



Global Trends in Hantavirus Research: GIS Mapping and Visualization Analysis

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Dear Editor-in-Chief

Hantaviruses, single-stranded, enveloped, negative-sense RNA viruses of Bunyaviridae family, are important zoonotic pathogens and distributed worldwide (1). Since the first hantavirus, Hantaan virus (HTNV), was isolated in 1977, the research on hantavirus has developed dramatically, involves many fields: the hantavirus biology, the epidemiology, pathogenesis, diagnostics, therapy, and prevention of human hantavirus infections. However, the evolution of scientific outputs has rarely been analyzed systematically in this field.

We aimed to provide an overview of recent studies in hantavirus, identify its hotspots, and predict its emerging trends, through geographical information system (GIS) mapping and visualization analysis.

The data of publications were downloaded from the Web of Science Core Collection (WoSCC). The time span was set to between January 1988 and July 2018. Online retrieval was performed with keywords “hantavirus”, or “hemorrhagic fever with renal syndrome”, or “hantavirus pulmonary syndrome”, or “hantavirus cardiopulmonary syndrome”. The publication type was not limited. The following information was downloaded for each publication: authors, titles, keywords, institutions and cited references.

A total of 4128 publications in hantavirus were identified from January 1988 to July 2018 by 126 countries or territories. The largest number of publications were published by the United States (1410), followed by China (422), Germany (371), Finland (349), and Sweden (285), accounting for 68.7% of the total number of publications. On a country-level world map (Fig. 1A), all countries were grouped into five categories using the Jenks natural breaks classification method, according to the number of publications in this country. North America, Europe, and East Asia contributed the most publications. Research projects need collaborations. Co-authorship analysis could evaluate this research status in a particular field. Country co-authorship analysis reflects the influential countries as well as the co-operation between countries. The country co-authorship network in 2017 is shown in Fig. 1B. One red node represented a paper, the links between nodes represented cooperative relationships among countries or institutes, and the thickness of links represented the degree of cooperation. The United States was not only a research center but also closely cooperated with many countries in hantavirus research, North America, Europe, and China had close cooperative relationships.



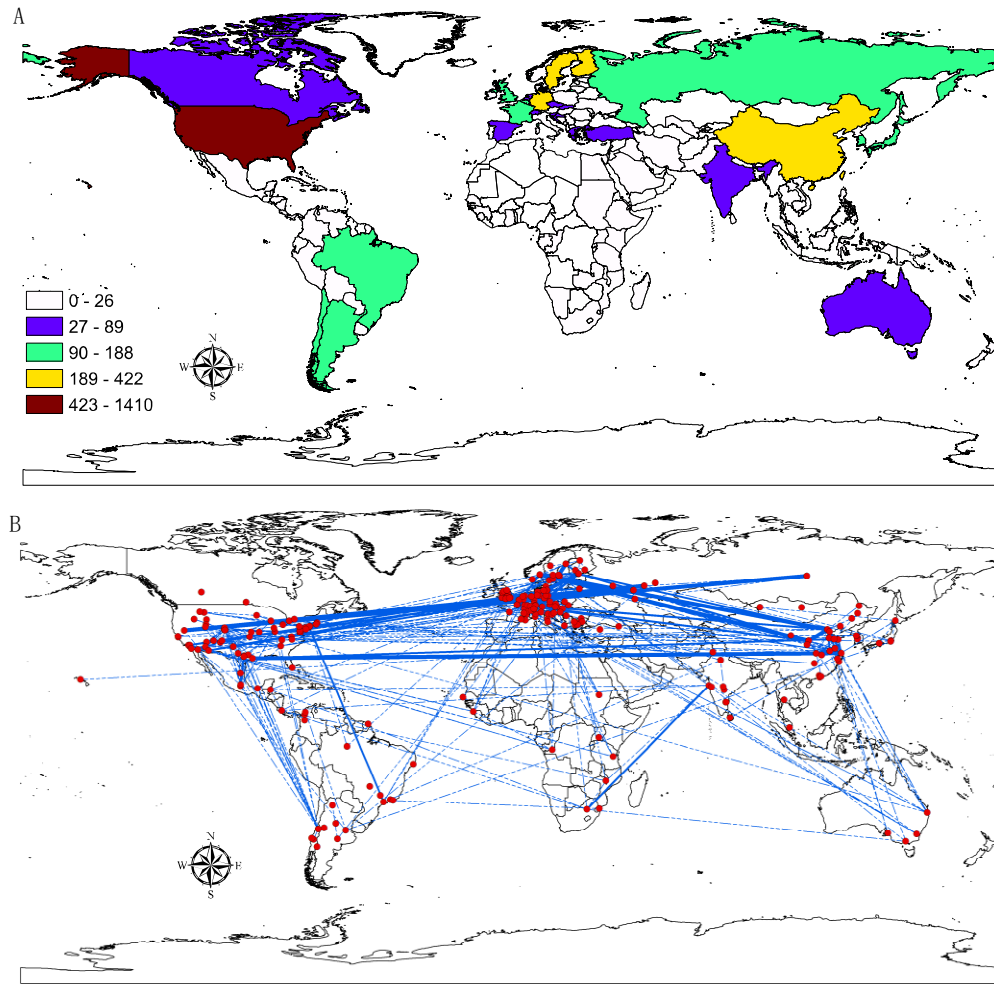


Fig. 1: GIS mapping of publications in hantavirus. A) Global distribution from January 1988 to July 2018, B) The country co-authorship network in 2017

Keywords provide a reasonable description of research hotspots, thus burst keywords represent research frontiers and predict emerging trends (3,4). Here, the keywords with the strongest citation bursts were identified as research frontiers from January 1988 to July 2018. The time intervals were plotted on the green lines, while the periods of burst keywords were highlighted in red, indicating the beginning and end of the time interval of each burst(5). The top 25 research frontiers of hantavirus research were listed in Fig. 2. From 1988 to 2005, the keywords “Korean hemorrhagic fever”, “nucleotide sequence analy-

sis”, “hantaan virus”, “bunyaviridae”, “antigen” and “genetic identification” were the research hotspots. Since 1997, more species of hantaviruses were found and identified, such as “creek canal virus” and “dobrava virus”, with novel reservoir hosts (e.g., “deer mice”, “shrew”, and “myodes glareolus”), these viruses and reservoir hosts together result in “cardiopulmonary syndrome” (HCPS) in Americas, and HFRS in Asia (e.g., “China”) and Europe (e.g., “Germany”) with main clinical symptom “acute kidney injury”. In recent years, research hotspots have switched to “climate change”.

Keywords	Strength	Begin	End	1988 - 2018
korean hemorrhagic fever	28.4969	1988	1999	
etiologic agent	27.3718	1988	2002	
hantaan virus	15.7396	1988	1995	
coding strategy	14.4813	1988	1996	
nucleotide sequence analysis	13.4667	1988	1997	
genome segment	13.1683	1988	1996	
bunyaviridae	11.7314	1988	2004	
prospect hill virus	16.5056	1992	1997	
rna	16.4795	1992	2001	
nucleotide sequence	14.0798	1992	2005	
antigen	11.1245	1992	2002	
genetic identification	28.3502	1996	2003	
creek canal virus	14.1919	1997	2005	
dobrava virus	10.7148	1999	2004	
argentina	15.2759	2000	2006	
endothelial cell	11.7121	2005	2008	
cardiopulmonary syndrome	13.4232	2006	2014	
ecology	10.7122	2009	2016	
deer mice	10.6091	2009	2012	
china	14.6236	2012	2018	
shrew	13.7835	2012	2016	
germany	12.3577	2013	2018	
acute kidney injury	13.7915	2015	2018	
climate change	10.5357	2015	2018	
myodes glareolus	10.9481	2016	2018	

Fig. 2: The keywords with the strongest citation bursts of hantavirus related publications, January 1988 to July 2018

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Competing interests

The authors have declared that no competing interests exist.

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