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Hantavirus infection in East Asia

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Abstract

Hantaviruses are enveloped RNA viruses that belong to the *Hantavirus* genus of the family *Bunyaviridae*. These viruses persistently infect their rodent reservoirs without causing disease. The virus is transmitted to humans via the inhalation of infectious aerosols generated from contaminated animal secretions or through the contaminated saliva of animal bites. Hantaviruses cause haemorrhagic fever with renal syndrome in Euro-Asia, and hantavirus pulmonary syndrome (HPS) in North and South America. Here, we review the epidemiology and epizootiology of hantavirus infection in Asian countries.

Keywords: Zoonosis; Bunyavirus; Rodent; HFRS; HPS; Renal; Pulmonary; Persistent infection

Résumé

L'Hantavirus est un virus, enveloppé d'ARN, classé comme une espèce de Hantavirus de la famille Bunyaviridae. Ce virus infecte constamment des réservoirs rongeurs sans provoquer immédiatement la maladie. Le virus est transmis aux humains par l'intermédiaire de l'inhalation d'aérosols infectieux, qui sont fabriqués des sécrétions animales contaminées, ou par l'intermédiaire de la salive contaminée des animaux lorsque les humains sont mordus par un animal. La fièvre hémorragique sera provoquée par l'infection à Hantavirus et cette

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fièvre est souvent accompagnée du syndrome rénal (HFRS) dans les régions Euro-Asies, tandis qu'elle provoque le syndrome pulmonaire à Hantavirus (SPH) dans l'Amérique du Nord et du Sud. Dans ce document, nous révisons l'épidémiologie et l'épizootiologie de l'infection à Hantavirus dans les pays asiatiques.

Mots clés: Zoonose; Bunyavirus; Rongeur; HFRS; HPS; Renal; Pulmonaire; Persistant infection

1. Introduction

Hantaviruses form a separate genus, *Hantavirus*, within the family *Bunyaviridae*. To date, 22 *Hantavirus* species have been registered within this genus based on comparisons of nucleotide sequence similarity and evolutionary classifications of viral genomes [1].

Hantavirus infection includes two different forms of severe febrile diseases, haemorrhagic fever with renal syndrome (HFRS) [2] and hantavirus pulmonary syndrome (HPS) [3]. The virus is maintained in persistently infected rodents, which therefore serve as natural viral reservoirs. Transmission of the virus to humans and rodents occurs via the inhalation of infectious aerosols generated from hantavirus-containing animal secretions [4–6] or by the contaminated saliva of animal bites [7]. Other viruses in the *Bunyaviridae* are transmitted by arthropod vectors [8].

Each *Hantavirus* species is predominantly carried by one species of rodent [9]. Phylogenetic analysis of the hantavirus genome has demonstrated three distinct clades, each composed of viruses isolated from rodent hosts belonging to the same subfamily. Thus, viral clades for the subfamilies *Murinae* (Old World rats and mice), *Arvicolinae* (voles and lemmings of the Northern Hemisphere) and *Sigmodontinae* (New World mice and rats) have been identified [10]. Thottapalayam virus (TPMV) is the only hantavirus isolated from a non-rodent host, the house musk shrew *Suncus murinus*, which was first captured in southern India in 1964 [11]. The phylogeny of the hantaviruses, including TPMV, has been shown to mirror the genealogical relatedness of their host animals, suggesting their co-evolution [12,13].

Due to the close relationship between hantavirus and rodent species, the distribution of cases of HFRS and HPS has been confined to the geographic distributions of the viral host species. Thus, since the reservoir animal species for the virus that causes HPS inhabits North and South American countries, the disease has only been reported in those regions [10]. Similarly, reservoir animals for Hantaan (HTNV) [14], Dobrava (DOBV) [15,16], and Puumala (PUUV) [17] viruses, which cause HFRS, live primarily in eastern Asia, northern and eastern Europe, central Europe, and central to northern Europe, respectively, and cases of disease caused by infections with these viruses are confined to the corresponding region. However, the HFRS-causing Seoul virus (SEOV) [18] is found worldwide, probably due to the distribution of its infected host, the brown rat, through international freight transportation. Nonetheless, HFRS resulting from SEOV infection has been confined, thus far, to Asian countries [19].