

Zoonotic risk of hantavirus infection in Sri Lanka: evidence from rodent surveillance in a rural agricultural area

Rathnayake N¹, Muthusinghe D², Vijeyakumaran R¹, Senarathne P^{3,4}, Herath T¹,
Koizumi N⁵, Urata S², Yoshimatsu K^{3,4}, Gamage C^{1,6}, Dissanayake N¹

Introduction and Objectives: Hantaviruses are rodent-borne zoonotic viruses belonging to the family *Hantaviridae*, order *Elliovirales*. Hantavirus infections in Eurasia can cause haemorrhagic fever with renal syndrome (HFRS) in humans. In Sri Lanka, the infection has been reported since 1988, while novel distinct hantavirus genomes of Lanka virus (LNKV) and Anjzorobe virus (ANJZV) were identified recently in rodents. This study aimed to investigate the presence and spread of hantaviruses in rural agricultural areas of Medawachchiya, Sri Lanka. The specific objectives were to identify the hantavirus species circulating in the area and determine the rodent host species involved.

Methods: Rodents were live trapped from farmlands, chena and paddy fields, and surrounding households in the study area. Trapped rodents were euthanised, and blood, lung, and kidney tissue samples were collected. Indirect Immunofluorescence Assay (IFA) was performed for all the serum samples using Thailand orthohantavirus-infected Vero E6 cell antigens to detect anti-hantavirus antibodies. RNA was extracted from lung tissues, and cDNA was synthesised. Hemi-nested PCR targeting a conserved region in the L-segment of hantaviruses was performed. Positive PCR amplicons were sequenced using the Sanger method, and a neighbor-joining phylogenetic tree was constructed to identify the viral strains. Rodent species were identified by the mitochondrial cytochrome-b (*cytb*) sequencing.

Results: A total of 61 rodents representing four species were captured: *Mus booduga* (n=47), *Rattus rattus* (n=10), *Tatera indica* (n=3), and *Bandicota bengalensis* (n=1). Anti-hantavirus IgG antibodies were found in 10 rodents (*Mus booduga*), while hantavirus RNA was detected in six of them. Sequencing and phylogenetic analysis confirmed that all six genome fragments belong to LNKV.

Conclusion: This study provides molecular and serological evidence for the presence of LNKV among rodent populations in a rural agricultural region of Sri Lanka, indicating a potential threat to farming communities in the area. The detection of LNKV after its first report in 2019 suggests a wider distribution in the country, particularly associated with its natural host, *Mus booduga*. Despite its apparent spread, the clinical features of LNKV infection remain unclear. Further clinical investigations are needed to clarify the disease manifestations of LNKV, along with the establishment of hantavirus diagnostic facilities in healthcare settings.

Keywords: Hantavirus infection, Sri Lanka

Acknowledgement: Royal Society of Tropical Medicine and Hygiene (RSTMH24-04), University of Peradeniya (URG/2024/27/M), Heiwa Nakajima Foundation

¹ Department of Microbiology, Faculty of Medicine, University of Peradeniya, Sri Lanka.

² National Research Center for the Control and Prevention of Infectious Diseases, Nagasaki University, Japan.

³ Graduate School of Infectious Diseases, Hokkaido University, Japan.

⁴ Laboratory of Animal Experimentations, Institute for Genetic Medicine, Hokkaido University, Japan.

⁵ National Institute of Infectious Diseases, Tokyo, Japan.

⁶ Department of Pathobiological Sciences, School of Veterinary Medicine, Louisiana State University, USA.

Address for correspondence: N Rathnayake: Department of Microbiology, Faculty of Medicine, University of Peradeniya, Sri Lanka ;
Telephone: +94778668893; Email: nipun.rathnayake1998@gmail.com;  <https://orcid.org/0000-0002-6918-9601>