Hantavirus infection in Taiwan: the experience of geographically unique area

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摘要.

Abstract

Hantaviruses are rodent-borne viruses, and they, mainly the Hantaan (HTN) serotype, are the causative agents of a group of febrile nephropathies known as hemorrhagic fever with renal syndrome (HFRS). Despite the fact that HFRS is frequently reported in China, with an annual incidence of 50,000-100,000 cases, one puzzling observation that no local case of HFRS has been confirmed in Taiwan has yet to be explained. We hypothesized that the hantavirus strain prevailing in Taiwan mainly belongs to the mild strain, the Seoul (SEO) strain, and the absence of severe disease was related to the absence of HTN. To test these hypotheses, this epidemiologic study was performed, including a seroprevalence survey and phylogenetic analysis on hantavirus isolated from the rodent population trapped in major seaports, rural, and mountainous areas of Taiwan. This study also included rodents and viruses from two isolated islands, Kinmen and Matzu, which are geographically adjacent to the east coast of mainland China. There were a total of 5,461 rodents of 16 species captured, and R. norvegicus was the most common species, with an antibody prevalence much higher in international seaports (20%) than in rural regions (approximately 5%) and intermediate in some domestic seaports. By reverse transcriptase polymerase chain reaction (RT-PCR), 33.9% of the seropositive R. norvegicus were found to have amplifiable hantavirus sequences in their lung tissues, and subsequent phylogenetic analyses indicated that almost all hantavirus in Taiwan was most closely related to the prototype SEO strain, and no HTN strain was recovered from any rodent species indigenous to Taiwan. The seroprevalence of SEO infection in R. norvegicus on Kinmen and Matzu was also different from that in southern provinces of China but closely resembled that in seaports in Taiwan, and the SEO identified was genetically linked to Taiwanese SEO strains. These results substantiate our hypotheses, and suggest that the epidemiology of hantavirus infection in Taiwan are different from that in China, where the

HTN and SEO strains and HFRS concurrently prevail.