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# WHO Drinking Water Guidelines

Aja Jagne

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# WHO DRINKING WATER GUIDELINES

By

AJA FATOU JAGNE

SPRING 2019

**INTRODUCTION:** The World Health Organization has a published collection of Guidelines for Drinking Water Quality. These Guidelines are the outcome of the input of various experts in this subject matter from all over the world. This capstone project focuses on providing updated data for three specific viruses: Coronaviruses, Orthomyxoviruses and Filoviruses.

**AIM:** The project aims to provide updated general descriptions, overviews on human health effects, background on specific epidemiology, transmission, environmental significance and control measures for Coronaviruses, Orthomyxoviruses and Filoviruses. This information will be presented in a way that is consistent with the fact sheets that are already published in the collection.

**METHODS:** Relevant information for each subsection of the virus outlines was obtained through searches within online databases. The search engines used were PubMed, The Georgia State University Library, and GoogleScholar. To ensure that the most recent data for each virus was found, only information within a 15-20-year time frame was cited. Search terms initially remained broad to ensure that applicable data was not overlooked and was gradually condensed to remain consistent with the information provided in other fact sheets in the collection.

**RESULTS:** The information provided from these factsheets will be synthesized from the literature review and will be presented in language accessible to a variety of audiences.

**DISCUSSION:** The WHO identifies the primary purpose of the Guidelines for Drinking Water as the “protection of Public Health”. With the data provided in these fact sheets, the public can make informed decisions regarding the maintenance of potable drinking water and controlling these three specific viruses that affect drinking water.

WHO DRINKING WATER GUIDELINES

by

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A Capstone Submitted to the Graduate Faculty  
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of the  
Requirements for the Degree

MASTER OF PUBLIC HEALTH

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# WHO Drinking Water Guidelines

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## Author's Statement Page

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Aja Fatou Jagne

A handwritten signature in black ink, appearing to read "Aja Fatou Jagne". The signature is written in a cursive style with a prominent initial "A".

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Methods

A separate systematic search of published literature for Coronaviruses, Orthomyxoviruses, and Filoviruses, respectively, was conducted.

To obtain data for “General Descriptions”, the words “Coronavirus classification” were typed in PubMed. Search results were first filtered by selecting the “Free full text” availability, then filtered again by entering “from 1998/01/01 to 2018/06/30” in Publication dates. These steps were repeated for each subsection of the fact sheet, using the search terms “Coronavirus health effects”, “Coronavirus epidemiology” “Coronavirus transmission”, “Coronavirus in environment” and “Coronavirus control measures”.

The following table shows the search details that were generated from PubMed for Coronavirus virus:

<b><u>Subsection</u></b>	<b><u>Search Result</u></b>
General Description	: (("coronavirus"[MeSH Terms] OR "coronavirus"[All Fields]) AND ("classification"[Subheading] OR "classification"[All Fields] OR "classification"[MeSH Terms])) AND ("loattrfree full text"[sb] AND ("1998/01/01"[PDAT] : "2018/06/30"[PDAT])).
Human Health Effects	(("coronavirus"[MeSH Terms] OR "coronavirus"[All Fields]) AND ("health"[MeSH Terms] OR "health"[All Fields]) AND effects[All Fields]) AND ("loattrfree full text"[sb] AND ("1998/01/01"[PDAT] : "2018/06/30"[PDAT]))
Epidemiology	(("coronavirus"[MeSH Terms] OR "coronavirus"[All Fields]) AND ("epidemiology"[Subheading] OR "epidemiology"[All Fields] OR "epidemiology"[MeSH Terms])) AND



	("loattrfree full text"[sb] AND ("1998/01/01"[PDAT] : "2018/06/30"[PDAT]))
Transmission	((("coronavirus"[MeSH Terms] OR "coronavirus"[All Fields]) AND ("transmission"[Subheading] OR "transmission"[All Fields])) AND ("loattrfree full text"[sb] AND ("1998/01/01"[PDAT] : "2018/06/30"[PDAT]))
Environmental Significance	((("coronavirus"[MeSH Terms] OR "coronavirus"[All Fields]) AND ("environment"[MeSH Terms] OR "environment"[All Fields] OR "environmental"[All Fields]) AND ("Signif (Oxf)"[Journal] OR "significance"[All Fields])) AND ("loattrfree full text"[sb] AND ("1998/01/01"[PDAT] : "2018/06/30"[PDAT]))
Control Measures	((("coronavirus"[MeSH Terms] OR "coronavirus"[All Fields]) AND ("prevention and control"[Subheading] OR ("prevention"[All Fields] AND "control"[All Fields]) OR "prevention and control"[All Fields] OR "control"[All Fields] OR "control groups"[MeSH Terms] OR ("control"[All Fields] AND "groups"[All Fields]) OR "control groups"[All Fields]) AND ("weights and measures"[MeSH Terms] OR ("weights"[All Fields] AND "measures"[All Fields]) OR "weights and measures"[All Fields] OR "measures"[All Fields])) AND ("loattrfree full text"[sb] AND ("1998/01/01"[PDAT] : "2018/06/30"[PDAT]))

This procedure was repeated for each virus and subsection.

Within the General Description subsection, the objective was to answer the following:

1. What family and order does the virus belong to?
2. What genera and species have the virus been classified into?
3. By which process does the virus enter cells?

Within the Human Health Effects subsection, the objective was to answer the following:

1. What part of the body does the virus affect?
2. What are the clinical manifestations in humans?

Within the Epidemiology subsection, the objective was to answer the following:

1. When was the virus first detected?
2. When does the virus peak in number of infections/ outbreaks?
3. Does the virus circulate in other animals?

Within the Transmission subsection, the objective was to answer the following:

1. What is the route in which the virus is spread?
2. What is the infectious dose of the virus?
3. What vectors are associated with the virus?

Within the Environmental Significance subsection, the objective was to answer the following:

1. How does the virus persist in sludge and sewage, waste water, surface waters, ground and drinking water, soil and crops, and surfaces?
2. How long can the virus persist in each?

Within the Control Measures subsection, the objective was to answer the following:

1. What can we do to avoid the spread of these viruses?
2. What public health interventions can be implemented to prevent onward transmission?

For information that was not found in PubMed, the Google Scholar search engine was utilized, using the same search terms. These results were filtered by selecting the “Custom range option and entering “1998-2018”.

The Georgia State University online database was also used to obtain necessary information on the viruses. These results were refined by placing the filters “Scholarly (Peer Reviewed) Journals” and “1998-2018” for Publication Date.

## Coronaviruses

### 1. General Description

Coronaviruses, abbreviated as CoVs, are apart of the Coronaviridae family. They are large, enveloped, single-stranded, positive-sense RNA viruses (Bruning, A. H. L., Aatola, H., Toivola, H., Ikonen, N., Savolainen-Kopra, C., Blomqvist, S., ... Koskinen, J. O., 2018). Coronaviruses are further classified into the Nidovirales order. This order is made up of the Coronaviridae, Arteriviridae, and Roniviridae families. The Coronavirinae are one of two subfamilies in the Coronaviridae family- the other being the Torovirinae (Fehr, A. R., & Perlman, S., 2015). The Coronavirinae are subdivided into four groups: the alpha, beta, gamma and delta coronaviruses.

There are the two human coronaviruses that cause the common cold: HCoV-229E and HCoV-OC43. Both were identified in the mid-1960s. An outbreak of severe acute respiratory syndrome lead to more attention drawn to this virus family. This lead to the identification of two additional human coronaviruses: HCoV-NL63 and HCoV-HKU1. (Krzysztof Pyrc, Ben Berkhout & Lia van der Hoek, 2007). Outbreaks of The Middle East respiratory syndrome coronavirus, abbreviated as MERS-Cov, in 2012 was proof that these pathogens can cross the species border and may pose a significant healthcare risk (Owczarek, K., Szczepanski, A., Milewska, A., Baster, Z., Rajfur, Z., Sarna, M., & Pyrc, K., 2018).

Coronavirus enters the cell through a complex process that require a series of cellular factors and a variety of fusion receptors. Most of the alphacoronaviruses, except for HCoV-NL63, use aminopeptidase N (CD13) for cell entry. The human angiotensin-converting enzyme 2HCoV-OC43, enters the cell by endocytic route. This enzyme is what is typically utilized. (Owczarek, K., Szczepanski, A., Milewska, A., Baster, Z., Rajfur, Z., Sarna, M., & Pyrc, K., 2018).

### 2. Human Health Effects

Coronaviruses are pathogens that usually infect the upper respiratory tract and are mainly associated with common colds. Literature has shown, however, that “ in more vulnerable populations such as newborns, infants, the elderly, and immune-compromised individuals, these pathogens can also affect the lower respiratory tract and lead to pneumonia, intensification of asthma, and several types of respiratory distress syndromes” (Marc Desforges, Alain Le Coupanec, Jenny K. Stodola, Mathieu Meessen-Pinard, Pierre J. Talbot, 2014). Coronaviruses have neuro-invasive capacities. This means that they can spread from the respiratory tract to the central nervous system. It has also been found that “infection of central nervous system cells could lead to human health problems, such as encephalitis and long-term neurological diseases”,

(Marc Desforges, Alain Le Coupanec, Jenny K. Stodola, Mathieu Meessen-Pinard, Pierre J. Talbot, 2014).

SARS-associated coronavirus differs from other coronaviruses, as it causes an illness of two phases. Gastrointestinal symptoms are mostly common in the first phase, and respiratory distress syndrome is common in the second phase. (Lessler, J., Reich, N. G., Brookmeyer, R., Perl, T. M., Nelson, K. E., & Cummings, D. A. T., 2009).

Coronaviruses are usually detected with other respiratory viruses- namely, human respiratory syncytial virus (Gaunt ER, et al. *J Clin Microbiol*, 2010). Though there is proven high morbidity and mortality associated with infections caused by some CoVs, it has been noted that “there is no rapid method available to detect clinically relevant CoVs in humans”, (Bruning, A. H. L., Aatola, H., Toivola, H., Ikonen, N., Savolainen-Kopra, C., Blomqvist, S., ... Koskinen, J. O., 2018).

### **3. Epidemiology**

HCoV-OC43 is considered the most common human coronavirus worldwide. This virus is linked to many respiratory tract infections. The highest incidence is seen during winter and spring months (Owczarek, K., Szczepanski, A., Milewska, A., Baster, Z., Rajfur, Z., Sarna, M., & Pyrc, K., 2018).

The epidemiology of coronavirus colds is not as widely studied. Patterns show that waves of infection affect communities during the winter months, and cause small outbreaks in families, schools, etc. It is possible for people to be re-infected, sometimes within a year. This pattern is different from rhinovirus infections, which peak in the fall and spring. This also typically results in long-lasting immunity. About one in five colds is due to coronaviruses (Tyrrell, David A.J. and Myint, Steven H. 1996).

### **4. Transmission**

One article states that, “Transmission of coronavirus is usually via airborne droplets to the nasal mucosa. Virus replicates locally in cells of the ciliated epithelium, causing cell damage and inflammation” (Tyrrell, David A.J. and Myint, Steven H. 1996). Another article found that “Middle East respiratory syndrome coronavirus (MERS-CoV) is also contracted via close contact with infected individuals”, (Adegboye, O. A., & Elfaki, F., 2018). The SARS coronavirus (SARS Co-V) is found in droplets from the respiratory secretions of an infected person, and spread from their secretions. The presence of coronavirus in the stool also suggests the possibility of oral-fecal transmission (Drosten C, Gunther S, Preiser W, et al., 2003). A lot of articles suggest the zoonotic transmission of MERS-CoV from camels. One article in particular expresses the primary mode of transmission to be “through saliva during direct contact with infected camels or through consumption of milk or uncooked meat” (Durai, P., Batool, M., Shah, M., & Choi, S., 2015).

Evidence also shows that Chinese horseshoe bats are natural reservoirs of SARS-CoV like viruses (*Reusken, Chantal BEM, Raj, V Stalin, P Koopmans, Marion, L Haagmans, Bart., 2016*). Studies show that “animal-to-human zoonotic transmissions can led to worldwide spread of viruses such as hCoV-OC43 and NL63”, (*Reusken, Chantal BEM, Raj, V Stalin, P Koopmans, Marion, L Haagmans, Bart., 2016*).

It is possible for coronavirus to remain in an infectious state on common surfaces for a number of days. One study, (*Warnes, S. L., Little, Z. R., & Keevil, C. W., 2015*), showed that “an inoculum of  $10^3$  plaque forming units (PFU) persisted on polyfluorotetraethylene (Teflon; PTFE), polyvinyl chloride (PVC), ceramic tiles, glass, and stainless steel for at least 5 days (and 3 days for silicon rubber) at 21°C and a relative humidity of 30% to 40%”.

The infectious dose of MERS-CoV has been studied in mice for data to be extrapolated to humans. The results of one study showed that “Evolving MERS-CoV in mouse lung maintains disease at lower infectious doses”, (*Madeline G. Douglas, Jacob F. Kocher, Trevor Scobey, Ralph S. Baric, Adam S. Cockrell., 2018*). The results of another study showed that “Fatal disease was routinely observed at the  $5 \times 10^6$  PFU dose”, (*A.S. Cockrell, B.L. Yount, T. Scobey, K. Jensen, M. Douglas, A. Beall, X.C. Tang, W.A. Marasco, M.T. Heise, R.S. Baric., 2016*).

Most published data estimate that human coronavirus are consistent with an incubation period ranging between 2–5 days. Most estimates for SARS associated coronavirus are consistent with an incubation period ranging between 2–10 days (*Lessler, J., Reich, N. G., Brookmeyer, R., Perl, T. M., Nelson, K. E., & Cummings, D. A. T., 2009*).

## **5. Environmental significance**

### *Sludge and sewage*

One article brings to light the fact that in other regions of the world, exotic animals are sold for human consumption. For example, in some Chinese markets, bats and civets are sold. This article also states that, “In southern China, the consumption of exotic animals is especially common during the winter months, and this when most respiratory tract infections are highly prevalent”, (*Sheahan, T., Rockx, B., Donaldson, E., Corti, D., & Baric, R., 2008*).

This article also brings attention to the fact that a significant number of zoonotic viral pathogens are shed in stool. This is important because birds and mammals shedding excreta in the wet marketplace create the perfect atmosphere for zoonotic virus transmission to the human consumer populations (*Sheahan, T., Rockx, B., Donaldson, E., Corti, D., & Baric, R., 2008*).

### *Waste water*

When studying the relation of CoVs to waste water, One article found the following results:

“In vitro experimentation shows that at 4 °C, the SARS-CoV could persist for 14 days in wastewater and at least 17 days in feces or urine. SARS-CoV is more susceptible to disinfectants than Escherichia coli and f2 phage. Free chlorine was found to inactivate SARS-CoV better than chlorine dioxide” (*Xin-Wei Wang, Jin-Song Li, Min Jin, Bei Zhen, Qing-Xin Kong, Nong Song, Wen-Jun Xiao, Jing Yin, Wei Wei, Gui-Jie Wang, Bing-yin Si, Bao-Zhong Guo, Chao Liu, Guo-Rong Ou, Min-Nian Wang, Tong-Yu Fang, Fu-Huan Chao, Jun-Wen Li., 2005*).

### *Ground water and drinking water*

Biofilms in drinking-water distribution systems carry the potential of accumulating a variety of human pathogenic viruses, CoVs included. Viruses that attach to biofilm are routinely removed from the water phase. This step is taken to improve the water quality. However, if they are released in slough, there is still a risk of infection.

## **6. Control Measures**

Vaccination serves as one of the most effective public health control measures for coronaviruses.

A recent study, (*Tang, J., Zhang, N., Tao, X., Zhao, G., Guo, Y., Tseng, C.-T. K., ... Zhou, Y., 2015*), examined the immunization potential of different doses of S377-588-Fc and compared their ability to induce specific humoral and cellular immune responses, against infection of MERS-CoV. The results proved that S377-588-Fc at 1 mg was able to induce strong humoral immune responses.

## **Orthomyxovirus**

### **1. General description**

The Orthomyxoviridae family is comprised of a total of seven genera. These genera are inclusive of four types of influenza viruses (Influenza virus A, B, C, and D), Thogotovirus, Quaranjavirus, and Isavirus—all of which are segmented negative-strand RNA viruses (Peng, R., Zhang, S., Cui, Y., Shi, Y., Gao, G. F., & Qi, J., 2017). The make up of the influenza A and B virus genomes is explained as “each being made up of eight negative-sense, single-stranded viral RNA (vRNA) segments, while influenza C virus has a seven-segment genome”, (Cook, J. D., Sultana, A., & Lee, J. E., 2017). Isavirus is explained as “consisting of eight single-stranded RNA segments that encode for at least 10 proteins”, (Friedemann Weber, Enrique Jambrina, Susana González, Johannes T Dessens, Michael Leahy, Georg Kochs, Agustín Portela, Patricia A Nuttall, Otto Haller, Juan Ortín, Thomas Zürcher, 1998). Influenza A Virus, abbreviated as ISAV, has its own unique mechanism of viral entry (Friedemann Weber, Enrique Jambrina, Susana González, Johannes T Dessens, Michael Leahy, Georg Kochs, Agustín Portela, Patricia A Nuttall, Otto Haller, Juan Ortín, Thomas Zürcher, 1998). Tick-borne Thogoto virus, abbreviated as THOV, and Quaranjavirus each “contain six single-stranded RNA segments of negative polarity”, (Sediri, H., & Klenk, H. (. D., 2015) & (Neumann G., Shinya K., Kawaoka Y., 2007).

The classification of Influenza A viruses are further explained in an article that states that they are “classified into subtypes based on the antigenicity of their haemagglutinin (HA) and neuraminidase (NA) molecules”, (Langat, P., Raghwan, J., Dudas, G., Bowden, T. A., Edwards, S., Gall, A., ... Watson, S. J., 2017). Influenza B viruses are explained to be “classified into two cocirculating phylogenetically- and antigenically-distinct lineages, named after viruses B/Yamagata/ 16/88 (Yamagata-lineage) and B/Victoria/2/87 (Victoria-lineage) that diverged in the 1970s”. (Salem, E., Cook, E. A. J., Lbacha, H. A., Oliva, J., Awoume, F., Aplogan, G. L., ... Ducatez, M. F., 2017).

### **2. Human Health Effects**

Influenza A virus greatly contributes to global mortality and morbidity rates. This is because it is a virus that continuously re-emerges. (Buttignol, M., Pires-Neto, R. C., Rossi e Silva, R. C., Albino, M. B., Dolhnikoff, M., & Mauad, T., 2017). IAV usually only infects airways, but can also infect resident immune cells (Buttignol, M., Pires-Neto, R. C., Rossi e Silva, R. C., Albino, M. B.,

Dolhnikoff, M., & Mauad, T., 2017). The effects of Influenza A virus can range widely, from mild/no symptoms, to respiratory failure. One article emphasizes that “IAV infection results in increased susceptibility to secondary bacterial infections, which also contribute to mortality”, (Soni, p., yasuhara, a., takenaga, t., iwatsuki-horimoto, k., uraki, r., ito, m., ... kawaoka, y., 2018). The influenza A (H5N1) viruses that have infected humans have all been from avian transmission and reflect strains that circulate among poultry and wild birds (Vangeti, S., Yu, M., & Smed-Sørensen, A., 2018).

Influenza B virus also mainly infects humans, but has been known to infect seals as well (Paul Glezen, W., Schmier, J. K., Kuehn, C. M., Ryan, K. J., & Oxford, J., 2013). Influenza B virus is a major cause of morbidity each season, posing a disproportionate health burden on susceptible populations (Jen-Jan Hu<sup>1</sup>, Chuan-Liang Kao<sup>2</sup>, Ping-Ing Lee<sup>3</sup>, Chung-Ming Chen<sup>3</sup>, Chin-Yun Lee<sup>3</sup>, Chun-Yi Lu<sup>3</sup>, Li-Min Huang<sup>3</sup>, 2003). Signs and symptoms of influenza A and influenza B virus infection include fever, cough, and rhinorrhea (Horm, S. V., Gutiérrez, R. A., Sorn, S., & Buchy, P., 2012). Influenza virus infections have the potential to manifest to mild upper respiratory tract infection, bronchiolitis and/or pneumonia (Horm, S. V., Gutiérrez, R. A., Sorn, S., & Buchy, P., 2012).

Thogotoviruses circulate in domestic animals, such as sheep, cattle, and camels. The viruses can cause neural diseases and abortion (Peng, R., Zhang, S., Cui, Y., Shi, Y., Gao, G. F., & Qi, J., 2017).

### **3. Epidemiology**

Rates of Influenza show a trend of peaking during winter months. One articles states that, “epidemics involving all age groups occur each winter, and worldwide pandemics appear irregularly”, (Jen-Jan Hu<sup>1</sup>, Chuan-Liang Kao<sup>2</sup>, Ping-Ing Lee<sup>3</sup>, Chung-Ming Chen<sup>3</sup>, Chin-Yun Lee<sup>3</sup>, Chun-Yi Lu<sup>3</sup>, Li-Min Huang<sup>3</sup>, 2003). Influenza B epidemics were noted to occur at intervals of 2 to 4 years. Clinic visits and hospitalizations from influenza B are common in all age groups (Killingley, B., & Nguyen Van Tam, J., 2013). There are new factors that have changed patterns of Influenza B. One articles states, “the emergence of a second lineage of influenza B, along with changing demographics and rapid movement of human populations, has changed the epidemiology of influenza B”. (Jen-Jan Hu<sup>1</sup>, Chuan-Liang Kao<sup>2</sup>, Ping-Ing Lee<sup>3</sup>, Chung-Ming Chen<sup>3</sup>, Chin-Yun Lee<sup>3</sup>, Chun-Yi Lu<sup>3</sup>, Li-Min Huang<sup>3</sup>, 2003). Since 2001, both influenza B lineages have been co circulating each influenza season. This is in contrast to the pattern of seeing a single lineage that occurred between 1985 and 2000 (Jen-Jan Hu<sup>1</sup>, Chuan-Liang Kao<sup>2</sup>, Ping-Ing Lee<sup>3</sup>, Chung-Ming Chen<sup>3</sup>, Chin-Yun Lee<sup>3</sup>, Chun-Yi Lu<sup>3</sup>, Li-Min Huang<sup>3</sup>, 2003).

### **4. Transmission**

There are a lot factors that makes studying the transmission of Influenza very difficult. They include seasonality, unpredictable attack rates, and environmental factors, such as temperature



and humidity (Nidzworski, D., Siuzdak, K., Niedziałkowski, P., Bogdanowicz, R., Sobaszek, M., Ryl, J., ... Ossowski, T., 2017).

Transmission of *Influenza A virus* in the avian reservoir (waterfowl, shorebirds) is believed to be through the fecal-oral route (Glezen WP, Decker M, Joseph SW, Mercready RG., 1987). Human-to human transmission of Influenza A is through respiratory aerosols/droplets and by direct contact (Webster RG, Bean WJ, Gorman OT, Chambers TM, Kawaoka Y., 1992). Both *Influenza B virus* and *Influenza C virus* are respiratory-borne human viruses. This means that these viruses have the potential to infect other mammals, such as swine, they do not naturally circulate in birds (Allison, A. B., Ballard, J. R., Tesh, R. B., Brown, J. D., Ruder, M. G., Keel, M. K., ... Dwyer, C., 2015).

The genus *Isavirus* is comprised of just one species, *Infectious salmon anemia virus- abbreviated as ISAV*. ISAV infects fish and is believed to be water transmitted or possibly through sea lice as a vector (Allison, A. B., Ballard, J. R., Tesh, R. B., Brown, J. D., Ruder, M. G., Keel, M. K., ... Dwyer, C., 2015). ISAV can be spread with the transport networks of live fish and with harvesting operations (Leo Heijnen, Gertjan Medema, 2011).

The transmission of Influenza D virus is not fully understood, but recent experimental infection of calves proved that “IDV can cause moderate respiratory disease” (Abdel-Ghafar AN, Chotpitayasunondh T, Gao Z, Hayden FG, Nguyen DH, de Jong MD, Naghdaliyev A, Peiris JS, Shindo N, et al. *N Engl J Med.*, 2008).

Thogotoviruses differ from influenza viruses, as thogotoviruses are transmitted mainly through tick vectors. They are also called “tick-borne viruses” because of this (Peng, R., Zhang, S., Cui, Y., Shi, Y., Gao, G. F., & Qi, J., 2017). It has also been reported that Dhori Virus, a species abbreviated as DHOV, caused human infections in a vector-free manner, possibly by an aerosol route (Peng, R., Zhang, S., Cui, Y., Shi, Y., Gao, G. F., & Qi, J., 2017).

## 5. Environmental Significance

### *Sludge and sewage*

One article found that, “it is possible for the influenza virus particles to be shed from feces, saliva and nasal discharge, then subsequently contaminate the water, soil, and related environmental components”, (Perry, K. A., Coulliette, A. D., Rose, L. J., Shams, A. M., Edwards, J. R., & Noble-Wang, J. A., 2016).

### *Waste water*

Monitoring of influenza viruses in sewage and surface water during a pandemic in The Netherlands in 2009 (Turner, J. C. M., Feeroz, M. M., Hasan, M. K., Akhtar, S., Walker, D., Seiler,

P ... Webster, R. G., 2017), showed that influenza A viruses were detected in sewage and surface water.

One study, (Brankston G, Gitterman L, Hirji Z, Lemieux C, Gardam M., 2007), showed that the vast majority of Avian Influenza Viruses detected (99.7%) have come from apparently healthy birds. This study also showed that, “poultry drinking water served as a reservoir of Avian Influenza Viruses with a prevalence of 32.5% in collected samples” (Brankston G, Gitterman L, Hirji Z, Lemieux C, Gardam M., 2007).

### *Surfaces*

One study showed that, “Influenza A virus has been shown to be transferred from stainless steel (SS) countertops to hands for up to 24 hours after surface contamination”, (Murray AG, Munro LA, Wallace IS, Berx B, Pendrey D, Fraser D, Raynard RS., 2010).

## **6. Control measures**

An inactivated virus vaccine is developed each year against the strains most likely to cause disease the next winter. It has been proven that the drugs amantadine and rimantadine can be used for “prophylaxis and treatment of influenza A infections”, (Allison, A. B., Ballard, J. R., Tesh, R. B., Brown, J. D., Ruder, M. G., Keel, M. K., ... Dwyer, C., 2015).

Early detection of the virus is a critical control measure. An influenza patient’s pharynx would be examined to detect the virus during initial development. During development is when tens to hundreds of virus-associated molecules are present. (Nidzworski, D., Siuzdak, K., Niedziałkowski, P., Bogdanowicz, R., Sobaszek, M., Ryl, J., ... Ossowski, T., 2017).

## **Filovirus**

### **General description**

Filoviridae is a part of the order Mononegavirales. Within the family there is a single genus-filovirus, and a separation into two sero-genotypes: Marburg and Ebola (Feldmann H, Klenk., 1996). To date, there have been five different Ebolavirus strains identified. They are: Zaire Ebolavirus, abbreviated as EBOV, Sudan Ebolavirus, abbreviated as SUDV, Tai Forest Ebolavirus, abbreviated as TAFV, Bundibugyo Ebolavirus, abbreviated as BDBV, and Reston Ebolavirus, abbreviated as RESTV. (Chowell, G., & Nishiura, H., 2014). There is one Marburgvirus species- Lake Victoria marburgvirus (LVMARV) (Kash, J. C., Mühlberger, E., Carter, V., Grosch, M., Perwitasari, O., Proll, S. C., ... Katze, M. G., 2006).

All viruses within this order are enveloped and contain a “non-segmented negative-strand (NNS) RNA genome” (Mühlberger E., 2007). The different filoviruses are all similar in genome organization. There are a total of viral genes arranged on the negative-sense RNA genome, which is about 19 kb in length (Mühlberger E., 2007).

Nucleoprotein (NP), glycoprotein (GP), RNA-dependent RNA polymerase (L), and four structural proteins: VP24, VP30, VP35, and VP40 are the proteins expressed by Filoviruses (Olival, K. J., & Hayman, D. T. S., 2014). Ebolavirus is able to express a shortened soluble glycoprotein (sGP) through RNA editing. The ribonucleoprotein comes from the RNA genome, NP, VP30, VP35, and L protein, though Marburgvirus is reported to be able to replicate in the absence of VP30. The VP35 protein is known to block interferon induction in both Marburg and Ebola viruses (Brauburger, K., Hume, A. J., Mühlberger, E., & Olejnik, J., 2012).

### **Human health effects**

EBOV and MARV both cause frequently fatal disease in humans (Yen, B. C., & Basler, C. F., 2016). It only takes an incubation period of about a week before victims develop symptoms of high fever, diarrhea, vomiting, respiratory disorders, and hemorrhaging. Death is usually the result within a few days (Xavier Pourrut, Brice Kumulungui, Tatiana Wittmann, Ghislain Moussavou, André Délicat, Philippe Yaba, Dieudonné Nkoghe, Jean-Paul Gonzalez, Eric Maurice Leroy., 2005). One study shows that, “disease outbreaks associated with the Zaire EBOV subtype have resulted in mortality rates of up to 90%; while MARV and Sudan EBOV result in mortality

rates of 25 to 90%”, (Kash, J. C., Mühlberger, E., Carter, V., Grosch, M., Perwitasari, O., Proll, S. C., ... Katze, M. G., 2006).

The onset of illness begins with common flu-like symptoms- high fever, severe headache, chills, muscle pain, exhaustion, and discomfort. For many infected people, this is followed by gastrointestinal symptoms including anorexia, abdominal pain, severe nausea, vomiting, and watery diarrhea. Starting on day four to five patients commonly develop a rash, dysphasia (a language disorder), and pharyngitis (Brauburger, K., Hume, A. J., Mühlberger, E., & Olejnik, J., 2012).

Fatalities typically occur 8–16 days following the onset of these symptoms, with death usually the result of shock and multiorgan failure. Non-fatal cases are represented by an extensive recovering period, during which, exhaustion, sweating, peeling of the skin at the sites of rash, partial amnesia, and secondary infections are all common (Brauburger, K., Hume, A. J., Mühlberger, E., & Olejnik, J., 2012).

### **Epidemiology**

It has been noted that the first cases of filovirus hemorrhagic fever were reported in 1967 in Germany and the former Yugoslavia. The causative agent was identified as Marburg virus. In this outbreak, laboratory workers in Marburg, Germany and Belgrade, Yugoslavia (now Republic of Serbia) were exposed to the virus after contact with infected, imported green monkeys (Olival, K. J., & Hayman, D. T. S., 2014). Similar cases were described in 1976 from outbreaks in two neighboring locations: first in southern Sudan, then in northern Zaire, now Democratic Republic of the Congo (Feldmann, H., & Geisbert, T. W., 2011). After a 15-year period of no further recorded cases, Ebola re-emerged in 1994 for a 3-year period. In this new phase, there was identification of a new subtype- E. Ivory Coast. (Xavier Pourrut, Brice Kumulungui, Tatiana Wittmann, Ghislain Moussavou, André Délicat, Philippe Yaba, Dieudonné Nkoghe, Jean-Paul Gonzalez, Eric Maurice Leroy., 2005).

One study shows that the two largest outbreaks of Marburg virus occurred in the Democratic Republic of Congo, between 1998–2000, where “128/154 infected people died; and in Angola between 2004–2005 where 227/252” patients also succumbed to this virus (Olival, K. J., & Hayman, D. T. S., 2014).

The 2013–2015 Western African Ebola virus disease epidemic, caused by the Ebola virus of the Makona variant is the largest EVD outbreak to date, with “26,648 cases and 11,017 deaths documented as of May 8, 2015”, (Park, D. J., Dudas, G., Wohl, S., Goba, A., Whitmer, S. L. M., Andersen, K. G., ... Sabeti, P. C., 2015). It has been suggested that this outbreak was caused by Zaire ebolavirus, which is the first time that this virus has been detected in West Africa (Olival, K. J., & Hayman, D. T. S., 2014).

## **Transmission**

Marburg and Ebola viruses are zoonotic pathogens. The Egyptian rousette bat (*Rousettus aegyptiacus*) is the natural reservoir of MARV. The reservoir of EBOV is unknown, but it is believed to be another bat species (Kuzmin, I. V., Schwarz, T. M., Ilinykh, P. A., Jordan, I., Ksiazek, T. G., Sachidanandam, R., ... Bukreyev, A., 2017). Fruit bats of the species *Hypsignathus monstrosus*, *Epomops franqueti*, and *Myonycteris torquata*, which are present in large parts of West Africa (Leroy EM, Kumulungui B, Pourrut X, et al., 2005), are all reservoirs of the virus.

Filovirus transmission among humans occurs through direct human-to-human contact or contact with their infectious bodily fluids, (Carroll, S. A., Towner, J. S., Sealy, T. K., McMullan, L. K., Khristova, M. L., Burt, F. J., ... Nichol, S. T., 2013). Ebola virus can be excreted in bodily fluids, including “vomit, stool, blood, saliva, semen, and breast milk”, (Bibby, K., Fischer, R. J., Casson, L. W., Stachler, E., Haas, C. N., & Munster, V. J., 2015). The transmission of Ebola virus via environmental routes, like droplets, aerosols, or fomites, has been thought to be unlikely due to epidemiological evidence and environmental sampling (Bibby, K., Fischer, R. J., Casson, L. W., Stachler, E., Haas, C. N., & Munster, V. J., 2015). Hospital transmission can often occur through the reuse of needles and syringes that were not properly sterilized (Piercy, T., Smither, S., Steward, J., Eastaugh, L. and Lever, M., 2010).

Like Ebola virus infections, MARV infections usually occur by direct contact with infected body fluids or direct personal contact with infected animals or humans. The viruses enter the body through small skin lesions or mucosal membranes (Mehedi, M., Groseth, A., Feldmann, H., & Ebihara, H., 2011). Excreta of an EBOV-infected patient enables viral persistence in the environment, which leads to the the potential for fomite transmission.

Administration of medical care to infected individuals as well as handling of corpses without use of proper protection are where typical risk of exposure lie. The virus has been found in tears, semen, and in a liver biopsy week to months following the onset of symptoms. This reiterates the importance of monitoring recovering patients (Brauburger, K., Hume, A. J., Mühlberger, E., & Olejnik, J., 2012). Socio-cultural factors have contributed significantly to Ebola spread, and has also complicated the implementation of control interventions. Cultural practices that involve touching the body of the deceased naturally contributes to the spread of the Ebola virus (Chowell, G., & Nishiura, H., 2014).

## **Environmental significance**

One study, (Nikiforuk, A. M., Cutts, T. A., Theriault, S. S., & Cook, B. W. M., 2017), showed that Ebola-Makona virus “persisted on PPE and materials found in outbreak settings for less than 72 hours at 27 °C and 80% relative humidity”. A difference in virus penetration was observed between dry (5%, 1/21 tests) and saturated (33%, 7/21 tests) samples of PPE. Theses result

proved that “infectious virus particles can penetrate through saturated coupons of Tyvek Micro Clean, Tychem QC, whole surgical masks and N95 respirators”.

### **Wastewater**

Individuals infected with Ebola virus shed the virus in bodily fluid and may produce up to nine liters of bodily waste per day (Bibby, K., Fischer, R. J., Casson, L. W., de Carvalho, N. A., Haas, C. N., & Munster, V. J., 2017). The World Health Organization initially recommended that liquid waste from Ebola patients be directly disposed into the sanitary sewers or latrines without disinfection (Bibby K, Casson LW, Stachler E, Haas CN., 2015). The results of one Ebola disinfection experiment, (Bibby, K., Fischer, R. J., Casson, L. W., de Carvalho, N. A., Haas, C. N., & Munster, V. J., 2017), highlighted the value of considering wastewater disinfection before disposition in response to infectious disease outbreaks. This is to minimize the risk of secondary transmission, as well as to address public concern.

### **Control measures**

The first measure in response to an outbreak include setting up isolation wards in hospitals to assure the quick isolation of infected patients and prevent person-to-person transmission (Brauburger, K., Hume, A. J., Mühlberger, E., & Olejnik, J., 2012). One article recommends that “basic infection control measures in health care settings are essential to avoid further spread of the disease to other patients, health care workers and visitors “(Chowell, G., & Nishiura, H., 2014).

To avoid the spread of filoviruses by tourists, the Python cave, which housed 40,000 Egyptian fruit bats, was closed to the public following the diagnosis of the Dutch patient in 2008 (Timen, A., Koopmans, M. P. G., Vossen, A. C. T. M., van Doornum, G. J. J., Günther, S., van den Berkmortel, F., ... Coutinho, R. A., 2009).

Because there is a lack of licensed therapeutic treatment regimens and vaccines, major control measures are a combination of “early diagnosis, case isolation, contact precaution, awareness campaigns, and sanitary burial practices”, (Shen, M., Xiao, Y., & Rong, L., 2015).

Infection control measures also include standard precautions in health care settings, rapid contact tracing and isolation of infectious individuals, and social distancing interventions in the community. This may include awareness campaigns to inform the population on how to avoid contracting the disease, quarantining individuals that are potentially exposed to infectious individuals, and restricting the movement of communities that have cases of local transmission, to prevent onward transmission (Chowell, G., & Nishiura, H., 2014).

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