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Editorial

Hantaviruses in the One Health era: strengthening surveillance before the next spillover

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Abstract

Keywords

Hantaviruses, One Health, wildlife surveillance, rodent reservoirs, zoonotic spillover

Hantavirus infections are emerging zoonotic diseases of increasing global public health concern, although their relevance in Europe remains less recognised than in other endemic regions. Renewed attention has recently focused on these viruses following media reports describing a suspected hantavirus outbreak on a cruise ship anchored off the coast of Cape Verde, associated with multiple fatalities. Of particular concern is the reported involvement of the Andes orthohantavirus (ANDV), currently the only hantavirus known to be capable of documented human-to-human transmission (Disease Outbreak News, WHO, 8 May 2026; Taylor, 2026).

Orthohantaviruses, hereafter referred to as hantaviruses, are negative-sense RNA viruses belonging to the subfamily *Mammantavirinae* within the family *Hantaviridae* (ICTV; https://ictv.global/). These viruses are primarily maintained in nature by rodent reservoirs, although hantavirus-like viruses have also been detected in insectivores, including shrews and moles, as well as bats (Chen et al., 2023). Reservoir hosts are generally chronically and asymptomatically infected and may shed the virus in urine, faeces, and saliva for prolonged periods (Bi et al., 2008). To date, more than 50 hantaviruses have been identified in rodent species worldwide, and phylogenetic analyses suggest that each virus has likely co-evolved with a specific host species. This long-term evolutionary relationship may have favoured the establishment of persistent lifelong infections in which viral replication and host immune responses remain relatively balanced, allowing survival of both the pathogen and its reservoir host (Easterbrook & Klein, 2008).

Text

Within reservoir populations, hantaviruses are transmitted horizontally either directly, through aggressive or grooming behaviour, or indirectly through inhalation of infectious particles released into the environment. Humans are accidental hosts, and infection generally occurs through inhalation of aerosolised viral particles originating from contaminated excreta. Activities such as harvesting crops, handling hay, cutting wood in poorly ventilated woodsheds, or cleaning barns, sheds, and rural seasonal dwellings are considered major risk factors for transmission. Consequently, occupational groups with frequent exposure to rodents, including farmers, forestry workers, mammalogists, animal trappers, and military personnel, are regarded as being at increased risk of infection (Vapalahti et al., 1999; Deutz et al., 2003; Mustonen et al., 2024).

Environmental conditions may influence both reservoir host abundance and the persistence of viral particles in the environment, potentially increasing viral circulation within rodent populations and consequently the risk of zoonotic transmission to humans (Khalil et al., 2014; Maroli et al., 2018). Traditionally, hantaviruses are divided into two major

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groups: Old World hantaviruses, mainly distributed in Europe and Asia, and New World hantaviruses, circulating in the Americas. Old World hantaviruses are primarily associated with rodent genera such as *Myodes*, *Microtus*, *Apodemus*, and *Rattus*, and are responsible for haemorrhagic fever with renal syndrome (HFRS), with disease severity varying according to the viral species involved. Clinically important representatives include Puumala orthohantavirus (PUUV), Dobrava-Belgrade orthohantavirus (DOBV), Seoul orthohantavirus (SEOV), and Hantaan orthohantavirus (HTNV). In contrast, New World hantaviruses were first recognised following outbreaks of hantavirus cardiopulmonary syndrome (HCPS) in the Americas in 1993 and are mainly associated with New World rodent species. Among them, Sin Nombre orthohantavirus (SNV) and ANDV are considered the most clinically relevant (Jonsson et al., 2010).

Currently, more than 28 hantavirus species associated with human disease have been identified worldwide. While HFRS represents the major global clinical burden, with more than 100,000 estimated cases annually and mortality rates reaching up to 15% depending on the viral species involved, several thousand HCPS cases have also been reported in the Americas since the syndrome was first recognised (Vaheri et al., 2013; Kruger et al., 2015). The greatest disease burden is reported in China, which accounts for more than 90% of all HFRS cases globally and has remained the most affected country since the early 2000s (Jiang et al., 2017). Other endemic areas include South Korea, Russia, and several European countries, particularly within the Balkan and Northern European regions, where different hantavirus species continue to circulate in wild rodent populations (Heyman et al., 2011; Avšič-Županc et al., 2019).

Growing evidence also indicates that hantaviruses circulate in Africa, where their diversity, ecology, and public health significance remain largely unexplored (Klempa et al., 2006). Since the identification of the first African hantaviruses, including the Sangassou virus (SANGV) in rodents and the Tanganya virus (TGNV) in shrews, additional investigations have revealed an unexpectedly broad host range involving rodents, insectivores, and bats. Nevertheless, little is currently known regarding the pathogenicity, epidemiology, and zoonotic potential of these viruses in African settings (Castel et al., 2023). Limited surveillance programmes, restricted diagnostic capacity, and the frequent overlap with other febrile diseases may contribute to substantial underdiagnosis and underreporting across the continent. Furthermore, the recent detection of novel hantaviruses in wildlife species from Sierra Leone and Côte d'Ivoire highlights the complex evolutionary history of these pathogens and raises concerns regarding their potential emergence as an underrecognised threat to both human and animal health in Africa (Castel et al., 2023).

Although Italy is geographically close to several endemic regions and hosts recognised reservoir species, no confirmed autochthonous human infections have been officially reported during the last decade. To date, only a limited number of cases have been documented, mostly involving tourists or cross-border workers likely infected abroad (Riccò et al., 2021). However, serological evidence of exposure to PUUV and DOBV has previously been reported in both humans and rodents, especially in mountainous areas close to the Austrian and Slovenian borders (Kallio-Kokko et al., 2006; Rizzoli et al., 2015). In addition, the molecular detection of DOBV in *Apodemus flavicollis* in north-eastern Italy in 2021 further supports the likelihood that hantaviruses are circulating, at least locally, within the country (Leopardi et al., 2022). Nevertheless, the presence of competent wildlife reservoirs across Europe highlights the importance of maintaining active surveillance systems capable of detecting potential viral circulation before the occurrence of human outbreaks. In this context, genomic and metagenomic surveillance of wild rodents should be increasingly considered a public health priority, similarly to what has already been implemented for other wildlife-associated zoonotic threats, including bat-borne viruses and arboviruses. Lessons learned from the SARS-CoV-2 pandemic highlight the urgent need to strengthen and expand surveillance systems for emerging viruses. This should be achieved through an integrated One Health approach, encompassing not only known reservoirs and vectors, but also poorly investigated wildlife hosts and ecological niches that may represent critical starting points for future spillover events and, potentially, new pandemic threats (Lorusso et al., 2020). Continuous monitoring of rodent populations, combined with ecological and environmental data, may provide valuable insights into viral diversity, host distribution, and the early identification of emerging hantaviruses with zoonotic potential.

Within the One Health framework, veterinarians and veterinary virologists play a central role in the surveillance of pathogens circulating at the human–animal–environment interface. Beyond their contribution to animal health, veterinary laboratories increasingly represent essential components of early warning systems for emerging zoonotic threats. In the case of hantaviruses, strengthening surveillance activities in wildlife reservoirs and integrating molecular epidemiology, genomics, and ecological investigations will be crucial to improve preparedness and risk assessment strategies in Europe.

During recent decades, substantial progress has been made in the understanding and recognition of hantavirus infections worldwide, largely driven by improved clinical awareness, the availability of more sensitive diagnostic methods, and increased research focused on wildlife reservoirs and viral ecology. Although many hantaviruses have only recently been identified, these viruses are considered ancient pathogens that have likely circulated in wildlife hosts for centuries. Nevertheless, ongoing environmental and climatic changes may alter the distribution, density, and population dynamics of reservoir hosts, particularly rodents, thereby influencing the transmission patterns and epidemiology of hantavirus-associated diseases (Avšič-Županc et al., 2019).

In this context, the integration of advanced diagnostic technologies, including next-generation sequencing, metagenomics, and large-scale data analysis, represents a cornerstone of modern public health preparedness and early warning systems. The increasing frequency of pathogen spillover events, driven by environmental changes, ecosystem disruption, intensified wildlife–human interactions, global trade, and international travel and tourism, further emphasises the importance of multidisciplinary collaboration among veterinarians, physicians, ecologists, epidemiologists, and public health professionals. Strengthening integrated One Health surveillance systems, particularly those based on wildlife genomic surveillance and multidisciplinary collaboration, will be essential to improve early detection and preparedness against future hantavirus emergence and other zoonotic threats in an increasingly interconnected world.

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