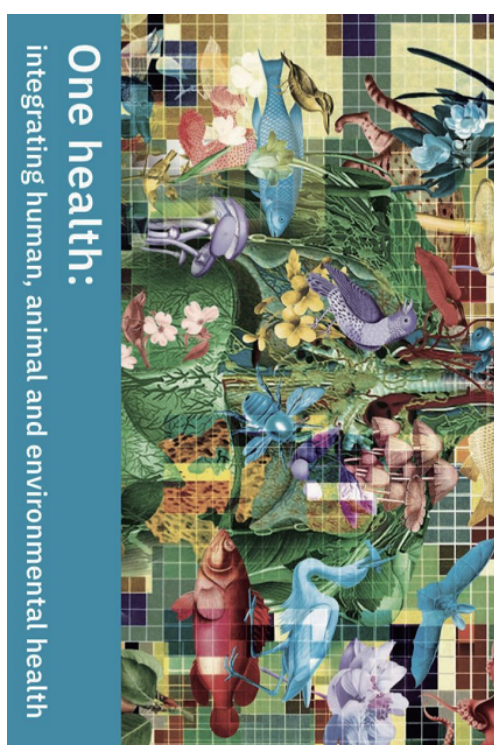


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中国疾病预防控制中心周报



One health:
integrating human, animal and environmental health

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Foreword

Insight on Infectious Diseases from the Perspective of One Health

Zhongwei Jia^{1,2,3,#}

Pathogenic organisms, animals, and humans have always existed in the same ecosystem, but people rarely think of this when they are engaged in specific research regarding human health. However, people often argue on which of heredity or environment is more important to human health, and they never doubt the importance of environments on health. The unifying concepts of One Health are not entirely new as it has reemerged and been recognized again in recent years. One Health was formally endorsed by 3 bodies of the United Nations in 2010 including the Food and Agriculture Organization (FAO), the World Organization for Animal Health (OIE), and the World Health Organization (WHO) (1). Moreover, November 3 has been designated as One Health Day in 2016 (2).

In one ecosystem, whether disease-causing pathogens can successfully invade humans is dominated by genetics and the ecological environment, which is a complex interaction. One Health is an approach that recognizes that the health of people is closely connected to the health of animals and to the health of the environment, which provides an opportunity for people to work on one thing together (3). Coronavirus disease 2019 (COVID-19) is not the last pandemic which humans are co-infected with other animal species, and yet human beings cannot solve all health problems between humans, animals, and the environment in a short time. Conversely, it is more likely for human to struggle with new health problems all the time. But, COVID-19 makes people realize the importance of uniting against infectious diseases and further realize the importance of One Health.

Everyone has a role to play on earth. Collaboration and coordination among experts working in animal, human, and environmental health and other relevant areas are the foundation of the One Health approach (4). To this end, we organized this special issue to explore the potential risks of public health from different ecological perspectives based on a variety of research methods and data sources, which might be a slight challenge for traditional studies of public health. For example, Zhao MC et al. analyzed the distribution and evolution of viruses and hosts globally (5). Xu M et al. estimated relationship between ocean environment and infectious diarrheal disease (6). Hong Z et al. provided a perspective to eliminate schistosomiasis through the One Health approach (7). The findings rising from the issue highlight the necessity and importance to promote interdisciplinary research as the foundation of One Health.

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Preplanned Studies

A Landscape Analysis on Virus: based on NCBI Database

Mingchen Zhao¹; Jingyuan Chen²; Qiang Wang³; Zuhong Lu⁴; Zhongwei Jia^{1,5,6,#}**Summary****What is already known about this topic?**

Studies indicate that viruses could spread across species, but it is difficult to know when and where such small probability events occur because it is almost impossible to design an observational study on the whole landscape.

What is added by this report?

We did a comprehensive analysis on the The National Center for Biotechnology Information database and tried to find the time, place, and host that the viruses stayed in their long evolutionary history.

What are the implications for public health practice?

Public databases are helpful to understand the risk of virus infection in humans and also a cost-effective method for monitoring public health and safety events.

According to the International Committee on Taxonomy of Viruses Master Species List 2020, more than 9,000 virus species have been identified on earth (1), of which the World Health Organization (WHO) announced that more than 200 species were known as zoonotic viruses (2). Previous studies have also shown that zoonoses (hantavirus, Ebola virus, highly pathogenic avian influenza, West Nile virus, Rift Valley fever virus, norovirus, severe acute respiratory syndrome coronavirus 1, Marburg virus, influenza A virus) infected more than 2.5 billion people every year, among which 2.7 million died (3). Zoonotic viruses have aroused broad concerns in recent years so that people have been encouraged to avoid eating wild animals, and a series of animal protection laws and regulations were enacted, such as the Convention on International Trade in Endangered Species of Wild Fauna and Flora (4). Researchers from different fields and countries have tried to collaborate to explore virus associations between animals and humans worldwide (5). However, many studies only focused on investigating a specific virus when it received enough attention as in a localized or global epidemic, such as Ebola virus, H1N1, Zika virus, and severe acute

respiratory syndrome coronavirus 2 (SARS-CoV-2) (6). Even so, it's difficult for people to know exactly when, where and how the virus jumped from animal or environment to humans because it is impossible to design an observational study on the whole landscape around a virus. To understand the overall evolution law of viruses, this study aimed to find the spatial and temporal distribution of viruses and related hosts through the public database.

The National Center for Biotechnology Information (NCBI) virus database is a database of gene sequences maintained by the National Institutes of Health that aggregates and annotates all publicly available nucleotide and protein sequences, and it has been used for studies exploring of quantitative snapshots of viral genomic trends and overviewing virus real-time quantitative polymerase chain reaction (RT-qPCR) method performance (7–8). In this study, we performed a spatiotemporal analysis on the viruses in the NCBI database and tried to disclose the potential time, place, and hosts that the virus appeared or stayed in their long evolutionary history. Our study indicated that the top five widely distributed viruses and found that no virus has been reported in all countries/regions. In addition, the reported areas of viruses did not completely overlap with areas where their suspected hosts live. We also found that the 249 viruses isolated from humans were also isolated from 705 other mammals and 938 non-mammals. We attempted to map the distribution and evolution of viruses and identify suspected hosts globally based on the NCBI database, which was helpful for understanding the risk of virus infection in humans and was also a cost-effective method for monitoring and predicting public health and safety events globally.

The data were downloaded from the NCBI Virus database and covered available data up to September 2021 (www.ncbi.nlm.nih.gov/labs/virus). The data included virus genomic sequence submission information (accession number, submitter, and release date), virus types (species, genus, and family), and biological sample description (location, organisms of sample, isolation, and collection date). Data that were

duplicated, missing, or had unidentified collected dates, locations, or organisms of the biological samples were excluded. Because the NCBI only reported that the virus was isolated from an organism, not whether the organism was the host of the virus, we referred to the organisms as suspected hosts. Based on the standard of NCBI taxonomy, suspected hosts were classified into animals, plants, and microbes.

The numbers were calculated by virus species, suspected hosts, suspected host locations, and collection time. The spatiotemporal distribution was mapped in country/region units and the path was analyzed by linking the reported location of the viruses or suspected hosts. Potential zoonotic diseases were explored by observing the suspected hosts from which the viruses were isolated.

All statistical analyses were performed in R statistical software (version 4.1.0, The R Foundation for Statistical Computing, Vienna, Austria). Animal silhouettes representing hosts were downloaded from PhyloPic (<http://www.phylopic.org>). All maps were made by using ArcGIS (version 10.7, Esri Inc, Redlands, CA, USA).

A total of 605,504 records covering 24,234 viruses from 240 countries/regions with sample collection date from 1865 to September 22, 2021 were involved in the final analysis. We observed that 12,243 viruses were isolated from 4,187 animals, 2,856 from 2,074 plants, and 9,176 from 965 microbes (Figure 1). However, more than 90% viruses (21,845 of 24,234) were reported in a single country/region, and the remaining 10% (2,389 of 24,234) of viruses were from 236 countries/regions and were isolated from 4,742 suspected hosts in 238 countries/regions.

The top five widely distributed viruses were influenza A virus, human immunodeficiency virus 1, hepatitis B virus, rabies lyssavirus, dengue virus, and measles morbillivirus (dengue virus and measles morbillivirus tied for fifth place), which were reported in 155, 151, 145, 128, 122, and 122 countries/regions, respectively (Supplementary Table S1, available in <http://weekly.chinacdc.cn/>). Influenza A virus was reported over approximately 118 years, ranging from the first report in Italy in 1902 to the last report in Tanzania in 2020, and was reported in 155 countries/regions from 422 suspected hosts living in 231 countries/regions. Human immunodeficiency virus 1 was reported over approximately 120 years, ranging from Russia in 1899 to Iraq in 2019, and was reported in 151 countries/regions from 1 suspected

host (*Homo sapiens*) in 225 countries/regions; Hepatitis B virus was reported over approximately 120 years, ranging from Indonesia in 1900 to Ireland in 2020, and was reported in 145 countries/regions from 35 suspected hosts in 229 countries/regions; Rabies lyssavirus was reported over approximately 138 years, ranging from France in 1882 to Equatorial Guinea in 2020, and was reported in 128 countries/regions from 192 suspected hosts in 233 countries/regions; Dengue virus was reported over approximately 75 years, ranging from Colombia in 1944 to Sudan in 2019, and was reported in 122 countries/regions from 25 suspected hosts in 227 countries/regions; Measles morbillivirus was reported over approximately 101 years, ranging from New Zealand in 1919 to United Arab Emirates 2020, and was reported in 122 countries/regions from 3 suspected hosts (*Chlorocebus aethiops*, *Homo sapiens*, and *Macaca fascicularis*) in 225 countries/regions (Figure 2, Supplementary Figure S1A, available in <http://weekly.chinacdc.cn/>).

The top five widely distributed suspected hosts were *Homo sapiens*, *Bos taurus*, *Canis lupus familiaris*, *Gallus gallus*, and *Sus scrofa*, which were reported in 225, 143, 123, 122 and 110 countries/regions, respectively (Supplementary Table S1). *Homo sapiens* were reported in 225 countries/regions in the past 154 years (from the United States in 1866 to the Faroe Islands in 2020), and approximately 1,075 viruses were isolated from this host. *Bos taurus* were reported in 143 countries/regions during the past 138 years (from France in 1882 to Luxembourg in 2020) and from which 273 viruses were isolated; *Canis lupus familiaris* were reported in 123 countries/regions during the past 89 years (from China in 1931 to Ghana in 2020) and from which 106 viruses were isolated; *Gallus gallus* were reported in 122 countries/regions during the past 118 years (from Italy in 1902 to Timor-Leste in 2020) and from which 287 viruses were isolated; *Sus scrofa* were reported in 110 countries/regions during the past 99 years (from China in 1921 to Paraguay in 2020) and from which 276 viruses were isolated (Supplementary Figure S1B, available in <http://weekly.chinacdc.cn/>).

There were 27 viruses in the database reported to be isolated from animals as well as plants (animals-plants). Similarly, 9 and 5 viruses were isolated from animals-microbes and plants-microbes, respectively (Figure 3A). Specifically, 249 viruses from humans were also isolated from the other 1,643 animals, among which 705 were mammals. Most of the 249

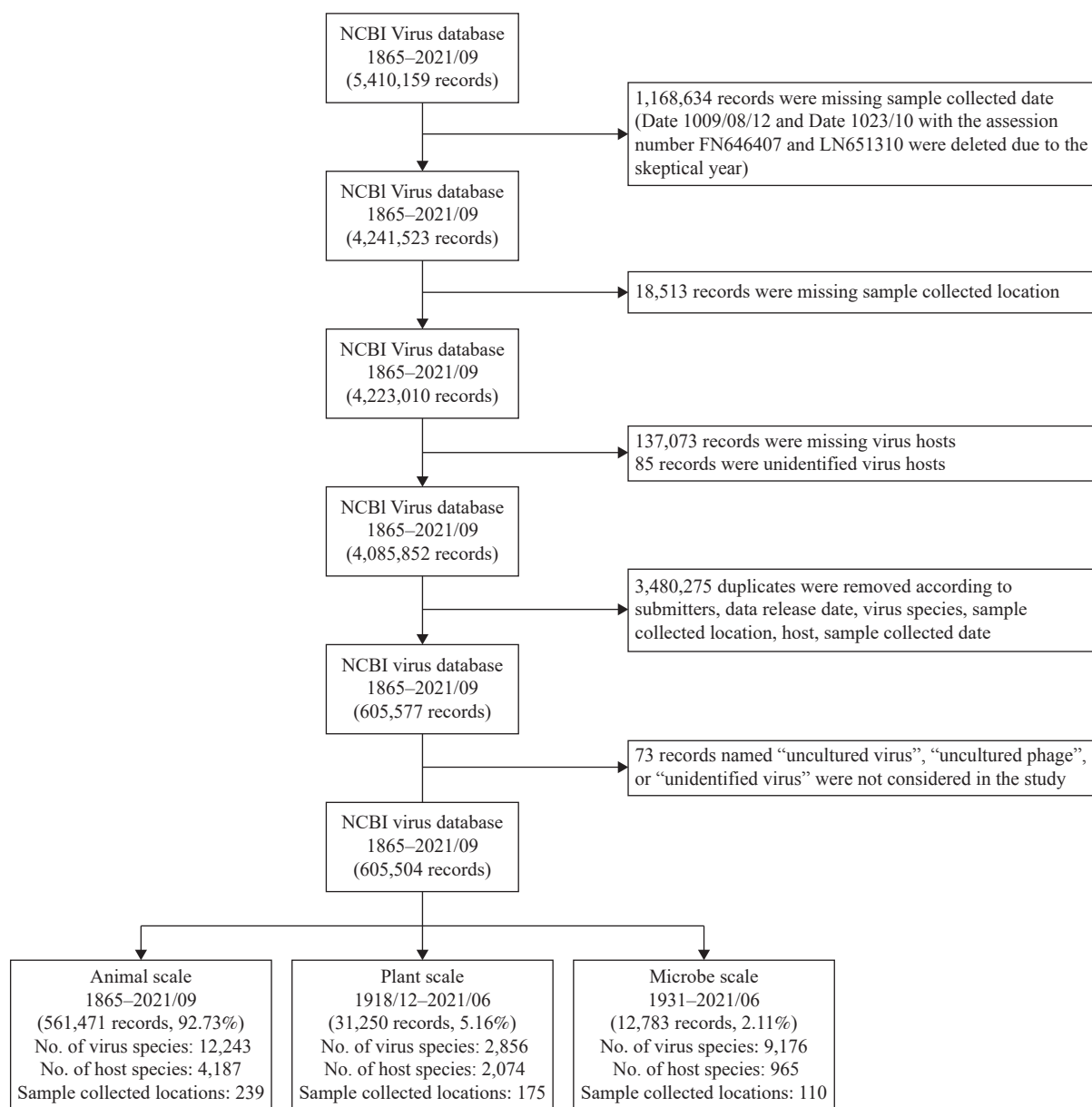


FIGURE 1. Flow diagram depicting the process of identification and inclusion of selected records.
Abbreviation: NCBI=National Center for Biotechnology Information.

multi-suspected host viruses were reported in the United States (125 of 249), China (141 of 249), and Brazil (107 of 249), with 402, 344, and 187 suspected hosts, respectively (Figure 3B). The first reported human-animal multi-suspected host virus was the Vaccinia virus, isolated from *Homo sapiens* in the United States in 1866 (Supplementary Table S2, available in <http://weekly.chinacdc.cn/>).

In the study period, 181 countries/regions reported at least 1 new virus. The top 5 countries reporting the highest number of new virus species were the United States, China, Brazil, Australia, and Italy, with 6,628,

4,518, 1,032, 994, and 730 new virus species, respectively. Newly reported viruses showed a rapid increase since 2003, peaking in 2013, and then showed a jump decline until the bottom of 2019 (Supplementary Figure S2, available in <http://weekly.chinacdc.cn/>). In 2021, 14 new viruses were reported, of which Belarus, Canada, South Africa, the Republic of Korea, Spain, and Switzerland reported 1 new virus, Vietnam reported 2 new viruses, and the United States and China both reported 3 new virus species (Supplementary Table S3, available in <http://weekly.chinacdc.cn/>).

DISCUSSION

To our knowledge, this is the first systematic, global landscape analysis of viruses utilizing the NCBI virus database. Although the database may not cover all known viruses, the NCBI includes almost all viruses that have had significant impact on humans. The study indicates that approximately 24,234 viruses have been investigated as of September 22, 2021, covering 240 countries/regions and involving suspected hosts of 4,187 animals, 2,074 plants and 965 microbes (Figure 1). The top five most widely distributed viruses were influenza A virus, human immunodeficiency virus 1, Hepatitis B virus, rabies lyssavirus, dengue virus and measles morbillivirus, and the top five most widely distributed suspected hosts were *Homo sapiens*, *Bos taurus*, *Canis lupus familiaris*, *Gallus gallus*, and *Sus scrofa*, which all covered more than 100 countries/regions (Supplementary Table S1, available in <http://weekly.chinacdc.cn/>). These outcomes pose several concerning issues.

First, the top five most widely distributed viruses have been investigated and reported in most countries/regions (Supplementary Table S1, available in <http://weekly.chinacdc.cn/>), but no virus has been reported in all countries/regions. The surprising finding is the distribution of influenza A virus — a respiratory virus closely related to humans. We presumed it should be distributed everywhere and reported by all 240 countries/regions. Our study indicates that influenza A virus is the most reported location but 85 countries/regions have not yet reported it. It is possible that the NCBI database has not collected these viruses in these countries/regions or that these areas have not covered these viruses. In either case, these countries/regions deserve attention from the perspective of virus monitoring.

Second, the reported areas of viruses do not completely overlap with areas where their suspected hosts live. For example, influenza A virus has been reported in 155 countries/regions, but its 422 hosts live in 231 countries/regions. The results have two explanations: first, the 76 countries/regions may have influenza A virus but do not investigate and report it; second, the 76 countries/regions could have no influenza A virus, which implies that these areas are susceptible to influenza A virus. However, both viruses and suspected hosts all take approximately one hundred years to survive in a region (Supplementary Figure S1, available in <http://weekly.chinacdc.cn/>).

This long period of history leaves many opportunities for people to find and be involved in their evolution.

Third, we found that 249 viruses from humans were also isolated from other 705 mammals and 938 non-mammals. It is not surprising that most mammals' zoonoses are from *Sus scrofa*, *Gallus gallus*, *Anas platyrhynchos*, *Canis lupus familiaris*, and *Bos taurus*, because these domestic mammals have a close relationship with humans. Bats (152 kinds of species in the database) and *Paguma larvata* covered 44 zoonoses and 3 zoonoses with humans in the reported data. We also found 27 viruses from animals and plants that are involved in insects, whether it is related with humans has not been reported (Figure 2).

This study was subject to some limitations. First, NCBI is a public database, and the data quality may be uneven. However, NCBI has a form for submitted data, which guarantees that the basic information of submitted data is consistent at some level, and these data can meet the requirements of our spatiotemporal analysis. Second, we classified viruses and suspected hosts according to their submitted names. It will be regarded as two different viruses or suspected hosts if their names are spelled differently. For example, *Enterovirus A*, *Enterovirus B*, *Enterovirus C*, and *Enterovirus* sp. are regarded as different viruses in this study. This might be a slight overestimation of the virus species and suspected hosts submitted in the NCBI database but cannot change their whole spatiotemporal distribution, especially in the long history of their evolution. Further, we identified 249 zoonotic viruses in NCBI, which was consistent with the figure published by the WHO (2). Third, data reported by countries may not be complete, which could lead to bias in the analysis. Also, the advent of next generation sequencing (NGS) would cause bias on the temporal discovery of viruses because it was hard to perform large-scale genome sequencing of viruses before NGS became relative affordable. Fourth, we did not analyze the path of each virus and their suspected hosts. Analysis of the overlap of viruses and their hosts is important for predicting the risk of a new virus outbreak in local areas, but beyond the scope of this study.

In conclusion, we attempted to map the distribution and evolution of viruses and suspected hosts globally based on the NCBI database, which is helpful for understanding the risk of virus infection in humans and is also a cost-effective method for monitoring and predicting public health and safety events globally.

Conflicts of interest: No conflicts of interest.

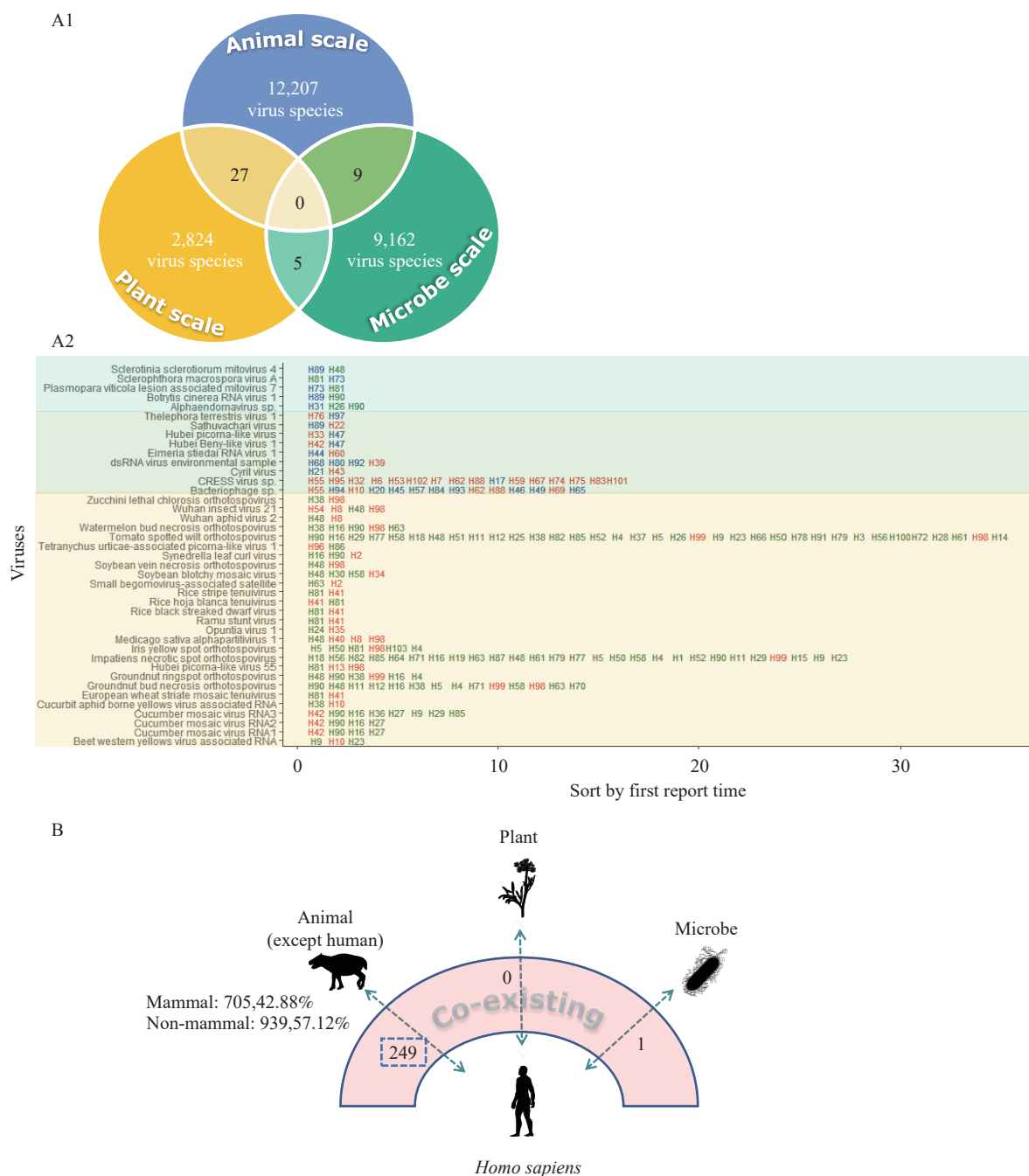


FIGURE 2. Coexisting virus species among animals, plants, and microbes. (A1) The number and intersection of virus species reported from NCBI Virus Database between 1865 and 2021/9. (A2) First reported host family sorted by first report time among coexisting virus species; (B) Coexisting virus species between *Homo sapiens* and animals, plants, or microbes. Notes: The host families represented by the tags were shown in Supplementary Table S4, available in <http://weekly.chinacdc.cn/>.

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SUPPLEMENTARY TABLE S1. The top five widely distributed viruses and hosts.

Virus species	Distributed countries/regions
Influenza A virus	Afghanistan; Albania; Algeria; Angola; Antarctica; Argentina; Australia; Austria; Azerbaijan; Bahrain; Bangladesh; Belarus; Belgium; Benin; Bhutan; Bolivia; Bosnia and Herzegovina; Brazil; Bulgaria; Burkina Faso; Cambodia; Cameroon; Canada; Central African Republic; Chad; Chile; China; Colombia; Cook Islands; Costa Rica; Cote d'Ivoire; Croatia; Cuba; Cyprus; Czech Republic; Czechoslovakia; Democratic Republic of the Congo; Denmark; Djibouti; Dominican Republic; Ecuador; Egypt; El Salvador; Estonia; Ethiopia; Fiji; Finland; France; French Guiana; French Polynesia; Georgia; Germany; Ghana; Gibraltar; Greece; Greenland; Guatemala; Haiti; Honduras; Hong Kong, China; Hungary; Iceland; India; Indonesia; Iran; Iraq; Ireland; Israel; Italy; Jamaica; Japan; Jordan; Kazakhstan; Kenya; Kosovo; Kuwait; Kyrgyzstan; Laos; Latvia; Lebanon; Libya; Lithuania; Luxembourg; Macao, China; Madagascar; Malaysia; Mali; Mauritius; Mexico; Moldova; Mongolia; Montenegro; Montserrat; Morocco; Myanmar; Namibia; Nepal; Netherlands; New Caledonia; New Zealand; Nicaragua; Niger; Nigeria; Democratic People's Republic of Korea; Norway; Oman; Pakistan; Palestine; Panama; Papua New Guinea; Paraguay; Peru; Philippines; Poland; Portugal; Qatar; Republic of Serbia; Reunion; Romania; Russia; Saudi Arabia; Senegal; Singapore; Slovakia; Slovenia; Solomon Islands; South Africa; Republic of Korea; Spain; Sri Lanka; Sudan; Suriname; Sweden; Switzerland; Taiwan, China; Tajikistan; Thailand; Togo; Tonga; Tunisia; Turkey; Turkmenistan; Uganda; Ukraine; United Arab Emirates; United Kingdom; United Republic of Tanzania; United States of America; Uruguay; Uzbekistan; Venezuela; Vietnam; West Bank; Zambia; Zimbabwe (155)
Human immunodeficiency virus 1	Afghanistan; Algeria; Angola; Argentina; Armenia; Australia; Austria; Azerbaijan; Bangladesh; Barbados; Belarus; Belgium; Belize; Benin; Bolivia; Bosnia and Herzegovina; Botswana; Brazil; Bulgaria; Burkina Faso; Burundi; Cambodia; Cameroon; Canada; Cape Verde; Central African Republic; Chad; Chile; China; Colombia; Costa Rica; Cote d'Ivoire; Croatia; Cuba; Cyprus; Czech Republic; Democratic Republic of the Congo; Denmark; Djibouti; Dominican Republic; Ecuador; Egypt; El Salvador; Equatorial Guinea; Eritrea; Estonia; Ethiopia; Fiji; Finland; France; French Guiana; Gabon; Gambia; Georgia; Germany; Ghana; Greece; Greenland; Guadeloupe; Guatemala; Guinea; Guinea-Bissau; Haiti; Honduras; Hong Kong, China; Hungary; Iceland; India; Indonesia; Iran; Iraq; Ireland; Israel; Italy; Jamaica; Japan; Kazakhstan; Kenya; Kuwait; Kyrgyzstan; Laos; Latvia; Liberia; Libya; Lithuania; Luxembourg; Macao, China; Madagascar; Malawi; Malaysia; Mali; Martinique; Mauritania; Mauritius; Mexico; Mongolia; Morocco; Mozambique; Myanmar; Nepal; Netherlands; Niger; Nigeria; Norway; Pakistan; Panama; Papua New Guinea; Paraguay; Peru; Philippines; Poland; Portugal; Republic of Serbia; Romania; Russia; Rwanda; Saudi Arabia; Senegal; Seychelles; Sierra Leone; Singapore; Slovakia; Slovenia; Somalia; South Africa; Republic of Korea; Spain; Sri Lanka; Sudan; Suriname; Swaziland; Sweden; Switzerland; Taiwan, China; Tajikistan; Thailand; Togo; Trinidad and Tobago; Tunisia; Turkey; Uganda; Ukraine; United Kingdom; United Republic of Tanzania; United States of America; Uruguay; Uzbekistan; Venezuela; Vietnam; Zambia; Zimbabwe (151)
Hepatitis B virus	Afghanistan; Albania; Algeria; Angola; Argentina; Armenia; Australia; Azerbaijan; Bangladesh; Belarus; Belgium; Bhutan; Bolivia; Bosnia and Herzegovina; Botswana; Brazil; Bulgaria; Burkina Faso; Burundi; Cambodia; Cameroon; Canada; Cape Verde; Central African Republic; Chad; Chile; China; Colombia; Comoros; Cote d'Ivoire; Croatia; Cuba; Czech Republic; Democratic Republic of the Congo; Dominican Republic; Ecuador; Egypt; Eritrea; Estonia; Ethiopia; Fiji; Finland; France; French Guiana; French Polynesia; Gabon; Gambia; Germany; Ghana; Greece; Greenland; Guadeloupe; Guinea; Guinea-Bissau; Guyana; Haiti; Hong Kong, China; Hungary; India; Indonesia; Iran; Iraq; Ireland; Israel; Italy; Japan; Jordan; Kenya; Kiribati; Kuwait; Kyrgyzstan; Laos; Latvia; Lebanon; Liberia; Libya; Lithuania; Macedonia; Madagascar; Malaysia; Maldives; Mali; Mauritania; Mauritius; Mayotte; Mexico; Moldova; Mongolia; Morocco; Mozambique; Myanmar; Nepal; Netherlands; New Caledonia; New Zealand; Niger; Nigeria; Norway; Pakistan; Palestine; Panama; Papua New Guinea; Paraguay; Peru; Philippines; Poland; Portugal; Republic of Serbia; Reunion; Romania; Russia; Rwanda; Samoa; Saudi Arabia; Senegal; Sierra Leone; Singapore; Slovakia; Slovenia; Somalia; South Africa; Republic of Korea; Spain; Sri Lanka; Sudan; Suriname; Sweden; Switzerland; Syria; Taiwan, China; Thailand; Tonga; Tunisia; Turkey; Uganda; Ukraine; United Kingdom; United Republic of Tanzania; United States of America; Uruguay; Uzbekistan; Vanuatu; Venezuela; Vietnam; Zimbabwe (145)
Rabies lyssavirus	Afghanistan; Algeria; Argentina; Austria; Azerbaijan; Bangladesh; Belgium; Benin; Bhutan; Bosnia and Herzegovina; Botswana; Brazil; Bulgaria; Burkina Faso; Burundi; Cambodia; Cameroon; Canada; Central African Republic; Chad; Chile; China; Colombia; Costa Rica; Cote d'Ivoire; Croatia; Cuba; Czech Republic; Democratic Republic of the Congo; Dominican Republic; Ecuador; Egypt; El Salvador; Equatorial Guinea; Estonia; Ethiopia; Finland; France; French Guiana; Gabon; Gambia; Georgia; Germany; Ghana; Greece; Greenland; Grenada; Guatemala; Guinea; Guyana; Haiti; Honduras; Hungary; India; Indonesia; Iran; Iraq; Israel; Italy; Japan; Jersey; Jordan; Kazakhstan; Kenya; Laos; Latvia; Lebanon; Lesotho; Liberia; Lithuania; Macedonia; Madagascar; Malaysia; Mali; Mauritania; Mexico; Mongolia; Montenegro; Morocco; Mozambique; Myanmar; Namibia; Nepal; Netherlands; Niger; Nigeria; Norway; Oman; Pakistan; Paraguay; Peru; Philippines; Poland; Qatar; Republic of Serbia; Romania; Russia; Rwanda; Saudi Arabia; Senegal; Sierra Leone; Slovenia; Somalia; South Africa; Republic of Korea; Spain; Sri Lanka; Sudan; Svalbard; Swaziland; Switzerland; Syria; Taiwan, China; Tajikistan; Thailand; Tunisia; Turkey; Uganda; Ukraine; United Arab Emirates; United Kingdom; United Republic of Tanzania; United States of America; Uruguay; Vietnam; Zaire; Zambia; Zimbabwe (128)

TABLE S1. (Continued)

Virus species	Distributed countries/regions
Dengue virus	<p>Angola; Anguilla; Antigua and Barbuda; Arctic Ocean; Argentina; Aruba; Australia; Bangladesh; Barbados; Belize; Benin; Bhutan; Bolivia; Borneo; Brazil; British Virgin Islands; Brunei; Burkina Faso; Cambodia; Cameroon; Cape Verde; Chile; China; Colombia; Comoros; Cook Islands; Costa Rica; Cote d'Ivoire; Cuba; Democratic Republic of the Congo; Djibouti; Dominica; Dominican Republic; East Timor; Ecuador; El Salvador; Eritrea; Federated States of Micronesia; Fiji; France; French Guiana; French Polynesia; Gabon; Germany; Ghana; Grenada; Guadeloupe; Guatemala; Guinea; Guyana; Haiti; Honduras; India; Indonesia; Iran; Ireland; Italy; Jamaica; Japan; Kenya; Kiribati; Laos; Madagascar; Malaysia; Maldives; Mali; Marshall Islands; Martinique; Mauritania; Mexico; Mozambique; Myanmar; Nauru; Nepal; New Caledonia; Nicaragua; Nigeria; Niue; Pacific Ocean; Pakistan; Palau; Panama; Papua New Guinea; Paraguay; Peru; Philippines; Portugal; Reunion; Russia; Saint Barthelemy; Saint Kitts and Nevis; Saint Lucia; Saint Vincent and the Grenadines; Samoa; Saudi Arabia; Senegal; Seychelles; Singapore; Solomon Islands; Somalia; Republic of Korea; Spain; Sri Lanka; Sudan; Suriname; Sweden; Taiwan, China; Thailand; The Bahamas; Timor-Leste; Togo; Tonga; Trinidad and Tobago; Tuvalu; United Republic of Tanzania; United States of America; Uruguay; Vanuatu; Venezuela; Vietnam; Wallis and Futuna; Yemen (122)</p>
Measles morbillivirus	<p>Afghanistan; Algeria; Angola; Argentina; Australia; Austria; Bahrain; Bangladesh; Belarus; Belgium; Benin; Bhutan; Bosnia and Herzegovina; Botswana; Brazil; Brunei; Bulgaria; Cameroon; Canada; Central African Republic; Chile; China; Colombia; Cote d'Ivoire; Croatia; Cuba; Cyprus; Czech Republic; Democratic Republic of the Congo; Ecuador; Estonia; Ethiopia; Fiji; Finland; France; Gabon; Germany; Ghana; Gibraltar; Greece; Guatemala; Hong Kong, China; Hungary; Iceland; India; Indonesia; Iran; Iraq; Ireland; Israel; Italy; Japan; Kazakhstan; Kenya; Kyrgyzstan; Latvia; Lebanon; Lesotho; Liberia; Lithuania; Luxembourg; Macedonia; Malawi; Malaysia; Mali; Mauritania; Mexico; Moldova; Mongolia; Montenegro; Morocco; Mozambique; Myanmar; Namibia; Nepal; Netherlands; New Caledonia; New Zealand; Niger; Nigeria; Norway; Oman; Pakistan; Panama; Papua New Guinea; Philippines; Poland; Portugal; Qatar; Republic of Serbia; Romania; Russia; Rwanda; Senegal; Sierra Leone; Slovakia; Slovenia; Solomon Islands; Somalia; South Africa; Republic of Korea; Spain; Sri Lanka; Sudan; Swaziland; Sweden; Switzerland; Taiwan, China; Thailand; Togo; Tunisia; Turkey; Uganda; Ukraine; United Arab Emirates; United Kingdom; United States of America; Uzbekistan; Venezuela; Vietnam; Zambia; Zimbabwe (122)</p>
Host	Distributed countries
<i>Homo sapiens</i>	<p>Afghanistan; Albania; Algeria; Andorra; Angola; Anguilla; Antigua and Barbuda; Arctic Ocean; Argentina; Armenia; Aruba; Australia; Austria; Azerbaijan; Bahrain; Bangladesh; Barbados; Belarus; Belgium; Belize; Benin; Bermuda; Bhutan; Bolivia; Borneo; Bosnia and Herzegovina; Botswana; Brazil; British Virgin Islands; Brunei; Bulgaria; Burkina Faso; Burundi; Cambodia; Cameroon; Canada; Cape Verde; Cayman Islands; Central African Republic; Chad; Chile; China; Colombia; Comoros; Cook Islands; Costa Rica; Cote d'Ivoire; Croatia; Cuba; Cyprus; Czech Republic; Democratic Republic of the Congo; Denmark; Djibouti; Dominica; Dominican Republic; East Timor; Ecuador; Egypt; El Salvador; Equatorial Guinea; Eritrea; Estonia; Ethiopia; Faroe Islands; Federated States of Micronesia; Fiji; Finland; France; French Guiana; French Polynesia; Gabon; Gambia; Georgia; Germany; Ghana; Gibraltar; Greece; Greenland; Grenada; Guadeloupe; Guatemala; Guinea; Guinea-Bissau; Guyana; Haiti; Honduras; Hong Kong, China; Hungary; Iceland; India; Indonesia; Iran; Iraq; Ireland; Israel; Italy; Jamaica; Japan; Jordan; Kazakhstan; Kenya; Kiribati; Kosovo; Kuwait; Kyrgyzstan; Laos; Latvia; Lebanon; Lesotho; Liberia; Libya; Liechtenstein; Lithuania; Luxembourg; Macao, China; Macedonia; Madagascar; Malawi; Malaysia; Maldives; Mali; Malta; Marshall Islands; Martinique; Mauritania; Mauritius; Mayotte; Mexico; Moldova; Mongolia; Montenegro; Montserrat; Morocco; Mozambique; Myanmar; Namibia; Nauru; Nepal; Netherlands; New Caledonia; New Zealand; Nicaragua; Niger; Nigeria; Niue; Norway; Oman; Pacific Ocean; Pakistan; Palau; Palestine; Panama; Papua New Guinea; Paraguay; Peru; Philippines; Poland; Portugal; Qatar; Republic of Serbia; Reunion; Romania; Russia; Rwanda; Saint Barthelemy; Saint Kitts and Nevis; Saint Lucia; Saint Martin; Saint Vincent and the Grenadines; Samoa; Sao Tome and Principe; Saudi Arabia; Senegal; Seychelles; Sierra Leone; Singapore; Slovakia; Slovenia; Solomon Islands; Somalia; South Africa; Republic of Korea; South Sudan; Spain; Sri Lanka; Sudan; Suriname; Swaziland; Sweden; Switzerland; Syria; Taiwan, China; Tajikistan; Thailand; The Bahamas; Timor-Leste; Togo; Tokelau; Tonga; Trinidad and Tobago; Tunisia; Turkey; Turkmenistan; Turks and Caicos Islands; Tuvalu; Uganda; Ukraine; United Arab Emirates; United Kingdom; United Republic of Tanzania; United States of America; Uruguay; Uzbekistan; Vanuatu; Venezuela; Vietnam; Wallis and Futuna; West Bank; Western Sahara; Yemen; Yugoslavia; Zaire; Zambia; Zimbabwe (225)</p>
<i>Bos taurus</i>	<p>Afghanistan; Albania; Algeria; Angola; Argentina; Armenia; Australia; Austria; Azerbaijan; Bahrain; Bangladesh; Belarus; Belgium; Benin; Bhutan; Bolivia; Bosnia and Herzegovina; Botswana; Brazil; Bulgaria; Burkina Faso; Cambodia; Cameroon; Canada; Chad; Chile; China; Colombia; Costa Rica; Cote d'Ivoire; Croatia; Cuba; Cyprus; Denmark; Ecuador; Egypt; El Salvador; Eritrea; Estonia; Ethiopia; France; French Guiana; Gaza Strip; Georgia; Germany; Ghana; Greece; Guatemala; Guinea; Honduras; Hong Kong, China; Hungary; India; Indonesia; Iran; Iraq; Ireland; Israel; Italy; Japan; Jordan; Kazakhstan; Kenya; Kosovo; Kuwait; Kyrgyzstan; Laos; Latvia; Lebanon; Lesotho; Libya; Liechtenstein; Lithuania; Luxembourg; Madagascar; Malawi; Malaysia; Mali; Martinique; Mauritania; Mauritius; Mayotte; Mexico; Moldova; Mongolia; Montenegro; Morocco; Mozambique; Myanmar; Namibia; Nepal; Netherlands; New Zealand; Niger; Nigeria; Democratic People's Republic of Korea; Norway; Oman; Pakistan; Palestine; Panama; Papua New Guinea; Paraguay; Peru; Poland; Portugal; Republic of Serbia; Romania; Russia; Rwanda; San Marino; Saudi Arabia; Senegal; Slovakia; Slovenia; Somalia; South Africa; Republic of Korea; Spain; Sri Lanka; Sudan; Sweden; Switzerland; Syria; Taiwan, China; Tajikistan; Thailand; Togo; Trinidad and Tobago; Tunisia; Turkey; Uganda; Ukraine; United Arab Emirates; United Kingdom; United Republic of Tanzania; United States of America; Uruguay; Venezuela; Vietnam; Yemen; Zambia; Zimbabwe (143)</p>

TABLE S1. (Continued)

Virus species	Distributed countries/regions
<i>Canis lupus familiaris</i>	Afghanistan; Albania; Algeria; Argentina; Australia; Austria; Azerbaijan; Bangladesh; Belgium; Benin; Bhutan; Bosnia and Herzegovina; Botswana; Brazil; Bulgaria; Burkina Faso; Cambodia; Cameroon; Canada; Central African Republic; Chad; Chile; China; Colombia; Costa Rica; Cote d'Ivoire; Croatia; Cuba; Czech Republic; Democratic Republic of the Congo; Dominican Republic; Ecuador; Egypt; Estonia; Ethiopia; Finland; France; French Guiana; Gabon; Gambia; Georgia; Germany; Ghana; Greece; Greenland; Grenada; Guatemala; Guinea; Guyana; Haiti; Honduras; Hong Kong, China; Hungary; India; Indonesia; Iran; Iraq; Ireland; Israel; Italy; Japan; Kazakhstan; Kenya; Laos; Latvia; Lesotho; Liberia; Lithuania; Luxembourg; Madagascar; Malaysia; Mali; Mauritania; Mexico; Mongolia; Morocco; Mozambique; Myanmar; Namibia; Nepal; Netherlands; New Zealand; Nicaragua; Niger; Nigeria; Oman; Pakistan; Paraguay; Peru; Philippines; Poland; Portugal; Republic of Serbia; Romania; Russia; Rwanda; Saint Kitts and Nevis; Senegal; Slovenia; Somalia; South Africa; Republic of Korea; Spain; Sri Lanka; Sudan; Swaziland; Switzerland; Taiwan, China; Tajikistan; Thailand; Tunisia; Turkey; Uganda; Ukraine; United Arab Emirates; United Kingdom; United Republic of Tanzania; United States of America; Uruguay; Vietnam; Zaire; Zambia; Zimbabwe (123)
<i>Gallus gallus</i>	Afghanistan; Algeria; Argentina; Australia; Austria; Azerbaijan; Bangladesh; Belgium; Belize; Benin; Bhutan; Botswana; Brazil; Bulgaria; Burkina Faso; Burundi; Cambodia; Cameroon; Canada; Chile; China; Colombia; Costa Rica; Cote d'Ivoire; Croatia; Czech Republic; Democratic Republic of the Congo; Denmark; Dominican Republic; Ecuador; Egypt; El Salvador; Ethiopia; Fiji; Finland; France; Georgia; Germany; Ghana; Greece; Grenada; Guatemala; Honduras; Hong Kong, China; Hungary; India; Indonesia; Iran; Iraq; Ireland; Israel; Italy; Japan; Jordan; Kazakhstan; Kenya; Kuwait; Kyrgyzstan; Laos; Latvia; Lebanon; Libya; Luxembourg; Macedonia; Madagascar; Malaysia; Mali; Mexico; Morocco; Mozambique; Myanmar; Namibia; Nepal; Netherlands; New Zealand; Nicaragua; Niger; Nigeria; Democratic People's Republic of Korea; Oman; Pakistan; Peru; Philippines; Poland; Portugal; Republic of Serbia; Romania; Russia; Saudi Arabia; Senegal; Singapore; Slovakia; Slovenia; South Africa; Republic of Korea; Spain; Sri Lanka; Sudan; Sweden; Switzerland; Syria; Taiwan, China; Tajikistan; Thailand; Timor-Leste; Togo; Trinidad and Tobago; Tunisia; Turkey; Uganda; Ukraine; United Arab Emirates; United Kingdom; United Republic of Tanzania; United States of America; Uruguay; Venezuela; Vietnam; West Bank; Yemen; Zambia; Zimbabwe (122)
<i>Sus scrofa</i>	Afghanistan; Albania; Angola; Argentina; Armenia; Australia; Austria; Bangladesh; Belarus; Belgium; Benin; Bhutan; Bolivia; Brazil; Bulgaria; Burkina Faso; Burundi; Cambodia; Cameroon; Canada; Chile; China; Colombia; Costa Rica; Cote d'Ivoire; Croatia; Cuba; Czech Republic; Democratic Republic of the Congo; Denmark; Dominican Republic; Egypt; Estonia; Ethiopia; Finland; France; Gambia; Germany; Ghana; Greece; Guatemala; Haiti; Hong Kong, China; Hungary; India; Indonesia; Ireland; Israel; Italy; Japan; Kazakhstan; Kenya; Laos; Latvia; Lithuania; Luxembourg; Madagascar; Malawi; Malaysia; Mali; Malta; Mauritius; Mexico; Mongolia; Mozambique; Myanmar; Namibia; Nepal; Netherlands; New Caledonia; New Zealand; Nicaragua; Nigeria; Democratic People's Republic of Korea; Norway; Paraguay; Peru; Philippines; Poland; Portugal; Republic of Serbia; Romania; Russia; Saint Kitts and Nevis; Sao Tome and Principe; Senegal; Singapore; Slovakia; Slovenia; South Africa; Republic of Korea; Spain; Sri Lanka; Sweden; Switzerland; Taiwan, China; Thailand; Togo; Turkey; Uganda; Ukraine; United Kingdom; United Republic of Tanzania; United States of America; Uruguay; Venezuela; Vietnam; Zaire; Zambia; Zimbabwe (110)

SUPPLEMENTARY TABLE S2. Characteristics of first reported viruses.

Virus species	Type	Why report	First reported time	First reported location	First reported host
Avipoxvirus	Animal virus	First animal virus reported in database	1865	Peru	Leptotila rufaxilla
Cotton leaf curl Multan virus	Plant virus	First plant virus reported in database	1918	China	Hibiscus rosa-sinensis
Saccharomyces paradoxus virus	Microbe virus	First microbe virus reported in database	1931	Russia	Saccharomyces paradoxus
Influenza A virus	Animal virus	The most widely distributed virus in database	1902	Italy	Gallus gallus and unspecified Aves
SARSr-Cov	Animal virus	The most submitted virus in database	2003	China	Homo sapiens
Aeromonas phage PZL-Ah8	Microbe virus	Latest new virus reported in database	2021	China	Aeromonas hydrophila
Vaccinia virus	Animal virus	The earliest reported human-animal co-virus	1866	the United States	Homo sapiens

SUPPLEMENTARY TABLE S3. New viruses reported times of each country or region.

Country/region	No. of report times
United States of America	6628
China	4518
Brazil	1032
Australia	994
Italy	730
Germany	590
Spain	552
India	529
United Kingdom	424
Japan	379
France	304
Canada	300
Republic of Korea	297
New Zealand	291
Denmark	264
Mexico	248
South Africa	230
Hungary	220
Russia	212
Bangladesh	207
Kenya	198
Sweden	195
Thailand	167
Zambia	162
Cameroon	158
Antarctica	157
Netherlands	151
Finland	143
Ghana	137
Taiwan, China	133
Argentina	122
Iran	119
Pakistan	119
Portugal	108
Czech Republic	107
Nigeria	97
Austria	91
Switzerland	86
Colombia	85
Vietnam	83
Turkey	79
Uganda	77

Continued

Country/region	No. of report times
Poland	75
Cote d'Ivoire	74
Belgium	73
Tunisia	71
Malaysia	70
Indonesia	69
Hong Kong, China	65
Philippines	63
Gabon	62
Bulgaria	57
Bermuda	56
Democratic Republic of the Congo	55
Ireland	54
Madagascar	54
Peru	53
Tonga	51
Norway	49
United Republic of Tanzania	49
Israel	48
Panama	47
Egypt	45
Venezuela	41
Chile	39
Greece	37
Costa Rica	36
Central African Republic	34
Cuba	34
Slovenia	34
French Guiana	29
Senegal	29
Ecuador	27
Kuwait	27
Liberia	27
Rwanda	27
Nepal	25
South Georgia and the Islands	25
Trinidad and Tobago	25
United Arab Emirates	24
Croatia	22
Malawi	22
Saudi Arabia	22
Republic of Serbia	21
Georgia	20

Continued

Country/region	No. of report times
Papua New Guinea	20
Bolivia	19
Cambodia	19
Guadeloupe	19
Burkina Faso	18
Lithuania	18
Reunion	18
Myanmar	17
Ethiopia	16
Mauritius	16
Sudan	16
Pacific Ocean	14
Uruguay	14
Mozambique	12
Singapore	12
Ukraine	12
Azerbaijan	11
Iraq	11
Morocco	11
Vanuatu	11
Guatemala	10
Saint Kitts and Nevis	10
Gambia	9
Iceland	9
Oman	9
Sri Lanka	9
Benin	8
Guinea	8
Slovakia	8
Laos	7
Namibia	7
Saint Vincent and the Grenadines	7
Afghanistan	6
Algeria	6
Arctic Ocean	6
Dominican Republic	6
Nicaragua	6
The Bahamas	6
Belarus	5
Honduras	5
Jamaica	5
Jordan	5

Continued

Country/region	No. of report times
Mongolia	5
Romania	5
Yemen	5
Albania	4
Estonia	4
Kazakhstan	4
Kyrgyzstan	4
Mali	4
Mayotte	4
Solomon Islands	4
Cayman Islands	3
Latvia	3
Paraguay	3
Samoa	3
South Sudan	3
Syria	3
Togo	3
Turkmenistan	3
Zimbabwe	3
Angola	2
Armenia	2
Bhutan	2
Bosnia and Herzegovina	2
Christmas Island	2
Comoros	2
Cyprus	2
Czechoslovakia	2
Indian Ocean Territories	2
Lebanon	2
Libya	2
Moldova	2
Niger	2
Saint Barthelemy	2
Seychelles	2
Sierra Leone	2
Barbados	1
Belize	1
Botswana	1
Chad	1
East Timor	1
Faroe Islands	1
Fiji	1
Grenada	1

Continued

Country/region	No. of report times
Haiti	1
Kiribati	1
Mediterranean Sea	1
Midway Islands	1
Montenegro	1
New Caledonia	1
Somalia	1
Suriname	1
Uzbekistan	1
Yugoslavia	1

SUPPLEMENTARY TABLE S4. Co-existed viruses host family and tags.

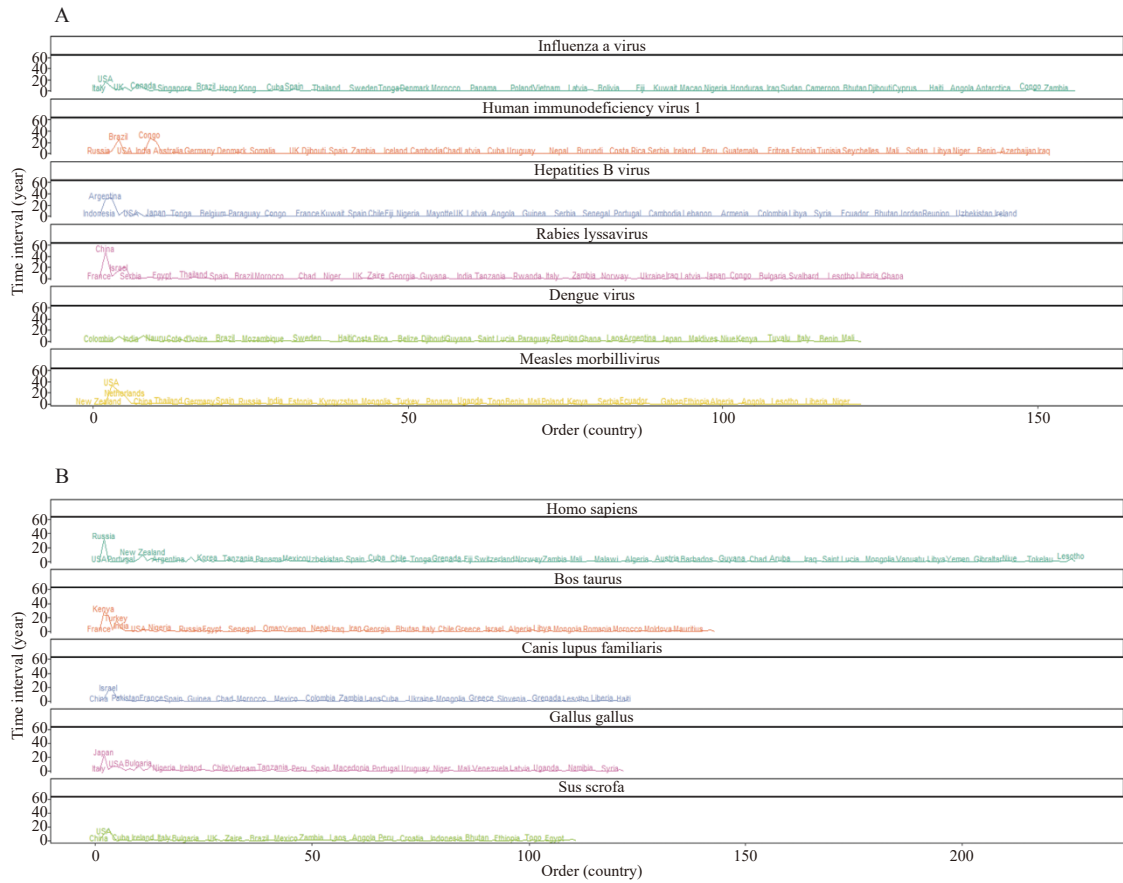
Host family	Tag
Aleyrodidae	H2
Alstroemeriaceae	H3
Amaranthaceae	H4
Amaryllidaceae	H5
Anatidae	H6
Animalia	H7
Aphididae	H8
Apiaceae	H9
Apidae	H10
Apocynaceae	H11
Araceae	H12
Araneae	H13
Arecaceae	H14
Asparagaceae	H15
Asteraceae	H16
Bacteria	H17
Balsaminaceae	H18
Begoniaceae	H19
Bifidobacteriaceae	H20
Botryosphaeriaceae	H21
Brassicaceae	H22
Bovidae	H23
Cactaceae	H24
Calceolariaceae	H25
Campanulaceae	H26
Cannaceae	H27
Caprifoliaceae	H28
Caryophyllaceae	H29
Celastraceae	H30
Ceratobasidiaceae	H31

Continued

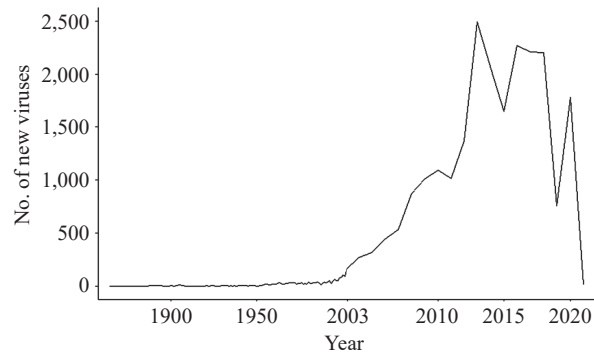
Host family	Tag
Cervidae	H32
Chiroptera	H33
Cicadellidae	H34
Coccoidea	H35
Commelinaceae	H36
Convolvulaceae	H37
Cucurbitaceae	H38
Culicidae	H39
Curculionidae	H40
Delphacidae	H41
Diptera	H42
Drosophilidae	H43
Eimeriidae	H44
Enterobacteriaceae	H45
Enterococcaceae	H46
Entomophthoraceae	H47
Fabaceae	H48
Firmicutes	H49
Gentianaceae	H50
Geraniaceae	H51
Gesneriaceae	H52
Gruidae	H53
Hexapoda	H54
Homo sapiens	H55
Iridaceae	H56
Lactobacillaceae	H57
Lamiaceae	H58
Laniidae	H59
Leporidae	H60
Liliaceae	H61
Lutjanidae	H62
Malvaceae	H63
Marantaceae	H64
Microcystaceae	H65
Moringaceae	H66
Muscicapidae	H67
Mycosphaerellaceae	H68
Nymphalidae	H69
Oleaceae	H70
Orchidaceae	H71
Pedaliaceae	H72
Peronosporaceae	H73
Phasianidae	H74

Continued

Host family	Tag
Phoenicopteridae	H75
Phthiracaridae	H76
Piperaceae	H77
Pittosporaceae	H78
Plantaginaceae	H79
Pleosporaceae	H80
Poaceae	H81
Primulaceae	H82
Prunellidae	H83
Pseudomonadaceae	H84
Ranunculaceae	H85
Rosaceae	H86
Rubiaceae	H87
Salmonidae	H88
Sclerotiniaceae	H89
Solanaceae	H90
Spermatophyta	H91
Sporormiaceae	H92
Staphylococcaceae	H93
Streptococcaceae	H94
Suidae	H95
Tetranychidae	H96
Thelephoraceae	H97
Thripidae	H98
Thysanoptera	H99
Tropaeolaceae	H100
Turdidae	H101
Viverridae	H102
Zygophyllaceae	H103



SUPPLEMENTARY FIGURE S1. Top 5 widely distributed (A) viruses and (B) hosts sorted by first report country or region.



SUPPLEMENTARY FIGURE S2. The trend of new reported viruses sorted by year.

Preplanned Studies

Exploring the Association Between Infectious Diarrheal Diseases and Sea Surface Temperatures — Coastal Areas of China, 2009–2018

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Summary

What is already known about this topic?

Coastal areas of China have a higher reported incidence of other infectious diarrheal diseases (OIDD; excluding cholera, dysentery, typhoid, and paratyphoid) than inland areas of China.

What is added by this report?

The incidence of OIDD in high latitude coastal provincial-level administrative divisions (PLADs) nearby Bohai Sea was positively correlated with sea surface temperatures (SSTs), while in coastal PLADs nearby the South China Sea was negatively correlated.

What are the implications for public health practice?

The marine environmental risk factors acquired by remote sensing provide a new way for diseases surveillance and early warning. SSTs can be employed as predictor of OIDD in some coastal areas in China.

Infectious diarrhea is an important public health problem worldwide (1). As a type of common and important infectious disease, it poses a serious threat to human health and was ranked as the leading cause of death among people of all ages, especially young children in developing countries (2). Other infectious diarrheal diseases (OIDD) refer to a group of intestinal infectious diseases with diarrhea that exclude cholera, bacterial and amoebic dysentery, typhoid, and paratyphoid. Spatial analysis and Pearson's correlation was employed to explore the association between the monthly OIDD incidence of the each coastal provincial-level administrative divisions (PLADs) and the average monthly sea surface temperature (SST) of its nearby offshore based on ten years data of China from 2009 to 2018. The results showed that the incidence of OIDD in coastal PLADs was higher than that of inland PLADs in China; coastal PLADs of high latitude areas nearby Bohai Sea had significant positive correlations with the SSTs, but those of low latitude areas nearby South China Sea were negatively

correlated with the SSTs. SSTs can be potential predictor of OIDD in some coastal areas in China.

Meteorological conditions have been confirmed to impact pathogen exposures, in particular those associated with waterborne transmission. Several epidemiological studies used time series analysis to show that temperature or precipitation factors had a strong triggering effect on diarrhea (3). Extreme rainfall caused floods may contaminate drinking water by flushing diarrhea-causing pathogens from pastures and dwellings into drinking water supplies (4). High ambient temperatures can further promote diarrhea transmission by enhancing pathogen replication rates or by changing water usage behaviors and hygiene and sanitation practices (5). The ocean is the largest reservoir of viruses and bacteria globally. The marine environmental parameters including sea surface temperature, sea surface height anomaly and sea chlorophyll concentration are potential predictors of many infectious diseases such as cholera to coastal regions (6). SSTs in the central equatorial Pacific Ocean have been proved to be linked to diarrhea outbreaks to the many Asian and South American countries including Bangladesh, Peru, and Japan (5). While the association between meteorological factors and diarrhea incidence has been well documented in China, limited attention has been directed at whether the marine environmental factors especially the SST have an influence on the incidence of OIDD in coastal areas of China.

Ten years monthly-recorded OIDD data of China from 2009 to 2018 were extracted from the Data-center of China Public Health Science. This database included all data since the initiation of network reporting system, which are number of cases, incidence by PLAD. Only the diarrhea cases confirmed clinically or by laboratory tests, including microscopic examination and biochemical identification, were included in the database. SSTs data of the same period were acquired from NASA'S Jet Propulsion Laboratory (<http://podaac.jpl.nasa.gov>). The data were produced

using the satellite images from the National Oceanographic and Atmospheric Administration Advanced Very High Resolution Radiometer (AVHRR). The SSTs data used in the study were monthly AVHRR Oceans Pathfinder SST data with a spatial resolution of 4 km.

Descriptive statistics methods were used to describe the study variables in coastal PLADs of China. ArcGIS software (version 10.2, ESRI, Redlands, USA) was employed for the spatialization of the OIDD incidence data. Meanwhile, Pearson's correlation analysis was conducted to assess the associations between SSTs and OIDD incidence and a two-tailed test of significance was used. Offshore China were divided into four seas including Bohai Sea, Yellow Sea, East China Sea, and South China Sea. The 31 PLADs of the mainland of China were divided into 11 coastal PLADs and 20 non-coastal PLADs. The coastal PLADs near the Bohai Sea include Liaoning, Hebei, Tianjin, and Shandong; near the Yellow Sea include Liaoning, Shandong, and Jiangsu; near the East China Sea include Shanghai, Jiangsu, and Zhejiang; near the South China Sea include Fujian, Guangdong, Hainan, and Guangxi.

The total cases and monthly OIDD incidence of each PLAD in the mainland of China was shown in Table 1. The average incidence of OIDD in coastal PLADs was significantly higher than that in inland PLADs. A total of 9,527,747 OIDD cases were reported in China from 2009 to 2018, including 5,124,303 cases in the 11 coastal PLADs that accounted for 54% of the total cases. The average monthly incidence in China was 5.817/100,000. While the monthly incidence in coastal PLADs was higher than the average, which reached 7.230/100,000. Tianjin Municipality had the highest incidence of monthly OIDD, which was 19.846/100,000. Because the consultation rate of OIDD in China was estimated to be between 50% to 80%, some cases were missed, and the true incidence was higher than the reported incidence.

The dynamic curve of monthly OIDD incidence in coastal PLADs and China from 2009 to 2018 was shown in Figure 1. The data exhibit a clear seasonality with the outbreaks concentrated in summer and winter. The monthly OIDD incidences between 2009 and 2018 in coastal PLADs were always higher than that in inland PLADs all the year around. The time series monthly SSTs extracted from the four offshore areas vary greatly from each other. The average monthly SST in Bohai Sea was 13.2 °C and varied

TABLE 1. The total cases and monthly OIDD incidence of each PLAD in the mainland of China from 2009 to 2018.

Areas	PLADs	Total OIDD cases	OIDD incidence (1/100,000)
Coastal PLADs	Tianjin	370,781	19.846
	Zhejiang	1,059,099	15.602
	Guangdong	1,334,039	9.953
	Guangxi	529,972	9.041
	Hebei	535,975	5.940
	Fujian	255,043	5.434
	Shandong	603,132	5.023
	Liaoning	186,186	3.551
	Hainan	39,326	3.270
	Shanghai	52,878	1.822
	Jiangsu	157,872	1.638
Inland PLADs	Beijing	437,431	16.793
	Ningxia	87,545	10.701
	Anhui	738,954	9.845
	Chongqing	317,852	8.613
	Jiangxi	310,117	5.591
	Xinjiang	154,375	5.262
	Shaanxi	241,495	5.247
	Qinghai	35,155	4.896
	Hubei	334,722	4.726
	Henan	504,081	4.394
	Gansu	118,912	3.774
	Shanxi	161,360	3.632
	Hunan	270,434	3.285
	Sichuan	323,674	3.249
	Yunnan	173,563	3.013
	Guizhou	90,778	2.113
	Inner Mongolia	35,157	1.159
	Heilongjiang	50,075	1.101
	Jilin	17,022	0.522
	Xizang (Tibet)	742	0.200

Abbreviations: OIDD=other infectious diarrheal diseases; PLADs=provincial-level administrative divisions.

from 1 °C to 27 °C; the characteristics of SST in Yellow Sea were similar to that of the Bohai Sea; the average value of SSTs in Yellow Sea was 15.3 °C and it varied from 5 °C to 28 °C, both of which had seasonality. While average monthly SST in the South China Sea was 27.9 °C and varied only from 25 °C to 30 °C. In the East China Sea, the average monthly SST was 22.2 °C and varied only from 16 °C to 30 °C.

Pearson's correlation coefficient was employed to analyze the association between the monthly OIDD

incidence of the each coastal PLAD and the average monthly SST of its adjacent offshore sea. Marine environmental factors may have a delayed effect on the OIDD outbreaks, so one-month lag effects for SST were created in the study. The correlation analysis was used for both the current and one-month lag OIDD with the SST. As shown in Table 2, the PLADs of Liaoning, Hebei, Tianjin, Shandong, and Shanghai had significant correlations with the SSTs. The monthly OIDD incidences in Fujian and Guangdong were significantly negative correlated with the SSTs. However, Jiangsu, Zhejiang, Hainan, and Guangxi had little or no significant correlation with SSTs.

DISCUSSION

Our findings confirm the average OIDD incidence in coastal PLADs was higher than in inland areas of China and demonstrated an association between coastal SSTs and local OIDD incidence. Specifically, we found that coastal PLADs of high latitude areas near Bohai Sea had significant positive correlations with the SSTs, but that of low latitude areas nearby South China Sea were negatively correlated with the SSTs. No matter in coastal PLADs or inland areas, reported cases mostly occurred in summer and winter, and the incidence dynamic curve showed bimodal fluctuation.

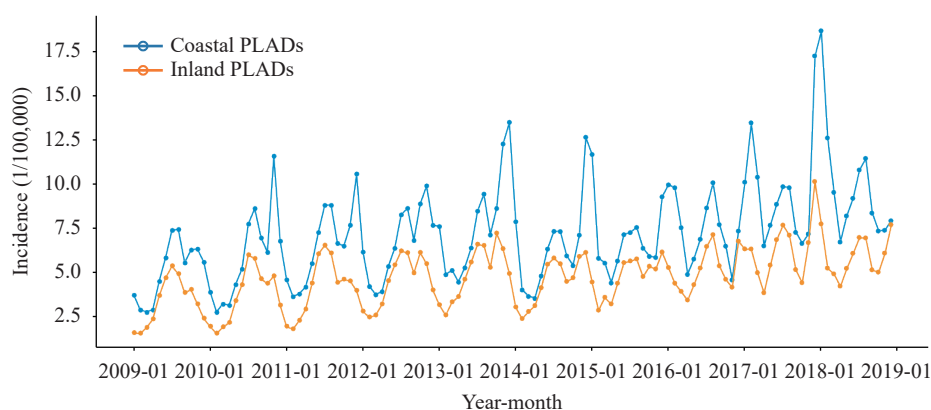


FIGURE 1. The dynamic curve of monthly OIDD incidence in coastal and inland PLADs of mainland China from 2009 to 2018. Abbreviations: OIDD=other infectious diarrheal diseases; PLADs=provincial-level administrative divisions.

TABLE 2. Pearson's correlation analysis between SSTs and OIDD in coastal PLADs of mainland China.

Coastal seas	Coastal PLADs	Pearson's correlation coefficient between SSTs and OIDD incidence	Pearson's correlation coefficient between SSTs and one month lag OIDD incidence
Bohai Sea	Liaoning	0.674*	0.451*
	Hebei	0.712*	0.583*
	Tianjin	0.834*	0.578*
	Shandong	0.447*	0.343*
Yellow Sea	Liaoning	0.679*	0.413*
	Shandong	0.442*	0.306*
	Jiangsu	0.024 [†]	0.128 [†]
East China Sea	Jiangsu	0.044 [†]	0.154 [†]
	Zhejiang	0.193 [¶]	0.327*
	Shanghai	0.579*	0.322*
	Fujian	-0.385*	-0.120 [†]
South China Sea	Guangdong	-0.457*	-0.131 [†]
	Hainan	-0.187 [¶]	-0.081 [†]
	Guangxi	-0.184 [¶]	-0.096 [†]

Abbreviations: SSTs=Sea surface temperatures; OIDD=other infectious diarrheal diseases; PLADs=provincial-level administrative divisions.

* Significant correlation at 0.05 level.

[†] No significant correlation.

[¶] Significant correlation at 0.01 level.

The incidence of OIDD in coastal PLADs from 2009 to 2018 was higher than that of inland PLADs. A possible reason should be related to the impact of marine environmental factors. Although the underlying mechanisms by which marine environmental factors influence infectious diarrheal diseases have not been fully clarified, these marine environment, such as SST, can impact the production or transmission of some pathogens in coastal areas. Pathogens may spread quickly through the contaminated water after flooding. In addition, the consumption and improper preservation of seafood in coastal PLADs may also be important factors affecting the OIDD incidence.

There is a spatial heterogeneity of OIDD distribution in China that the incidence of OIDD in different latitude coastal PLADs varies from each other. This further reinforced results of a former study that suggested the difference of the health effects of temperature in different regions is related to latitude. The effect of temperature on OIDD could be modified by latitude (7). The risk of OIDD was higher in high latitude areas at low temperatures, suggesting that high latitude areas were vulnerable areas in cold seasons (8). For these areas, we should improve the public's awareness of OIDD protection and medical treatment and enhance the supply of medical resources. Many former studies have shown that high temperatures may increase the risk of infectious diarrhea by affecting pathogen activity, accelerating food decomposition, and increasing drinking water demand (9). However, some areas have shown that infectious diarrhea is negatively correlated with temperature.

This study was subject to some limitations. First, the SSTs were extract from satellite retrieved products, which itself is subject to a certain level of error. Second, the mechanism of the impact of the marine environment on the incidence of diarrhea is not clear yet, and the optimal impact of the marine environment on it is unknown. Therefore, we only calculate the average value of the sea surface temperature in each offshore sea area for analysis of the association with OIDD. Finally, sea surface temperature plays an important role in the survival and reproduction of infectious diarrhea in host environments a side from humans and will affect the transmission speed of diarrhea, so there are still some other marine variables that maybe impact on the incidence of OIDD in coastal PLADs. Sea surface height can reflect the characteristics of climate change such as drought stress, water surface rise, and flooding caused by El Niño

events. Seawater salinity and seawater chlorophyll concentration are important factors for the transmission and reproduction of pathogenic microorganisms in coastal PLADs. All these impact factors can be predictors for OIDD in coastal PLADs of China.

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Recollection

Elimination of Schistosomiasis Japonica in China: From the One Health Perspective

Zhong Hong¹; Lu Li¹; Lijuan Zhang¹; Qiang Wang¹; Jing Xu^{1,†}; Shizhu Li¹; Xiao-nong Zhou^{2,†}

ABSTRACT

Schistosomiasis japonica is caused by infection of *Schistosoma japonicum* (*S. japonicum*), which infected 12 million residents in the 1950s in China and was a heavy burden to public health and socioeconomic development (1). After more than seven decades of effort to control schistosomiasis, the prevalence of schistosomiasis has been reduced dramatically in China. Among the 450 endemic counties (including city and district-level jurisdictions), 74.89% (337/450), 21.87% (98/450), and 3.33% (15/450) have achieved the criteria of elimination, transmission interruption, and transmission control of schistosomiasis, respectively. As the overall endemic status of schistosomiasis remains at a low level, the strategies shifted from snail control to morbidity control and then to an integrated strategy that emphasized infection source control. However, being a vector-borne and zoonotic disease, schistosomiasis japonica is intricately linked to multiple factors including biological, natural, and socioeconomic risk factors. In order to eliminate schistosomiasis earlier and more thoroughly, the One Health approach should be adopted, which focuses on solving complex health problems from a macro-level perspective of interactions among human, animal, and environment, emphasizing multi-institution, interdisciplinary, and cross-regional collaboration and communication.

Human schistosomiasis is a water-borne infectious disease caused by infection with blood flukes of the genus *Schistosoma*. The disease occurs worldwide in 78 countries and regions in Asia, South America, the Middle East, and Africa. Globally, over 780 million people are at risk of infection and 250 million people are infected, of which 90% are concentrated in sub-Saharan Africa (2–4). The estimated global burden of schistosomiasis is 3.31 million disability-adjusted life years (DALYs) (5). In China, human schistosomiasis is

only caused by *S. japonicum*. Like other human-hosting *Schistosoma* spp., the life cycle of *S. japonicum* includes adult worm, egg, miracidium, sporocyst, cercariae, and schistosomula, requiring an intermediate host and a definitive host to complete its asexual and sexual production separately (Figure 1). *Oncomelania hupensis*, an amphibious snail, is the only intermediate host of *S. japonicum*. Humans and over forty other mammals serve as definitive hosts of *S. japonicum* and play a role in spreading infections when they excrete feces containing schistosome eggs to the environment.

The control of schistosomiasis was a high priority in China soon after the founding of the People's Republic of China in 1949, and schistosomiasis japonica was largely brought under control through 7 decades of effort. However, great challenges still exist to completely eliminate schistosomiasis from the country by 2030 due to climate change, natural disasters, socioeconomic development, environmental protection, etc. The progress of the national schistosomiasis control program and the experience accumulated over past several decades in China is reviewed in this article, and solutions to achieve the elimination of schistosomiasis through a One Health approach are explored, which addresses complex health issues from a holistic perspective of human-animal-environment interaction.

Progress of the National Schistosomiasis Control Program in China

From Figure 2, we can see that the systematic and large-scale control activities against schistosomiasis have been initiated since the mid-1950s in China. During the whole process, the selection and implementation of control strategies were in accordance with socioeconomic level, the health needs of the people in the epidemic area, and the law of epidemic change. The great achievements in the prevention and control of schistosomiasis in China are

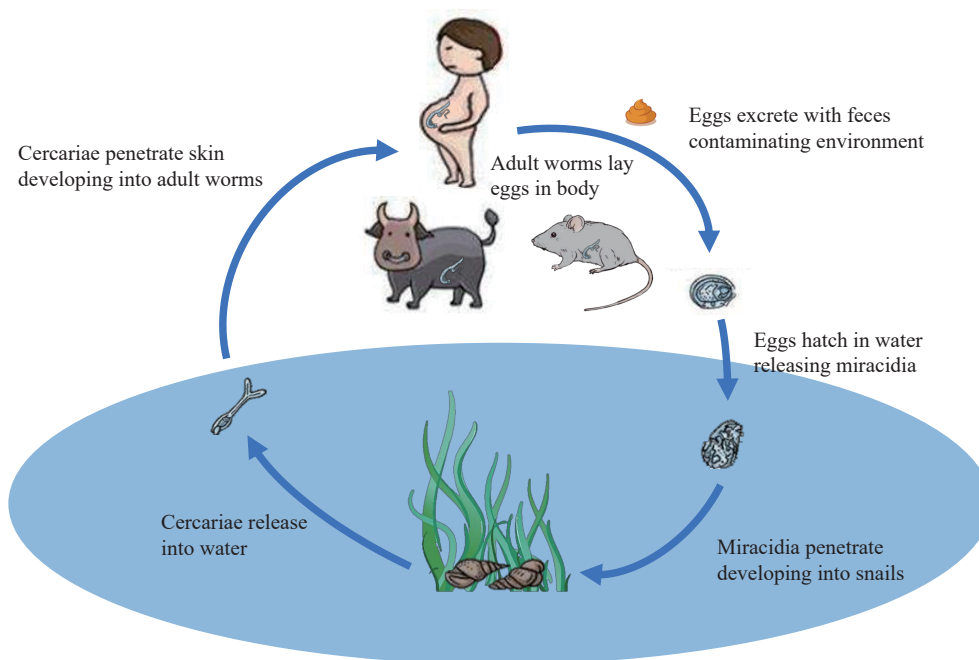
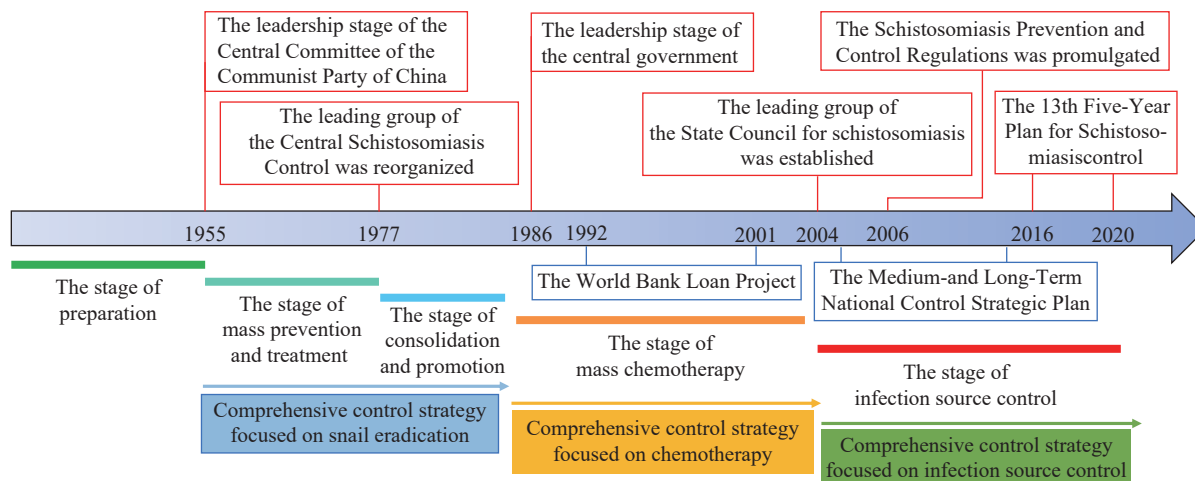
FIGURE 1. The life cycle of *S. japonicum*.

FIGURE 2. Different stages of schistosomiasis control in China.

closely related to the timely adjustment of the control strategy, which has gone through the following three stages.

Strategy Focused on Snail Elimination (mid-1950s to the early 1980s)

From the 1950s to the early 1980s, because of the slow economic growth, scarce health resources, lack of low toxicity medicine, and insufficient understanding of epidemiology towards schistosomiasis, large scale chemotherapy could not be implemented and transmission was difficult to be interrupted. Therefore,

snail control was the most suitable way to reduce the damage caused by schistosomiasis. The main countermeasures against schistosomiasis were to eliminate snails through environmental modification in combination with massive agricultural activities and molluscicide using pentachlorophenol sodium and other chemical drugs. In addition, human patients and infected animals were treated, and interventions such as personal protection, feces management, safe water usage, and government publicity were conducted. This strategy had great achievements. The snail breeding areas decreased significantly nationwide, especially in waterway network regions, and 4 provincial-level

administrative divisions including Shanghai, Guangdong, Guangxi, and Fujian had interrupted the transmission of schistosomiasis by 1985. However, this strategy required a large quantity of manpower that was not possible after the economic system reforms in the late 1970s. In addition, this strategy was not practical in marshland and lake regions where water levels fluctuated and mountainous areas where economic development was slowed.

Strategy Focused on Morbidity Control (mid-1980s to 2003)

With the recognition of the impossibility of reaching schistosomiasis elimination under the circumstances at that time and the availability of praziquantel, the drug effective against schistosomiasis that had low toxicity, China adjusted its strategy from snail control to morbidity control following guidelines from the World Health Organization (WHO) and supported by the World Bank Loan Project (WBLP) in the mid-1980s. Mass drug administration (MDA) was conducted simultaneously to human beings and domestic animals, supplemented by snail control and government publicity. The morbidity control strategy was boosted nationwide by the WBLP for schistosomiasis control in China, which spanned from 1992 to 2001 and covered 8 endemic PLADs. The number of cases with schistosome infection decreased from 1.64 million in 1989 to 0.82 million by 2001, with a reduction rate of 49.94%. However, the morbidity control strategy that focused on chemotherapy could not prevent re-infection of schistosomes in human beings and livestock. Moreover, schistosomiasis rebounded significantly after the termination of WBLP, especially after the occurrence of serious flooding in 1998 along the Yangtze River Valley (6). The lag effect of flood disasters and the implementation of the strategy of “returning farmland to lakes and removing embankments for flood discharge” further increased the distribution area of snails in China, expanded the scope of epidemic areas, and increased the population threatened by infection.

Strategy Focused on Infection Source Control (Since 2004)

Because of the low-level incidence, a comprehensive strategy was formulated to interrupt transmission via controlling schistosome egg contamination or infectious sources' exposure to the environment, particularly in snail habitats (7). In addition to

implementing conventional countermeasures such as chemotherapy on human beings and livestock, molluscicide, and health education, interventions focusing on the control of the source of infection were strengthened, such as raising livestock in pens, herding bovine in snail-free areas (avoiding eggs polluting the snail environment), replacing bovine with machines (reducing the number and kind of susceptible animals), reconstructing the sanitary toilets (conducting harmless treatment of excrement), and collecting the excrement of fishermen (avoiding eggs polluting water). In addition, engineering projects conducted by local ministries of agriculture, forestry, water conservancy, land resources, and others were integrated with the snail control projects to remove the snail breeding areas and prevent environmental pollution from the feces of human beings and animals (8). China reached transmission control criteria issued by the Chinese government as well as criteria of schistosomiasis elimination as a public health problem defined by the WHO by 2015.

Perspectives to Eliminate Schistosomiasis Through the One Health Approach

Being a vector-borne and zoonotic disease, schistosomiasis japonica is intricately linked to multiple factors including biological, natural, and socioeconomic risk factors, such as widespread snail habitats, a variety of animal hosts, frequent occurrences of floods, increased population mobilization, and transportation of goods, which are all threatening the obtained achievements and hindering the process of schistosomiasis elimination. The One Health approach, focusing on solving complex health problems from the overall perspective of human-animal-environmental interaction, advocates for multisectoral, cross-regional, and trans-disciplinary collaborations in all aspects (9–10). Thus, to realize the goal set by the strategic plan of healthy China 2030 to eliminate schistosomiasis in China, the One Health approach should be applied in national control program.

Integrated Surveillance and Response System

It was reported that about 75% of emerging infectious diseases of humans have emerged from animals during the past few decades (11). Thus, the

importance of surveillance of schistosome-susceptible animals should not be neglected. Therefore, there must be a merger of monitoring clinical practice, veterinary practice, vector surveillance, and environmental surveillance to more effectively evaluate and plan an appropriate response to the transmission of schistosomiasis. In order to promote integrated surveillance and response systems, general reference laboratories, surveillance centers based on epidemiological and big data related to schistosomiasis would be useful for pooling resources and providing rapid access information (5). Some surveillance indicators, such as observed risk factors, newly identified infected cases in humans and animals, and infection status of wild animals following examination, would allow for rapid responses before an outbreak occurs (12).

Multisectoral Collaboration

The transmission and distribution of schistosomiasis are influenced by many types of factors including the environments, pathogens, vectors, local economic conditions, and level of societal development. Interventions such as blocking the transmission of schistosomiasis from infection source to surroundings, treating or culling infected livestock, raising schistosome-unsusceptible poultry, replacing cattle with machines, and herding livestock in snail-free areas are imperative in order to control animal reservoir hosts. All of these need veterinarians, livestock producers, health workers, and political decisionmakers to work together. For snail control, there are two major approaches, which are chemical control by molluscicide and environmental modification. The former faces great challenges due to increasing environmental protection laws that prohibit controlling snail habitats along the Yangtze River and wetland eco-zones. The latter mainly relies on the projects being chaired by the ministries of water conservancy, agriculture, forestry, land resources, etc. (13).

Interdisciplinary Research

Interdisciplinary research, with the collaboration of scientists in the field of biology, ecology, computer science, and more, is a key component in understanding the complex transmission patterns and exploring interventions against schistosomiasis. Understanding the transmission dynamics of schistosomiasis in human-environment-animal interface will benefit schistosomiasis elimination (14).

Furthermore, interdisciplinary research will help connect schistosomiasis control with information technology and big data organically, establishing an efficient and sensitive early warning system worldwide (15). Moreover, increased emphasis on comparative diseases etiology, pathology, genomics, proteomics, and metabolomics is important to potentially discover novel treatments for humans and animals.

CONCLUSION

Schistosomiasis japonica is a vector-borne zoonotic disease, requiring integrated approaches for prevention and elimination to deal with the relationship among animals, the environment, and humans. Although great achievements have been reached in China through more than 70 years of effort, the elimination of schistosomiasis is a constant challenge complicated by many different biological and environmental factors involved in the circulation of the diseases, including widespread snail habitats, various animal hosts, frequent occurrence of flooding, and increased population mobilization and goods transportation. As human influence on the environment increases and the transmission of disease becomes more complex, adopting the One Health approach is an essential key to elimination of this disease. Therefore, strengthening multi-institution, interdisciplinary, and cross-regional cooperation and conducting further research to this disease are important to accelerate process of schistosomiasis elimination.

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Notifiable Infectious Diseases Reports

Reported Cases and Deaths of National Notifiable Infectious Diseases — China, January 2022

Diseases	Cases	Deaths
Plague	0	0
Cholera	1	0
SARS-CoV	0	0
Acquired immune deficiency syndrome*	3,109	1,294
Hepatitis	132,430	54
Hepatitis A	956	0
Hepatitis B	109,531	38
Hepatitis C	18,704	14
Hepatitis D	27	0
Hepatitis E	2,530	2
Other hepatitis	682	0
Poliomyelitis	0	0
Human infection with H5N1 virus	0	0
Measles	40	0
Epidemic hemorrhagic fever	781	6
Rabies†	13	14
Japanese encephalitis	9	0
Dengue	0	0
Anthrax	10	0
Dysentery	2,169	0
Tuberculosis	61,697	304
Typhoid fever and paratyphoid fever	405	0
Meningococcal meningitis	13	0
Pertussis	2,354	0
Diphtheria	0	0
Neonatal tetanus	1	0
Scarlet fever	3,232	0
Brucellosis	4,396	0
Gonorrhea	9,273	1
Syphilis	39,586	5
Leptospirosis	8	0
Schistosomiasis	4	0
Malaria	26	0
Human infection with H7N9 virus	0	0
COVID-19§	3,825	0
Influenza	230,714	5
Mumps	6,570	0

Continued

Diseases	Cases	Deaths
Rubella	70	0
Acute hemorrhagic conjunctivitis	1,811	0
Leprosy	32	0
Typhus	63	0
Kala azar	22	0
Echinococcosis	347	0
Filariasis	0	0
Infectious diarrhea [¶]	80,364	1
Hand, foot and mouth disease	44,183	1
Total	627,558	1,685

* The number of deaths of Acquired immune deficiency syndrome (AIDS) is the number of all-cause deaths reported in the month by cumulative reported AIDS patients.

† Among the 14 death cases, 7 deaths were reported in January 2022, the other were reported before.

§ The data were from the website of the National Health Commission of the People's Republic of China.

¶ Infectious diarrhea excludes cholera, dysentery, typhoid fever and paratyphoid fever.

The number of cases and cause-specific deaths refer to data recorded in National Notifiable Disease Reporting System in China, which includes both clinically-diagnosed cases and laboratory-confirmed cases. Only reported cases of the 31 provincial-level administrative divisions in the mainland of China are included in the table, whereas data of Hong Kong Special Administrative Region, Macau Special Administrative Region, and Taiwan are not included. Monthly statistics are calculated without annual verification, which were usually conducted in February of the next year for de-duplication and verification of reported cases in annual statistics. Therefore, 12-month cases could not be added together directly to calculate the cumulative cases because the individual information might be verified via National Notifiable Disease Reporting System according to information verification or field investigations by local CDCs.

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