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RAPID REVIEW

Genomic Epidemiology and Molecular Characteristics of Andes Virus

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Key Findings

- A multi-country hantavirus outbreak originating on a cruise ship, the MV *Hondius*, is ongoing. Canadians who were on the vessel or those in contact with symptomatic passengers on flights are currently being monitored by local public health authorities
- Preliminary genomic analyses are consistent with Andes virus (ANDV) as the causative agent of the current outbreak
- ANDV is endemic to Southern South America, where rodents serve as the primary reservoirs
- ANDV is a distinct from hantaviruses identified in Canada, including Sin Nombre virus in western Canada and New York virus detected in deer mice in eastern Canada
  - Neither virus has been associated with person-to-person (PTP) transmission
  - No hantavirus pulmonary syndrome (HPS) cases were reported in Ontario between 2015–2024
- Although ANDV is the only hantavirus with documented PTP transmission, no single mutation has been conclusively shown to independently confer efficient human transmissibility
- Genome sequences from 2026 cases in Switzerland, the Netherlands, South Africa and Canada form a monophyletic cluster, with segments sharing either identical sequences or nearly identical sequences
- Genomic analyses of the 2026 sequences associated with the MV *Hondius* outbreak showed the absence of mutations, Q40R and N47S in the non-structural protein (NSs) encoded within the small (S) segment, and T641I in the glycoprotein precursor encoded within the medium (M) segment, previously reported in prior ANDV infection outbreaks

Scope

Public Health Ontario is providing evidence-based information on the ANDV to understand whether any recent changes in the viral genome may alter or enhance its ability to transmit person-to-person.

This report summarizes current knowledge of the genomic epidemiology and molecular characteristics of the ANDV, a hantavirus species implicated in an international outbreak on board the MV *Hondius* cruise ship. The analysis described here includes a recently sequenced Andes virus genome from the plasma of a symptomatic Swiss individual that was on board the MV *Hondius*.

Since departing Ushuaia, Argentina, in early April 2026, publicly available information (current as of May 17, 2026) indicates that 11 individuals who were on board the ship at various times were either confirmed to have or suspected of Andes virus infection, including three fatalities.

Background

Hantaviruses (genus: *Orthohantaviruses*) are a diverse group of rodent-borne viruses with a near worldwide distribution, comprising 37 recognised species.[1-4] Human infections most frequently occur from exposure to aerosolised secreta or excreta containing infectious virions from infected rodent reservoirs.[5-6] Only Andes virus (ANDV; *Orthohantavirus andesense*) infection is known to transmit person-to-person (PTP). PTP outbreaks occurred in Argentina in 1996, and again in 2018.[5, 7-8] In April–May 2026, an ongoing ANDV outbreak linked to the cruise ship, the MV Hondius involve at least 6 confirmed and two suspected cases with three fatalities as of May 10, 2026.[9-11]

Methods

We reviewed the published and preprint literature for ANDV mutations potentially associated with PTP, outbreak dynamics, and viral evolution. PubMed searches were performed using combination of the following keywords: (“Hantavirus” OR "Andes virus" OR "Andes orthohantavirus" OR ANDV) AND (human OR rodent OR reservoir) AND (outbreak OR cluster OR "person-to-person transmission" OR superspreading) AND (mutation OR variant OR genomics OR phylogeny OR evolution). Sequence data from the 2026 outbreak and previously reported outbreak-associated strains were retrieved from the Pathoplexus (SeqSet: https://doi.org/10.62599/PP_SS_1783.1) and analyzed for genomic relatedness.

Results

Characteristics of Hantavirus

Hantaviruses are enveloped, single-stranded, negative-sense RNA viruses with a tripartite genome (total genome size: ~11-13 kb)[12]:

- The small (S, ~1.8–2.1 kb) segment encodes a nucleocapsid (N) protein involved in viral replication and assembly
    - In some hantaviruses including ANDV viruses, it also encodes a non-structural protein (NSs) that modulates host innate immune responses
- The medium (M, ~3.6–3.8 kb) segment encodes a glycoprotein precursor (GPC), is responsible for host cell attachment and viral entry
- The large (L, ~6.5–6.7 kb) segment encodes the RNA-dependent RNA polymerase (RdRp) responsible for viral replication and transcription.

Hantaviruses exhibit substantial genomic diversity across rodent reservoir populations and associated human infections, with viral evolution influenced by host ecology and geographic separation. Multiple genetically distinct ANDV lineages have been identified in both rodents and humans, although available evidence suggests relative genomic stability during short-term transmission chains and outbreaks.[13-15] Genome sequences from Switzerland, the Netherlands, South Africa and Canada form a monophyletic cluster, with segments sharing either identical sequences or nearly identical sequences.

Although ANDV is the only hantavirus with documented PTP transmission, no single mutation has been conclusively shown to independently confer efficient human transmissibility (Table 1). Current evidence instead supports genomic signatures associated with prior PTP outbreaks, particularly the 2018–2019 Epuyén outbreak in Argentina.[5] Comparative phylogenetics and outbreak genomic studies identified recurrent candidate mutations, especially M segment T641I and NSs substitutions Q40R and N47S, within a monophyletic PTP-associated linages (Table 1).[16-18] These mutations are repeatedly observed in Argentine PTP-associated ANDV outbreak but remain correlative and lack definitive functional validation.[16-18]

Genomic analyses of the 2026 sequences associated with the MV *Hondius* outbreak showed absence of mutations previously reported in prior ANDV outbreaks, including NSs Q40R and N47S and M segment T641I. Instead, the 2026 sequences retained mutations more commonly observed in non-PTP reference sequences. M and S gene phylogenies further demonstrated that the 2026 outbreak sequences do not cluster within the previously characterized 2018–2019 Epuyén outbreak PTP associated lineage, as per a preliminary report and ANDV nextstrain.[9, 19]

Table 1: ANDV Mutations Proposed to Be Associated with Person-to-Person Transmission and Supporting Experimental or Genomic Evidence

No mutation has been conclusively demonstrated to independently confer efficient person-to-person transmission in ANDV; most associations remain correlative and require functional validation.

Gene: Mutation	Context	Evidence type	Interpretation (reference)	Strength of evidence
M: P97S	Human outbreak-associated ANDV strains and Chilean reservoir surveillance	• WGS • Selection analysis	Possible effect on receptor interaction or immune recognition (2025 preprint)[16, 17]	Speculative/not proven
M: L247S	2018–2019 Epuyén outbreak, Argentina	WGS phylogenetics	Observed in outbreak network but no evidence for increased transmission[5]	Observed only – not proven
M: V499L	2018–2019 Epuyén outbreak and related PTP-associated strains	Comparative analysis	Identified as a PTP outbreak-related substitution; functional role unknown[16,18]	Candidate association
M: T641	Multiple PTP-associated outbreaks	• WGS • Phylogenetics • Hamster studies • Selection analysis	• Most consistently discussed PTP- associated mutation[5, 16-18] • Shared among several ANDV strains associated with PTP transmission. (2025 preprint)[16]	Candidate PTP-associated mutation
M: T938A	Human transmission clusters in Argentina	WGS	• Near antibody escape-associated region; biological significance uncertain (2025 preprint)[5, 16-18]	Candidate mutation - not proven
S-NS: Q40R	PTP-associated ANDV clade	Comparative WGS phylogenetics	Potentially affecting innate immune modulation[16]	Candidate PTP-associated mutation

Gene: Mutation	Context	Evidence type	Interpretation (reference)	Strength of evidence
S-NS: N47S	PTP-associated ANDV clade	Comparative WGS phylogenetics	Proposed PTP-associated mutation[16]	Candidate PTP-associated mutation
L: Q1965H	Chile/Argentina PTP-associated clade	WGS phylogenetics	Conservative substitution with likely limited functional impact (2025 preprint)[17]	Weak candidate association
M codons 265, 699, 721, 743, 994	Chilean reservoir surveillance	Selection analysis	Positive selection signal within Gn/Gc antibody-targeted domains; Possible antigenic relevance (2025 preprint)[17]	Evolutionary signal only

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