HANTAVIRUS

CONTAINED THREAT OR EMERGING PANDEMIC?

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On May 2, 2026, a cruise ship in the Atlantic Ocean reported the outbreak of Andes virus, a type of Hantavirus that already existed in the Americas and Europe. Casualties, symptoms, and the spread of the virus renewed global attention surrounding it while bringing back the memories of the initial outbreak of COVID-19.

Since then, it has been linked to how COVID-19 is transmitted between humans, leading to the spread of the pandemic. However, evidence suggests human-to-human transmission is different in both cases; the SARS-CoV-2 virus was transmitted to an average of two or more people within populations that had not previously been exposed. As for the Andes virus, the transmission on the ship happened under very specific conditions of human-to-human interaction: the presence of symptomatic individuals in crowded, poorly ventilated spaces with direct and continuous contact.

Some experts from the World Health Organisation (WHO) note that the current Hantavirus outbreak on the cruise ship doesn’t qualify as the next “COVID-19” pandemic. Although it signals risks for affected people, it replicates slowly, spreads mainly through close contact, and appears to be most effective when symptoms appear. Nevertheless, other experts warn about the implications of the outbreak of the virus, citing its fatal symptoms and its shift in its traditional method of transmission. This raises a crucial question about whether Hantavirus can realistically become a pandemic.

This paper examines the potential for Hantavirus to evolve into a global pandemic threat by assessing its biological characteristics, transmission patterns, mortality rates, as well as its current global situation, including geographic distribution. It also assesses whether Hantavirus meets the established criteria for a pandemic, including sustained human-to-human transmission, international spread potential, asymptomatic transmission, urban transmission, and containment challenges.

In addition, the paper explores potential future trajectories for Hantavirus outbreaks by analysing scenarios ranging from continued local outbreaks to expanded regional transmission, as well as the low-probability but potentially high-impact pandemic driven by mutations. The report also addresses policy implications, early warning indicators, and lessons learned from the COVID-19 pandemic to assess gaps in preparedness and response capacity.

Methodologically, this paper adopts both qualitative and quantitative approaches that rely primarily on primary data/numbers and secondary sources. It draws on reports and data from international health organizations, such as the WHO, statistical facts, along with peer-reviewed academic literature, epidemiological studies, and expert analyses. The study also employs a comparative analysis of Hantavirus and COVID-19 to identify similarities and differences in defined indicators, such as transmissibility, mortality rates, and pandemic capability. Furthermore, the paper utilises scenario-building and risk assessment methods to evaluate potential future outbreak trajectories and preparedness indicators as well as challenges.

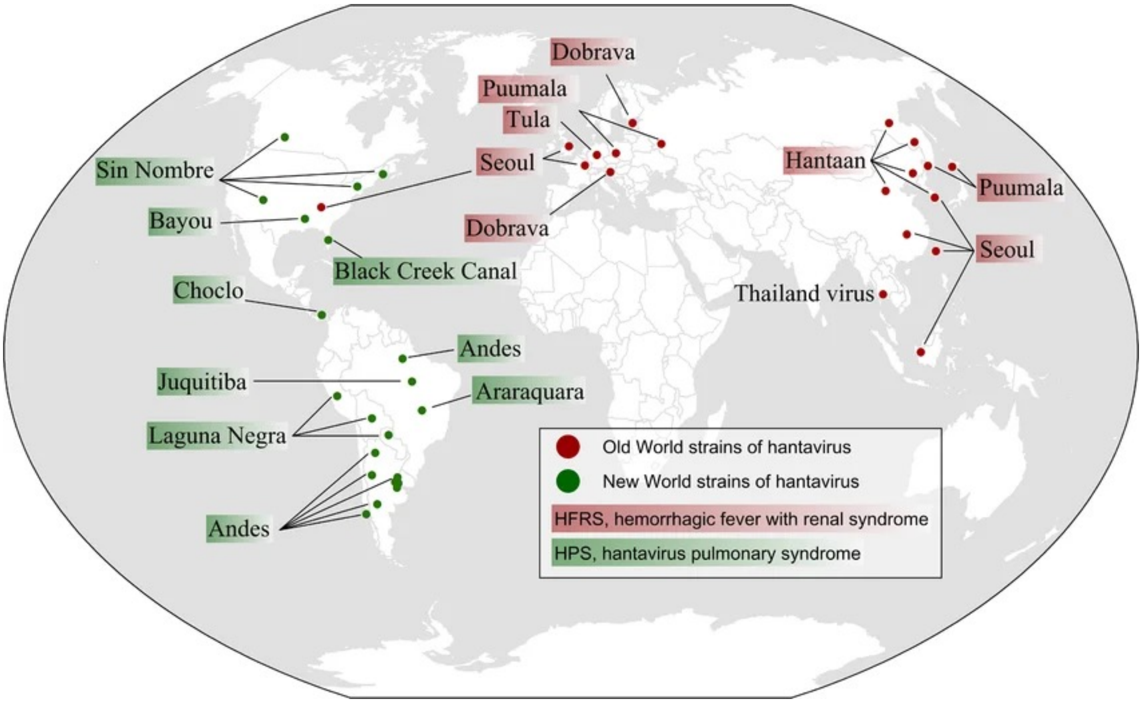
1. Understanding Hantavirus: Background and Symptoms

Hantaviruses are a group of viruses that naturally infect rodents and are sometimes transmitted through human-to-human contact, causing serious illness affecting the respiratory system or disturbing kidney functions, and could lead to death. The virus is largely found in the Americas and can cause hantavirus cardiopulmonary syndrome (HCPS) or hantavirus pulmonary syndrome (HPS), a severe respiratory illness with a mortality rate of up to 50%. Also, it is found in Europe and Asia, where it can cause hemorrhagic fever with renal syndrome (HFRS), an illness that could cause kidney failure and affect blood vessels.

Hantaviruses belong to the Hantaviridae family within the Bunyaviricetes order. Each Hantavirus strain is typically associated with a specific rodent species, in which it causes a prolonged infection without noticeable symptoms. Although the virus family includes numerous strains, only a limited number are capable of infecting humans. HCPS is primarily found in North, Central, and South America, while HFRS is found in Europe and Asia. Even though HFRS has no documentation for its transmission, the Andes virus, part of the HCPS family, has been documented through limited human-to-human transmission among close and prolonged contact, particularly in Argentina and Chile.

The symptoms of both diseases impose serious consequences for human health. HCPS's symptoms typically start 1 to 8 weeks after exposure to the disease, and it includes fatigue, fever, and muscle aches. While nearly 50% of people with HCPS also experience headache, dizziness, chills, and abdominal problems, such as nausea, vomiting, diarrhoea, and abdominal pain. As the disease progresses, symptoms may include coughing, shortness of breath, and chest tightness due to fluid in the lungs. HCPS is particularly fatal once respiratory symptoms emerge, with mortality rates reaching up to 38%.

On the other hand, HFRS' degree of fatality depends on the virus causing the infection. Hantaan and Dobrava virus infections usually cause severe symptoms, with a mortality rate of 5% to 15%. In contrast, infections with Seoul, Saaremaa, and Puumala viruses are usually less severe, with a mortality rate of less than 1%. Its initial symptoms include severe headache, back and abdominal pain, fever/chills, nausea, blurred vision, and patients may experience facial flushing, inflammation, or red eyes, or a rash. As the disease progresses, symptoms may include low blood pressure, lack of blood flow, internal bleeding, and acute kidney failure.



Source: Tian, Huaiyu and Nils Chr. Stenseth. (2019). The ecological dynamics of hantavirus diseases: From environmental variability to disease prevention largely based on data from China. PLOS Neglected Tropical Diseases, 13(2).

Hantaviruses are primarily transmitted to humans through contact with the urine, saliva, or droppings of infected rodents. In some cases, infection can also occur through rodent bites, although this is less common. The risk of infection increases when people engage in activities that increase their exposure to rodents, such as cleaning enclosed or poorly ventilated spaces, working in agriculture or forestry, or living in areas infested with rodents.

An earlier 2012 study, titled In Search for Factors that Drive Hantavirus Epidemics, identifies Hantavirus transmission as the result of a complex interaction between ecological, climatic, and biological factors related to rodents. Human behavioural factors also play a role, rather than a single factor being responsible. The study explains that the higher the rodent density, the higher the possibility for rodent-to-rodent transmission and human infection through rodents' urine and saliva. The study traces the beech and tree seeds to increasing rodent numbers. It also links specific weather conditions, such as mild winters and warm springs and summers, to rodents' survival and reproduction.

Also, it suggests that certain human behavioural factors increase the probability of transmission, including living near forests, cleaning sheds, attics, garages, camping and hiking, forestry work, farming, military exercises, and recreational forest visits. The virus is primarily transmitted through inhalation of rodent droppings. Until now, human-to-human transmission has only been documented in cases of the Andes virus in the Americas, and this type of transmission remains rare. Its transmission is usually associated with close and prolonged contact with infected individuals, particularly among family members or partners, and especially during the early stages of the illness when the virus is most contagious.

Furthermore, a more recent 2020 study titled "Super-Spreaders" and Person-to-Person Transmission of Andes Virus in Argentina, analyses the outbreak of Hantaviruses in Argentina in 2018 and 2019, indicating that although the virus becoming a pandemic is somewhat unlikely, the spread of it is more common than solely through direct and intimate contact. That's due to the widespread social activities and various ways humans contact each other on a daily basis, hence making community transmission highly possible. The study explains that the virus was transmitted during a birthday party with 100 people when one person developed a fever, and it spread to people sitting next to this person and others who had been in contact with at least one person of whom has shown symptoms were infected as well. Argentine public health authorities imposed mandatory self-quarantine on contacts of confirmed cases, which proved to limit person-to-person "super-spreading" and reduce the number of cases.

Moreover, an analysis titled Andes hantavirus: Deadly 2018 outbreak shows that it is not only transmitted through close contact, argues that the virus won't transform into a pandemic, unlike COVID-19, citing its limited transmission extent to 3 rounds in the birthday incident, then it stops spreading. Nevertheless, it raises concerns about the lack of approved medical treatments, the potential for its widespread transmission, and the high mortality rate.

Although Hantaviruses are not new, there is no licensed antiviral treatment or vaccine specifically made for human infection. The WHO and the U.S. Centers for Disease Control and Prevention (CDC) recommend supportive care. This includes rest, hydration, and clinical monitoring for respiratory, cardiac, and renal complications. However, evidence suggests a possibility for medicinal and vaccination developments for Hantavirus, citing the need for immunity vaccination and antiviral, such as polyclonal antibody treatment.

Potential Vaccine Development Against Hantavirus

Vaccine type	Antigen	Animal model	Immunogenicity evaluation
Inactivated vaccine	Formalin inactivated HNTV	Humans	Humoral response Neutralizing antibodies
Virus-like particles	HTNV-VLP with CD40L or GM-CSF	Mice	Cytotoxic response Neutralization antibody Cytolytic activity
	M	DHFR-deficient CHO cells	Antigen-specific IFN-γ production
			Effective against HTNV Still in developing phases
Virus-vector vaccines	Replication-competent VSV-vectored SNV or ANDV glycoproteins	Syrian Hamster	Cross-reactive IgG antibodies
			Neutralizing antibodies
	Replication-competent VSV-vectored ANDV glycoproteins	Syrian Hamsters	Neutralizing antibodies
	Non-replicating Ad vector expressing N, Gn, Gc, or Gn/Gc	Syrian Hamsters	CD8+ cell response Neutralizing antibodies
Recombinant vaccines	Yeast-expressed DOBV nucleoprotein	Mice	NP-specific IgG response
			Th1/Th2 response
			Cross-reactivity with HTNV and PUUV
	Nucleoproteins from ANDV, TOPV, DOBV or PUUV	Bank voles	Specific CD8+ cell production

Potential Vaccine Development Against Hantavirus

Vaccine type	Antigen	Animal model	Immunogenicity evaluation
			Cross-reactive response against PUUV
	Truncated recombinant PUUV nucleoprotein linked to bacterial membrane protein	Mice	CD8+ T-cell response NP IgG response
DNA vaccines	HTNV/PUUV/SNV/ANDV M gene segment mix	Rabbits	Neutralizing antibodies
	HTNV M segment	Rhesus macaques	Neutralizing antibodies Cross-reactivity with SEOV and DOBV
	ANDV and HNTV M gene segments	Rhesus macaques	Neutralizing antibodies
	SNV M gene segment	Syrian hamsters	Neutralizing antibodies
	PUUV M gene segment	Syrian hamsters	Protection against lethal ANDV infection, without nAbs
			Neutralizing antibodies

2. Current Global Situation of Hantavirus

This section maps the current global distribution of hantavirus, analyses dominant regional dynamics across North America, South America, East Asia, and Europe, and evaluates the ecological, climatic, and surveillance factors shaping its trajectory. It argues that while hantavirus remains far from pandemic in its current form, it represents a strategically significant biosecurity concern, one whose risks are consistently underestimated because of its relatively low absolute case counts, but whose lethality, environmental drivers, and emerging transmission anomalies demand sustained attention.

2.1 Where Is Hantavirus Today?

Hantavirus is not a disease of any single country or continent. It is, rather, a family of rodent-borne viruses, currently comprising more than 50 known species, distributed across virtually every inhabited region of the world, bound to specific reservoir rodents with whom individual strains have co-evolved over millennia. What distinguishes hantavirus from many other zoonotic pathogens is the intimacy of this reservoir relationship: each virus is typically associated with a single rodent host, and disease burden in human populations closely tracks the density, distribution, and behavioural patterns of those animals. This ecological dependency makes hantavirus simultaneously predictable and volatile, predictable in its endemic zones, volatile in response to environmental disruption.

The global picture recently is one of persistence across known hotspots, moderate surveillance pressure, and several emerging signals that warrant strategic attention. The virus continues to circulate heavily in East Asia, where China alone accounts for an estimated 50% of all global HFRS cases. It maintains a steady endemic presence across Northern and Central Europe. In the Americas, case numbers remain modest in absolute terms but carry disproportionate lethality. And crucially, the recent MV Hondius outbreak underscored an important and often overlooked dimension of Andes virus risk, namely its documented, if rare, capacity for limited human-to-human transmission.

Global Incidence Overview

The WHO estimates between 10,000 and 100,000 annual hantavirus infections worldwide, with the true burden likely higher given significant underreporting in resource-limited settings. This range reflects genuine epidemiological heterogeneity: different strains, different clinical syndromes, and vastly different surveillance capacity across regions. The two principal disease syndromes, Hemorrhagic Fever with Renal Syndrome (HFRS), dominant in Asia and Europe, and Hantavirus Cardiopulmonary Syndrome (HCPS), predominant in the Americas, carry markedly different mortality profiles, making cross-regional comparisons inherently complex.

Global Hantavirus Burden by Region

Region	Primary Syndrome	Annual Case Estimate	CFR Range	Primary Strain(s)	Surveillance Quality
East Asia (China, South Korea)	HFRS	~50,000–70,000	0.3–5%	Hantaan, Seoul, Puumala	Moderate–High
Europe	HFRS / NE	~2,000–5,000	<1–8%	Puumala, Dobrava-Belgrade	High (EU/EEA)
North America	HCPS	~15–40/year (US)	~38%	Sin Nombre	High (US, Canada)
South America	HCPS	~200–300/year	20–50%	Andes, others	Variable
Central Asia / Russia	HFRS	Several thousand	1–10%	Puumala, Hantaan	Limited
Africa / Middle East	Unknown/Emerging	Largely unreported	Unknown	Seoul (limited)	Very Low

Table: Al Habtoor Research Centre • Source: Multiple Sources • Created with Datawrapper

A major feature of this distribution is the inverse relationship between case volume and fatality rate. Europe and Asia together account for the vast majority of reported cases but experience relatively lower mortality—particularly in Europe, where the Puumala strain causes a mild form of HFRS known as nephropathia epidemica, with fatality rates below 1% in most surveillance settings. Conversely, the Americas report far fewer cases but see fatality rates of 20–50% for New World strains, and up to 50% for the Andes virus specifically. This geographic asymmetry has significant implications for risk communication and preparedness: public health authorities and health security planners in high-incidence, low-mortality regions may underestimate the lethal potential of strains circulating elsewhere.

Why Hantavirus Continues to Attract Global Attention

Given relatively modest case counts compared to other diseases, hantavirus commands public health attention for reasons that extend beyond raw epidemiology. Three structural features make it a subject of genuine strategic concern:

- **High and consistent fatality rates,** particularly for New World strains, mean that even small outbreaks translate into significant mortality. The 2025 Americas data recorded 59 deaths from 229 reported cases, a case fatality rate of 25.7%. For the Andes strain, case fatality rates have ranged from 35% to 50% in documented outbreaks. By comparison, the 2009 H1N1 influenza pandemic had an estimated CFR well below 1%. Hantavirus is a disease where infection frequently means death.
- **The potential for spillover expansion is real and ecologically grounded.** As climate change reshapes rodent habitats, disease boundaries are not static. If reservoir species migrate into new zones—or if novel strains emerge in previously unaffected host populations—the human exposure risk profile will shift accordingly. Scientists have already warned that warming temperatures in Argentina are effectively making parts of the Southern Cone more hospitable to the rodents that carry Andes virus.
- **Concerns regarding viral adaptation and future transmissibility are not hypothetical.** Andes virus already demonstrates limited human-to-human transmission—the only hantavirus strain for which this has been documented. While the mechanism is not fully understood, and current transmission remains dependent on close and prolonged contact, the existence of this capability marks Andes as a strain that warrants disproportionate monitoring investment relative to its current case count.
- **Underreporting and surveillance gaps mean the true burden of hantavirus is almost** certainly higher than official figures suggest, particularly in South America, Central Asia, and sub-Saharan Africa, where diagnostic capacity is limited and cases may be misclassified as influenza, leptospirosis, or dengue.

2.2 Global Spread Mapping: Regional Patterns and Strategic Assessment

The global distribution of hantavirus is neither random nor static. It follows the geography of its reservoir hosts, is shaped by land use and climate, and is mediated, in both directions, by the quality of national surveillance systems. The following regional analysis draws on current epidemiological data to assess where hantavirus stands today, what the dominant transmission dynamics look like, and what signals are emerging from each region.

North America

Dominant strains: Sin Nombre virus (SNV); Seoul virus (limited, cosmopolitan)

Hantavirus in North America is primarily a phenomenon of the rural American West, defined by Sin Nombre virus (SNV) transmitted by the deer mouse (Peromyscus maniculatus). From 1993, when HPS was first identified following an outbreak in the Four Corners region of the American Southwest, through 2023, the United States recorded 890 laboratory-confirmed cases—an average of roughly 30 per year. The vast majority occurred west of the Mississippi River, with New Mexico, Colorado, Arizona, and California accounting for the highest cumulative totals. The case fatality rate for HPS in the United States has remained consistently around 38%, a figure unchanged by decades of supportive care advances and unchanged in the absence of any approved antiviral treatment.

Public awareness of hantavirus in the United States has historically been limited, though episodic events, most recently the 2025 death of Betsy Arakawa, wife of actor Gene Hackman, from confirmed hantavirus infection, periodically elevate national attention. The CDC maintains active surveillance for hantavirus, classifies it as a nationally notifiable disease, and has established clear case reporting protocols. Surveillance quality in the United States is high relative to global standards, though reporting is still passive and likely captures only a fraction of true incidence, particularly for milder cases that do not progress to full HPS.

Canada records a small number of cases annually, primarily in British Columbia, Manitoba, and Saskatchewan, linked to the same deer mouse reservoir. Mexico and Central America report sporadic HCPS cases, though surveillance infrastructure is considerably weaker, and cases are routinely underdiagnosed.

The environmental outlook for North America carries moderate concern. Drought-and-moisture cycles driven by El Niño events have historically correlated with deer mouse population surges in the Southwest. Climate projections suggest increasing variability in these patterns, which may expand the geographic range of susceptible rodent populations into higher elevations and previously cooler latitudes where hantavirus transmission has not historically occurred.

South America

Dominant strains: Andes virus (ANDV); multiple regional strains including Araraquara, Laguna Negra, and others across Brazil, Bolivia, Paraguay, Uruguay, and Chile.

South America is the most strategically significant region for global hantavirus risk assessment, not because it has the highest case burden, but because it harbors the Andes virus: the only hantavirus strain in the world for which human-to-human transmission has been documented. This single epidemiological fact sets South America apart from all other endemic regions and elevates Andes virus from a serious regional health concern to a global biosecurity consideration.

In 2025, eight countries across the Americas, Argentina, Brazil, Bolivia, Chile, Panama, Paraguay, Uruguay, and the United States, reported a combined 229 confirmed HCPS cases and 59 deaths, yielding a regional CFR of 25.7%. Argentina and Brazil consistently account for the majority of cases, with Argentina's Patagonian and northwestern regions representing the highest-density transmission corridors. Bolivia's 2025 season saw 48 cases and 11 deaths by mid-November, roughly double the 2023–2024 average.

The Andes virus cluster aboard the MV Hondius in 2026 warrants particular analytical attention. The index case, a Dutch national who had spent more than three months traveling through Argentina, Chile, and Uruguay before boarding the ship in Ushuaia, developed symptoms on April 6. Over the following three weeks, at least seven additional cases were identified among passengers and crew from 23 countries, with three confirmed deaths and a case fatality rate of approximately 38%. The cluster's international character, with cases subsequently identified in the Netherlands, the United Kingdom, Germany, Switzerland, and South Africa, prompted IHR notifications across multiple continents and a coordinated WHO response.

East Asia

Dominant strains: Hantaan virus (HTNV); Seoul virus (SEOV); Puumala (Russia border regions)

East Asia, and China in particular, bears by far the largest absolute burden of hantavirus disease globally. China alone is estimated to account for approximately 50% of all annual HFRS cases worldwide, driven primarily by Hantaan virus (spread by the striped field mouse, Apodemus agrarius) and Seoul virus (spread by the globally distributed brown rat, Rattus norvegicus). From 1950 to 2007, China recorded more than 1.5 million HFRS cases and over 45,000 deaths. While these figures have declined substantially, HFRS incidence fell from 0.99 per 100,000 in 2010 to 0.31 per 100,000 in 2024, and the case fatality rate fell from 1.27% to 0.28% over the same period—the absolute burden remains large.

This decline is attributable to several factors: widespread deployment of bivalent HFRS vaccines (against Hantaan and Seoul viruses) in high-risk rural populations; improvements in early clinical recognition and supportive care; urbanization and rodent control programs in endemic provinces; and intensified surveillance following China's experience with SARS in 2003. China's national HFRS surveillance system is among the most comprehensive for this disease globally, covering hundreds of sentinel sites and producing reliable seasonal trend data.

South Korea records approximately 400–600 HFRS cases annually, concentrated in rural and military populations, a legacy of the disease's first formal identification among UN soldiers near the Hantan River during the Korean War in the 1950s. South Korea has also deployed bivalent vaccination programs and maintains robust surveillance. Russia, bordering both the Chinese and European endemic zones, reports several thousand HFRS cases per year, primarily from Puumala virus in the Far East and Hantaan virus in the Russian Far East.

The primary strategic concern for East Asia is not current trajectory, which is declining, but latent risk. Seoul virus, whose reservoir is the globally distributed brown rat, has the theoretical capacity to spread hantavirus beyond its current endemic boundaries through rat migration along commercial shipping and trade routes. Cases of Seoul virus infection have been recorded in the Americas, Europe, and Oceania, making it a uniquely cosmopolitan hantavirus strain. While Seoul virus HFRS is generally mild (CFR 1–2%), it represents the primary mechanism by which hantavirus could emerge in regions currently considered non-endemic.

Europe

Dominant strains: Puumala virus (PUUV, bank vole); Dobrava-Belgrade virus (DOBV, yellow-necked mouse and striped field mouse)

Europe's hantavirus burden is defined by cyclical epidemiology: cases surge in years when rodent populations peak, typically following bumper seed and beech mast years, and decline in the intervening periods. In 2023, the European Region reported 1,885 hantavirus infections, a rate of 0.4 per 100,000, the lowest recorded in the 2019–2023 surveillance window. This figure masks significant variation: Finland consistently ranks as the most affected European country, recording 1,000–3,000 cases per year in high-incidence years, with Sweden, Germany, Belgium, and France also reporting regular seasonal caseloads.

Puumala virus, the dominant European strain, causes nephropathia epidemica (NE), a generally mild form of HFRS with fatality rates below 1% in most reported series. Dobrava, Belgrade virus, circulating primarily in the Balkans and southeastern Europe, causes more severe disease, with CFRs reaching 5–12% for its most pathogenic genotype (DOBV-Aa). Both strains are transmitted by small rodents, bank voles for Puumala, yellow-necked mice and striped field mice for Dobrava, whose population cycles are strongly influenced by forest mast production and winter temperature.

European surveillance is generally robust, with the European Centre for Disease Prevention and Control (ECDC) publishing annual epidemiological reports and maintaining standardized case definitions across EU/EEA member states. However, surveillance capacity drops sharply beyond the EU/EEA boundary, particularly in the Caucasus, Central Asia, and parts of the Western Balkans, creating regional blind spots of moderate concern.

Climate projections for Europe suggest that warming winters, which historically limit vole populations, could disrupt established rodent population cycles, leading to more prolonged transmission seasons and potentially expanding the geographic range of endemic zones northward and to higher elevations. Several studies have identified a correlation between increasing temperatures in Northern and Central Europe and multi-year rodent population booms that have historically preceded major HFRS outbreak years.

Regional Hantavirus Assessment Matrix

Indicator	North America	South America	East Asia	Europe
Primary strain(s)	Sin Nombre	Andes + regional	Hantaan, Seoul	Puumala, Dobrava
Annual cases (approx.)	15–40	200–300	50,000–70,000	2,000–5,000
CFR range	~38%	20–50%	0.3–5%	<1–8%
Syndrome type	HCPS	HCPS	HFRS	HFRS/NE
Human-to-human transmission	None documented	Andes only (limited)	None documented	None documented
Surveillance strength	High	Variable	Moderate–High	High (EU/EEA)
Climate risk trajectory	Moderate↑	High↑↑	Declining (vaccines)	Moderate↑
Urbanization pressure	Low–Moderate	Moderate–High	Declining	Low–Moderate
Vaccine availability	None	None	Yes (China, Korea)	None

Table: Al Habtoor Research Centre • Source: Multiple Sources • Created with Datawrapper

Selected Major Hantavirus Outbreaks and Epidemiological Milestones (1993–2026)

Year	Location / Event	Strain	Cases / Deaths	Strategic Significance
1993	Four Corners, USA	Sin Nombre	48 cases; ~50% CFR	First identification of HPS; triggered global strain surveys
1995–1996	Argentina/Chile	Andes virus	Cluster with H2H transmission	First documented human-to-human transmission of any hantavirus
1999–2001	Panama (Azuero Peninsula)	Choclo virus	71 cases; ~23% CFR	Confirmed novel New World strain; rural-to-peri-urban spread
2003	Chile (Aysén)	Andes virus	Multiple H2H clusters	H2H transmission confirmed via contact tracing; healthcare worker infection
2010–2012	Yosemite NP, USA (2012)	Sin Nombre	10 cases; 3 deaths	Visitor exposure in tent cabins; international exposure of tourists
2013	Germany/France (Seoul)	Seoul virus	Cluster in lab workers	Seoul virus in laboratory rat colonies; EU-wide alert
2016–2017	Bolivia	Laguna Negra	Elevated caseload	Drought-linked rodent irruption; diagnostic gap highlighted
2019–2020	China (Shaanxi)	Hantaan virus	37 cases/1 death (bus cluster)	Non-H2H; media amplification raised misplaced pandemic fears
2025 season	Argentina	Andes virus	101 cases; 32 deaths	Double prior-year rate; climate-driven rodent surge implicated
2025 (full year)	Americas (8 countries)	Multiple HCPS	229 cases; 59 deaths; CFR 25.7%	Highest Americas-wide lethality in recent surveillance windows
May 2026	MV Hondius (multi-country)	Andes virus	8 cases; 3 deaths; CFR 38%	First international maritime cluster; IHR notifications across 10+ countries

The evidence presented in this section establishes a clear and consistent picture: hantavirus is geographically concentrated, ecologically dependent, and currently far from pandemic in any conventional epidemiological sense. It does not spread efficiently between humans; it does not achieve urban transmissibility; and its absolute case counts remain modest relative to the major global infectious disease burdens. Yet it is also a virus with a lethal record, an ecological substrate that is actively being reshaped by climate change and land use transformation, and at least one strain, Andes virus, that has already demonstrated, in controlled and now international settings, a capacity for human-to-human transmission that is unique among its family.

3. From Outbreak to Pandemic: A Risk Assessment

Defining the Scale: The Outbreak

An outbreak refers to a sudden increase in cases of a disease or infection within a localized area, specific population, or linked group of individuals. It may involve two or more connected cases, a number of cases exceeding expected levels, or even a single case caused by a serious pathogen such as diphtheria or viral haemorrhagic fever. Outbreaks are usually limited in geographic scope and can often be controlled through public health measures such as isolation, sanitation, vaccination, and contact tracing. They may remain confined to one family or spread locally, nationally, or internationally (e.g. diphtheria or viral haemorrhagic fever). In this context, it is important to distinguish between three related terms:

- **Endemic:** An endemic disease is consistently present within a specific geographic area or population at relatively stable levels. This does not necessarily mean the disease is harmless, but rather that it is regularly found in that region. For example, malaria is endemic in several parts of sub-Saharan Africa.
- **Epidemic:** An epidemic occurs when the number of disease cases rises rapidly above the normal expected level within a community, region, or country over a certain period of time. Epidemics are generally limited to a particular area or population. For example, the 2014 Ebola virus disease outbreak in West Africa was considered an epidemic.
- **Pandemic:** A pandemic is an epidemic that spreads across multiple countries or continents and affects a large number of people, involving sustained global transmission rather than remaining confined to one region. For example, COVID-19 was declared a pandemic by the World Health Organization in 2020.

Main Pandemic Criteria:

Sustained Human-to-Human Transmission, for a disease to reach pandemic potential, it must pass reliably between people without needing an animal as an intermediary host. This is considered the single most important criterion. As Professor William Hanage of Harvard T.H. Chan School of Public Health stated, the case fatality rate is secondary, what truly determines pandemic risk is the efficiency of human-to-human transmission. A pathogen that spreads easily between people, even with low lethality, poses far greater global threat than a deadly but poorly transmissible one.

International spread requires that a pathogen moves freely across national borders through human mobility, travel, trade, and migration, faster than public health systems can detect and respond. The disease must establish transmission chains in multiple countries simultaneously, not merely be carried by isolated travellers. Crucially, spread must occur before any alert is issued, exploiting the gap between exposure and diagnosis. The 2026 MV Hondius outbreak exposed exactly this vulnerability. Before the cluster was identified, passengers from 23 countries had been potentially exposed. Confirmed cases subsequently emerged in South Africa, Switzerland, the Netherlands, Germany, Spain, and the United States, demonstrating how a single point-source event aboard one vessel can seed a pathogen across multiple continents within days

Large-scale community transmission occurs when a pathogen spreads freely within general populations through unknown or untraceable contact chains, moving well beyond the reach of individual case identification. It is characterised by simultaneous, self-sustaining outbreaks across multiple communities, hospitals, and social settings without a common exposure source. At this stage, containment strategies shift from isolation of known contacts to broad mitigation measures. COVID-19 demonstrated this criterion clearly, by the time community transmission was confirmed in most countries, the virus had already embedded silently across entire cities.

Difficulty of containment is characterised by a pathogen's ability to outpace standard public health responses, where isolation, quarantine, and contact tracing prove fundamentally insufficient to interrupt transmission chains. This occurs when the virus spreads faster than cases can be identified, when infectious individuals are mobile before symptoms appear, or when healthcare systems become overwhelmed. Containment failure is typically marked by exponential case growth despite active interventions. The 1918 influenza pandemic is the defining example, quarantine measures slowed but could not stop a virus spreading silently through asymptomatic carriers across every continent.

Silent or asymptomatic transmission occurs when infected individuals spread a pathogen before experiencing any symptoms or without ever becoming visibly ill, making detection and containment extremely difficult. This characteristic is what allows a pandemic virus to embed deeply into populations before authorities recognise the threat. The infectious window precedes diagnosis, meaning standard symptom-based screening fails entirely. Carriers move freely through airports, workplaces, and households unknowingly seeding transmission chains. SARS-CoV-2 demonstrated this most acutely, modelling estimated that over 50% of its transmission occurred pre-symptomatically.

Urban transmissibility, refers to a pathogen's capacity to spread efficiently within densely populated human environments, cities, transport hubs, workplaces, and healthcare facilities. High population density accelerates transmission by increasing the frequency of human contact, while shared infrastructure such as public transport, ventilation systems, and crowded indoor spaces creates ideal conditions for rapid spread. A pandemic pathogen must sustain itself in these settings to reach global scale. The 1918 influenza pandemic demonstrated this acutely, dense urban military camps and civilian cities became the engine of its worldwide propagation.

Overall assessment of Current Pandemic Capability

The following table assesses the current pandemic potential of the Andes virus against each of the six established pandemic criteria:

Pandemic Criterion	Hantavirus Assessment
Human-to-human transmission	Limited – Andes virus is the only known hantavirus capable of person-to-person spread, but requires close, prolonged contact with a symptomatic person. On a cruise ship with 147 passengers in close quarters, only 9 cases resulted. Infectious window is approximately one day around symptom onset.
International spread capability	Moderate – International travel enabled rapid geographic dispersal before detection. Passengers from 23 countries were aboard; confirmed cases reached South Africa, Switzerland, Netherlands, Germany, Spain, and 5 US states. However, no secondary community transmission has been reported in any destination country.
Silent transmission	Weak – Hantavirus settles deep in the lungs rather than the upper airways, limiting airborne spread. Patients are typically only infectious once symptomatic and severely ill. There is currently no strong evidence of sustained pre-symptomatic transmission, unlike COVID-19 or influenza.
Urban spread potential	Low – Rodent reservoir (long-tailed pygmy rice rat) is confined to rural South America. Rodents carrying Andes virus have not been found in the United States or Europe. Primary transmission route remains contact with rodent urine, faeces, or saliva – not urban person-to-person spread.
Containment difficulty	Relatively manageable – Standard isolation, quarantine, and contact tracing effectively contain outbreaks. In the 2018–2019 Argentina outbreak, R_0 (basic reproduction number) measures the average number of secondary infections generated by one infected person. interventions reduced R_0 from 2.12 to 0.96 (below epidemic threshold). The 2026 cruise ship evacuation involved coordinated contact tracing across 23 countries and a 42-day monitoring period per WHO guidance.
Mutation potential	Uncertain – No evidence of mutation toward increased transmissibility in the 2026 outbreak. The virus sequence (ANDV/Switzerland/Hu-3337/2026) was published on virological.org on 8 May 2026 and is under active Nextstrain phylogenetic surveillance. Experts note that most research on zoonotic viruses remains reactive: "We study them after they spill over into humans instead of understanding how they circulate in wildlife beforehand".

Overall assessment of current pandemic capability, as current assessments remain limited by the relatively small number of documented human-to-human transmission events. WHO classifies the 2026 hantavirus outbreak as low global risk. The Andes virus currently lacks the key features of a pandemic pathogen: efficient airborne spread, long pre-symptomatic infectious window, and broad urban reservoir. With a case fatality rate of 38% and an R_0 of 1.19 (reduced to 0.96 post-intervention), it is dangerous but containable. Experts at Harvard, CDC, and WHO agree this is “not a virus that spreads like flu or like COVID – it's quite different” (Dr. Maria Van Kerkhove, WHO; CNN, 8 May 2026).

4. Covid-19 and Hantavirus- A Comparison

Early Case Accumulation Comparison

COVID-19 vs Andes Hantavirus

One useful way to assess the trajectory of an emerging outbreak is to compare the number of confirmed infections recorded within the same timeframe following the first detected case. This does not imply that different pathogens share identical transmission dynamics. Rather, it helps evaluate the speed of outbreak growth, the effectiveness of containment efforts, and whether transmission is accelerating or remaining contained.

COVID-19 was first officially reported to the WHO on 31 December 2019. In the weeks that followed, confirmed infections increased rapidly despite significant underreporting during the early phase of the outbreak. By Day 7, authorities had reported 44 pneumonia cases in Wuhan. By Day 14, official confirmed infections had reached 41 cases. One week later, on Day 21, the number had risen sharply to 278 confirmed cases across China. By Day 30, China alone had recorded 7,711 confirmed infections and 170 deaths, while international spread had already reached 18 countries with 83 confirmed cases outside China.

By contrast, the current Andes hantavirus cluster linked to the cruise ship Hondius has followed a significantly slower trajectory. During the first week following detection, confirmed infections remained limited to two cases. By Day 14, the number had risen to four confirmed cases, before reaching seven cases around Day 21. Approximately one month after the first detection, the outbreak remained confined to only 8–9 confirmed cases, with three reported deaths and no evidence thus far of sustained large-scale transmission.

Comparative Timeline of Confirmed Cases

Overall assessment of current pandemic capability, as current assessments remain limited by the relatively small number of documented human-to-human transmission events. WHO classifies the 2026 hantavirus outbreak as low global risk. The Andes virus currently lacks the key features of a pandemic pathogen: efficient airborne spread, long pre-symptomatic infectious window, and broad urban reservoir. With a case fatality rate of 38% and an R_0 of 1.19 (reduced to 0.96 post-intervention), it is dangerous but containable. Experts at Harvard, CDC, and WHO agree this is “not a virus that spreads like flu or like COVID – it’s quite different” (Dr. Maria Van Kerkhove, WHO; CNN, 8 May 2026).

4. Covid-19 and Hantavirus- A Comparison

Days Since First Detection	COVID-19 (China, 2019–2020)	Andes Hantavirus (2026)
Day 7	44 reported pneumonia cases in Wuhan	2 confirmed cases
Day 14	41 confirmed cases officially identified	4 confirmed cases
Day 21	278 confirmed cases in China	7 confirmed cases
Day 30	7,711 confirmed cases in China, 83 cases across 18 countries	11 confirmed cases
Reported deaths by Day 30	170 deaths	3 deaths

The comparison reveals two fundamentally different outbreak trajectories. COVID-19 demonstrated rapid exponential expansion driven by efficient respiratory transmission, dense urban interaction, and international mobility networks. The outbreak moved from a localised health event to an international crisis within weeks, making containment increasingly difficult.

The Andes hantavirus outbreak, meanwhile, continues to appear cluster-based and geographically concentrated. The slower accumulation of confirmed infections suggests that transmission remains linked primarily to specific exposure settings rather than broad community spread. The outbreak also remains comparatively traceable from an epidemiological perspective, unlike COVID-19, which quickly generated transmission chains that became difficult to monitor.

At the same time, the comparison highlights an important distinction between transmissibility and lethality. Although hantavirus has produced far fewer confirmed infections, the mortality-to-case ratio remains significantly higher. This means that even limited outbreaks can generate substantial concern and strategic attention despite the absence of rapid exponential spread.

The comparison, however, should not be interpreted as evidence that hantavirus could replicate COVID-19's pandemic trajectory. COVID-19 spread primarily through efficient airborne respiratory transmission, whereas hantavirus transmission is generally associated with rodent exposure and, in rare cases, prolonged close human contact. The purpose of the comparison is therefore analytical rather than predictive. It helps measure outbreak acceleration and containment dynamics, not equal pandemic potential.

4.1 Doubling-Time Comparison

Measuring the Speed of Outbreak Expansion

Beyond total case accumulation, one of the most important indicators in outbreak forecasting is the doubling time, namely the period required for confirmed infections to double in number. This metric helps determine whether an outbreak is showing signs of exponential growth or remaining relatively contained.

During the early phase of COVID-19, researchers estimated that infections were doubling approximately every 2.5 to 6.4 days in Wuhan before strict containment measures were introduced.

Some retrospective studies later suggested that the true doubling rate may have been even faster due to limited testing capacity and delayed detection during December 2019 and January 2020. The rapid doubling pattern reflected efficient airborne human-to-human transmission, high population density, and extensive domestic and international mobility networks.

This rapid acceleration became visible very quickly. Officially confirmed cases rose from 41 cases on 11 January 2020 to 278 cases by 20 January, before surging to more than 7,700 confirmed infections by 30 January. In practical terms, the outbreak repeatedly doubled several times within a single month, overwhelming early containment efforts and transforming a local outbreak into an international crisis.

The Andes hantavirus cluster presents a markedly different picture. Approximately one month after the first confirmed cases linked to the Hondius cruise ship outbreak, total infections remained below 10 confirmed cases. Although the number of cases increased gradually from two to four and later to seven cases, the outbreak has not yet displayed the sharp exponential acceleration typically associated with self-sustaining respiratory pandemics.

Comparative Doubling Dynamics

Indicator	COVID-19	Andes Hantavirus
Estimated early doubling time	2.5–6.4 days	No stable exponential doubling pattern observed
Cases after ~30 days	7,711 in China	8–9 confirmed cases
Main driver of spread	Airborne human transmission	Environmental exposure / limited close contact
Transmission traceability	Rapidly lost	Largely traceable clusters

This distinction is critical from an early-warning perspective. Outbreaks become strategically dangerous not only because of lethality, but because of their ability to sustain repeated cycles of rapid transmission. COVID-19 demonstrated exactly this dynamic during its first month. Hantavirus, by contrast, still appears dependent on relatively narrow transmission pathways tied to environmental exposure or close-contact conditions. Nevertheless, monitoring the doubling rate remains important because a sudden reduction in doubling time could indicate that transmission dynamics are changing. Such a shift could suggest either undetected exposure chains, delayed reporting, or the emergence of more sustained human-to-human spread.

4.2 Geographic Spread Comparison

Global Mobility vs Localised Clusters

Another major difference between COVID-19 and hantavirus lies in the geographic pattern of spread. COVID-19 spread internationally with extraordinary speed. Within one month of the first reported cluster in Wuhan, confirmed infections had already reached at least 18 countries across Asia, Europe, North America, and the Middle East. Major transport hubs, international air travel, and dense urban networks accelerated transmission far beyond the original outbreak zone. By late January 2020, cases had already been identified in countries including Thailand, Japan, South Korea, the United States, France, Germany, and the United Arab Emirates.

The speed of geographic diffusion reflected one of COVID-19's defining characteristics: infected individuals could travel while asymptomatic or mildly symptomatic, allowing the virus to move silently across borders before authorities recognised the scale of transmission.

The current Andes hantavirus cluster has behaved very differently. Cases remain strongly linked to identifiable exposure networks connected to the Hondius cruise ship and associated close-contact chains. Unlike COVID-19, there has not yet been evidence of widespread urban transmission or simultaneous outbreaks across multiple unrelated regions.

Geographic Expansion Comparison

Indicator	COVID-19	Andes Hantavirus
Countries affected within ~30 days	18+ countries	6–9 countries
Confirmed international spread by Day 30	83 confirmed cases outside China	Fewer than 10 confirmed cases globally

This geographic distinction matters strategically because outbreaks driven by mobility networks are significantly harder to contain than those tied to identifiable environmental exposure points. COVID-19 spread through interconnected urban systems, airports, and dense social interaction. Hantavirus outbreaks, meanwhile, generally remain concentrated around specific environmental conditions, including rodent habitats, enclosed contaminated spaces, or prolonged close-contact exposure. As a result, geographic spread patterns currently suggest that the hantavirus outbreak resembles a contained epidemiological cluster rather than a globally mobile pandemic event.

4.3 Mortality-to-Case Ratio Comparison

High Spread vs High Fatality

Although COVID-19 spread far more rapidly than hantavirus, its early mortality-to-case ratio was significantly lower.

By 30 January 2020, COVID-19 had caused 170 reported deaths out of approximately 7,711 confirmed cases in China, producing a crude fatality ratio of roughly 2.2% during the early phase. While mortality later varied substantially across countries, age groups, and healthcare systems, COVID-19's strategic danger stemmed primarily from its enormous transmission scale rather than exceptionally high lethality.

Hantavirus presents the opposite dynamic. The current Andes hantavirus cluster has produced approximately three deaths among fewer than 10 confirmed infections, implying a fatality ratio exceeding 30%. Historically, hantavirus pulmonary syndrome in the Americas has often recorded fatality rates between 35% and 40%, depending on healthcare access and the specific viral strain involved.

Mortality Comparison

Indicator	COVID-19 (Early Phase)	Andes Hantavirus
Approximate early cases	7,711	8–9
Approximate early deaths	170	3
Estimated fatality ratio	~2.2%	~33–38%
Strategic risk profile	Massive spread	High lethality

This distinction is important because outbreaks generate strategic disruption through different pathways. COVID-19 destabilised healthcare systems through overwhelming case volume, even when most infections were mild or moderate. Hantavirus outbreaks, meanwhile, can create concern through severe clinical outcomes despite relatively limited transmission. The higher mortality-to-case ratio also explains why even small hantavirus outbreaks attract significant international attention. A pathogen does not need to infect millions of people to generate strategic anxiety if the probability of severe illness or death remains high.

Projected Trajectory

Days Since First Detection	COVID-19 Confirmed Cases	Andes Hantavirus Confirmed Cases
Day 0	2	2
Day 7	44	4
Day 14	41	7
Day 21	278	9
Day 30	7,711	12 (projected if current pace continues)
Day 45	~50,000+	16 (projected)
Day 60	~80,000+	20 (projected)

Note: First symptomatic passenger death occurred around 11 April 2026

Thus, it is evident that the current trajectory of the Andes hantavirus outbreak remains significantly slower than the early expansion pattern observed during COVID-19. Based on presently available data, confirmed cases have increased gradually from approximately two initial cases to fewer than 10 infections within the first month, suggesting a relatively contained and traceable outbreak structure. If the current transmission dynamics continue without major epidemiological change, projections indicate that total confirmed infections could remain below 20–30 cases within the next 60 days. However, even a moderate increase in transmission efficiency or delayed detection could produce a substantially steeper growth curve, potentially pushing cases into the dozens or low hundreds over the same period. By contrast, a COVID-like acceleration pattern, characterised by rapid respiratory transmission and silent community spread, would generate exponential growth capable of producing thousands of infections within weeks. The comparison therefore highlights that the current hantavirus outbreak continues to behave more like a constrained cluster event than a self-sustaining pandemic wave. At the same time, the exercise demonstrates how sensitive outbreak trajectories can become if transmission conditions shift, surveillance weakens, or wider exposure networks emerge.

5. Assessing the Future Trajectory of Hantavirus

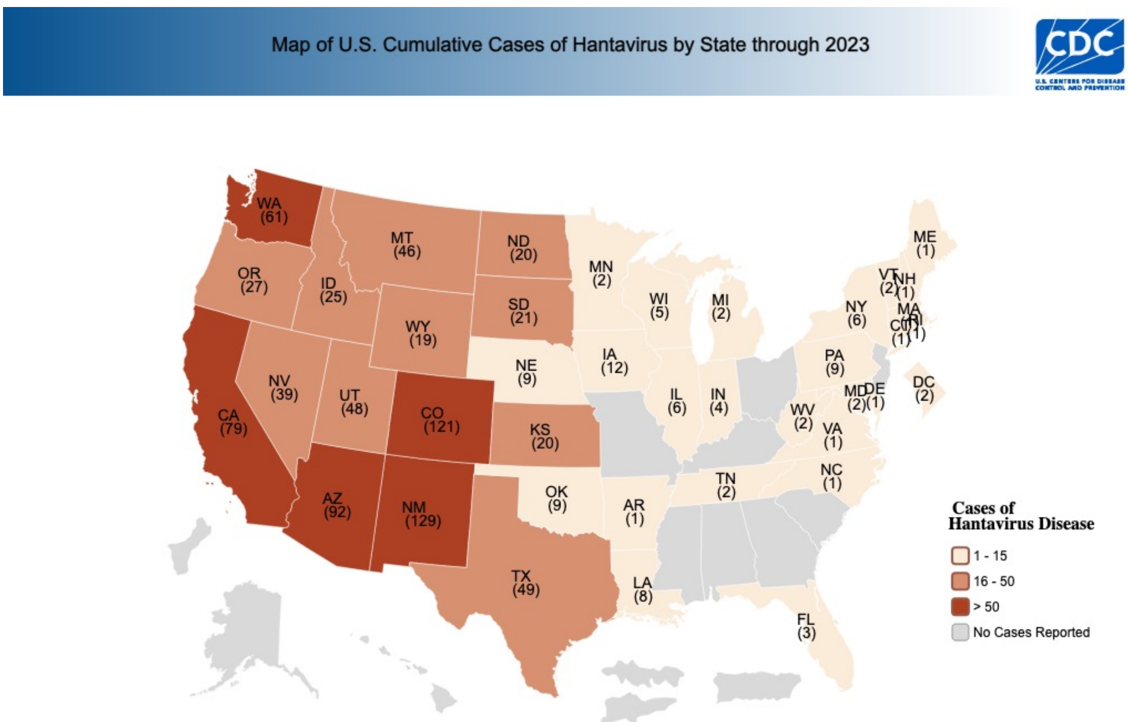
Scenario 1: Continued Localized Outbreaks

The first scenario that should be considered is the scenario that nothing comes from the current Hantavirus outbreak. This can be attributed to the fact that the Hantavirus itself is a rare disease and is mainly transmitted from direct contact between rodents and humans. The rarity of this disease is evident as according to the CDC, between 1993 and 2023, there has been a reported 890 confirmed cases of Hantavirus in the United States. Moreover, the World Health Organization maintains that in South American countries such as Brazil, Argentina, and Chile the number is significantly lower, with the disease being most found in areas within Europe and Asia. While this disease is uncommon there are quite a few strains that exist.

The most worrisome is the Andes strain from South America, which can be transmitted from human-to-human. According to Giulia Gallo, postdoctoral scientist at Pirbright Institute, UK mentions that the most likely scenario is that two passengers on the cruise ship afflicted with the Hantavirus caught the disease while on a trip to South America (Andes strain), which can explain how the virus was able to spread among the passengers.

In this case, there is a possibility that there will be localized outbreaks, however, due to the circumstances for transmission, it is possible people will have limited exposure to the virus, which reduces the chances of these localized outbreaks transitioning into an epidemic or pandemic on a similar scale to COVID-19.

In terms of a response, the WHO have maintained that the chances of the Hantavirus turning into a COVID like pandemic are quite low and recommend there is no need to enact any restrictions on everyday activities. However, the WHO are currently monitoring the situation and do recommend vigilance to potentially stop the Hantavirus from spreading further.



All cases were confirmed between 1993-2023 and met the NNDSS case definition applicable at the time of reporting. Included in the sum total are 31 historical cases that occurred prior to 1993, but were confirmed retrospectively. Five cases had presumed exposure outside the United States.

Under this scenario, the economic impact would remain localized and limited. Governments would likely strengthen public health surveillance, rodent control programs, and hospital preparedness, particularly in rural regions with previous outbreaks. These expenditures would resemble routine infectious disease management rather than emergency economic intervention. Industries such as pest control, sanitation services, and diagnostic laboratories could experience modest gains due to heightened prevention efforts.

Scenario 2: Expanded Regional Transmission (Epidemic)

While the most probable scenario is that the Hantavirus can occur in localized areas, one cannot ignore the possibility that the outbreak can become regionalized, hence, an epidemic. The evolution of the Hantavirus from localized to epidemic can stem from several factors. One of these factors can be the spread of the virus from an infectious agent, which is usually an asymptomatic human or an infected animal. A notable example is the Bubonic Plague, which was carried through rodents and infected fleas, where the disease was transferred to humans through bites or contact with such carriers. In the case of the Hantavirus, it is possible the disease can become more an epidemic if there is an increase of contact between humans and rodents. According to Jorge Salinas, MD, medical director of infection prevention at Stanford Health Centre, the Hantavirus is more likely to spread in areas where there are higher rodent populations, such as rural areas in the western areas of the United States and as the human population continues to grow and society continues to increase its exposure to wildlife, the chances of human to rodent contact also increases. As a result, increased contact between humans and possibly infected rodents contributes to the scenario that the Hantavirus can become epidemic in areas where the rodent population is prevalent.

A contributing factor to the increased infections from rodents to humans is climate change. The link between increasing temperatures and rodent populations also serves as a link to increased infections among humans. This correlation is clear, as areas with higher levels of rainfall and lower temperatures lay the foundation for an increase in the populations of rodents in areas such as Europe, Asia, and the Americas, thus leading to increased risks of a Hantavirus epidemic taking place. For example, the Hantavirus outbreak in 1993 in the United States can be attributed to the increase in rainfall due to the El Nino storm, which resulted in increased food supplies and contributed to a boom in the rodent population. The consequence was an invasion of rodents into civilian populations hence increasing the number of Hantavirus infections at the time. Moreover, increased infections can also be attributed to agricultural expansion, which also could provide rodents with a suitable food source and environment to increase their populations. Therefore, it can be argued that climatic factors can play a role in increasing the chances of regional outbreak.

With ecological and climatic factors contributing to potentially increased rates of infections, naturally, it can also result in higher probabilities of cross-border spread. Naturally, cross-border infections can occur for a host of reasons including migration of rodents into new environments, or through infected humans traveling to different regions. In the current case of the cruise ship Hantavirus infections making the news, the variant identified was the Andes strain, which is spread by prolonged human-to-human contact, however, is limited in transmission. As the passengers on the cruise ship have been exposed to the Andes strain of the virus, it is possible that cross-border contamination can occur and result in a greater risk of infection. However, once again, the possibility of a mass transmission event akin to COVID-19 is limited due to the lack of efficiency in the way the virus spreads. According to Stephen Bradfute, immunologist and Hantavirus researcher from the University of New Mexico Health Sciences Center "Unlike measles and Covid, which can be spread by viruses lingering in the air after an infected person has left a room, Andes virus is spread by close contact…". As the virus does not have an efficient spread rate, the likelihood that it could transform into COVID-19 level event is not high and therefore cross-border spread will also be limited.

In terms of surveilling the spread of the Hantavirus, there is a significant amount of pressure to adequately track and contain the virus. One reason is that it is difficult to assess where the origin of the first infection, which in turn makes it difficult to respond rapidly to the onset of an outbreak. This difficulty in determining the origin of infection is usually associated with emerging viruses. Moreover, there is also pressure to surveil the disease effectively as the virus is difficult to diagnose. This is clear as the symptoms of the virus mimic the symptoms of other viruses such as the flu, and there is no adequate test to effectively confirm a case of Hantavirus. As of now, the only method to diagnose the Hantavirus is through a blood test. Therefore, the surveillance of the virus is difficult and puts pressure on the system to adequately trace the spread of the virus to prevent a possible pandemic scenario.

Under this scenario, economically, the first pressure points would emerge within healthcare systems. Governments in affected countries would likely increase emergency healthcare spending to expand ICU capacity, improve laboratory testing, strengthen epidemiological surveillance, and enhance outbreak response coordination. Public health agencies could also implement targeted quarantine measures and contact-tracing operations in outbreak clusters, increasing operational costs for local authorities.

Labour market disruptions would likely be moderate but noticeable. Workers in affected areas could face absenteeism due to illness, quarantine requirements, caregiving responsibilities, or fear of infection. Productivity losses would be most visible in sectors dependent on physical presence, including agriculture, manufacturing, logistics, and hospitality. Rural economies could be particularly vulnerable because rodent exposure remains closely linked to hantavirus transmission. Furthermore, the long-Hantavirus effect, the need for prolonged pulmonary or renal rehabilitation in survivors, would create a multi-year drain on workforce productivity and social security systems.

Tourism and transportation sectors would likely face sharper disruption if outbreaks emerged simultaneously across multiple countries. Airlines could reduce routes to affected regions, while travellers might postpone or cancel trips due to infection concerns. Cruise tourism has already demonstrated vulnerability following the 2026 hantavirus cluster aboard the MV Hondius, where multiple cases and deaths were reported.

Consumer behaviour would also shift during regional outbreaks. Households typically reduce discretionary spending and increase precautionary savings during periods of uncertainty. Retail sectors dependent on physical foot traffic, including restaurants, shopping centres, and entertainment venues, could therefore experience declining revenues. In contrast, pharmaceutical companies, telemedicine providers, protective equipment manufacturers, and sanitation businesses would likely benefit economically. A significant secondary impact would be the risk-premium hike in the insurance sector; insurers might rewrite force majeure clauses and increase premiums for shipping and agribusinesses operating in high-risk biomes, raising the cost of doing business regardless of case counts.

Financial markets would likely experience heightened but regionally concentrated volatility as investors reacted to concerns over disrupted trade, weaker consumption, and slower economic activity. Countries heavily dependent on tourism or international mobility could face disproportionate losses. At the macroeconomic level, the epidemic scenario would likely reduce growth rates in affected economies by fractions of a percentage point rather than trigger a synchronized global recession. Inflationary pressures could emerge if labour shortages or transportation disruptions affected supply chains, particularly in food and healthcare products. Nevertheless, most economies would likely continue functioning without nationwide lockdowns.

Scenario 3: Mutation Driven Pandemic Event

The final scenario, which is the least probable but the highest impact scenario, the case that the Hantavirus evolves to COVID-19 like pandemic event. There is one way the virus can become contagious enough to result in a pandemic level event, and that is if the virus evolves enough to pass efficiently from rodent-to-humans and/or human-to-human. The Harvard T.H. Chan School for Public Health mentions that experts believe that the Hantavirus can only become contagious enough to result in a pandemic level event if it were to go through "...multiple evolutionary changes..." to pose a realistic threat to global health. For this to happen, the virus would have to evolve over a short period of time, which can only happen through the processes of "first spillover, then adaptation to the new host...", which is necessary for the virus to acquire mutations to become more viral. If that were to happen, the result can be a worrisome scenario akin to the COVID-19 pandemic. Ultimately, it is due to its lack of transmission efficiency and slow evolution that experts believe it will not result in the next pandemic.

However, unlike COVID-19, global health agencies and experts are in the process of monitoring the progress of the current outbreak as preparation for the unlikely case the result is a pandemic. This is clear as experts are monitoring worrying signs such as "...a deadly virus originally in a confined setting, evidence of person-to-person transmission, and international passengers being repatriated around the world". Moreover, the Coalition for Epidemic Preparedness Innovations stated that this case of Hantavirus is important to show why pandemic readiness needs to take place well before a pandemic level event arrives. CEPI are engaged in such readiness by studying high-risk viral families. The belief is that "By studying these families in advance, researchers can develop tools, knowledge and vaccine building blocks that could speed up the response if a pandemic threat emerges". Therefore, the current steps taken to deal with the limited outbreak of the Hantavirus is vital to understanding emerging viruses and potential pandemics.

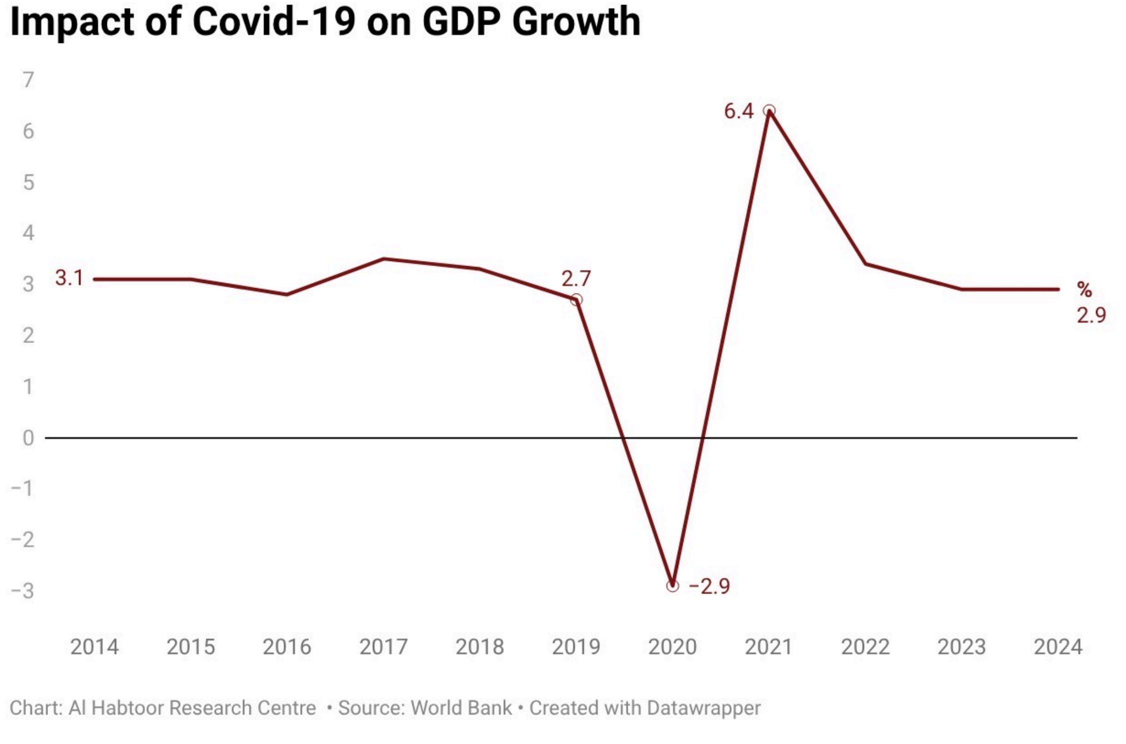
Under this scenario, the immediate policy response would likely include travel restrictions, quarantines, school closures, and large-scale lockdowns. Governments would rapidly expand spending on hospitals, intensive care units, vaccine development, and emergency social support programs. Public debt levels would likely rise sharply as states attempted to stabilize collapsing economic activity. Unlike the 2020 crisis, however, the 2026 economic environment suffers from "fiscal exhaustion.

Because interest rates are already high and government debt is at an all-time peak, central banks have very little emergency fuel left to pump money into the economy and prevent a deep depression.

Global supply chains would face severe disruption. Manufacturing hubs could temporarily shut down because of workforce shortages or lockdown measures, interrupting the production of electronics, pharmaceuticals, automobiles, and industrial goods. Shipping delays and shortages of essential products could generate inflationary pressures worldwide. Food supply systems could also become vulnerable if agricultural labor forces were significantly affected.

Labour markets would experience major shockwaves. Sectors dependent on physical interaction, including aviation, tourism, hospitality, entertainment, retail, and commercial real estate, would likely suffer large-scale job losses. Similar to the COVID-19 crisis, millions of workers globally could face unemployment or reduced working hours within a short period, potentially intensified by higher mortality fears.

The broader macroeconomic consequences could be severe. The World Bank estimated that COVID-19 caused the global economy to contract by approximately 3% in 2020, marking the deepest recession since World War II.



Advanced economies shrank by around 7%, while emerging markets experienced their first collective contraction in decades. A true hantavirus pandemic accompanied by widespread lockdowns could produce comparable contractions in GDP, international trade, and investment. A true hantavirus pandemic, layered over the fragile 2026 geopolitical landscape, would likely trigger a contraction far exceeding that 3% decline of 2020. With the world currently fractured by kinetic warfare and medical nationalism, the cooperative response seen in the past would be replaced by weaponized supply chains and the hoarding of strategic resources. This fragmentation tax, combined with an estimated 50% mortality rate, would paralyze labour-intensive sectors like agriculture and shipping, which are already strained by conflict-related logistics hurdles. Ultimately, a hantavirus-driven lockdown would not just pause the global economy; it would risk a permanent fracture of the international trade system as governments, already exhausted by high debt and defence spending, struggle to choose between biological survival and economic continuity.

Financial markets would likely experience sharp selloffs, with investors shifting toward safe-haven assets such as gold and government bonds. Consumer confidence could decline substantially as uncertainty and mortality fears suppressed spending. Governments and central banks would probably intervene aggressively through stimulus programs, interest rate cuts, and emergency liquidity measures. Long-term structural changes could also emerge. Businesses might accelerate automation to reduce reliance on human labour, governments could localize supply chains to improve resilience, and remote work infrastructure would likely expand further. Digital healthcare, biotechnology, AI-driven diagnostics, and pharmaceutical research sectors could experience major investment growth.

Probable Scenario

Out of these scenarios, the most likely scenario is that the virus will remain localized to a degree and will not result in an existential crisis like the one produced by COVID-19. This is clear as the Hantavirus lacks the efficiency to effectively transmit from human-to-human, which requires prolonged and direct human contact. For the virus to reach a level of virality that compares to COVID-19, it will have to undergo multiple extensive evolutionary changes and mutations in a short period to pose an effective threat to society. While this virus will most likely remain localized the second scenario is also somewhat probable due to climate and ecological factors, which can result in increased rodent populations, hence leading to more cross-border infections.

Also travel among humans can also contribute to the spread of the virus, however, there would have to be direct and prolonged human contact for this spread to take place. Therefore, the most likely scenario is that the virus will remain localized.

6. Policy Implications and Early Warning Preparedness

The preceding analysis has established that hantavirus does not currently meet the epidemiological thresholds required to constitute a global pandemic threat. Nevertheless, its high case fatality rate, ecological sensitivity to climate conditions, and the existence of at least one strain (Andes virus) with documented person-to-person transmission capacity demand sustained policy attention. The 2025 Andes virus outbreak aboard the MV Hondius cruise ship, which activated international health coordination mechanisms across multiple countries and the World Health Organization (WHO),demonstrated how rapidly a localised zoonotic event can acquire global visibility in an interconnected world. This section examines the policy and preparedness architecture necessary to manage hantavirus risk, drawing on current surveillance frameworks and the lessons of the COVID-19 pandemic.

6.1 Public Health Preparedness

Effective preparedness for hantavirus rests on three interlocking pillars: strengthened surveillance, hospital readiness, and community, level prevention. Each addresses a distinct phase of risk, detection, response, and exposure reduction, and all three must be reinforced simultaneously if preparedness is to be meaningful.

Strengthening Surveillance Systems

Current hantavirus surveillance in most affected regions relies primarily on passive case detection, meaning infections are typically identified only after a patient presents with severe symptoms. This approach systematically undercounts the true disease burden. A twenty-year review of United States hantavirus data found that requiring pulmonary symptoms as a condition for reporting excludes milder laboratory, confirmed infections, leaving public health authorities with an incomplete epidemiological picture. The authors proposed that all laboratory-confirmed hantavirus infections, not only those presenting with pulmonary or renal syndrome, should be reportable to health authorities. A broader and more sensitive case definition would better capture the full spectrum of disease and improve situational awareness regarding where and how transmission is occurring.

Active surveillance, proactive testing of at-risk populations and rodent reservoirs, offers a substantially more powerful tool than passive reporting alone. Research applying genomic epidemiology and targeted rodent trapping has demonstrated that active surveillance can identify infection sites and trace phylogeographic relationships between rodent-derived and patient, derived viral strains, providing high-resolution intelligence on transmission dynamics. Embedding this approach within national surveillance frameworks, particularly in endemic regions and ecological corridors where rodent populations are expanding, would represent a significant upgrade over the status quo.

Rodent Population Monitoring

Because hantavirus is fundamentally an ecological disease transmitted through contact with infected rodents or their excreta, controlling human exposure depends on understanding and anticipating rodent population dynamics. Research from Argentina's endemic northwestern region has demonstrated that rodent abundance anticipates human infection outbreaks by approximately three months, and that rainfall events precede rodent population explosions by roughly eight months. This sequential relationship provides a scientifically grounded framework for a two-tier early warning system: tracking rainfall anomalies first, then rodent density indicators, to generate advance warning of elevated human infection risk.

Such an approach requires investment in systematic rodent monitoring networks in high-risk zones. Multiple trapping methods, including live trapping, removal trapping, and proxy indicators such as domestic cat predation rates, can provide triangulated estimates of local rodent density. When populations surge beyond baseline thresholds, public health authorities can proactively issue exposure advisories, intensify community outreach, and pre-position diagnostic and clinical resources.

Hospital Preparedness and Rapid Diagnostics

Hantavirus pulmonary syndrome (HPS) and haemorrhagic fever with renal syndrome (HFRS) are medical emergencies requiring intensive care. With no approved specific antiviral therapy currently available, clinical outcomes depend heavily on the speed and quality of supportive care, including mechanical ventilation, fluid management, and renal support.

Current confirmatory testing, including hantavirus-specific IgM serology, RT-PCR for viral RNA, and immunohistochemical assays, requires laboratory infrastructure unevenly distributed across endemic regions. Developing point-of-care diagnostics deployable at primary and district health facility level, particularly in rural areas where exposure risk is highest, would reduce the diagnostic delay that currently impedes timely clinical management and public health response.

6.2 Early Warning Indicators

An effective early warning architecture for hantavirus must integrate signals from ecological, epidemiological, virological, and climatic domains. No single indicator is sufficient; rather, it is the convergence of multiple signals that should trigger escalating public health responses. The table below sets out the principal indicator categories, their specific manifestations, and suggested response thresholds.

Indicator Category	Specific Signal	Response Threshold
Epidemiological	Sudden clustering of human-to-human transmission	2+ linked cases without rodent exposure
Geographic	Cases appearing in dense urban or peri-urban zones	First confirmed urban cluster
Ecological	Rapid rodent population surge following rainfall	Rodent density exceeds regional baseline by 3x
Virological	Novel strain with altered glycoprotein receptor binding	Any detected mutation in glycoprotein region
Climatic	Anomalous rainfall or temperature shifts in endemic zones	Rainfall 40%+ above seasonal average
Healthcare	Unexplained severe pneumonia in high-risk occupations	Cluster of ≥3 unexplained severe respiratory cases

The most consequential early warning signal would be the detection of sustained human-to-human transmission, particularly in an urban setting, as this would represent a fundamental departure from the virus's established epidemiological behaviour. Equally significant would be the genomic detection of mutations in the viral glycoprotein, which governs host cell entry and could, if altered, affect transmissibility. Genomic sequencing of clinical and rodent-derived samples on a routine basis, rather than solely during recognised outbreaks, is therefore an indispensable component of any serious preparedness architecture.

Climatic signals deserve particular weight. Research has consistently linked elevated rainfall to subsequent rodent population growth and, with further lag, to increases in human infection rates. Climate projections for many hantavirus-endemic regions, including parts of South America, East Asia, and Central Europe, suggest increasing rainfall variability, which may translate into more frequent and intense rodent population surges. Integrating meteorological data into epidemiological forecasting platforms, ideally through automated alert systems, would enable proactive rather than reactive public health action.

6.3 Lessons from COVID-19

The COVID-19 pandemic was, among other things, a comprehensive audit of the world's preparedness architecture. Several of its failure modes are directly applicable to hantavirus preparedness, even though the two pathogens differ substantially in their transmission characteristics.

The Imperative of Early Detection

COVID-19 spread for weeks before it was recognised as a novel pathogen, and for further weeks before effective containment measures were activated. The critical window for early containment, before community transmission becomes self-sustaining, was missed in most countries due to insufficient surveillance sensitivity. For hantavirus, the analogous risk lies in the quiet early phase of an outbreak: unexplained fever clusters in farming communities, dengue-negative febrile illness in rural clinics, or severe pneumonia among travellers returning from endemic regions. Public health systems must be explicitly trained to consider hantavirus in differential diagnoses for severe unexplained respiratory or renal illness, particularly among high-risk occupational groups such as farmers, miners, forestry workers, and healthcare staff.

International Coordination and Data Sharing

COVID-19 exposed profound weaknesses in international mechanisms for sharing epidemiological intelligence quickly and equitably. The 2025 hantavirus cruise ship outbreak immediately triggered coordination between multiple national health authorities and the WHO — a more responsive reaction than the early days of COVID-19, reflecting the institutional learning of the preceding years. Sustaining and deepening these coordination mechanisms, including resolving outstanding disagreements around the WHO pandemic treaty, is essential before rather than during a health emergency.

Pathogen genomic data sharing is particularly critical. The number of countries with in-country sequencing capacity increased by 40% between February 2021 and July 2022, largely as a consequence of COVID-19 investments. This capacity should be extended to hantavirus and other zoonotic pathogens, with sequences deposited in open repositories such as GISAID or NCBI GenBank on a routine basis. Sharing hantavirus genomic data in real time enables the global scientific community to track viral evolution and detect the emergence of variants with altered biological properties far more rapidly than traditional surveillance would permit.

Public Communication and Misinformation Management

The COVID-19 pandemic was accompanied by a parallel infodemic — a flood of misinformation that complicated public health messaging and eroded public trust. Hantavirus is not immune to this dynamic. The 2025 cruise ship outbreak generated widespread media coverage, with some outlets drawing explicit and epidemiologically misleading comparisons to COVID-19. The WHO's Maria Van Kerkhove was compelled to issue a direct public statement clarifying that the outbreak did not represent "the next COVID," while affirming that hantavirus remains a serious disease warranting vigilance.

Clear, calibrated, and timely public communication is therefore a preparedness function, not merely a communications afterthought. Health authorities should develop standing communication protocols for hantavirus events that distinguish between the elevated lethality of hantavirus (which is real) and its low transmissibility (which sharply limits pandemic risk under current conditions). Failure to make this distinction risks both under-reaction and disproportionate alarm, neither of which serves public health objectives.

Pandemic Readiness Gaps: Treatment and Countermeasures

COVID-19 demonstrated the transformative potential of advance investment in platform technologies. Hantavirus currently has no internationally approved vaccine and no specific antiviral therapy; clinical management remains entirely supportive. This represents a serious vulnerability. The biopharmaceutical industry, drawing on the COVID-19 experience, has made commitments under frameworks such as the Berlin Declaration to reserve production capacity and ensure equitable access to countermeasures for lower-income countries. Extending these commitments explicitly to priority zoonotic pathogens including hantavirus, under "Disease X" preparedness frameworks, would represent meaningful progress. The stated goal of developing effective pandemic products within 100 days of a new pandemic declaration is achievable only if the underlying research and manufacturing infrastructure for relevant pathogen families is developed in advance.

6.4 Strategic Recommendations

The following recommendations are organised by priority level and reflect an integrated One Health approach, recognising that hantavirus risk sits at the intersection of ecological, animal, and human health systems, and that effective preparedness must address all three domains simultaneously.

Priority Level	Recommendation	Lead Stakeholders
High	Expand real-time rodent and wildlife surveillance in endemic and border zones	WHO, Ministries of Health, PAHO
High	Standardise hantavirus case definitions and reporting protocols globally	WHO, CDC, national laboratories
High	Develop rapid diagnostics deployable at primary care level	Research institutions, MoH
Medium	Integrate climate modelling with epidemiological forecasting platforms	Academic bodies, WHO
Medium	Establish cross-border data-sharing agreements for zoonotic disease signals	Regional health authorities
Medium	Conduct occupational risk assessments for high-exposure groups	Labour and health ministries
Long-term	Invest in AI-assisted surveillance for anomaly detection in disease signals	Tech sector, public health bodies
Long-term	Fast-track vaccine and antiviral research under pandemic preparedness frameworks	Pharmaceutical industry, governments

Integrating Ecological and Epidemiological Monitoring

The strongest preparedness investment is the integration of ecological surveillance, tracking rodent populations, rainfall patterns, land-use change, and vegetation indices, with human epidemiological data streams. This One Health approach, endorsed by the WHO, FAO, and UNEP as the appropriate paradigm for zoonotic disease preparedness, means building platforms that can ingest rodent density data from field monitors, rainfall anomaly data from meteorological services, and clinical notification data from health facilities, and synthesise them into risk assessments actionable at the national and sub-national level.

Improving Global Reporting Systems

PAHO's 2024 initiative to align surveillance protocols and laboratory strategies across the Americas, convened in Panama and involving Argentina's INEVH, the US CDC, and PAHO, represents precisely the kind of regional coordination infrastructure that should be replicated and sustained. Standardising case definitions, laboratory methods, and data reporting formats across jurisdictions reduces friction that currently impedes comparative epidemiological analysis. The WHO's Bunyavirales Collaborative Open Research Consortium (CORC), led by the UK Health Security Agency and including ANRS MIE in France, provides a model for international scientific collaboration on hantavirus that should be expanded to more endemic regions.

Enhancing Regional Cooperation

Border regions are often where epidemiological risks are highest and institutional coordination weakest. Many hantavirus-endemic areas span national boundaries, the Patagonian corridor shared by Argentina and Chile, the Balkans region of Europe, and the Korean peninsula. Effective outbreak response in these zones requires pre-negotiated protocols for information sharing, joint field investigations, and cross-border patient management. Bilateral and multilateral health security agreements that specifically address zoonotic disease preparedness, including hantavirus, should be formalised and exercised regularly through simulation drills.

Investing in Predictive Modelling and AI-Supported Surveillance

Artificial intelligence and machine learning offer significant potential for enhancing the sensitivity and speed of hantavirus surveillance. Anomaly detection algorithms applied to syndromic surveillance data, flagging unusual clusters of respiratory or renal illness in real time, could identify outbreak signals days or weeks earlier than traditional reporting systems. Predictive models integrating climate variables, rodent population dynamics, and historical outbreak data could generate probabilistic risk maps updated on a rolling basis, enabling anticipatory public health action rather than reactive response.

Conclusion

This paper finds that hantavirus, in its current biological and epidemiological form, does not constitute a pandemic-level threat comparable to COVID-19. Despite the international attention generated by the 2026 MV Hondius outbreak and the documented capacity of the Andes strain for limited human-to-human transmission, the virus remains structurally constrained by several factors: inefficient interpersonal spread, the absence of sustained community transmission, limited urban transmissibility, and continued dependence on ecological exposure pathways linked primarily to rodent reservoirs.

Nevertheless, dismissing hantavirus as merely a localized zoonotic disease would underestimate its strategic significance. The virus combines exceptionally high case fatality rates with expanding ecological risk factors driven by climate change, environmental disruption, urban expansion into wildlife habitats, and increasing global mobility. These conditions increase the likelihood of more frequent regional outbreaks and create opportunities for cross-border transmission events capable of testing international surveillance and response systems.

The paper further demonstrates that the primary risk posed by hantavirus is not its current pandemic capability, but the possibility that future viral adaptation, ecological shifts, or surveillance failures could alter existing transmission dynamics. The documented person-to-person transmission of the Andes strain, although limited, represents a critical warning that zoonotic pathogens cannot be assessed solely according to their present behaviour.

Ultimately, the central lesson of the 2026 outbreak is not that hantavirus is the next COVID-19, but that global preparedness systems remain largely reactive rather than preventive. Effective preparedness therefore requires sustained investment in early-warning systems, genomic surveillance, rodent population monitoring, rapid diagnostics, and international coordination frameworks before a more transmissible zoonotic threat emerges. In an era increasingly defined by climate instability, ecological disruption, and rapid global interconnectedness, pathogens once considered geographically contained can no longer be treated as strategically insignificant.

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