

Chapter 3

HANTAVIRUS INFECTIONS

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INTRODUCTION

Hantaviruses are a diverse group of RNA having a place in the Bunyaviridae family, named after the Hantan River in South Korea, from which this virus was first isolated in 1970 (1). The link between the virus and hemorrhagic fever with renal syndrome (HFRS) was first discovered during the Korean War, when in excess of 3,000 soldiers affiliated with the United Nations were afflicted with an illness, resulting in sickness and death (2).

Since then, numerous strains of Hantaviruses have been identified worldwide, each associated with a specific rodent species. The principal transmission mode to humans is inhaling aerosolized virus in rodent urine, feces, or saliva (3). They are considered significant zoonotic pathogens, causing two major human diseases, namely HFRS, mainly in Europe and Asia, and Hantavirus Cardiopulmonary Syndrome (HCPS) in the Americas (4).

Despite ongoing research, no specific antiviral treatments or vaccines against Hantavirus infections exist. Thus, they pose significant threats to public health, particularly in endemic regions. Hantaviruses' prevalence and geographical distribution appear much more significant than previously thought, increasing the potential for human exposure and subsequent disease (5).

BIOLOGY AND CLASSIFICATION OF HANTAVIRUS

Hantaviruses are viruses composed of a non-recombinant RNA genome. The genetic makeup of the pathogen is trifurcated into three distinct regions, specifically the small (S), medium (M), and large (L) segments. The S segment encodes the nucleocapsid (N) protein involved in encapsulating the viral genome and infection. The M segment encodes two envelope glycoproteins, Gn and Gc, which play essential roles in bacterial entry and penetration; the L segment

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Nevertheless, these ailments continue to present a significant obstacle to public health on account of their extensive prevalence, elevated fatality rate, and dearth of targeted antibodies and responses (7).

Comprehensive and multidisciplinary research is required to gain insights into multiple aspects of Hantavirus infections. This includes a deeper understanding of virus-host interactions, which can reveal the complex dynamics of how these viruses subvert host immune responses, replicate, and cause disease (5).

Research to identify predictors of severe disease, such as biomarkers or specific clinical characteristics, could facilitate early intervention strategies and improve patient outcomes. Furthermore, studying the socio-ecological factors contributing to outbreaks can help formulate better preventive measures and risk assessments (23).

Efforts toward developing specific antiviral treatments and vaccines should remain a priority. This includes the design and testing of potential therapeutic candidates and the establishment of infrastructure for conducting clinical trials in areas where outbreaks occur (25).

In conclusion, the global impact of hantavirus infections underscores the need for continuous and coordinated efforts in research, public health interventions, and education. Efforts such as these play a crucial role in the management of the impact of perilous pathogens on human health. This is particularly significant in a world that is progressively influenced by environmental transformations and population shifts (26).

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