



EDITORIAL

From the Andes to the world: Hantavirus outbreaks reported in Argentina

De los Andes al mundo: brotes de hantavirus relacionados con Argentina

Zoonoses are diseases transmitted from animals to humans and represent a major public health concern. Many zoonotic diseases are derived from mammals¹. In this editorial, I address the zoonosis known as Hantavirus Pulmonary Syndrome (HPS), with special attention to notable cases in Argentina.

HPS is caused by different variants of the genus *Orthohantavirus* (family Hantaviridae), with over 30 genotypes identified, of which 11 have been officially recognized as viral species by the International Committee on Taxonomy of Viruses (ICTV); <https://ictv.global/report/chapter/hantaviridae/hantaviridae/mamantavirinae/orthohantavirus>). The New World is a hotspot for orthohantavirus infections, which are associated with rodents of the family Cricetidae (subfamilies Sigmodontinae and Neotominae)¹. The current taxonomy of orthohantaviruses established by the ICTV has been the subject of debate because, under this classification, distinct genotypes associated with different rodent reservoirs and geographic distributions are often grouped together as if they were a single species. Consequently, this editorial will refer to genotypes rather than viral species. Studies on South American rodent reservoirs have discovered new genotypes and host species, providing insights into viral ecology and epidemiology². Since no specific treatment exists for hantavirus infection, prevention measures are essential to decrease HPS cases; thus, the following recommendations have been proposed³: (i) identifying the reservoir host, (ii) delineating the geographical range of the host and the distribution of pathogen infection within that range, and (iii) assessing the relative risk to humans by determining host and pathogen distribution across distinct habitats.

In light of these recommendations, I collaborated with colleagues from the Instituto Nacional de Enfermedades Humanas Virales, INEVH, Pergamino (special thanks to Dr. Gladys Calderón, Dr. Silvana Levis, Dr. María Laura Martín, and Dr. Julia Brignone) and the Instituto de Diversidad

y Ecología Animal, IDEA, CONICET-UNC, Córdoba (special gratitude to Dr. Cristina Noemí Gardenal, Dr. Paula Rivera, Dr. Natalia Ortiz and Dr. Juan Diego Pinotti), to identify four distinct areas of Argentina where HPS cases are documented annually. Through molecular identification of both the sampled rodents and viruses, we established the following host-virus associations in the four areas. (1) The region comprising Salta, Jujuy, and Tucumán provinces have the following rodent/virus genotype associations: *Calomys fecundus*/Laguna Negra, *Oligoryzomys chacoensis*/Orán, *Oligoryzomys occidentalis*/Bermejo and HU39694, *Oligoryzomys brendae*/a novel genotype for which no formal name has yet been assigned (María Laura Martín, INEVH, personal communication). (2) Misiones province: *Oligoryzomys nigripes*/Jujituba genotype. (3) The area comprising northern Buenos Aires, southern Entre Ríos and Santa Fe provinces and southwestern Uruguay, where associations between *Oligoryzomys flavescens* has been linked to the Lechiguana, Buenos Aires, Central Plata and HU39694 genotypes, while *O. nigripes* has been associated only with the Lechiguana genotype. (4) The region involving the provinces of Neuquén, Río Negro and Chubut, where the association *Oligoryzomys longicaudatus*/Andes has been established. However, cases of HPS have also been reported beyond these four areas. In central Buenos Aires province, the *O. flavescens*/Lechiguana association is responsible for most cases; in the province of Formosa, the *Calomys callosus*/Laguna Negra association has been reported; and in northern Santa Fe province, the rodent *Holochilus chacarius* is the reservoir of the Alto Paraguay genotype^{1,4}.

Orthohantaviruses are transmitted to humans through inhalation of aerosolized rodent excreta (urine, saliva, and feces), contaminated surfaces or bites. Within rodent populations, both horizontal (e.g., through aggressive interactions) and vertical transmission occur. Most human infections present as isolated cases and do not result in outbreaks. However, numerous studies have reported person-to-person transmission of the Andes genotype¹,

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although such cases remain rare and generally involve close contact or familial outbreaks⁴. In these cases, the virus is initially transmitted from *O. longicaudatus* to humans and then from person-to-person, occasionally causing high-mortality outbreaks. *Oligoryzomys longicaudatus* inhabits a wide range of environments including forests, scrublands, grasslands, and river margins, and is distributed from the Atacama Desert to the south in Chile, and from Mendoza to Tierra del Fuego in Argentina. For this species, I conducted several population-genetic studies in collaboration with colleagues from the “Grupo de Investigaciones en Ecología Poblacional y Comportamental” (GIEPCO), belonging to the Universidad Nacional de Río Cuarto (I am especially grateful to Dr. Jaime J. Polop, Dr. Francisco J. Polop, Dr. Verónica C. Andreo, Dr. M. Cecilia Provencal, Dr. Ernesto Juan and Dr. José Priotto). The distribution of the Andes genotype, in contrast, is more limited. In Argentina, it has been recorded only in Neuquén, Río Negro, and Chubut, and occasionally in Santa Cruz provinces. In Chile, the virus spans a wider area in the regions of Coquimbo, Valparaíso, O’Higgins, Maule, Ñuble, Biobío, La Araucanía, Los Ríos, and Los Lagos⁵.

There have been three major outbreaks of HPS in Argentina. In 1996, 18 cases of HPS were reported among residents or visitors to El Bolsón, Bariloche, and Esquel, resulting in nine deaths. During this period, two physicians from Buenos Aires who had not visited El Bolsón, but had been in contact with patients from the area contracted HPS, and one of them subsequently died. In total, the case fatality rate was 50% (10 of 20 infected persons). In late 2018, an outbreak occurred in Epuyén, Chubut, which began when a person who had visited a rural area and was experiencing nonspecific fever, attended a 15th birthday party with a large number of guests. This person was subsequently diagnosed with HPS. Following the event, five individuals who attended the party developed symptoms consistent with the disease, and seven additional cases were reported shortly after. All cases had an epidemiological link to one of the previous cases. In early January 2019, 13 more cases were reported. Ultimately, 34 people were infected, including 11 deaths (case fatality rate: 32%). Finally, the last outbreak was that associated with the MV Hondius Cruise ship in 2026. The ship departed from Ushuaia, Argentina, on April 1, following an itinerary across the South Atlantic with 147 people onboard, including 88 passengers and 59 crew members, from 23 nationalities. On May 2, a cluster of passengers with severe respiratory illness was reported to the World Health Organization. By May 4, seven cases were identified, including three deaths. The outbreak was linked to a couple from the Netherlands (both of whom died), who had traveled through southern Chile and Argentina, where they were likely infected with the Andes genotype. Based on the currently available epidemiological information, the most likely viral exposure had occurred prior to arrival in Ushuaia or Tierra del Fuego, where no HPS cases have ever been reported. Furthermore, the incubation periods are not consistent with this location being the site of infection. Since the passengers arrived at their isolation places, three additional confirmed cases have been reported: one in Canada, one in the Netherlands, and another in Spain. By May 27, 13 cases (11 confirmed and 2 probable) were reported, including three deaths. This outbreak received global attention

because of the large number of countries involved. As part of my research into the viral reservoirs and genotypes, I spent two intense weeks giving interviews to media outlets from France, Spain, the Netherlands, the United States, the United Kingdom, Thailand, Mexico, Uruguay, Peru, Chile, and Argentina.

Now that the brief period of fame has passed, I can say that prevention is paramount, as no vaccine is currently available. Efforts should focus on early detection, public education, and reducing human-rodent contact through simple, low-cost interventions, including the use of personal protective equipment, rodent-proofing of dwellings, and safe cleaning of rodent excreta. Community education should promote hygiene, rodent avoidance practices, and the maintenance of clean peridomestic environments. Furthermore, combining ecological and epidemiological research through modeling and long-term field studies is essential for predicting outbreaks and developing sustainable control strategies. However, achieving this requires investment in healthcare, which remains a critical aspect that unfortunately does not appear to be a priority in our country’s current government agenda. This hinders the development of effective, long-term public health strategies and responses.

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