#### **REVIEW ARTICLE**



# Transmission of SARS-CoV-2 virus and ambient temperature: a critical review

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#### Abstract

The coronavirus disease 2019 (COVID-19) pandemic has brought unprecedented public health, and social and economic challenges. It remains unclear whether seasonal changes in ambient temperature will alter spreading trajectory of the COVID-19 epidemic. The probable mechanism on this is still lacking. This review summarizes the most recent research data on the effect of ambient temperature on the COVID-19 epidemic characteristic. The available data suggest that (i) mesophilic traits of viruses are different due to their molecular composition; (ii) increasing ambient temperature decreases the persistence of some viruses in aquatic media; (iii) a 1°C increase in the average monthly minimum ambient temperatures (AMMAT) was related to a 0.72% fewer mammalian individuals that would be infected by coronavirus; (iv) proportion of zoonotic viruses of mammals including humans is probably related to their body temperature difference; (v) seasonal divergence between the northern and southern hemispheres may be a significant driver in determining a waved trajectory in the next 2 years. Further research is needed to understand its effects and mechanisms of global temperature change so that effective strategies can be adopted to curb its natural effects. This paper mainly explores possible scientific hypothesis and evidences that local communities and authorities should consider to find optimal solutions that can limit the transmission of SARS-CoV-2 virus.

Keywords COVID-19 · Ambient temperature · Global seasonal change · Mammals · Trend prediction

# Introduction

Since December 2019, a novel corona virus, severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2), has exhibited unprecedented human-to-human transmissibility, with more than 156 million confirmed cases of the coronavirus disease 2019 (COVID-19) and 3.26 million deaths in 220 countries and regions on May 8, 2021 (from the World

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Health Organization (WHO) COVID–19 Dashboard: https:// covid19.who.int/). To date, there is no consensus on whether temperature can mitigate spreading of the virus, so efforts at control have focused on implementation of extensive public health interventions, such as social distancing, wearing of protective clothing, including face masks, and disinfection of surfaces and hands. To understand the effects of temperature and humidity on behavior of the SARS-CoV-2 virus, the first

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rapid response research fund was launched by the United States National Science Foundation for supporting decisionmaking on disease control.

From a perspective of environmental geosciences using a regression framework, results of previous studies on relationships between spatial and temporal distributions of SARS-CoV-2 and temperature have been summarized. Newly confirmed cases, in China and other countries worldwide, have been examined to show significantly relationships with ambient temperature (Wang et al. 2020a; Wang et al. 2020b). The optimal temperature for peak rate of transmission was centered at 8.72 °C, which indicates that cold environments facilitate survival and spread of droplet-mediated viral diseases and contributes to spreading the epidemic. Based on analysis of some countries where wide-spread infections have occurred, warm and humid weather in Singapore and Thailand might have been a factor in the more moderate trajectories of epidemics, which is compared to the relatively severe viral transmission in Japan, South Korea, Europe, and Iran. Based on results of a recent statistical study, the global pandemic was primarily between latitudes of  $30^{\circ}$  N ~  $50^{\circ}$  N, a corridor with average temperatures of  $5 \sim 11$  °C. The number of cumulative cases in countries with an average temperature of more than 18 °C and an absolute humidity of more than 9 g/m<sup>3</sup> from January to March 2020 is less than 6% of the total number of global confirmed cases (Bukhari and Jameel 2020). Due to limited and early-stage results on the current pandemic, the relative importance of climate drivers need to be further characterized (Baker et al. 2020).

Epidemic disease emergence cannot occur without certain conditions being met, including the presence of the pathogen, humans, and environment media in which the virus can survive. A conceptual framework of viral outbreaks, transmission and occurrences of diseases that they cause, through interplay of these three essentials is provided (Fig. 1). There is a scientific hypothesis that the change of ambient temperature might affect infection tendency of different types of viruses, survival capacity in environmental media, and spreading among mammals as well as humans. The main objective of the present study is to review the limited temperature-dependent spatial and temporal distributions of the COVID-19 pandemic through existing data analyses. Viral mesophilic trait, survival in aquatic environment, body temperatures of hosts, and infected ratio of mammals were mainly discussed. Furthermore, based on global change of ambient temperature that differs from two hemispheres, we also predict the prevalent trend of COVID-19 epidemics in the next 2 years and demonstrate the seasonal epidemic characteristics of SARS-CoV-2 virus.

# Data analysis and discussion

#### Mesophilic traits of different viruses

Several viruses that have caused outbreaks of infectious diseases such as Zika and Ebola show certain geographical distribution characteristics (Kraemer et al. 2019). Bibliometrics results show that optimal temperature ranges for survival and spreading can vary among seven major types of viruses that have caused public health emergency (Fig. 2). The optimal temperature range for transmission of coronavirus and influenza virus is usually below 20 °C, while some thermophilic viruses, including Zika, dengue fever virus (DFV), yellow fever virus (YFV), and Japanese encephalitis virus (JEV), tend to outbreak and spread in tropical areas (>25°C). For example, outbreak and spreading of Zika virus have been reported frequently in the past decades; however, the epidemic trajectory showed obvious geographical distribution characteristics. It was mainly located in tropical and subtropical areas, and did not cross into temperate zone (Caminade et al. 2017; Messina et al. 2016).

In our opinion, the probable reason of temperaturedependent characteristics of viruses can be explained from principle of structural biology. Chemical bonding and non-

Fig. 1 Ambient temperature can affect COVID-19 emergence through interactions among three essential elements of SARS-CoV-2 (purple), environmental media (blue), and uninfected humans (green). The red region represents emergence of an infective disease



V-SARS-CoV-2 virus; E-Environment; H-Humans; D-Disease emergence; I-Infection tendency; S-Survival in the environment; W-Wildlife Fig. 2 Mesophilic traits of viruses that have caused major public health emergencies in the last decades include severe acute respiratory syndrome (SARS) coronavirus, influenza (Flu), Ebola, yellow fever virus (YFV), Zika, dengue fever virus (DFV), and Japanese encephalitis virus (JEV)



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bonding forces that maintain the protein structure are inversely proportional to temperature, which results in loss of structural integrity of the whole virus or partial function areas at high temperatures (Pain 1987). Some in silico techniques, such as molecular docking and molecular dynamic simulation, have been used to assess the stability of critical main proteases of the SARS-CoV-2, which indicated that temperature could interfere with virus replication (Bhardwaj et al. 2021; Sharma et al. 2021). Structural denaturation of proteins that make up viruses may trigger subsequently irreversible inactivation (Bhardwaj et al. 2020; Han and Kral 2020).

#### Survival capacity of viruses in aquatic media

In the present study, we compared durations of survival of various pathogens in aquatic environments under different ambient temperatures (4 °C, 15 °C, and 20-25 °C), results of which suggested that temperature was a significant factor influencing viability and survival of viruses (Table S1). Most viruses such as CoV-229E, Poliovirus, Feline CoV, and Adenoviruses can survive longer in cooler environments. Therefore, disinfection of drinking water can prevent transmission of SARS-CoV-2 through aquatic media. These findings demonstrate that higher temperature and humidity can reduce durations of survival of most viruses in aquatic media. Based on an extreme case of cluster transmission in a toilet, some researchers, however, have come to different conclusions. For nine patients who were infected, within a week, after entering the same public bathroom (Luo et al. 2020), the authors alerted the public to the fact that higher temperature and humidity have limited ability to suppress spread of the novel coronavirus, and the spread might not be weakened.

The SARS-CoV-2 virus as well as other viruses has been reported to be shed outside bodies of infected organisms, through aerosol, feces, and urine, which ultimately enter environmental media (Banik and Ulrich 2020; Chen et al. 2020). Persistence in air, water, soil, or on physical surfaces is a vital determinant of transmissibility. In general, viruses transmitted in droplets tend to persist longer at low-temperature and lowhumidity environment (Chan et al. 2011), and on certain surfaces, including glass and steel (Wood et al. 2010). In the present study, we compared survival capacity of various viruses in aquatic environments under cold (4 °C) and warm (>15 °C) conditions (Fig. 3), which suggested that ambient temperature was a vital factor to influence the time to kill 99% of viruses ( $T_{99}$ ). Four corona viruses including 229E, Feline CoV, Porcine CoV, and Rat CoV can survive much longer in cold environments. These findings demonstrate that higher temperature and humidity can reduce durations of most of corona viruses in aquatic media. Median T<sub>99</sub> of Poliovirus and Adenoviruses in cold condition extended at 2.9 and 1.44 times, respectively. Hepatitis A does not show any difference under warm and cold conditions. Despite of this, higher ambient temperature cannot completely prevent the spread of virus through environmental media. Luo C. et al. (2020)



**Fig. 3** Durations of survival, based on 99% inactivation of virus ( $T_{99}$ , days) at different ambient temperatures (4 °C in blue and >15 °C in red). The horizontal lines represent the 95th centiles, and the boxes represent the 25th and 75th centiles. Median are shown as the hollow box (data sources: Table S1)

reported an extreme case of cluster transmission of SARS-CoV-2 in a public bathroom, where nine patients were confirmed to be infected through indirect contact. The authors alerted the public that higher temperature and humidity have limited ability to suppress spread of SARS-CoV-2 virus, and the spread might not be weakened.

Several direct testing on survival of SARS-CoV-2 in environmental media were reported in the past year. SARS-CoV-2 can survive for 7 days in outer layers of surgical masks. Absorbent materials like cotton are safer than unabsorbent materials for protection from virus infection. Risk of transmission via touching contaminated paper is low (Ren et al. 2020). The spread of the SARS-CoV-2 was reduced by increasing temperature from -13.2 to 19 °C and ambient concentration of ozone (Yao et al. 2020). More in-depth researches need to be performed as time goes on. Compared with other coronaviruses, SARS-CoV-2 may have greater survival capacity, which contributes to strong susceptibility. Therefore, it is very vital promoting effective environmental elimination in high-risk areas.

#### Infected ratio of mammals and ambient temperature

Mammals is an unneglected reservoir host to the SARS-CoV-2, and has opportunity in cross-species spillover to humans by close contact. To explore the relationships between ambient temperature and ratio of infection incidence in mammals, infected ratios of coronavirus (including  $\alpha$  and  $\beta$  subtype) through polymerase chain reaction (PCR) testing were reviewed from existing literatures and database (Table S2). For mammals in five orders, including Chiroptera, Rodentia, Carnivora, Artiodactyla, and Erinaceomorpha, ratios between number of positive samples and number of total samples in mammals were computed. The average monthly minimum ambient temperatures (AMMAT) at the sampling regions were calculated at the same time. As shown in Fig. 4, the Pos/Tot ratios of mammals were inversely proportional to AMMAT, with a coefficient of determination  $(R^2)$  of 0.6546 (F = 18.95, p = 0.001, RSS = 0.0166, RMSE = 0.0408). The internal validation had been performed to overcome overfitting  $(R^2 - Q_{CV}^2) = 0.2546 < 0.3$ ,  $RMSE_{CV} = 0.053$ ). Our finding indicates that a 1° increase in AMMAT was associated with 0.72% fewer mammalian individuals that were infected by the SARS-CoV-2.

If we regard humans as a member of mammals, the ratio of cumulative infected cases by SARS-CoV-2 was investigated and global average infection ratio was quantified as 0.4% ( $0\sim3.9\%$ ), which was lower than that of mammals (Table S3). Based on the linear correlation model, the corresponding AMMAT was 24.9°C, at which SARS-CoV-2 virus can spread in most geographic areas worldwide.

These results also suggested that some mammals are more susceptible hosts than humans. There are some evidences that



**Fig. 4** The relationship between average monthly minimum ambient temperatures (AMMAT) and ratio of infection incidence in mammals and human. Incidence of expression is expressed as the Pos/Tot ratio of mammals which was determined based on coronavirus detection by PCR. Red line is a linear fitting with minimum root mean square deviation (*RMSE*). Blue tape describes the range of cumulative infected ratio in top 31 countries worldwide. Animal silhouettes visually represent each mammalian order which were downloaded from PhyloPic (www.phylopic.org)

SARS-CoV-2 was detected in body of kitten, dog, tiger, and lion (Sabateeshan and Graham 2020; Sit et al. 2020). It was also found from ferret farms in Denmark, Spain, and the Netherlands, where cross-species transmission of SARS-CoV-2 has occurred from ferret to humans (Richard et al. 2020). Therefore, mutual infection between mammals and humans needs to be paid more attentions.

## Proportion of zoonotic viruses in mammals and their body temperature

Several studies have shown that mammals may carry a variety of zoonotic viruses, which are prone to cross-species spillover to humans (Carlson et al. 2019; Mollentze and Streicker 2020). However, it is not clear whether the capacity to carry zoonotic viruses is related to body temperature of mammals. Therefore, we are trying to explore the normal body temperature of mammals and humans. Normal body temperatures of 62 mammals in 7 orders and 20 families were obtained from the existing literatures, including Chiroptera, Rodentia, Cetartiodactyla, Carnivora, Didelphimorphia, Primates, and Lagomorpha. A human body's normal temperature, also referred to as euthermia or normothermia, is typically within the range of 36.5-37.5 °C, concerning race, circadian rhythm, age, and sex. The proportion of zoonotic viruses in 7 orders was predicted from a comprehensive analysis of mammalian hostvirus relationships, which suggests that Chiroptera, Primate, and Rodentia harbor a significantly higher proportion of zoonotic viruses than other mammalian orders (Olival et al. 2017). As shown in Fig. 5, mammals in four orders



**Fig. 5** Proportion of zoonotic viruses and normal body temperatures of 62 mammals in 7 orders and 20 families (data sources: Table S4). Horizontal lines represent the 95th centiles, and the boxes represent the 25th and 75th centiles. The range of human body temperature is shown between two dotted lines. Proportion of zoonotic viruses is from an existing literature reported by K. J. Olival et al. (2017)

(Primates, Chiroptera, Carnivora, and Rodentia), whose body temperatures were close to humans, had a higher proportion of zoonotic viruses and thus exhibited greater potential for viral spillover to humans. Body temperature of mammals, higher or lower than normal human body temperature, possesses fewer zoonotic virus. Although there is limited data on different species, it is a probable significant predictor of zoonotic potential to assess if a newly discovered mammalian virus could infect people.

#### Global epidemic trajectory and seasonal change

In the past year since the COVID-19 outbreak, SARS-CoV-2 virus has transmitted to more than 220 countries and regions worldwide. Variation of cumulative confirmed ratios between two hemispheres is a good indicator to indicate seasonal trends of the COVID-19 pandemic. Based on confirmed cases reported by the WHO (https://covid19.who.int/), cumulative ratios of the N hemisphere to those of global from Feb 29, 2020 to Feb 28, 2021 alternate in waves between two hemispheres (Fig. 6 and Table S5). A sinusoidal decay model was used to fit this trend, which suggested that under the current control measures, community communication will fluctuate with the seasons between two hemispheres. Then, the predicted cumulative ratios are going to stabilize at 82. 17% in the next 2 years. Seasonal alternation between the northern and southern hemispheres is one of the important climatic drivers for the spread of SARS-CoV-2 virus (Figure S1). In winter time of the S hemisphere (up to Aug 2020), cumulative ratio of the N hemisphere to global dropped to a minimum value of 75.89% for the high speed at which the SARS-CoV-2 virus spreads. Preliminary epidemiological results have also demonstrated a significant increase in the number of confirmed cases in Brazil, Argentina, Chile, Peru, South Africa, and southern Australia during that period. A latest study in Brazil also reported that a decrease of 1°C was associated with an increase of 4.89% of total, daily, confirmed cases of COVID-19, which suggests greater severity in winter (Prata et al. 2020).

# Conclusions

It is concluded that ambient temperature can play a role in influencing spatial and temporal distributions of viral transmission that has been usually overlooked in epidemiologic research. Three probable drivers to alter the pandemic trajectory are viral mesophilic traits, survival capacities in aquatic environmental media, and cross-species spillover from mammals to humans. Understanding the intrinsic connection and revealing the mechanism can help mitigate epidemic spread all over the world. It is the first reported study that infected ratio of mammals was inversely proportional to AMMAT at the sampling regions ( $R^2 = 0.6546$ , F = 18.95, p = 0.001). A 1°C increase in the AMMAT was related to a 0.72% fewer mammalian individuals that would be infected by SARS-CoV-2 virus. Our findings also indicate that seasonal alternations between the northern and southern hemispheres could be a significant factor in determining a waved trajectory of the COVID-19 pandemic.

Therefore, international cooperation and joint research are of paramount importance. Some key scientific issues need to be further developed in three areas. These include (1) behavior, effect, and toxicological mechanism in the multi-process from natural environment to human, animal to environment to human, and human to human; (2) in addition to temperature, multi-factors should be focused, such as humidity, lighting, wind speed, extreme climate, susceptible people, natural and man-made environment types, and environmental pollution characteristics; (3) developing in silico techniques and statistical models to assess spreading spatial and temporal distributions in local, regional, and global scales.

## Materials and methods

## **Data extraction**

Literatures were obtained from the ISI Web of Knowledge Core Collection (1975-2020) and Chinese Science Citation Database (1989-2020) databases on July 12, 2020. To investigate the mesophilic traits of viruses, reference search strategy is virus [Topic] AND transmission [Topic] AND optimal temperature [Topic] and 86 publications were obtained. After



**Fig. 6** Global COVID-19 epidemic trajectory between two hemispheres during the period between Feb 2020 and Feb 2023. Dotted line shows 95% confidence intervals. Robustness of fitting model was evaluated by use of the adjusted coefficient of determination (*adj*  $R^2$ ), sum of squares due to error (*SSE*), root mean square deviation (*RMSE*), and *F* value using

one-way analysis of variance (ANOVA) with the level of significance at  $\alpha = 0.05$ . Means and variances were compared with Bonferroni and Tukey's multiple tests. The red line represents the population ratio of the N hemisphere to global with 70.18%, published by the United Nations Population Division (UNPD) in 2019 (Table S4)

checking abstract and full text, 15 papers on seven types of viruses satisfied the following selection criteria (Brady et al. 2014; Chan et al. 2011; Fiszon et al. 1989; Fouque and Reeder 2019; Hamlet et al. 2018; Kiseleva et al. 2010; Lambrechts et al. 2011; Li et al. 2014; Mordecai et al. 2013; Ng et al. 2014; Tesla et al. 2018; Tramonte and Christofferson 2019; Watanabe et al. 2013; Zhang et al. 2015; Zhang et al. 2004).

Body temperatures of mammals in different orders were obtained under existing literatures. The searching strategy is mammal [Topic] AND normal body temperature [Topic] OR normothermia [Topic]. After reviewing full text of 189 publications, 34 papers on normal body temperature of 62 mammals in 7 orders and 20 families were selected for further analysis (An 2005; Bevanger and Broseth 1998; Chen and White 2006; Deavers and Hudson 1981; Duan et al. 2019; Fleming 1980; Fons and Sicart 1976; Geiser 1984, 1986; Geiser 1988; Geiser and Baudinette 1987; Harlow 1981; Heldmaier and Steinlechner 1981; Hudson 1965; Hudson and Scott 1979; Jensen et al. 2009; Jing and Sun 1982; Kennedy and Macfarlane 1971; Kulzer 1965; Lee et al. 1985; Liu 1983; Liu et al. 2004; Macmillen 1965; Morrison and McNab 1962; Morton and Lee 1978; Noll 1979; Sheng 1982; Sun 2005; Thompson 1985; Tucker 1965; Wang 2003; Wang and Hudson 1970; Wei and Huang 1983; Yang et al. 2012). And then, keywords were set as coronavirus [Topic] AND mammal [Topic] AND PCR [Topic] OR polymerase chain reaction [Topic] to search both databases. Twelve papers reporting total number of samples and coronavirus positive number for mammalian individuals were screened (August et al. 2012; Berto et al. 2018; Castanheira et al. 2014; Ge et al. 2017; McIver et al. 2020; Nziza et al. 2020; Ommeh et al. 2018; Quan et al. 2010; Saldanha et al. 2019; Tsoleridis et al. 2016; Valitutto et al. 2020; Wacharapluesadee et al. 2015). Information on sampling time and location is summarized in Table S1. Average ambient minimum and maximum temperatures at the sampling regions were extracted from available data on World Meteorological Organization website (https://public.wmo.int/en). Global cumulative confirmed cases are derived from WHO Coronavirus Disease (COVID-19) Dashboard (https://covid19.who.int/). Population data are publicly available from open data of the World Bank (https://data.worldbank.org.cn/). Animal silhouettes visually represent each mammalian order which were downloaded from PhyloPic (www.phylopic.org).

#### Statistical analysis

Linear regression analysis was performed between the Pos/ Tot ratio of different mammals and average monthly minimum ambient temperature (AMMAT). Robustness of fitting model was evaluated by use of the adjusted coefficient of determination (*adj*  $R^2$ ), sum of squares due to error (SSE), root mean square deviation (RMSE), and F value using one-way analysis of variance (ANOVA) with the level of significance at  $\alpha = 0.05$ . Means and variances were compared with Bonferroni and Tukey's multiple tests. To reduce the probability of overfitting the model to the training data, depending on presence/absence of one sample in the training set, models were internally validated by use of the cross-validated, leaveone-out technique ( $LOO_{CV}$ ) (Golbraikh et al. 2003; Tropsha et al. 2003). Following the  $LOO_{CV}$  algorithm, each mammal was removed, one at a time, from the training set. The crossvalidated correlation coefficient,  $Q_{CV}^2$ , and cross-validated root-mean-square errors of prediction, RMSE<sub>CV</sub>, were calculated from the sum of the squared differences between the observed and estimated toxicity. The recommended reference criteria stated that  $R^2$  should be greater than 0.6 and that the difference between  $R^2$  and  $Q_{CV}^2$  should be less than 0.3 (Eriksson et al. 2003). We used the QSAR toolbox in the SYBYL X1.1 program (Tripos, Inc., MO, USA) for leaveone-out calculations. Statistical analyses were completed with SPSS Statistics 17.0 (IBM Inc., NY, USA), G\*Power 3.1.9.2 (program written by Franz Faul, Kiel University, Germany), and Origin Pro 8.0 (OriginLab Inc., MA, USA).

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**Data availability** The datasets developed during the current study are available from the corresponding author on reasonable request.

#### Declarations

**Conflict of interest** The authors declare no competing interests.

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1 2	Submitted to Environmental Science and Pollution Research
3	<b>Transmission of SARS-CoV-2 virus and ambient</b>
4	temperature: A critical review
5	
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Figure S1 Global seasonal change of top 30 countries with maximum cumulative confirmed cases. 23 in

28 northern hemisphere (solid line) and 7 in southern hemisphere (dotted line).

Туре	Virus	<i>T</i> 99(d)	AT (°C)	Media type	Ref.
Enveloped	229E	6.76	23	Filtered tap water	(Gundy et al. 2009)
virus	229E	8.09	23	Tap water	(Gundy et al. 2009)
	229E	392	4	Filtered Tap water	(Gundy et al. 2009)
	229E	1.57	23	Primary effluent	(Gundy et al. 2009)
	229E	2.36	23	Primary effluent	(Gundy et al. 2009)
	229E	1.85	23	Secondary effluent	(Gundy et al. 2009)
	Feline CoV	6.67	23	Tap water	(Gundy et al. 2009)
	Feline CoV	8.32	23	Tap water	(Gundy et al. 2009)
	Feline CoV	87	4	Filtered tap water	(Gundy et al. 2009)
	Feline CoV	1.6	23	Primary effluent	(Gundy et al. 2009)
	Feline CoV	1.71	23	Primary effluent	(Gundy et al. 2009)
	Feline CoV	1.62	23	Secondary effluent	(Gundy et al. 2009)
	Porcine CoV	11	4	Reagent grade	(Casanova et al. 2009)
	Porcine CoV	110	25	water Reagent grade	(Casanova et al. 2009)
				water	
	Porcine CoV	4	4	Pasteurized	(Casanova et al. 2009)
				precipitated sewage	
	Rat CoV	9	25	Pasteurized	(Casanova et al. 2009)
				precipitated sewage	
	Rat CoV	>365	4	Pasteurized	(Casanova et al. 2009)
				precipitated sewage	
	Rat CoV	3	25	Reagent grade	(Casanova et al. 2009)
				water	
Non-envelo	Poliovirus	43.3	23	Filtered tap water	(Gundy et al. 2009)

**Table S1** Survival time (days) for ninety-nine percent of viruses inactive (T<sub>99</sub>) in aquatic environment

ped virus	Poliovirus	47.5	23	Tap water	(Gundy et al. 2009)
	Poliovirus	135	4	Filtered tap water	(Gundy et al. 2009)
	Poliovirus	23.6	23	Primary effluent	(Gundy et al. 2009)
	Poliovirus	7.27	23	Primary effluent	(Gundy et al. 2009)
	Poliovirus	3.83	23	Secondary effluent	(Gundy et al. 2009)
	Poliovirus	41	4	Tap water	(Enriquez et al. 1995)
	Poliovirus	24	15	Tap water	(Enriquez et al. 1995)
	Poliovirus	11	23	Tap water	(Enriquez et al. 1995)
	Poliovirus	49	4	Secondary effluent	(Enriquez et al. 1995)
	Poliovirus	19	15	Secondary effluent	(Enriquez et al. 1995)
	Poliovirus	36	4	Primary effluent	(Enriquez et al. 1995)
	Poliovirus	28	15	Primary effluent	(Enriquez et al. 1995)
	Poliovirus	18	23	saltwater	(Enriquez et al. 1995)
	Hepatitis A	56	4	Tap water	(Enriquez et al. 1995)
	Hepatitis A	87	15	Tap water	(Enriquez et al. 1995)
	Hepatitis A	27	23	Tap water	(Enriquez et al. 1995)
	Adenoviruses	92	4	Tap water	(Enriquez et al. 1995)
	Adenoviruses	87	15	Tap water	(Enriquez et al. 1995)
	Adenoviruses	60	23	Tap water	(Enriquez et al. 1995)
	Adenoviruses	58	4	Secondary effluent	(Enriquez et al. 1995)
	Adenoviruses	43	15	Secondary effluent	(Enriquez et al. 1995)
	Adenoviruses	44	4	Primary effluent	(Enriquez et al. 1995)
	Adenoviruses	40	15	Primary effluent	(Enriquez et al. 1995)
	Adenoviruses	77	23	Saltwater	(Enriquez et al. 1995)

 Adenoviruses	304	4	Tap water	(Enriquez et al. 1995)
Adenoviruses	124	15	Tap water	(Enriquez et al. 1995)
Adenoviruses	84	23	Tap water	(Enriquez et al. 1995)
Adenoviruses	47	4	Secondary effluent	(Enriquez et al. 1995)
Adenoviruses	45	15	Secondary effluent	(Enriquez et al. 1995)
Adenoviruses	48	4	Primary effluent	(Enriquez et al. 1995)
Adenoviruses	43	15	Primary effluent	(Enriquez et al. 1995)
Adenoviruses	85	23	Saltwater	(Enriquez et al. 1995)

31 **Table S2**. Coronavirus RNA-positive samples reported in the literature with their Positive : Total Ratio (i.e., Pos/Tot Ratio) and average monthly ambient minimum

Common	Orders	Sample	Positive	Pos/To	Minimum <sup>a</sup>	Maximum <sup>a</sup>	Location	Ref.
name		<b>(n)</b>	( <b>n</b> )	t Ratio	Temperature	Temperatur		
						e		
Bats	Chiroptera	464	7	0.015	23.7	30.1	Myanmar	(Valitutto et al. 2020)
Bats	Chiroptera	33	1	0.03	22.7	30	Nigeria	(Quan et al. 2010)
Bats	Chiroptera	626	47	0.075	19.5	29.8	Eastern Thailand	(Wacharapluesadee et al. 2015)
Bats	Chiroptera	503	27	0.054	15.8	30.5	Rwanda	(Nziza et al. 2020)
Bats	Chiroptera	112	26	0.232	2.6	20.9	Southwest England	(August et al. 2012)
Camel	Artiodactyla	1163	11	0.009	24.9	32.6	Kenya	(Ommeh et al. 2018)
Canine	Carnivora	53	1	0.019	16	28.8	Cape Verde	(Castanheira et al. 2014)
Hedgehogs	Insectivore	351	38	0.108	6.85	17.7	England	(Saldanha et al. 2019)
Rats	Rodentia	270	12	0.044	18.5	30.8	Southern Viet Num	(Berto et al. 2018)
Rats	Rodentia	513	11	0.021	10.4	19.4	East Midlands regions of the England	(Tsoleridis et al. 2016)
Rats	Rodentia	851	12	0.014	23.7	29.3	Lao People's Democratic Republic	(McIver et al. 2020)
Rats	Rodentia	177	23	0.13	9	22	Yunnan	(Ge et al. 2017)

32 and maximum temperatures at the sampling regions.

33 <sup>a</sup> Average monthly ambient temperature data was extracted from World Meteorological Organization website (https://public.wmo.int/);

Order	No.	Family	Latin name	BT (°C)	Ref.
Chiroptera	28	Molossidae	Eumops perotis	33.1	(Noll 1979)
			Tadarida teniotis	36.0	(Kulzer 1965)
			Tadarida condylura	36.8	(Kulzer 1965)
			Tadarida hindei	39.4	(Kulzer 1965)
			Tadarida pumila	39.1	(Kulzer 1965)
		Pteropodidae	Rousettus aegyptiacus	40.1	(Kulzer 1965)
			Rousettus angolensis	39.1	(Kulzer 1965)
			Pteropus giganteus	36.8	(Kulzer 1965)
			Epomophorus anurus	39.2	(Kulzer 1965)
			Asellia tridens	36.3	(Kulzer 1965)
		Rhinolophidae	Hipposideros speoris	34.8	(Kulzer 1965)
			Hipposideros bicolor	34.9	(Kulzer 1965)
			Rhinopoma microphyllum	33.9	(Kulzer 1965)
			Rhinopoma hardwickei	34.0	(Kulzer 1965)
			Rhinolophus ferrumequinum	38.3	(Kulzer 1965)
			Rhinolophus hipposideros	37.0	(Kulzer 1965)
		Emballonuridae	Taphozous melanopogon	37.5	(Kulzer 1965)
		Megadermatidae	Megaderma lyra	39.3	(Kulzer 1965)
		Vespertilionidae	Myotis myotis	39.5	(Kulzer 1965)
			Myotis nattereri	39.8	(Kulzer 1965)
			Myotis yumanensis	38.3	(Kulzer 1965)
			Pipistrellus pipistrellus	37.3	(Kulzer 1965)
			Nyctalus noctula	38.2	(Kulzer 1965)
			Eptesicus fuscus	38.2	(Kulzer 1965)
			Eptesicus sp. I (Bagdad)	38.0	(Kulzer 1965)
			Eptesicus sp. II (Bagdad)	36.5	(Kulzer 1965)
			Plecotus auritus	38.5	(Kulzer 1965)
			Antrozous pallidus	37.3	(Kulzer 1965)
Rodentia	17	Circetidae	Peromyscus leucopus	36.7	(Deavers & Hudson 1981
			Peromyscus eremicus	37.0	(Macmillen 1965)
			Phodopus sungorus	37.0	(Heldmaier &

34 ]	Fable S3.	Normal body	temper	ature (BT	) of 62	mammals	in 7	orders	and 20	families
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					Steinlechner 1981)
			Baiomys taylori	35.5	(Hudson 1965)
			Reithrodontomys megalotis	37.5	(Thompson 1985)
			longicaudatus		
			Reithrodontornys megalotis ravus	37.3	(Thompson 1985)
			Cricetulus triton	35.9	(Wei & Huang 1983)
			Eothenomys miletus	35.5	(Wei & Huang 1983)
			Meriones unguiculatus	34.7	(Jing & Sun 1982)
			Eothenomys olitor hypolitor	35.6	(Wei & Huang 1983)
			Microtus mandarinus	36.7	(Wei & Huang 1983)
		Heteromyidae	Perognathus hispidus	38.0	(Wang & Hudson 1970)
			Perognathus californicus	38.0	(Tucker 1965)
		Muridae	Mus musculus	37.4	(Hudson & Scott 1979)
			Rattus flavipeetus	35.4	(Wei & Huang 1983)
			Apodemus chevrieri	36.6	(Liu et al. 2004)
		Sciuridae	Ammospermophilus leucurusa	41.0	(Sheng 1982)
			Marmota bobak	38.0	(Sheng 1982)
Cetartiodactyla	3	Alpacaceae	Camelus dromedarius	38.0	(Sheng 1982)
		Suina	Sus scrofa domesticus	39.2	(Wang 2003)
		Bovidae	/	39.0	(An 2005)
Carnivora	7	Mustelidae	Taxidea taxus	37.0	(Harlow 1981)
			Melogale moschata	37.0	(Bevanger & Broseth
					1998)
			Arctonyx collaris	37.0	(Bevanger & Broseth
					1998)
			Meles meles	37.0	(Bevanger & Broseth
					1998)
		Canidae	Siberian Husky	38.0	(Sheng 1982)
			Lycaon pictus	38.5	(Liu 1983)
		Viverridae	Paguma larvata	37.0	(Sun 2005)
Didelphimorphia	1	Didelphidae	Marmosa sp.	34.7	(Morrison & McNab
					1962)
Primates	4	Hominidae	Pan troglodytes	37.2	(Jensen et al. 2009)
		Cercopithecidae	Rhesus macaques	38.2	(Duan et al. 2019)

			Macaca mulatta	37.1	(Yang et al. 2012)
			Macaca fascicularis	38.2	(Lee et al. 1985)
Lagomorpha	2	Leporidae	Oryctolagus cuniculus	39.3	(Chen & White 2006
			Oryctolagus cuniculus	39.0	(Chen & White 2006
Homo sapiens	/	/	/	36.2~37.3	/

Date	Cumulative confirmed	Global cumulative	Cumulative ratio of N	Population of N	Global population	Population ratio of N
	cases of N hemisphere <sup>a</sup>	confirmed cases <sup>a</sup>	hemisphere to global (%)	hemisphere (million) <sup>b</sup>	(million) <sup>b</sup>	hemisphere to global (%)
Feb 29, 2020	1,660,370	1,660,910	99.97%			
Mar 31, 2020	2,346,846	2,367,230	99.14%			
Apr 30, 2020	4,503,556	4,680,632	96.22%			
May 31, 2020	6,663,545	7,517,373	88.64%			
Jun 30, 2020	9,463,771	11,757,712	80.49%			
Jul 31, 2020	14,373,680	18,712,168	76.81%			
Aug 31, 2020	20,468,269	26,970,000	75.89%	5433.4	7673.5	70.81%
Sept 30, 2020	27,385,271	35,589,758	76.95%			
Oct 31, 2020	37,981,452	47,780,950	79.49%			
Nov 31, 2020	53,638,984	64,918,692	82.62%			
Dec 31, 2020	70,496,157	83,935,535	83.99%			
Jan 31, 2021	87,253,595	103,835,746	84.03%			
Feb 28, 2021	96,074,805	115,014,037	83.53%			

# **Table S4** Ratios of N hemisphere to global for cumulative confirmed cases and populations

- 37 a Data of cumulative confirmed case are from WHO Coronavirus Disease (COVID-19) Dashboard (https://covid19.who.int/); b Populations revised in 2019, by the United Nations Population
- 38 Division (UNPD), are from the world bank open data website (https://data.worldbank.org.cn).

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