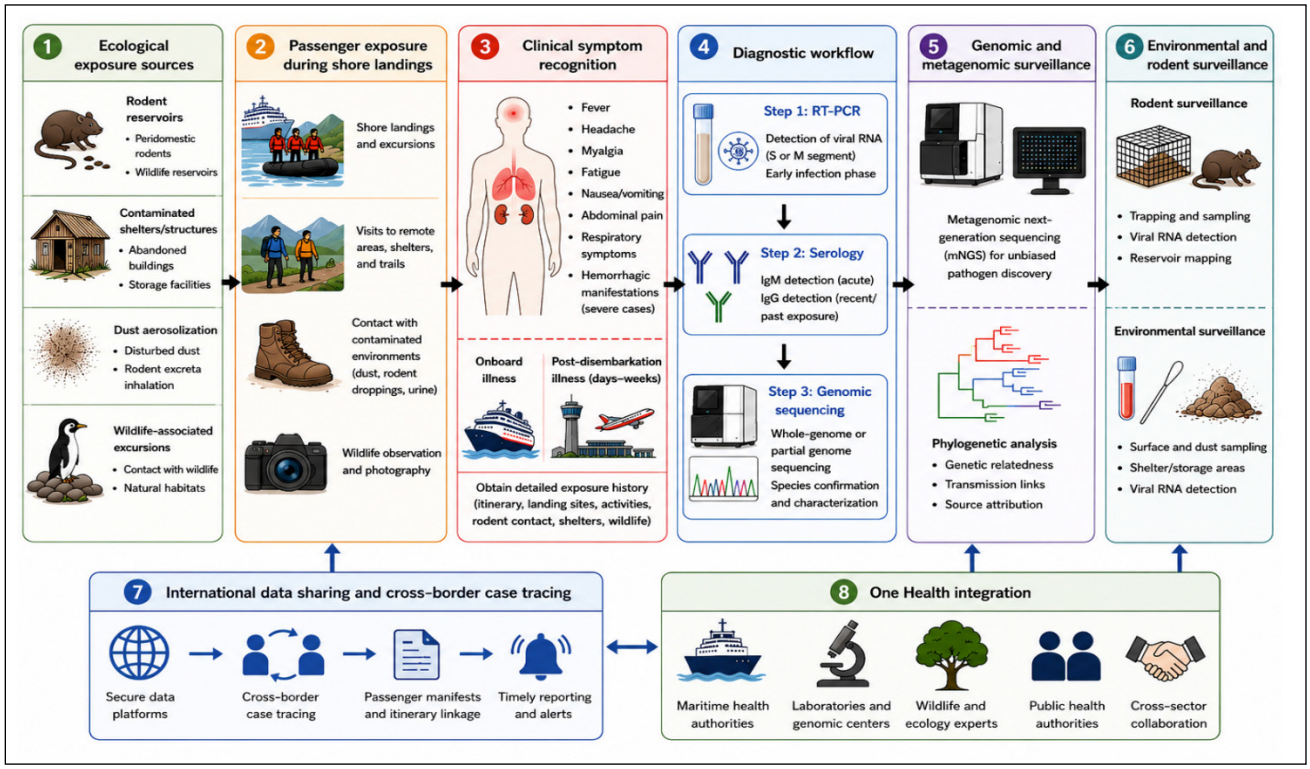


**Figure 4.** Integrated diagnostic, genomic, and One Health surveillance framework for hantavirus preparedness during expedition cruise travel.

get-enrichment sequencing can recover viral genomes directly from clinical or reservoir samples without culture, supporting species confirmation, phylogenetic placement, and comparison between human and rodent-derived sequences[33,34]. This can help distinguish three epidemiologically different possibilities: a shared exposure at one landing site, multiple independent zoonotic exposures along the itinerary, or limited secondary transmission after the voyage. This distinction is central for the Andes virus, where transmission control depends on separating environmental spillover from close-contact human transmission.

Metagenomic sequencing may be useful when severe illness has no clear microbiological diagnosis, particularly when the suspected pathogen is rare, unexpected, or absent from initial targeted panels. Its main advantage is hypothesis-free pathogen detection directly from clinical material. However, it should not be framed as a simple replacement for conventional diagnostics. Its performance depends on specimen quality, pathogen load, host-background nucleic acid, contamination control, bioinformatic interpretation, turnaround time, cost, and laboratory capacity. For maritime preparedness, a realistic tiered approach is therefore preferable: targeted RT-PCR and serology for rapid confirmation, followed by whole-genome or metagenomic sequencing in reference laboratories when outbreak reconstruction, source attribution, or pathogen discovery is required[35,36].

One Health surveillance should extend the investigation beyond human cases. For expedition cruise travel, the relevant surveillance unit is the itinerary-landing site-reservoir-passenger pathway. Rodent trapping, species identification, viral RNA screening, environmental assessment, and phylogeographic comparison of rodent and human sequences can identify whether a suspected site is epidemiologically plausible. Studies linking rodent abundance, rainfall, environmental conditions, and hantavirus activity show that reservoir dynamics may provide early warning signals before human cases appear, although such signals are region-specific and should not be generalized without local ecological validation[37,38].

The critical preparedness gap is operational integration. Maritime health teams, clinical laboratories, genomic centers, port authorities, ecologists, and wildlife-surveillance groups should not operate as separate systems during expedition cruises. A stronger preparedness model would link structured exposure documentation, passenger and excursion records, rapid referral to reference laboratories, ecological or reservoir surveillance, and the sharing of sequence-linked epidemiological data. In this framework, sequencing is not simply a research tool; it provides the link between clinical diagnosis, ecological source attribution, and multi-country outbreak investigation[39,40].

This figure illustrates an integrated diagnostic, genomic, and One Health surveillance framework for hantavirus preparedness during expedition cruise travel. It presents a proposed surveillance pathway linking ecological exposure sources, shore-landing activities, symptom recognition, laboratory confirmation, genomic/metagenomic analysis, environmental and rodent surveillance, international data sharing, and One Health coordination. The framework highlights how these integrated components can support early detection, source attribution, and preparedness for travel-associated hantavirus events.

## CROSS-BORDER COORDINATION AND FUTURE PREPAREDNESS

Cross-border coordination remains one of the most difficult operational challenges during expedition cruise-associated zoonotic events. Unlike conventional shipboard outbreaks, where illness is usually recognized and managed aboard the vessel, hantavirus exposure may occur briefly during shore excursions and only become clinically apparent after passengers and crew have returned to other countries. This delayed and geographically dispersed presentation can weaken outbreak recognition, complicate exposure reconstruction, and fragment public-health response across multiple healthcare systems. Recent reviews[6,8] published between 2025 and 2026 examining infectious-disease preparedness on passenger ships indicate that current maritime response frameworks remain focused mainly on respiratory and gastrointestinal outbreaks, while ecologically linked zoonotic threats receive comparatively less operational attention.

For expedition cruise travel, preparedness should therefore move beyond a purely ship-centered approach toward an itinerary-centered model. In this context, epidemiologically important information includes not only onboard contacts but also landing sites, wildlife-associated excursions, environmental conditions, rodent exposure opportunities, and shared excursion activities. Preserving detailed excursion and passenger records may become critical when cases are detected after disembarkation, particularly because hantavirus incubation periods may extend beyond the voyage itself[22]. Early recognition also depends heavily on clinical awareness. Febrile or respiratory illness that develops after travel through ecologically sensitive areas should prompt consideration of a history of zoonotic exposure, especially when conventional respiratory pathogens are not identified. Future preparedness will likely require stronger integration between maritime authorities, clinical laboratories, port-health systems, ecologists, and wildlife-surveillance teams. One Health coordination should not remain only a theoretical framework, but should function operationally through structured exposure assessment, rapid laboratory referral, environmental investigation, and coordinated international communication. In suspected hantavirus events, molecular diagnostics and sequencing may provide important support for distin-

guishing shared environmental exposure from possible secondary transmission, particularly in the context of Andes virus infection[32,39]. Risk communication should remain proportionate. Hantaviruses are primarily ecology-linked, rodent-associated zoonoses, and current evidence does not justify presenting expedition cruise ships as major settings for efficient onboard transmission. The more realistic concern is that expedition travel may bring mobile international travelers into remote environments where rodent reservoirs and zoonotic spillover potential may exist, while diagnosis and surveillance may be delayed or fragmented. Preparedness should therefore focus on pre-excursion ecological risk assessment, careful recording of exposure history and travel itineraries, rapid access to reference laboratory testing, and timely interjurisdictional communication when rare zoonotic infections are suspected. This approach strengthens detection and response without exaggerating the public-health risk of expedition cruise tourism[16,41].

## CONCLUSIONS

The hantavirus cluster linked to expedition cruise travel reported by WHO and ECDC in May 2026 should not be dismissed as an isolated maritime curiosity, nor should it be exaggerated as evidence that cruise ships are efficient platforms for hantavirus transmission. Its real importance lies elsewhere: it exposes a preparedness blind spot at the intersection of exposure to wildlife-associated settings, delayed clinical recognition, international passenger mobility, and fragmented international surveillance. Hantaviruses remain primarily rodent-associated zoonotic viruses, and most human infections arise from environmental exposure rather than sustained person-to-person spread. However, the suspected involvement of the Andes virus makes the event more consequential, because limited human-to-human transmission has been documented under close-contact conditions. For this reason, hantavirus infection should never be underestimated, particularly when severe febrile or respiratory illness follows travel through shore-based environments.

The central lesson is that expedition cruise travel is not only a shipboard health issue; it is an itinerary-linked environmental exposure system. Preparedness must therefore move beyond traditional cruise-outbreak models focused on norovirus, influenza, and other common respiratory or gastrointestinal infections. Future maritime protocols should include pre-landing ecological risk assessment, rodent-exposure warnings, structured documentation of shore-excursion participation, preservation of passenger and itinerary data, and early clinical prompts for zoonotic differential diagnosis after disembarkation. Rapid access to hantavirus RT-PCR, serology, reference laboratory confirmation, and sequencing should be integrated into response pathways when clinically indicated.

Future preparedness should also adopt a practical One Health model rather than a symbolic one. Maritime authorities, port-health services, clinicians, diagnostic laboratories, genomic-surveillance teams, ecologists, and wildlife authorities need predefined channels for information sharing during rare zoonotic events. Genomic and environmental investigation may help distinguish a shared zoonotic exposure from possible secondary transmission, which is especially important for the Andes virus. Looking ahead, expedition tourism will continue to expand into remote and environmentally sensitive regions. The public-health goal is not to discourage such travel, but to make it biologically informed, diagnostically prepared, and internationally coordinated. Increasing urbanization, expanding international mobility, and persistent rodent infestation in many metropolitan environments further emphasize the need to integrate urban ecological surveillance and rodent-control strategies into future zoonotic preparedness frameworks. A proportionate response should reassure the public while recognizing that rare hantavirus events can be severe, fatal, and operationally complex when detected late. This balanced approach may improve early recognition, protect travelers and crew, and strengthen maritime preparedness for future zoonotic threats emerging at the boundary between human mobility and changing ecosystems. Future maritime preparedness frameworks should therefore integrate ecological risk assessment, molecular diagnostics, and One Health surveillance into routine expedition-travel health planning.

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### Conflict of Interest

The author declares that he has no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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