Biomolecules & Biomedicine

OPINION

Hantaviruses in Southeast Europe: Climate change, rodent reservoirs, and One Health challenges

Jurica Arapović[1,2*], Luka Laura[3], and Maja Arapović[1]

Hantaviruses are not emerging pathogens in the strict sense, but their public health relevance is being reshaped by climate change, environmental disruption, land-use change, and increasing human mobility. In Southeast Europe, where Dobrava-Belgrade virus and Puumala virus remain endemic, these infections should no longer be viewed only as sporadic rodent-borne diseases of rural or forested environments. Changing ecological conditions can alter reservoir abundance, virus circulation, and human exposure, while fragmented surveillance and variable diagnostic capacity may obscure the true burden of disease. Although human infection is still driven primarily by environmental exposure to infected rodent excreta, rare person-to-person transmission of Andes virus and recent travel-associated clusters illustrate how traditionally localized zoonoses can acquire wider international relevance. This Opinion argues that hantaviruses should be approached as a climate-sensitive One Health challenge, requiring closer integration of human, veterinary, ecological, and meteorological surveillance. Strengthening regional preparedness is essential before environmental change further expands the conditions for transmission.

Keywords: Hantaviruses, One Health, Southeast Europe, hemorrhagic fever with renal syndrome, HFRS, hantavirus pulmonary syndrome, HPS, human-to-human transmission, Andes virus, emerging infectious diseases.

Introduction

Hantaviruses, though not novel pathogens, are gaining increased public health relevance. Traditionally, these zoonotic viruses were considered geographically restricted, maintained in specific rodent reservoirs, and primarily associated with sporadic human cases or localized outbreaks [1]. However, escalating climate variability, ecological disturbances, increased human-wildlife interaction, and recent reports of hantavirus infections linked to expedition travel have renewed interest in hantaviruses as climate-sensitive zoonotic pathogens [2].

Hantaviruses are enveloped, single-stranded RNA viruses belonging to the family *Hantaviridae*. The human pathogenic hantaviruses discussed herein are classified within the genus *Orthohantavirus* and are characterized by a strong ecological association with small mammal reservoirs, predominantly rodents [3]. Clinically relevant species include Hantaan virus, Puumala virus (PUUV), Dobrava-Belgrade virus (DOBV), Sin Nombre virus, and Andes virus. The latter is particularly noteworthy due to documented epidemiological evidence supporting rare human-to-human transmission during a 1996 outbreak in Argentina [4, 5]. Southeast Europe represents a historically significant region for hantavirus circulation, where the epidemiology of human disease is primarily driven by DOBV and PUUV. These viruses are responsible for most cases of hemorrhagic fever with renal syndrome (HFRS) reported in the region [6]. While DOBV predominates in much of the southern Balkan Peninsula and is generally associated with more severe disease, PUUV substantially contributes to the burden of infection in northern parts of the region and is typically linked to milder clinical presentations [7]. Given the close link between hantavirus transmission and reservoir ecology, these infections reflect the increasingly complex interplay among wildlife, environmental change, and human exposure.

Transmission and epidemiology of hantaviruses

Hantaviruses are rodent-borne viruses that establish persistent, typically asymptomatic, infections in their natural reservoir hosts [8]. Most hantavirus species exhibit a strong association with specific rodent reservoirs, which largely define their ecological niche and geographic distribution. Viral transmission among rodents commonly occurs through aggressive interactions, biting, and exposure to contaminated excreta. Humans, conversely, are incidental hosts infected through environmental exposure. Unlike many directly transmitted viral pathogens, the most common route of human infection is inhalation of aerosolized particles contaminated with urine, feces, or saliva from infected rodents [9]. Human-to-human transmission is exceptionally rare and has been primarily documented for Andes virus [4, 5].

The epidemiology of hantavirus infections is profoundly influenced by ecological and climatic factors affecting rodent population dynamics [10, 11]. Climate variability, food avail-

[1]Faculty of Medicine, University of Mostar, Mostar, Bosnia and Herzegovina; [2]Center for Disease Control and Geohealth Studies, Academy of Sciences and Arts of Bosnia and Herzegovina, Sarajevo, Bosnia and Herzegovina; [3]Faculty of Pharmacy, University of Mostar, Mostar, Bosnia and Herzegovina.

*Correspondence to Jurica Arapović: jurica.arapovic@mef.sum.ba

DOI: 10.17305/bb.2026.14499

© 2026 Arapović et al. This article is available under a Creative Commons License (Attribution 4.0 International, as described at https://creativecommons.org/licenses/by/4.0/).

Table 1. Distinctions between Old World and New World hantaviruses

Feature	Old World Hantaviruses	New World Hantaviruses
Geographic distribution	Europe and Asia	North and South America
Main clinical syndrome	HFRS	HPS
Organ involvement	Predominantly renal involvement	Predominantly pulmonary involvement
Major viruses (typical endemic regions)	Puumala (Northern Europe), Dobrava-Belgrade (Southeast Europe), Hantaan (East Asia), Seoul (worldwide)	Sin Nombre (North America), Andes (South America)
Typical disease severity	Usually mild to severe renal disease	Frequently severe cardiopulmonary disease
Mortality	Generally lower	Often higher
Reservoir hosts	Diverse rodent hosts, including *Murinae* and *Arvicolinae* species	Primarily *Sigmodontinae* rodents
Human-to-human transmission	Extremely rare	Documented mainly for Andes virus
Relevance in Southeast Europe	High	Minimal

Abbreviations: HFRS, hemorrhagic fever with renal syndrome; HPS, hantavirus pulmonary syndrome.

ability, habitat disturbances, and seasonal changes all impact rodent population density, migration patterns, and breeding activity, thereby increasing the risk of zoonotic transmission. Milder winters can prolong rodent survival and reproductive activity, while increased precipitation and vegetation growth often enhance food availability and support the expansion of reservoir populations [12]. Flooding events can also increase contact between humans and displaced rodents. This is particularly relevant in Southeast Europe, where extensive forested habitats and established rodent reservoir populations contribute to the endemic circulation of hantaviruses [7]. The principal hosts include rodents of the genera *Apodemus* and *Myodes*, particularly *Apodemus flavicollis* (yellow-necked mouse) and *Myodes glareolus* (bank vole), which serve as primary reservoirs for DOBV and PUUV and play a central role in hantavirus transmission dynamics in the region [13].

Long-term epidemiological observations indicate that HFRS remains endemic throughout much of the Balkan Peninsula, with both sporadic cases and epidemic outbreaks reported for decades [7, 13]. Regional patterns are not uniform; in southern Balkan countries, including Greece, Albania, Romania, North Macedonia, Serbia, and Montenegro, most reported HFRS cases are associated with DOBV. In contrast, PUUV substantially contributes to the disease burden in Slovenia, Bosnia and Herzegovina (BiH), and Croatia [7, 14].

Human infections are commonly associated with occupational and recreational exposure to contaminated environments, such as forests, rural households, storage facilities, agricultural settings, military training areas, and poorly ventilated buildings. Consequently, high-risk groups include forest workers, farmers, hunters, soldiers, and individuals frequently engaged in outdoor activities [15, 16].

However, disparities in surveillance systems, laboratory capacity, clinical awareness, and reporting practices complicate direct comparisons between countries. Furthermore, the relatively low incidence of reported hantavirus infections in Southeast Europe may contribute to reduced clinical suspicion, suggesting that the true burden of infection remains underestimated [6].

Clinical manifestations of hantavirus infections

Clinical manifestations of hantavirus infections vary considerably, depending on the viral species, host factors, and severity of endothelial dysfunction. Human disease presentation can range from mild febrile illness to rapidly progressive multiorgan failure [15]. Clinical severity differs substantially between hantavirus species, generally categorized into Old World and New World hantaviruses based on their geographic distribution and associated clinical syndromes (Table 1). Old World hantaviruses circulating in Europe and Asia are primarily associated with HFRS, whereas New World hantaviruses are linked to hantavirus pulmonary syndrome (HPS) [16].

Although these syndromes differ in their dominant organ involvement, both reflect the capacity of hantaviruses to cause severe disease through vascular dysfunction, capillary leakage, and systemic inflammatory responses. While PUUV infections are generally associated with milder forms of HFRS (often termed *nephropathia epidemica* in Northern Europe), DOBV infections, which account for a substantial proportion of HFRS cases in parts of Southeast Europe, are typically associated with more severe renal and hemorrhagic manifestations and higher reported case-fatality rates [16]. In contrast, HPS caused by New World hantaviruses can rapidly progress to severe respiratory failure and shock [15].

An additional challenge is the nonspecific clinical presentation of hantavirus infections, particularly during the early stages of disease. Initial manifestations often resemble influenza-like illnesses or other acute febrile syndromes, while severe forms may mimic leptospirosis, atypical pneumonias, sepsis, or viral hemorrhagic fevers [17]. Consequently, mild and moderate cases may remain undiagnosed, whereas severe infections are often recognized only retrospectively or during outbreak investigations. These diagnostic challenges underscore the importance of clinical awareness and access

Table 2. Environmental and ecological factors influencing hantavirus emergence and transmission

Environmental or Ecological Factor	Potential Impact on Hantavirus Transmission Dynamics
Mild winters	Increased rodent survival and prolonged breeding activity
Increased precipitation and vegetation growth	Improved food availability for reservoir hosts
Flooding events	Greater human exposure to displaced rodents
Deforestation	Altered reservoir habitats and increased wildlife-human interaction
Agricultural expansion	Increased occupational exposure in rural environments
Urban encroachment into natural habitats	Closer contact between humans and rodent reservoirs
Climate warming	Potential expansion of reservoir geographic range
Biodiversity and ecosystem disturbances	Altered host-pathogen dynamics and transmission patterns

Environmental and ecological factors may variably affect transmission risk depending on local ecological conditions, reservoir species composition, and patterns of human exposure. Therefore, these factors should not be interpreted as uniformly increasing transmission risk across all settings.

to appropriate laboratory diagnostics, particularly in endemic regions.

Environmental change and One Health implications

Beyond climatic influences, increasing human mobility, deforestation, agricultural expansion, and urban encroachment into natural habitats may further facilitate zoonotic transmission of hantaviruses [18] (Table 2). Such interactions among environmental change, wildlife reservoirs, and human exposure may be particularly relevant in Southeast Europe, where extensive forested habitats and shared ecological landscapes across national borders create favorable conditions for the circulation of hantaviruses and their rodent reservoirs [7, 19]. Reservoir population dynamics provide a clear example of these interactions. Environmental conditions influencing reservoir abundance and population dynamics can directly affect opportunities for viral transmission, and fluctuations in reservoir populations have been associated with variations in hantavirus outbreak occurrence and human infection risk [20]. This relationship has been particularly well documented for PUUV in Europe, where increased food availability following mast events can promote population growth of bank voles, leading to subsequent rises in human infections [21–23].

The growing recognition of hantaviruses as zoonotic infections shaped by environmental change further reinforces the relevance of the One Health approach [24] (Figure 1). Since transmission depends on interactions among reservoir hosts, environmental conditions, and human exposure patterns, prevention and surveillance strategies relying exclusively on human disease monitoring are insufficient. Therefore, environmental monitoring, rodent population studies and control, avoidance of exposure to rodent excreta, and epidemiological surveillance represent complementary components of risk assessment and prevention. Such an integrated approach may be particularly valuable in Southeast Europe, where differences in diagnostic capacity, surveillance strategies, and reporting systems between neighboring countries continue to complicate accurate assessment of hantavirus epidemiology and disease burden. Recent outbreaks in the region demonstrate the dynamic nature of hantavirus epidemiology. For example, a large PUUV outbreak reported in Croatia in 2021 involved transmission in areas not previously considered endemic, suggesting that human activity, reservoir dynamics, and environmental factors may alter the spatial distribution of infection risk [25].

The increasing confluence of climate change, land-use modification, and expanding human activity is altering contact patterns between humans, wildlife reservoirs, and their habitats. Consequently, integrated approaches are becoming progressively vital. The implementation of integrated surveillance systems, which combine epidemiological, veterinary, ecological, meteorological, and socioeconomic data, could facilitate earlier recognition of transmission risks and enhance outbreak preparedness.

Evolving contexts of hantavirus public health relevance

While hantaviruses have traditionally been regarded as zoonotic pathogens with limited epidemic potential, specific outbreaks have underscored their broader public health relevance in an increasingly interconnected world. In Southeast Europe, endemic hantaviruses such as DOBV and PUUV continue to be of paramount public health importance, accounting for the majority of reported human infections. However, reports involving other hantavirus species have revealed epidemiological features that extend beyond the conventional reservoir-to-human transmission model.

Unlike the hantaviruses prevalent in Southeast Europe, Andes virus is not endemic to the region. Nevertheless, it has garnered substantial scientific and public health attention due to its rare capacity for person-to-person transmission. Epidemiological investigations from Argentina and Chile have documented clustered infections among household contacts and those with close interpersonal exposures, including suspected nosocomial transmission in certain contexts [26, 27]. Molecular sequencing studies have further substantiated the possibility of person-to-person transmission during selected outbreaks [27].

The international significance of hantavirus preparedness was recently further emphasized by a multinational Andes virus cluster linked to cruise ship travel, reported by the



Figure 1. One Health framework for hantavirus epidemiology and risk dynamics in Southeast Europe. The diagram illustrates the interconnected environmental, animal, and human health domains that shape hantavirus emergence, transmission, and preparedness. Environmental drivers, including climate variability, extreme weather events, land-use change, habitat disturbance, forest ecosystems, and other determinants of human exposure, influence reservoir ecology and opportunities for virus spillover. Animal health components include monitoring of key rodent reservoirs, particularly *Apodemus flavicollis* and *Myodes glareolus*, assessment of reservoir population dynamics, and detection of DOBV and PUUV circulation at the wildlife–human interface. Human health components include HFRS surveillance and outbreak detection, clinical recognition and differential diagnosis, laboratory confirmation, regional data sharing, and preparedness. Together, these domains emphasize the need for integrated ecological, veterinary, epidemiological, and clinical surveillance to support earlier risk recognition and coordinated public health responses. **Abbreviations**: DOBV, Dobrava-Belgrade virus; HFRS, hemorrhagic fever with renal syndrome; PUUV, Puumala virus.

World Health Organization (WHO) in 2026 [2, 28]. According to WHO reports, 13 cases, including three fatalities, were identified among international travelers [2]. Epidemiological and sequencing data additionally suggested potential onboard person-to-person transmission. While sustained community transmission remains highly improbable, such events illustrate how international travel and population mobility can complicate outbreak investigations and expand the geographical scope of public health responses to traditionally localized zoonotic infections.

While endemic hantaviruses remain the primary concern in Southeast Europe, increasing human mobility and global connectivity underscore the importance of maintaining diagnostic awareness and supporting timely international information sharing. These measures are crucial for recognizing local transmission patterns and preparing for potential imported cases during unusual epidemiological events.

Conclusion

Hantaviruses persist as an important yet often underrecognized zoonotic threat in Southeast Europe, where DOBV and PUUV remain endemic and account for most reported human infections. Although the epidemiology of hantaviruses in the region is predominantly characterized by traditional rodent-to-human transmission, recent outbreaks and international investigations highlight the dynamic nature

of hantavirus emergence within a changing environmental and epidemiological landscape. Continued research, regional collaboration, and interdisciplinary surveillance are essential for enhancing our understanding of transmission dynamics and supporting effective public health preparedness.

Conflicts of interest: Authors declare no conflicts of interest.

Funding: Authors received no specific funding for this work.

Data availability: This review is based on published scientific literature and publicly available epidemiological data. No new data were generated specifically for this study. All information supporting the conclusions of this review is available within the manuscript and the cited references.

Editorial board member disclosure: Jurica Arapović is a member of the editorial board of Biomolecules & Biomedicine and was not involved in the editorial handling, peer review, reviewer selection, or decision-making process for this manuscript.

Submitted: 28 May 2026
Accepted: 17 June 2026
Published online: 22 June 2026

References

[1] Jonsson CB, Figueiredo LTM, Vapalahti O. A global perspective on hantavirus ecology, epidemiology, and disease. Clin Microbiol Rev 2010;23:412–41. https://doi.org/10.1128/CMR.00062-09
[2] World Health Organization. Hantavirus outbreak linked to cruise ship travel, multi-locations. Disease Outbreak News 2026 May 28 [cited 2026 Jun 10]. https://www.who.int/emergencies/disease-outbreak-news/item/2026-DON604
[3] Mir MA. Hantaviruses. Clin Lab Med 2010;30:67–91. https://doi.org/10.1016/j.cll.2010.01.004
[4] Enría D, Padula P, Segura EL, Pini N, Edelstein A, Posse CR, et al. Hantavirus pulmonary syndrome in Argentina. Possibility of person-to-person transmission. Medicina (B Aires) 1996;56:709–11. PMID: 9284576.
[5] An unusual hantavirus outbreak in southern Argentina: person-to-person transmission? Emerg Infect Dis 1997;3:171–4. https://doi.org/10.3201/eid0302.970210
[6] Lupuşoru G, Andronesi A, Lupuşoru M, Ailincăi I, Sfeatcu R, Văcăroiu I, et al. Hantavirus infections in the South Eastern European countries: a study of two cases and literature review. Exp Ther Med 2023;26:430. https://doi.org/10.3892/etm.2023.12129
[7] Avšič županc T, Korva M, Markotić A. HFRS and hantaviruses in the Balkans/South-East Europe. Virus Res 2014;187:27–33. https://doi.org/10.1016/j.virusres.2013.12.042
[8] Meyer BJ, Schmaljohn CS. Persistent hantavirus infections: characteristics and mechanisms. Trends Microbiol 2000;8:61–7. https://doi.org/10.1016/S0966-842X(99)01658-3
[9] Heyman P, Vaheri A, Lundkvist Å, Avšič-županc T. Hantavirus infections in Europe: from virus carriers to a major public-health problem. Expert Rev Anti Infect Ther 2009;7:205–17. https://doi.org/10.1586/14787210.7.2.205
[10] Luis AD, Douglass RJ, Mills JN, Bjørnstad ON. Environmental fluctuations lead to predictability in Sin Nombre hantavirus outbreaks. Ecology 2015;96:1691–701. https://doi.org/10.1890/14-1910.1
[11] Olsson GE, Leirs H, Henttonen H. Hantaviruses and their hosts in Europe: reservoirs here and there, but not everywhere? Vector Borne Zoonotic Dis 2010;10:549–61. https://doi.org/10.1089/vbz.2009.0138
[12] Beermann S, Dobler G, Faber M, Frank C, Habedank B, Hagedorn P, et al. Impact of climate change on vector- and rodent-borne infectious diseases. J Health Monit 2023;8:33–61. https://doi.org/10.25646/11401
[13] Hukić M, Nikolić J, Valjevac A, Seremet M, Tesić G, Markotić A. A serosurvey reveals Bosnia and Herzegovina as a Europe's hotspot in hantavirus seroprevalence. Epidemiol Infect 2010;138:1185–93. https://doi.org/10.1017/S0950268809991348
[14] Salimović-Bešić I, Hrvo S, Zahirović E, Đulić E-J, Baljić R, Dedeić-Ljubović A. Expansion of hantavirus infection during the SARS-CoV-2 pandemic in Bosnia and Herzegovina, 2021. J Med Microbiol 2023;72:001687. https://doi.org/10.1099/jmm.0.001687
[15] Vial PA, Ferrés M, Vial C, Klingström J, Ahlm C, López R, et al. Hantavirus in humans: a review of clinical aspects and management. Lancet Infect Dis 2023;23:e371–82. https://doi.org/10.1016/S1473-3099(23)00128-7
[16] Avšič-županc T, Saksida A, Korva M. Hantavirus infections. Clin Microbiol Infect 2019;21:e6–16. https://doi.org/10.1111/1469-0691.12291
[17] MacNeil A, Nichol ST, Spiropoulou CF. Hantavirus pulmonary syndrome. Virus Res 2011;162:138–47. https://doi.org/10.1016/j.virusres.2011.09.017
[18] Jones KE, Patel NG, Levy MA, Storeygard A, Balk D, Gittleman JL, et al. Global trends in emerging infectious diseases. Nature 2008;451:990–3. https://doi.org/10.1038/nature06536
[19] Guo J, Semenza JC, Ecke F, Rizzoli A, Dagostin F, Ulrich RG, et al. A pan-European assessment of multi-sector drivers of human hantavirus risk: climate, biodiversity, and socio-economic factors as key determinants. Environ Res 2026;298:124282. https://doi.org/10.1016/j.envres.2026.124282
[20] Kallio ER, Begon M, Henttonen H, Koskela E, Mappes T, Vaheri A, et al. Cyclic hantavirus epidemics in humans — predicted by rodent host dynamics. Epidemics 2009;1:101–7. https://doi.org/10.1016/j.epidem.2009.03.002
[21] Cunze S, Kochmann J, Kuhn T, Frank R, Dörge DD, Klimpel S. Spatial and temporal patterns of human Puumala virus infections in Germany. PeerJ 2018;6:e4255. https://doi.org/10.7717/peerj.4255
[22] Clement J, Vercauteren J, Verstraeten WW, Ducoffre G, Barrios JM, Vandamme A-M, et al. Relating increasing hantavirus incidences to the changing climate: the mast connection. Int J Health Geogr 2009;8:1. https://doi.org/10.1186/1476-072X-8-1
[23] Reil D, Imholt C, Eccard JA, Jacob J. Beech fructification and bank vole population dynamics — combined analyses of promoters of human Puumala virus infections in Germany. PLoS One 2015;10:e0134124. https://doi.org/10.1371/journal.pone.0134124
[24] Destoumieux-Garzón D, Mavingui P, Boetsch G, Boissier J, Darriet F, Duboz P, et al. The One Health concept: 10 years old and a long road ahead. Front Vet Sci 2018;5:14. https://doi.org/10.3389/fvets.2018.00014
[25] Tomljenovic M, Lakoseljac D, Knezevic L, Batista M, Vilibic-Cavlek T, Kaic B, et al. Spread of Puumala hantavirus to new areas in a large Croatian outbreak of hemorrhagic fever with renal syndrome, 2021. Vector Borne Zoonotic Dis 2024;24:773–83. https://doi.org/10.1089/vbz.2024.0032
[26] Martinez-Valdebenito C, Calvo M, Vial C, Mansilla R, Marco C, Palma RE, et al. Person-to-person household and nosocomial transmission of Andes hantavirus, southern Chile, 2011. Emerg Infect Dis 2014;20:1637–44. https://doi.org/10.3201/eid2010.140353
[27] Alonso DO, Pérez-Sautu U, Bellomo CM, Prieto K, Iglesias A, Coelho R, et al. Person-to-person transmission of Andes virus in hantavirus pulmonary syndrome, Argentina, 2014. Emerg Infect Dis 2020;26:756–9. https://doi.org/10.3201/eid2604.190799
[28] Hertelendy AJ, Gostin LO, Ciottone GR. The MV Hondius hantavirus outbreak — lessons for pandemic preparedness. JAMA 2026 May 26. https://doi.org/10.1001/jama.2026.10321