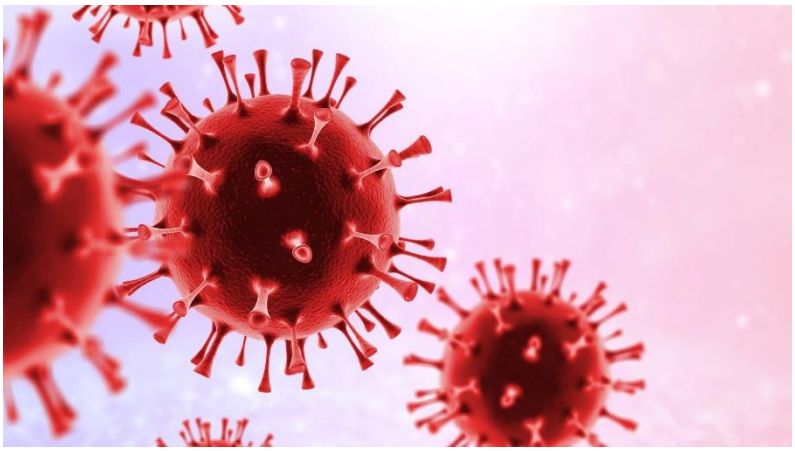
The Next COVID-19 is not consider as Andes Hantavirus

In May 2026, multiple countries identified cases of Andes hantavirus infection linked to the MV Hondius cruise ship. The individuals affected developed severe respiratory symptoms, leading to heightened international scrutiny and drawing parallels to the initial phase of the coronavirus disease 2019 (COVID-19) pandemic, when rapid transmission of SARS-CoV-2 created significant public health challenges.

Given the growing public concern and the potential for confusion between these two pathogens, it is essential to provide a clear scientific distinction between Andes hantavirus and SARS-CoV-2. This includes an examination of their respective transmission routes, mechanisms of disease development, and the overall level of risk each poses to the general population.



Study

Key risk factors for Andes hantavirus involve direct or indirect contact with infected rodent reservoirs, in contrast to the airborne and highly transmissible nature of SARS-CoV-2 outbreaks in closed environments. To clarify the fundamental differences between these two pathogens, the following sections provide a detailed comparison across five main domains: viral receptors, viral shedding, transmissibility, diagnostic strategies, and genomic characteristics.

Andes virus is a New World hantavirus maintained in nature by the long-tailed pygmy rice rat, a rodent native to Argentina and Chile. Human infection occurs mainly through inhalation of dust or aerosols contaminated with rodent excreta. The virus primarily enters cells via the protocadherin-1 (PCDH1) receptor, found on pulmonary endothelial cells, but may also use alternate pathways in airway epithelium, which could explain rare cases of person-to-person transmission. Nonetheless, the respiratory spread of Andes virus is less efficient than that of SARS-CoV-2.

In contrast, SARS-CoV-2 exploits the ACE2 receptor and the TMPRSS2 protease, both of which are plentiful in the respiratory tract. This facilitates efficient viral replication and person-to-person transmission via respiratory particles and aerosols. While Andes virus typically leads to severe disease by disrupting blood vessel integrity and causing fluid leakage into the lungs, severe COVID-19 primarily results from extensive viral replication in respiratory tissues and an intense inflammatory response.

The incubation period for SARS-CoV-2 has progressively shortened as new variants have emerged, ranging from 4–5 days for early strains to 3–4 days for Omicron. In contrast, Andes virus is characterized by a substantially longer incubation period, up to 6 weeks, with a median of about 20 days.

Andes virus RNA is primarily found in blood, with less frequent detection in saliva and nasopharyngeal secretions, indicating that transmission via respiratory secretions is rare and sustained person-to-person spread is unlikely. SARS-CoV-2, in contrast, is abundantly shed in saliva and respiratory tract samples, supporting efficient respiratory transmission.

For Omicron, viable virus shedding lasts about 5 days, and viral RNA is detectable for about 11 days. While SARS-CoV-2 RNA can be detected in other body fluids, the infectious virus is rarely found outside the respiratory tract.

Andes hantavirus transmission outside endemic regions is rare, with no evidence of sustained human-to-human spread, unlike SARS-CoV-2. Outbreaks of SARS-CoV-2 are marked by efficient respiratory transmission, high reproduction numbers, and rapid case doubling, especially in confined settings. In contrast, Andes virus outbreaks in closed environments produce fewer secondary cases over longer periods, reflecting lower transmissibility and longer incubation periods.

The Epuyen outbreak in Argentina provides the strongest evidence of Andes virus person-to-person transmission, but the reproduction number remained below that of SARS-CoV-2 and decreased further with control measures. Most introductions of Andes virus do not result in secondary cases, and onward transmission is usually limited to a single close or sexual contact. There is no evidence for asymptomatic spread or seroconversion.

Asymptomatic or mild Andes virus infections are poorly characterized, with limited data suggesting that some cases may be missed by surveillance systems focused on severe illness. Transmission likely occurs near symptom onset, but the timing and duration of infectiousness are not well defined. This contrasts with SARS-CoV-2, particularly Omicron, where pre-symptomatic transmission plays a major role in rapid spread.

Findings

For COVID-19, diagnosis relies on polymerase chain reaction (PCR) or antigen testing from upper respiratory tract samples, while serological testing has limited value due to delayed antibody response and high background seroprevalence. Viral load in SARS-CoV-2 typically peaks early, reducing the utility of antibody detection in acute settings.

In contrast, hantavirus diagnosis, including Andes virus, primarily relies on reverse transcription polymerase chain reaction (RT-PCR) of blood-derived specimens during the acute phase, with serology supporting diagnosis. Drawing largely on evidence from studies of Old World hantaviruses, IgM and IgG antibodies often become detectable within a week of symptom onset, with IgG persisting long term.

Molecular testing is most sensitive in the early symptomatic phase, and saliva testing may help assess transmission risk. PCR can detect infection before seroconversion, aiding early diagnosis in exposed contacts.

SARS-CoV-2 evolves primarily through ongoing human-to-human transmission and immune pressure, selecting spike protein mutations that enhance transmissibility, enable immune evasion, and, in certain variants, increase disease severity. Periods of rapid variant emergence are associated with accelerated evolutionary rates.

In contrast, Andes virus genetic diversity is largely determined by geographic distribution and the characteristics of local rodent reservoirs. Although short-term substitution rates can be high, recent outbreak analyses reveal limited overall diversity. To date, no specific mutation has been associated with enhanced human adaptation or transmissibility. Experimental studies indicate that Andes virus genomes remain stable during short transmission chains, with adaptive mutations accumulating slowly.

Conclusion

The current analysis aligns with World Health Organization (WHO) and European Center for Disease Prevention and Control (ECDC) assessments, confirming that Andes hantavirus poses a low risk to the general public, including during outbreaks in confined settings.

Unlike SARS-CoV-2, Andes virus is rodent-borne, causes disease through vascular mechanisms, relies on blood and serology for diagnosis, and has limited respiratory transmission. Public health responses should emphasize environmental investigation, case isolation, and thorough contact tracing, without conflating the risk of Andes virus with that of SARS-CoV-2.

This distinction is central to current guidance, reaffirming that Andes virus does not currently pose a SARS-CoV-2-like pandemic risk according to WHO and ECDC assessments.

Source:

https://www.news-medical.net/news/20260610/Why-Andes-hantavirus-is-not-the-next-COVID-19.aspx