Sources, fates and treatment strategies of typical viruses in urban sewage collection/treatment systems: A review

Jianju Li [a], Jing Liu [a,b], Hang Yu [a], Weixin Zhao [a], Xinhui Xia [a], Shijie You [a,*], Jun Zhang [a], Hailong Tong [a,c], Liangliang Wei [a,*]

[a] State Key Laboratory of Urban Water Resources and Environment (SKLUWRE), School of Environment, Harbin Institute of Technology, Harbin 150090, China
[b] School of Geosciences, China University of Petroleum, Qingdao 266580, China
[c] Harbin Veterinary Research Institute, Chinese Academy of Agricultural Sciences, Harbin 150069, China

HIGHLIGHTS

- Characteristic of sewer systems was the key factor affecting virus concentration.
- HAdV and NoV were most frequently detected viruses in the effluent of WWTPs.
- Aerosolization in sewer systems and at WWTPs might be a main reason for spreading.
- "Primary treatment+MBR+chlorine" was recommend for a better removal of SARS-CoV-2.

GRAPHICAL ABSTRACT
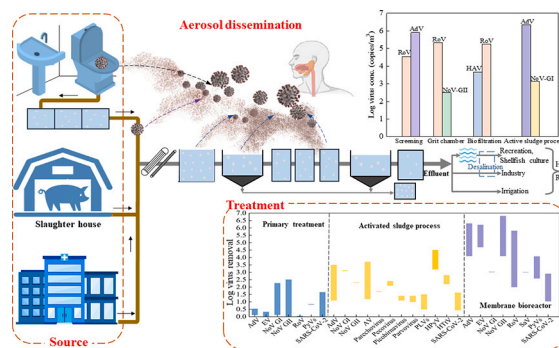
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ABSTRACT

The ongoing coronavirus pandemic (COVID-19) throughout the world has severely threatened the global economy and public health. Due to receiving severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) from a wide variety of sources (e.g., households, hospitals, slaughterhouses), urban sewage treatment systems are regarded as an important path for the transmission of waterborne viruses. This review presents a quantitative profile of the concentration distribution of typical viruses within wastewater collection systems and evaluates the influence of different characteristics of sewer systems on virus species and concentration. Then, the efficiencies and mechanisms of virus removal in the units of wastewater treatment plants (WWTPs) are summarized and compared, among which the inactivation efficiencies of typical viruses by typical disinfection approaches under varied operational conditions are elucidated. Subsequently, the occurrence and removal of viruses in treated effluent reuse and desalination, as well as that in sewage sludge treatment, are discussed. Potential dissemination of viruses is emphasized by occurrence via aerosolization from toilets, the collection system and WWTP aeration, which might have a vital role in the transmission and spread of viruses. Finally, the frequency and concentration of viruses in reclaimed water, the probability of infection are also reviewed for discussing the potential health risks.

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* Corresponding author.
E-mail addresses: sjyou@hit.edu.cn (S. You), weill333@163.com (L. Wei).

1. Introduction

The eruption of atypical pneumonia [coronavirus disease 2019 (COVID-19)] in December 2019 led to the global infection of over 429 million individuals and more than 5.9 million deaths as of February 2022. In addition to addressing the enormous economic damage incurred, a particular emphasis needs to be placed on environmental concerns and public health relevant to the fate of viruses. Thus, researches on the transmission of typical viruses in sewage collection, treatment, and desalination systems have attracted growing attention throughout the world.

The majority of viruses exhibit several unique characteristics, such as small size, resistance to disinfection, low infectious dose, refractoriness to antibiotics, and proclivity for adaptive mutation [1]. To date, more than 700 types of waterborne viruses have been detected in natural water and wastewater samples, and their long-range transmission from environmental media to hosts is the main cause of the outbreak of terrible waterborne diseases such as gastroenteritis, cardiac abnormalities, conjunctivitis, meningitis, respiratory diseases and hepatitis [2,3]. It is estimated that annually 1.4–1.9 million deaths are closely related to the prevailing waterborne diarrheal diseases associated with viruses already identified in natural or engineered water and wastewater systems [4,5].

The main sources of viruses released into wastewater may include hospitals, slaughterhouses, residential areas and so forth. In particular, the principal sources of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in wastewater systems are feces/urine of infected individuals and hospital sewage [6–8]. Once the viruses enter the sewer system, a subsequent decline in viral load is detected as a consequence of the dilution effect of other wastewater, reaction with the chemicals (e.g., disinfectants and detergents) and virus inactivation under water physicochemistry variation (e.g., pH, temperature, and solids content) [9–11]. Hence, septic and collection systems are extremely important with respect to the collection, storage, treatment, neutralization and stabilization of virus-containing wastewater [12]. Once viruses enter the wastewater treatment plants (WWTPs), conventional primary and secondary treatment may no longer be capable of achieving an absolute removal of viruses because viral genomes and extracellular proteins are unlikely to be denatured easily [13]. Thus, many advanced treatment units have been explored for the further treatment and elimination of these viruses within wastewater. For instance, the moving-bed biofilm reactor and sequencing batch reactor have been proven to be ideal secondary treatments for SARS-CoV-2 RNA removal from wastewater [14]. Chemical disinfection is a powerful way to inactivate viruses in tertiary treatment [15], where chlorination and UV irradiation are expected to provide high accessibility for SARS-CoV-2 inactivation based on experience with other classes of SARS viruses [16,17]. However, mechanistic insights into the removal trends of typical viruses during the operation of the available treatment units of WWTPs, as well as the dose-effect response of specific viruses to disinfectants and their inactivation kinetics of coronaviruses, still need further exploration. In addition, numerous studies have proven that typical enteric viruses and SARS-CoV-2 remain in WWTP effluent and present a high health risk during reuse and desalination [17]. Thus, obtaining further understanding of the effects of different treatment methods on virus removal in wastewater treatment, WWTP effluent reuse and desalination, and sewage sludge treatment is vital for controlling the spread of the virus and reducing the risk of wastewater-to-human transmission.

The main objectives of this study were to: (1) review the occurrence and concentration distributions of viruses in wastewater; (2) compare the efficiency and mechanisms of virus removal during the primary, secondary and tertiary treatments of WWTPs; (3) summarize the occurrence and removal of viruses in treated effluent reuse and desalination as well as in the different sewage sludge treatments; and (4) discuss the dissemination of viruses throughout the entire sewage collection, transmission and treatment process and assess the public health risks associated with reuse of treated wastewater. This work can aid us in risk assessment, virus inactivation and management during current and future viral outbreaks.

2. Methodology

The review was prepared based on a literature search for documents published until 14 February 2021 in the following databases: PubMed, Scopus, ScienceDirect, and Web Science Core Collection. The keywords employed for the search are presented in Table S1. In this first stage of the research, the title of each article was evaluated, and information about the quantification of typical viruses in wastewater, sewage, feces, urine samples and sewer system was selected, as well as information related to the concentration and removal of typical viruses found in sewage/sludge treatment units. In total, 618 articles were selected, and their abstracts were screened to verify whether they truly contained the information described above. Then, 412 articles were excluded because they did not contain the required information, and finally 246 eligible articles were screened and used as references for this review. In addition, another 25 articles were added due to a screening of the selected articles and the reviewers' suggestions.

3. Occurrence of viruses in wastewater

Viruses, generally with an average size ranging from 18 nm to 1500 nm, are microscopic pathogenic agents [18]. The reports of the International Committee for the Taxonomy of Viruses in 2016 revealed that 7 orders, 104 families, 505 genera, and 3286 species of viruses have been detected, including enveloped viruses, (such as severe acute respiratory syndrome coronavirus (SARS-CoV)) and other nonenveloped enteric viruses (including norovirus (NoV), rotavirus (RoV), hepatitis A virus (HAV), hepatitis E virus (HEV), adenovirus (AdV), polyomavirus (PyVs), astrovirus (AV), coxsackievirus (CV), poliovirus (PV), sapovirus (SaVs) and others) [19]. These viruses can be transmitted by contaminated water (SARS-CoV-2 can be transferred via both the waterborne and nonwaterborne pathways) [13], which lead to the spread of various human diseases, such as gastroenteritis, conjunctivitis, fever, meningitis, heart anomalies, paralysis, and hepatitis (Table 1).

Viruses cannot replicate in aquatic environments, thus the excretion of viruses via the feces and urine of humans/animals is their first entry point into the environmental cycle. Specifically, the nonenveloped particles excreted through the feces of infected humans or animals (slaughterhouses) have been regarded as one of the main pathways by which virus particles are released into the environment. Quasi-enveloped particles originating from blood might be another important pathway of virus excretion into aquatic environments, especially via slaughterhouse wastewater emissions. For instance, viral RNA from SARS-CoV-2 [42] has been recently detected in the feces of infected humans even 26 days after their recovery [31]. It is recognized that a person with an enteric viral infection may excrete as many as 10^{14} viral particles per day, and this may exceed 10^{15} for some infection cases [43,44].

Overall, eight viral families (*Astroviridae*, *Coronaviridae*, *Parvoviridae*, *Circoviridae*, *Herpesviridae*, *Anelloviridae*, *Caliciviridae*, and *Picobirnaviridae*) and six previously known viruses (feline CoV type 1, felid herpes 1, feline calicivirus, feline NoV, feline panleukopenia virus and picobirnavirus) detected in the feces of animals and are infectious to human beings [45]. For instance, the high concentrations of chicken/turkey parvoviruses detected in chicken stools (1.97×10^2–1.07×10^{10} genome copies·g^{-1}) and slaughterhouses (1.90×10^5–8.14×10^5 genome copies·mL^{-1}) highlight the importance of controlling virus emissions that occur via animal fecal contamination [46]. Furthermore, hospital wastewater has been described as another important source of disease-causing agents, particularly RoV, which is associated with diarrhea mortality among children younger than 5 years (128,515 deaths annually) and among all ages (228,047 deaths annually) [47]. The survey by

Kargar et al. revealed that RoV has frequently been detected in hospital sewage samples (40%), which is much higher than the level found in urban sewage samples (33.33%) [48]. Moreover, many hospitals do not properly treat their wastewater, especially those in developing countries, before it is discharged into their collection systems, seriously threatening the safety of aquatic environments [49].

According to the work of Korajkic et al. and Muirhead et al., the Zika virus exhibited a much higher decay rate under a temperature of >20 °C than under a temperature of <15 °C [50,51]. Prolonged viral persistence was observed at lower temperature for nonenveloped viruses [52]; in contrast, enveloped viruses are more susceptible to temperature as they contain a lipid bilayer membrane (envelope) surrounding the protein capsid [53,54]. Undoubtedly, viruses that enter the collection system via complex underground pipes partially maintain their infectivity before reaching WWTPs [55,56], despite the operational temperatures, pH and wastewater characteristics/composition that would influence their survival [57]. The survival times of typical viruses in sewage at different temperatures are shown in Fig. 1. The representative enveloped (SARS-CoV-2) and unenveloped (MNV) viruses were selected to linear fitting with temperatures (Fig. S1), and the R^2 were 0.98 and 0.82, respectively; and the obtained absolute values of slope were 0.613 and 0.055, respectively, which verified that enveloped viruses were more sensitive than nonenveloped viruses.

4. Species and concentrations of viruses in collection systems

Viruses have been widely detected in raw domestic wastewater, regardless of whether the wastewater is from urban or rural areas. For instance, some households in developed countries utilize drinking water from private wells and rely on onsite systems for wastewater treatment

[62,63]. A significant correlation has been reported between wastewater-borne illnesses and the presence of private wells and/or onsite wastewater systems [64]. On the other hand, the release of raw sewage, due to the overflow of combined sewers, also contributes to the emission of viruses into surface waters [65]. Information on the specifics and distributions of typical viruses in wastewater in sewer systems, especially those found in raw domestic wastewater, septic tanks, combined sewer systems and the influent of WWTPs, is collected and summarized in Table 2.

The concentration of the viruses within the wastewater of the different collection units varied widely. For instance, concentration of enterovirus (EV), RoV and NoV in raw domestic wastewater were 10^4–10^5·L^{-1}, 200–1000·L^{-1} and 2×10^5·L^{-1}, respectively [66,72]; in regard to septic tanks, the concentrations of the viruses in the influent were found to be 10–10^2 virus·L^{-1} [67], 10–10^2 virus·L^{-1} [70] and 10^5 virus·L^{-1}, respectively [67]. Although the viruses would be partially diluted in the septic tanks, it is estimated that the concentration of viruses in the septic tanks would reach 10^7–10^{10}·L^{-1} even with only one infected individual in a household [75,76]. Furthermore, those viruses would be transferred into WWTPs. For example, the concentrations (in genome copies·L^{-1}) of EV, AdV, RoV, NoV and AV detected in the influent of WWTPs were 2.2×10^3–7.9×10^3, 10^6–10^7, 10^6–8.9×10^6, 5.6×10^2–8.3×10^3 and 10^6–10^8, respectively [71,73,77,78].

Overall, the concentration distribution of viruses within the different collection units was seriously affected by pipeline quality, the areal percentage distribution of the combined collection system, extreme rainfall conditions, and the living standards of the households [68,79–81]. A publication revealed that rainfall in Chicago, which carries viruses in amounts comparable to those of sewers, led to a significant virus concentration increase in the influent of WWTPs as well as

Table 1
Virus concentrations in sewage from different sources.

Virus	Characteristics [20]	Symptoms and diseases [21,22]	Viral load at patients feces	Virus concentration in slaughterhouses	Virus concentration in hospital wastewater
Nov	27–35 nm; non-enveloped, spherical, non-segmented, positive-sense, ssRNA virus	Diarrhea, vomiting, nausea, dehydration, fever, abdominal pain, gastroenteritis	2.5×10^6–3.9×10^9 genome copies·g^{-1} [23]	NoV were not detected [24], while NoV GII were detected 14.2% of the pigs feces [25].	3.6×10^2, 3.1×10^2 genome copies·mL^{-1} [7].
RoV	70 nm; non-enveloped, icosahedral, segmented, positive-sense dsRNA virus	Diarrhea, gastroenteritis	10^{10} genome copies·g^{-1} [26]	GARV: 0.8% [25].	1.7×10^3, 4.1×10^6 genome copies·mL^{-1} [7].
HAV	27–34 nm; non-enveloped, icosahedral, non-segmented, positive-sense ssRNA virus	Inflammation of the liver which causes severe pain, fever, vomiting, incapacitation of the patient	/	/	2.1×10^4 genome copies·mL^{-1} [7].
HEV	27–34 nm; non-enveloped, spherical, non-segmented, positive-sense, ssRNA	Non-bacterial gastroenteritis in humans	2.1×10^4–7.7×10^7 genome copies·g^{-1} [27]	1.3×10^{-1}–6.4×10^3 genome copies·mL^{-1} [27]	55.6% [28].
AdV	60–90 nm; non-enveloped, icosahedral, non-segmented, dsDNA virus	Gastroenteritis, conjunctivitis, respiratory disease		PAdV: 1.56×10^3 genome copies·mL^{-1} [29]	5.0×10^3, 1.0×10^3 genome copies·mL^{-1} [7].
SARS-CoV	60–200 nm; enveloped, spherical, non-segmented, positive-sense, ssRNA virus	Respiratory and enteric symptoms	$10^{5.6}$–$10^{8.1}$ genome copies·g^{-1} [30,31]	/	0.633 genome copies·mL^{-1} in wastewater of the adjusting tank [32].
PyVs	40–50 nm; non-enveloped, icosahedral, non-segmented dsDNA virus	Sarcoma, cancer	/	OPyV: 9.81×10^{-1} genome copies·mL^{-1} [32]	45.0% [33].
AV	27–32 nm; non-enveloped, spherical, non-segmented, positive-sense, ssRNA virus	Gastroenteritis	2.8×10^5–1.6×10^{11} genome copies·mL^{-1} [34]	20.8% [25].	11.7% of the children stool samples with a diagnosis of gastroenteritis [35].
CV	20-30 nm; non-enveloped, icosahedral, non-segmented, positive-sense, ssRNA	Meningitis, respiratory disease	Ct value: 21.9–38.4 [36]		25×10^5 genome copies·mL^{-1} in CA6-infected children stool [37].
PV	20–30 nm; non-enveloped, icosahedral, non-segmented, positive-sense, ssRNA virus	Fever, paralysis, meningitis, poliomyelitis	4.7×10^2–2.1×10^5 genome copies·g^{-1} [38]		0.61% of pediatric patients stool [39].
SaVs	41–46 nm; non-enveloped, icosahedral, non-segmented, positive-sense, ssRNA virus	Dehydration, vomiting, abdominal pain	3.46×10^5–2.09×10^{10} genome copies·g^{-1} [23]	GIII SaVs:78% [40].	29.4% [41].

Notes: NoV, norovirus; RoV, rotavirus; HAV, hepatitis A virus; HEV, hepatitis E virus; AdV, adenovirus; SARS-CoV, severe acute respiratory syndrome coronavirus; PyVs, polyomavirus; AV, astrovirus; CV, coxsackievirus; PV, poliovirus; SaVs, sapovirus; dsRNA, double-stranded RNA; ssRNA, single-stranded RNA; dsDNA, double-stranded DNA; NoV GII, norovirus GII; GARV, group A rotavirus; PAdV, Porcine adenovirus; OPyV, Ovine polyomavirus; Ct, Cycle threshold.
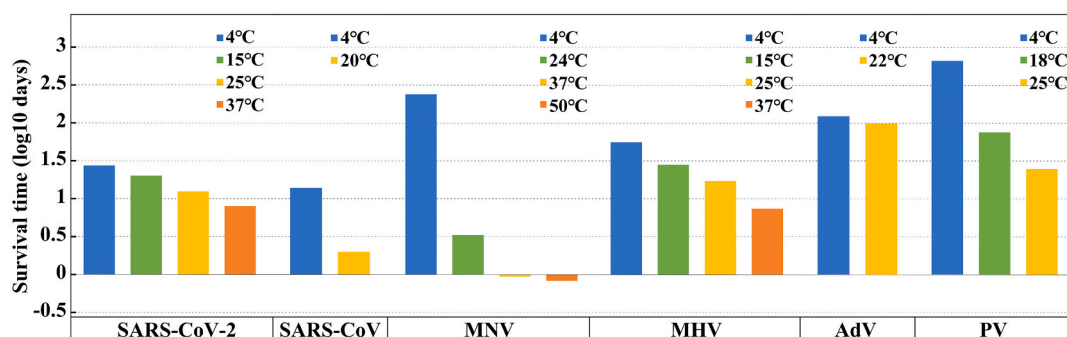
Fig. 1. Persistence of typical virus in wastewater at varying temperature [57–61].
(SARS-CoV-2, severe acute respiratory syndrome coronavirus 2; SARS-CoV, severe acute respiratory syndrome coronavirus; MNV, Murine Norovirus; MHV, Mouse hepatitis virus; AdV, adenovirus; PV, poliovirus)

Table 2
Concentration of the typical viruses in the collection system (per liter).

Virus	Raw domestic wastewater	Influent of septic tank	Combined sewer system	WWTPs influent
EV	10^4–10^5 [66]	10–10^2 [67]	6×10^3–1.74×10^5 [68]	3×10^2–1.1×10^6 [69]
RoV	2×10^2–10^3 [66]	10–10^2 [70]	/	10^6–8.9×10^6 [71]
AdV	/	/	5.3×10^3 [68]	2×10^4–6.7×10^8 [69]
NoV	2×10^5 [72]	10^5 [67]	2.3×10^3 [68] (NoV GI)	5.6×10^2–8.3×10^3 [73]
			6.31×10^5–1.61×10^6 [68] (NoV GI)	5.5×10^5–6×10^6 [74]

Notes: EV, enterovirus; RoV, rotavirus; AdV, adenovirus; Nov, norovirus.

in natural water bodies via overflows of the combined sewer [65]. In contrast, no obvious virus emission during rainfall was observed in Tokyo Bay due to the extensive construction of confluence systems [82,83]. In addition, Katayama et al. reported that significant seasonal concentration variation of EV was detected in wastewater [84]. For instance, NoV GI and NoV GII were found to be more abundant in wastewater during the winter (from Nov. to Mar.) than in the summer (190–$200 \cdot mL^{-1}$ vs. 4.9–$9.1 \cdot mL^{-1}$).

5. Removal trends of viruses in different WWTP unit processes

5.1. Primary treatment process

The primary treatment units of WWTPs mainly include bar screens and grit chambers, which involve a settling process under a very short hydraulic retention time (HRT) for the purpose of removing colloidal and other solid organic materials. Those viruses, exhibiting colloidal structures and a negative charge under neutral pH conditions [85] and thus can be easily removed via electrostatic adsorption [86] (Fig. 2), and the agglomerated particles always have a larger diameter and higher density, which benefit the sedimentation and subsequent virus removal. It was reported that as many as 75% of viruses, such as PV (serotypes 1, 2, and 3), CVB (serotypes 1, 2, 3, 4, and 5), echovirus (serotypes 3, 14, and 22), and reovirus, could be removed during the primary treatment of WWTPs [18,87], with a decrease in EVs, RoVs, and NVs of 0.2–0.4 log occurring through a fine screen [71]. In contrast, other publications showed that the primary treatments of WWTPs were less effective at virus removal, with an average removal rate of less than 10%, due to their short HRT [88,89]. The very recent work of Balboa et al. stated that the concentration of SARS-CoV-2 RNA of the primary settler effluent exhibited a lower value (<detection limit-4.2 genome copies·mL^{-1}) than that of the WWTP influent (2.15–9.8 genome copies·mL^{-1}), as well as the frequent detection of SARS-CoV-2 RNA in the sludge of the primary

setter (up to 24 genome copies·mL^{-1}), clearly revealing the adsorption of the positive charged amino groups of the virus onto the negative charged carboxyl groups of the sludge samples [90,91].

To further enhance the removal rate of typical viruses in primary treatment units of WWTPs, nanoparticles with different characteristics have been explored for the purpose of the in situ removal/inactivation of viruses [92]. The recent work of Mazurkow and Yuzbasi et al. found that the application of copper (copper oxide) nanoparticles as the active phase and plate-shaped porous alumina as the carrier material achieved 99.9% removal of bacteriophage MS2 [93]. Moreover, the formation of cation bridges between the metal Ca^{2+}/Mg^{2+} (Ca^{2+} exhibited a stronger tendency than Mg^{2+}) and carboxylate groups of both the natural organic matter and the MS2 capsids played a key role in MS2 reduction [94]. Overall, the two sorption mechanisms, hydrophobic interactions and electrostatic interactions, played major roles in the attachment of viruses to biosolids [95].

5.2. Secondary treatment processes

5.2.1. Performance of conventional biological treatment

The predominant mechanisms for virus removal in the secondary (biological) treatment units of WWTPs mainly include reversible binding/adsorption onto particles or flocs (such as suspended bacteria and algae, etc.) [96], filtration or internalization by larger organisms (e.g., nanoflagellates), and inactivation. Besides the characteristics of viruses [97], the binding, internalization and inactivation removal of viruses are closely related to the operational parameters and surrounding environmental conditions, such as pH, temperature, ionic strength and wastewater hardness [98–101].

For example, according to one of the earliest works by Clarke et al., approximately 90% of PV type 1 virus and 98% of CV A9 virus could be efficiently removed in an activated sludge system under a 6–7 h HRT [102]. In addition, the removal efficiency of NoV GI, under a high-purity oxygen-modified activated sludge system, was found to be lower than that of NoV GII, EV serotypes and male-specific coliphages (0.95 log vs. 1.48 log) [103]. On the other hand, the optimized Ludzack-Ettinger activated sludge system exhibited a much higher reduction of viruses (3.1 log or 99.92% for GI and 2.3 log or 99.5% for GII) than those of trickling filters, biological aerated filters and humus tanks [104]. Moreover, a case study conducted in Tunisia revealed that the upgrading of the traditional activated sludge process, via extended aeration in the oxidation channel, enhanced the bulk removal of HAV viruses from 32.43% to 91.47% [105].

In addition, long HRT WWTPs would benefit the overall removal of the viruses in wastewater. For instance, an as high as 1 log reduction of viruses in wastewater was achieved for a pond system under every 14.5–20.9 days of retention [106]. Theoretically, the initial rapid decline of virus concentration resulted from both adsorption and biodegradation by biomass, while the following gradual decline was due
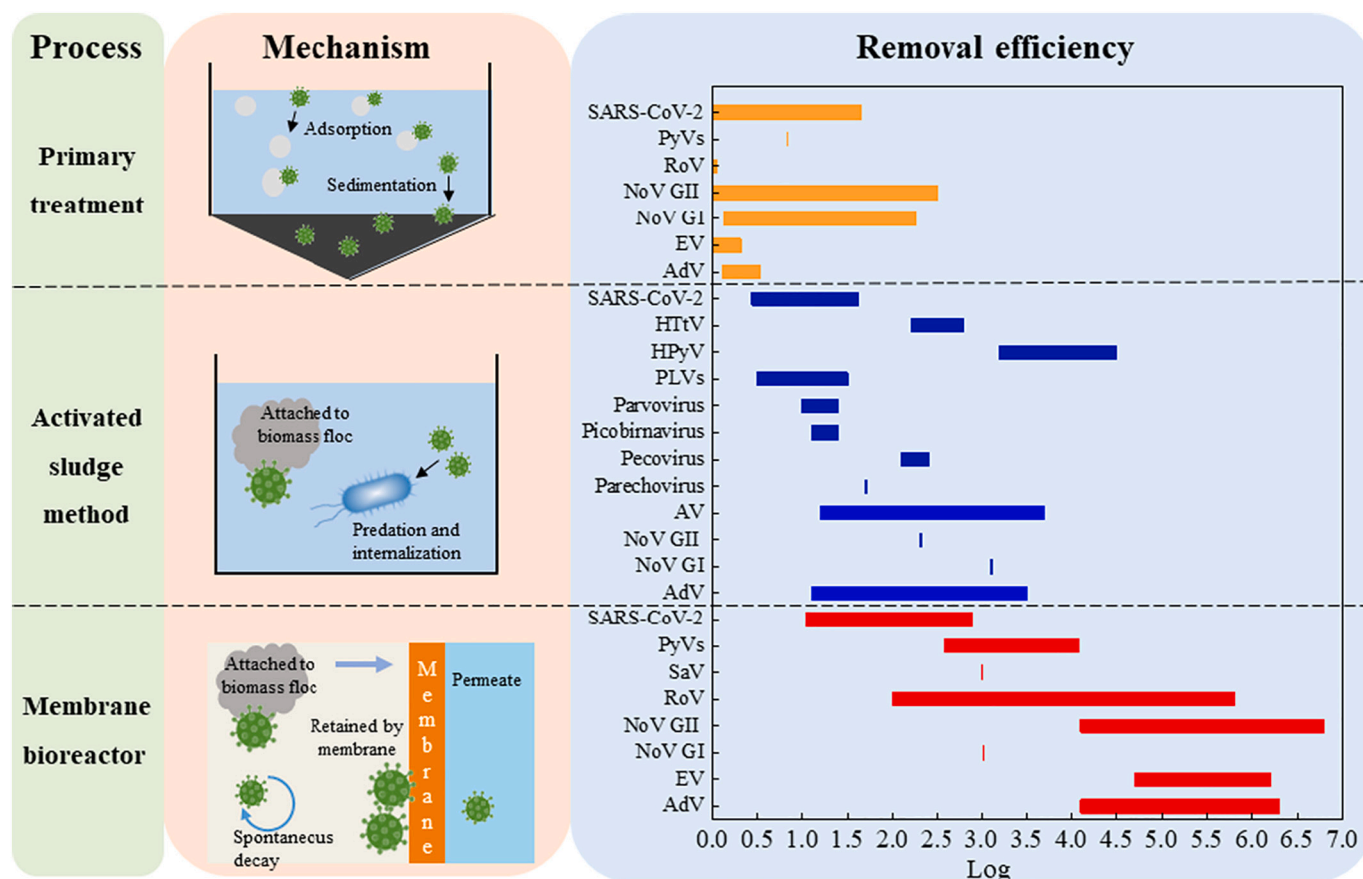
Fig. 2. Mechanism and log removal efficiency of different viruses during different WWTP units operation [69,73,104,108,121–129]. (SARS-CoV-2, severe acute respiratory syndrome coronavirus2; PyVs, polyomavirus; RoV, rotavirus; NoV GII, norovirus GII; NoV GI, norovirus GI; EV, enterovirus; AdV, adenovirus; HTtV, human torque teno virus; HPyV, Human polyomavirus; PLVs, primate lentivirus; AV, astrovirus; SaV, sapovirus).

to only degradation. Specifically, the biodegradation process could be well described by the Eckenfelder model (first order reaction), which might be the main reason for the excellent performance of the virus reduction under a longer HRT condition [107]. Furthermore, the performance of WWTP operation was deeply affected by virus characteristics, and a removal trend of human polyomavirus (HPyV) (3.65 log) > *Microviridae* (2.81 log) ≈ human adenovirus (HAdV) (2.79 log) was observed via a comparison of the operation of three WWTPs that employed Bardenpho processes [108]. It should be noted that complicating factors contribute to the wide disparity in virus removal, as evidenced by the relevant data on reduction (0.3–4.5 log) measured in the secondary treatment of WWTPs (Fig. 2).

5.2.2. Performance of membrane bioreactors

The majority of membrane bioreactors (MBRs) exhibit an excellent performance in virus removal [109], and the main mechanisms can be summarized as: (1) size exclusion, electrostatic repulsion, and sorption onto the membrane; (2) pore blocking and adsorption onto the biomass layer; (3) adsorption and predation by the suspended biomass; and (4) spontaneous decay and inactivation [110]. For example, an average removal rate of 4.1–6.3 log for AdV and 3.5–4.8 log for EV could be achieved in the operation of a full-scale aerobic MBR using a 0.04 μm membrane, whereas 3.67 and 3.40 log, respectively, were observed for a 0.4 μm membrane [110]. Moreover, the removal efficiency of viruses should greatly improve once the biofilm attaches to the membrane surface, as evidenced by the average 2.1 log virus removal rate of the 21-day continuously operated membrane, nevertheless, whereas it was only 0.3 log during the initial operational stage (9 h of continuous operation) [111]. Although membrane fouling contributes to virus rejection, it is

detrimental for WWTP operation because of the negative effect of the permeate flux [112,113]. Thus, backwashing is necessary for the operation of the MBR system; here, and it should be pointed out that backwashing partially deteriorated the overall performance of the MBR in virus removal (declined of 0.5 log) [114]. Hence, seeking a balance between virus particle rejection and membrane permeability will be an arduous task for the practical operation of WWTPs [115]. On the other hand, microorganism predation and enzymatic breakdown also contribute to virus removal [116], as evidenced by the noteworthy correlation between the bulk removal of SaVs and the mixed liquor suspended solids concentration in a pilot-scale MBR operation [117]. In summary, the abovementioned fluid flux, transmembrane pressure, chemical characteristics of biomass and the reduction of membrane pore size can significantly affect virus removal in the MBR system.

Overall, the removal efficiency of WWTP treatments is closely related to the characteristics of the viruses. Specifically, primary treatment was efficient for NoV GI (up to 2.26 log) and NoV GII (up to 2.5 log) removal and activated sludge treatment was efficient for HPyV (up to 4.5 log), AV (up to 3.7 log), NoV GI (up to 3.12 log) and AdV (up to 3.5 log) removal. It should be noted that primary treatment was more effective for the removal of SARS-CoV-2 than activated sludge treatment (1.65 log vs 1.62 log), emphasizing the importance of primary treatment in WWTPs especially during the COVID-19 pandemic. MBR systems exhibited better virus removal (2–6.8 log) than the traditional biological wastewater treatment systems (Fig. 2). Moreover, enveloped viruses are more likely to be removed in MBR system relative to nonenveloped viruses [118,119]. Thus, MBR has been recommended as one of the most effective approach for virus removal during WWTP operation [120].

5.3. Tertiary treatment processes

5.3.1. Ultrafiltration

Generally, as high as a >4 log reduction of viruses could be efficiently achieved in ultrafiltration (UF) membrane filtration via size exclusion [130], especially for SARS-CoV-2 virus [131]. The adsorption of viruses to solids, a formation of a cake layer on the membrane surface, and subsequent trapping of viruses played a key role in achieving a high removal efficiency of viruses in the UF system [132,133]. Specifically, UF membranes with a slightly negative charge benefit virus elimination more than those with a neutral charge [134]. It should be noted that the nominal pore size of UF membranes is not small enough to remove NoV [135], AdV [135], RoV [136], and bacteriophages [137,138]. Hence, the reduction of viruses can be improved via the use of coagulation as a pretreatment for UF systems. For example, Lee et al. [139] reported that the mean removal rate of MS2 during coagulation-UF operation in wastewater was 2.1 log higher than that with UF alone, and this was closely related to the efficient adsorption of MS2 onto aluminum floc particles and the subsequent trapping by UF.

5.3.2. Sand filtration

Viruses could be efficiently removed by slow sand filtration (SSF) via combined biological and physical treatment mechanisms [140–142], as evidenced by relatively high removal rates of 99.0% for MS-2 (28 nm) and 99.9% for PRD-1 (65 nm) [143]. The main mechanisms involved in the thin biologically active Schmutzdecke (filter cake formed on filter surface) are closely related to the combination processes of straining (related to filter bed resistance), attachment (association with sticking efficiency) and predation (related to biologic activity) [144]. The performance of SSF in virus removal also depended on the chemical characteristics of the water sources, operational temperature, the surface ripening of the Schmutzdecke and hydraulic parameters (e.g., filtering material, filter depth, hydraulic load (HL), HRT and feeding schedules) [145]. For instance, Anderson et al. [146] found virus removal to increase with a continuous increase in filter depth, water temperature, and operational HRT and with a decline in the HLs by evaluating the removal rate of sixteen MS2 during biologically mature pilot-scale slow sand filter operation. Since the majority of virus removal occurred within the Schmutzdecke, maintain a high operational efficiency of Schmutzdecke via the operational parameter optimization played a key role in enhancing virus removal [147].

5.3.3. Disinfection

The disinfection of viruses by damaging genome- and protein-mediated functions to inhibit their infectivity [148] has been proven to be the most efficient and convenient approach to virus elimination before WWTP effluent is discharged into aquatic environments. Powerful disinfection approaches, including ultraviolet (UV), ozonation, chlorination and chlorine dioxide oxidation, have been widely applied and proven to be efficient technologies for SARS-CoV deactivation [149].

i. UV disinfection

UV radiation inactivated the viruses mainly via the following two pathways: (1) damage of nucleic acids (DNA/RNA) through the formation of pyrimidine dimers, and (2) inhibition of virus replication and transcription through the reaction of photoproducts [150]. Overall, UV radiation exhibited excellent inactivation performance for RoV, HAV, calicivirus, PV and CVB5 [151], whereas it was less efficient for HAdV type 2 (one of the most UV light-resistant enteric viruses). Recent work shows that SARS-CoV-2 is highly susceptible to UV irradiation [152], and SARS-CoV-2 could be effectively inactivated by UVC within 9 min of operation even under a 5×10^6 TCID$_{50}$·mL^{-1} viral load. The inactivation of viruses during UV reaction is not only related to virus characteristics but also closely related to water turbidity [153]. Therefore, the elimination or reduction of the particles in the wastewater can significantly improve UV disinfection efficiency.

ii. Ozonation

Ozonation inactivated viruses by directly attacking the DNA or RNA [154] or via direct oxidation by the formed free radicals [155]. Generally, ozonation requires less contact time to achieve the same inactivation efficacy of viruses as traditional chlorination (1/10 times that of chlorine) [156]. Specifically, the susceptibility of the selected five enteric viruses [coxsackievirus B5 (CVF, CVEnv1, and CVEnv2), HAdV, and echovirus 11] toward ozone decreased in the following order: CVEnv2 > echovirus 11 > HAdV > CVF ≈ CVEnv1 [157]. The disinfection performance of ozonation is seriously affected by operating parameters, such as pH, alkalinity and organic content (as free radical triggers, promoters and scavengers).

iii. Chlorine-based disinfectants

Chlorine and chlorine dioxide have been widely applied for virus inactivation, especially for f2 bacteriophages, PV, and HAV. Specifically, chlorine exhibited excellent performance in destroying the genome and proteins of viruses [148], whereas the destruction of the genome has been regarded as the primary role involved in chlorine dioxide inactivation (especially for poliovirus, EV71 and hepatitis A virus) [158–160]. Meanwhile, the denaturation of virus proteins, such as human rotavirus (HRoV), also plays a key role in chlorine dioxide disinfection [161]. Cromeans et al. systematically compared the performance of chlorine on the inactivation of EV2, EV40, EV41, CVB3, CVB5, ekovirus 1, ekovirus 11 and murine NoV, and found CVB5 to show the strongest resistance to chlorine, whereas murine NoV exhibited the least resistance [162]. Similarly, the resistance of typical viruses to chlorine dioxide declined as follows: HRoV > coxsackie virus > echovirus > PV > f2 phages > monkey RoV [15,163–165]. Compared to chlorine dioxide, chlorine exhibited a much higher inactivation efficiency for SARS-CoV and SARS-CoV-2, which could be proven by the observation of complete inactivation of SARS-CoV by 20 mg·L^{-1} chlorine after a 1 min reaction [58,166]. Inactivation by chlorine dioxide for virus removal is temperature- and pH-dependent, and the virucidal efficiency of EV 71 was higher at pH 8.2 than at pH 5.6 and pH 7.2. Similarly, better inactivation was also observed at 36 °C than at 4 and 20 °C [159].

It should also be pointed out that the disinfection methods mentioned above still need further improvement during their practical utilization. For example, the decline in the light intensity of UV radiation after long-term operation [167] and the formation of reaction intermediates and stable disinfection byproducts (DBPs) (haloacetic acid, trihalomethanes, chloramines, chlorate, chlorite and other toxic byproducts) during the use of chlorine-based disinfectants [168] have been widely reported. To compare the sensitivity of typical viruses to disinfectants, the performance of typical disinfections under different operational parameters is summarized in Tables 3 and 4. The UV doses commonly applied for water and wastewater treatment are between 30 and 40 mJ/cm^2, and these doses were effective for many viruses except for AdV due to that double-stranded DNA viruses are likely the most resistant viruses to UV light disinfection [169]. In addition, chlorine dioxide was not as effective as expected in the inactivation of SARS-CoV at the disinfection dose applied for WWTPs, and ozone is a highly effective disinfectant for virus control (Table 4).

As noted above, traditional WWTPs are not specifically designed for the purpose of entirely removing viruses; thus, the viruses remaining in WWTP effluents negatively affect their recreational, irrigation, and potable- and nonpotable water reuse [170]. This has become the main challenge to most developing countries because they cannot be easily equipped with advanced wastewater treatment technologies [171]. Typical virus concentrations and positive detection rates in the effluent from WWTPs of different continents are shown in Fig. 3. According to

Table 3

Relative sensitivity of enteric viruses to chlorine, chlorine dioxide, and ozonation disinfections [15].

	Chlorine	Chlorine dioxide	Ozonation
HRoV	L	L	L
f$_2$	L	M	H
CV	M	L	H
Echo	M	L	H
PV	H	M	L
SA11	H	H	L

Note: HRoV, Human rotavirus; CV, coxsackievirus; Echo, echovirus; PV, poliovirus; SA11, simian rotavirus; H: high, M: middle, L: light.

the data of positive samples (%), viruses with a positive detection rate (%) more than 50 were AiVs (54), EVs (92), JCPyV (85.4), SaVs (88) for America Continent and were EVs (58.3), HAstV (83), HAdV (75), NoV GI (61.6), NoV GII (92.85), RoV (66.7), SARs-CoV-2 (75) for Europe and were HAdV (89), AiV (91.6), HAstV (66.7), NoV GII (58) for Asia and were HAdV (78), HBoV (57.5), HPyV (82.4), NoV (83.3) for Africa, respectively, in which HAdV and NoV were frequently detected in Europe, Asia and Africa; although they were occasionally detected in America Continent, the log concentrations (genome copies·L^{-1}) were as high as 6.45 and 6.1, respectively, highlighting their risks in WWTP effluent. In addition, it is worth noting that the frequency and concentration of SARS-CoV-2 were relatively high in Europe (with positive detection rates of 75%) and Aisa (with a concentration of 2×10^3 genome copies·L^{-1}).

5.4. Reuse and desalination

As mentioned above, typical enteric viruses have been frequently detected in treated WWTP effluent, which is of great concern in low-income and arid/semiarid countries, where have to reuse the effluents of WWTPs for agriculture and industry to alleviate serious water scarcity conditions [212,213]. In addition, the WWTP effluents are typically discharged into receiving water (sea, lake, river, etc.). Thus, we need to understand the occurrence and removal performance of viruses in sewage reuse and desalination. Briefly, the traditional treatment technologies of reclaimed water for irrigation mainly included coagulation, sedimentation, filtration and disinfection [214]. In contrast, membrane-based desalination technologies, especially reverse osmosis (RO) and nanofiltration (NF), have also been widely applied in agricultural applications throughout the world in recent years to meet salt content demands of agricultural irrigation water. Research has shown that NF membrane desalination technology can remove 95% of viruses [215]. Reclaimed water for industry used for cooling, district heating, etc. requires desalination according to the standard of water conductivity, and that for the steel industry is less than 400 μS·cm^{-1} [216]; and the technical route of "UF + RO" has been regarded as one of the best technologies for desalination [217], where as high as a 2.3–2.9 log reduction rate of viruses could be achieved [129].

In coastal areas, NoV GI, NoV GII, SaV, EV, RoV, HAdV, HAV, and HPyV can be detected in seawater due to the treated sewage discharge, with the concentration of $2 \times 10^2 – 1 \times 10^6$ genome copies·L^{-1} [218,219]. The recent work of Dias et al. identified viruses in all 48 water samples obtained from four beaches, among which 43% water

Table 4

Inactivation efficiency, operational parameters of the typical disinfectants for different viruses inactivation.

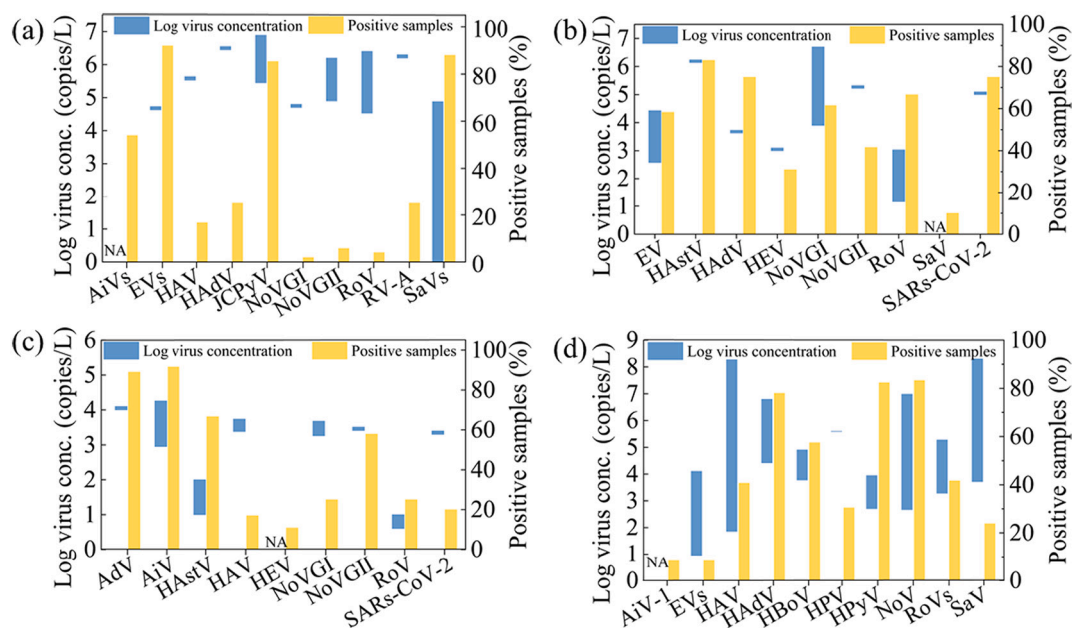| Viruses	UV			Ozonation					Chlorine dioxide			
	Dosage (mJ·cm^{-1})	Removal	Ref.	Parameters	Ozone	Contact time	Removal	Ref.	Concentration ppm	Treatment time	Removal	Ref.
PV-1	30	3.0 log	[196]	5 °C pH 7	0.37 mg·L^{-1}	5 min	4.5 log	[197]	85 μM	1 min	4.0 log	[198]
	9	2.0 log	[199]									
	18	3.43 log										
	24	4.75 log										
	35	5.7 log										
Ad 40	9	0.2 log	[199]	5 °C pH 7	0.60 mg·L^{-1}·min	/	4.0 log	[165]	15 °C, pH 6 0.92 mg·L^{-1}·min		4.0 log	[200]
	18	0.68 log										
	24	0.87 log							15 °C, pH 8 0.11 mg·L^{-1} min		4.0 log	
	35	1.21 log										
	90	3.0 log										
	120	4.0 log										
Ad 2	78	2.0 log	[169]	5.1×10^{-6}–4.1×10^{-3} mg·min·L^{-1}			2.0 log	[157]	1.0 ppm	15 s	1.5 log	[203]
	119	3.0 log										
	160	4.0 log							10 ppm	15 s	5.0 log	
	30 (medium-pressure)	2.19 log	[201]	0.7–0.9 mg·min·L^{-1}			3.0 log	[202]	100 ppm	15 s	>6.0 log	
	90 (medium-pressure)	5.36 log		0.77–1.10 mg·min·L^{-1}			4.0 log					
Simian Rotavirus (SA11)	42	4.0 log	[204]	4 °C pH 6	0.17 mg·L^{-1}	8 s	4.0 log	[205]	0.5 mg·L^{-1}; pH 10	15 s	>4.0 log	[206]
				4 °C pH 7	0.1 mg·L^{-1}	32 s	4.0log					
				4 °C pH 8	0.1 mg·L^{-1}	6 s	4.0 log					
FCV	36	4.0 log	[207]	5 °C pH 7 0.07	0.01–0.03 mg·L^{-1} min		4.0 log	[165]	0.8 mg·L^{-1}	2.1 min	4.0 log	[208]
									0.2 mg·L^{-1}	19.5 min	4.0 log	
HAV	16	4.0 log	[204]	pH 7.0,	1.0 mg·L^{-1}	24 s	4 log	[209]	0.8 mg·L^{-1}	0.43 min	4.0 log	[208]
									0.4 mg·L^{-1}	19.58 min	4.0 log	
CVB5	27	3.0 log	[201]	1.0×10^{-5}–8.0×10^{-3} mg·min·L^{-1}			2.0 log	[202]	0.6 mg·L^{-1}	1.00 min	4.0 log	[208]
	36	4.0 log							0.4 mg·L^{-1}	2.41 min	4.0 log	
	29	4.0 log	[204]						0.2 mg·L^{-1}	3.73 min	4.0 log	
SARS-CoV	3.75	0.9 log	[210]	/			/	/	10 mg·L^{-1}	1 min	0.25 log	[58]
	37.5	3.1 log								5 min	0.5 log	
	75	>3.3 log								10 min	>6.0 log	
	112.5	>3.3 log								20 min	>6.0 log	
	225	>3.3 log							40 mg·L^{-1}	1 min	1.25log	
	292	1.0 log	[211]							5 min	>6.0 log	
	1048	>4.0 log								10 min	>6.0 log	

Note: PV-1, poliovirus 1; Ad 40, adenovirus type 40; Ad 2, adenovirus type 2; FCV, feline calicivirus; HAV, hepatitis A virus; CVB5, coxsackievirus B5; SARS-CoV, severe acute respiratory syndrome coronavirus.

Fig. 3. Concentration and positive detection rates of typical viruses in WWTP effluent of (a) American Continent [7,129,172–176], (b) Europe [177–181], (c) Asia [182–190], (d) Africa [191–195]. (EVs, enterovirus; HAV, hepatitis A virus; HAdV, human adenovirus; JCPyV, JC Polyomavirus; NoV GII, norovirus GII; NoV GI, norovirus GI; RoV, rotavirus; RV-A, rotavirus A; SaVs, sapovirus; HAstV, Human astrovirus; HEV, hepatitis E virus; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2; AdV, adenovirus; AiVs, Avian influenza virus; HBoV, Human bocavirus; HPV, Human papillomavirus; HPyV, human polyomavirus; NoV, norovirus).

samples were positive for HAdV and 23% were positive for JC Polyomavirus (JCPyV) [220]. Similarly, Moresco et al. analyzed 132 samples of coastal water, and found that 55% were positive for HAdV, 51.5% for HAV, 7.5% for HuNoV GI, 4.5% for HuNoV GII, and 3% for JCPyV [218]. To obtain reclaimed water from seawater, RO, membrane distillation, forward osmosis (FO), and electrodialysis (ED) are sustainable and cost-effective desalination technologies. Specifically, RO was capable of achieving the highest log removal of viruses (3.52 to 4.40 log) among the different approaches (1.93 to 3.05 log virus removal for NF) due to its small "pore sizes" and significant size exclusion; it is interesting to note that operational pressure has a relatively weak effect on the log removal of viruses [221]. Practically, the adoption of hybrid system in seawater desalination, such as the FO-ED hybrid system, exhibits excellent performance and consumes very little energy compared to other hybrid systems [215]. Unfortunately, no data have been reported for hybrid systems in virus removal.

Recent work on the reliability of solar stills for wastewater treatment found that 90% of the virus can be removed by heating the WWTP effluent to 70 °C and denaturing proteins at high temperatures [17], and the pilot-scale solar could remove 4.5 log (99.997%) of HAdV-5 in the distillation process [222]. Furthermore, the emergence of nanotechnology improved the distillation mechanism greatly, and might help alleviate water issues by solving the technical challenges that removing viruses [223], creating potential avenues for addressing the virus concerns via the combination traditional desalination and emerging materials.

5.5. Sludge treatment and disposal

The majority of the viruses (including SARS-CoV-2) in the wastewater were eventually be transferred into the sewage sludge due to their excellent ability to bind to solids and colloids [224], as evidenced by the high and steady concentration of viruses observed in primary and thickened sludge (Table 5). The removal characteristics of the viruses in the sludge samples during subsequent treatment and disposal highly depended on the treatment techniques (composting, aerobic digestion, anaerobic digestion and air-drying) used.

The average survival time of viruses within a compost pile ranged from 34 to 44.5 h [225], and a long composting HRT (10–15 days) would lead to a 3–4 log reduction of viruses under an operational temperature of 55–70 °C [130]. Aerobic conditions, accompanied by the heat generated within composting systems, might be the main reason for virus inactivation [226]. Although the utilization of anaerobic digestion alone was ineffective in the elimination of EV (1 log reduction) and SARS-CoV-2, the combination of mesophilic anaerobic digestion and thermal hydrolysis has been regarded as one of the most effective approaches to virus inactivation [226]. Similarly, the recent work of Serra-Compte et al. found the log removal of viruses during traditional digestion to be negative (mean values of −0.17 ± 0.89), while it was 1.69 ± 0.27 for thermal hydrolysis+anaerobic digestion, which is closely related to the inactivation of the viruses by saturated steam at 150–160 °C [227]. For sludge air-drying, the infectivity of viruses declined with the continuous increase in solid content [228]; moreover, such inactivation was irreversible because of the disintegration of viral particles and release of RNA genomes. It should be pointed out that the proteases produced by indigenous microbes in sludge have a potentially significant role in the decay of enteric viruses in sewage sludge [229].

6. Dissemination of viruses during the entire wastewater collection, transmission and treatment process

The dissemination of viruses during the entire sewage wastewater collection, transmission and treatment process mainly includes fecal-oral transmission, aerosol transmission and direct contact [238–240]. The fecal-oral contamination route of viruses spreading via the improper treatment of wastewater plays a predominant role in the spread of viruses in low-income regions [241]. Due to a lack of wastewater sanitation and sewer systems in low-income regions, billions of people have limited or no toilet facilities and suffer from unsafe sanitation [242], and the consequential public contact with infected waste or wastewater facilitates the transmission of viral diseases via the incidental fecal-oral route. Importantly, an increasing number of researchers have proven that the fecal transmission is the main transmission route of SARS-CoV-2 [240]. Since high volumes of bioaerosols can be generated through the

Table 5
Concentration of typical viruses in sewage sludge samples.

Virus	Raw sludge (genome copies·kg^{-1})	Anaerobically digested sludge (genome copies·kg^{-1})	References
EV	10^5–10^7 (Primary sludge) 3×10^5 (Secondary sludge)	2×10^2–2.1×10^5	[230]
NoV GI	/	5.0×10^7	[231]
Nov GII	1.6×10^4–4.90×10^5[a] (Primary sludge)	1.50×10^8	[231,232]
RoV	8.00×10^3–8.00×10^5[a] (Primary sludge)	1.4×10^4–4.85×10^5	[230,232]
HAdV	1.80×10^5–1.20×10^{10}[a] (Primary sludge) 9.40×10^9–3.90×10^{11} (Thickened sludge)	9.10×10^7–6.90×10^9	[231–233]
HAV	Activated sludge: 3.10×10^5–5.20×10^5[a]	/	[232,233]
AdV	Activated sludge: 5×10^4–1.3×10^7[a]	/	[233]
EV	5.47×10^7–1.15×10^8 (Primary sludge) 5.66×10^6–1.44×10^7 (Activated Sludge) 1.44×10^7–2.40×10^8 (Thickened Sludge)	2.60×10^7–7.60×10^7	[231,234]
HPyV	/	7.40×10^7–2.5×10^8	[231]
Parechovirus	/	2.51×10^7–2.51×10^8	[235]
SARS-CoV-2	1.17×10^4–4.02×10^4[a] (Primary and activated sludge)	8.13×10^1–8.13×10^4	[236,237]

Note: EV, enterovirus; NoV GI, norovirus GI; NoV GII, norovirus GII; RoV, rotavirus; HAdV, human adenovirus; HAV, hepatitis A virus; AdV, adenovirus; HPyV, human polyomavirus; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

[a] Expressed in genome copies·L^{-1}.

high pressure and turbulence of toilet flushing, aerosol inhalation also plays a key role in sewage-associated virus transmission in communities because inhalation exposure of bioaerosols is approximately 10^5 times higher than dermal exposure [243]. In addition, the improperly sealed (dried out) floor drains lead to a vertical transmission of virus-laden aerosols throughout the building collection system, facilitating the spread of viruses [244] (Fig. 4a). Additionally, the leakage of wastewater from septic tanks and collection systems allows the direct discharge of viruses into receiving water bodies (such as streams, rivers, ponds, estuaries, lakes and groundwater) [245], which increases the incidence of direct human contact with virus-loaded sewage.

The mechanical rotation and aeration of wastewater during the primary and secondary treatment creates bubbles with diameters of approximately 60–600 μm that travel as much as ~8 cm above the wastewater surface of the aeration tanks [246,247]. Thus, aerosol inhalation or direct contact with infectious viral particles leads to a higher exposure risk of viruses for WWTP workers (Fig. 4b). Approximately 94% of viruses in wastewater have been detected in a liquid phase rather than on biosolid surfaces [248]; thus, aerosolization might be the main pathway of virus spread in WWTPs [249]. In addition, the microorganisms in sludge easily escape into the air and accumulate in the dewatering room during the sludge dewatering process, which also threatens the safety of workers in WWTPs [250]. Although accurate qualitative and quantitative studies of microbial concentrations in

WWTPs are currently lacking, it is clear that the concentration of microbial aerosols is significantly affected by temperature, wind speed and other factors [187]. The recent work of Gholipour et al. revealed that the annual infection risk ranged from 1.1×10^{-2} to 2.3×10^{-2} per person per year (PPPY) among wastewater workers and was higher than the WHO recommended level (10^{-3} PPPY) [251]. From the above, we can conclude that the aerosols generated during wastewater treatment contributed to the transmission of viral infections; thus, it is urgently necessary to further control the aerosol inhalation of viruses in WWTPs, especially during the ongoing global COVID-19 pandemic.

7. Public health risks associated with the reuse of (inadequately) treated wastewater

Discharge of treated or inadequately treated WWTP effluent into surface and natural water bodies poses a public health risk of viral infection, especially during the utilization of sewage-contaminated surface water for irrigation, recreation, shellfish culture, etc. due to the low infectious doses of viruses and their ability to persist for long periods of time outside their hosts [256,257]. Ingestion through food contamination and inhalation through the respiratory system were the means through which the pathogens viruses can enter the human body [258], evidenced by the investigation in the United States between 2009 and 2013 reporting that viruses caused 68% of foodborne outbreaks [259].

For agricultural irrigation, the probability of illness (DALY pppy) estimated of the concentrations of both HAdV and NoV GII in both tertiary effluents were 1.44×10^{-3} and 1.94×10^{-3} for WWTP1, respectively, whereas 2.09×10^{-4} and 2.99×10^{-4} were observed for WWTP2, which haven't met the threshold of $\leq 10^{-6}$ DALY pppy for an acceptable level of risk for irrigation [180]. To achieve an annual health-based target of the tolerable annual disease burden values, the concentration of AdV in irrigation water needs to $\leq 6.9 \times 10^{-5}$ genome copies·mL^{-1} and $< 1.5 \times 10^{-2}$ genome copies·mL^{-1} for EVs [260]; and the concentration of NoV GII in irrigation water needs to ≤ 1.8 log genome copies·mL^{-1} [261] Furthermore, in most developing regions, there is a concern that waterborne infection risk may increase from the reuse of untreated or partially treated sewage. The average DALY was 7.15×10^{-4} for maize, 7.09×10^{-4} for barley and 7.17×10^{-4} for paddy rice cultivation at the concentration of ADV, EV, NoV GI, NoV GII, NoV GIV, and RV in irrigation water that were almost the same virus concentrations in raw sewage [262]. Additionally, it is estimated that at least one type of virus has been detected (with the highest concentration of 7.8×10^5 GC·m^{-3}·h^{-1} found for HEV) in the air above irrigated plots, [263], which emphasized the risk of inhalation of pathogen bioaerosols to public health. These reports showed that polluted irrigation water is infectious to not only farmers but also crop consumers.

In the recreational surface waters, the daily risk of viral infection at either of the investigated beaches ranged from 0.2 to 2.4/1000 swimmers; moreover, as high as 0.9%–1.5% infection risk for child swimmers taking three swims per day over a season was obtained using AdV as the risk quantitative microbial assessment model [264]. According to a case study conducted in Singapore, the mean probability of illness caused by NoV was measured as 0.61% for adults and 0.89% for children during primary contact recreation, and as 0.28% and 0.48%, respectively, for HAdV; in contrast, the mean probability of illness were 0.16% for NoV and 0.068% for HAdV during secondary contact recreation [265]. In most developing countries, such as Bangladesh, wastewater enters directly into the rivers, which increase the people's vulnerability to waterborne diseases. The risks of illness were ranged from 7 to 10% for NoV and 12 to 17% for RoV from a single exposure of bathers. The overall risk of illness at the rivers was slightly higher in children (9–19%) compared to adults (7–16%), that was higher than that in developed countries/regions [266].

The improper intake of raw or lightly cooked bivalve shellfish (oysters, clams, and mussels) can lead to illness spreading if these
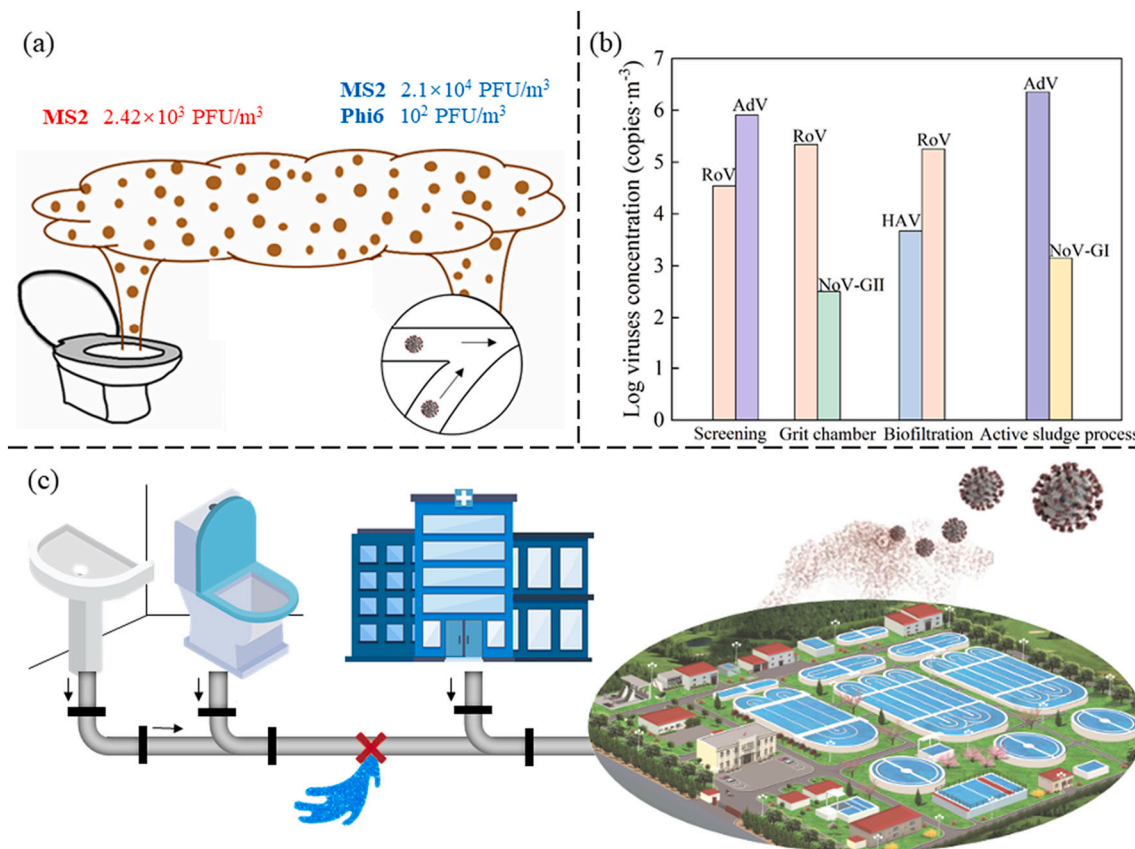
Fig. 4. Dissemination of virus via aerosol route in the whole process of sewage collection, transmission and treatment [252–255].
(a) Concentrations of MS2 and Phi6 in aerosols generated in lab-scale models of toilet and converging sewer pipes. (b) Concentrations of typical viruses in aerosols generated from different units of WWTP. (c) Overview of potential virus dissemination via aerosol route during wastewater collection, transmission and treatment. (Different font colors in (a) and column colors in (b) indicate that the data come from different articles)
(RoV, rotavirus; AdV, adenovirus; NoV GII, norovirus GII; HAV, hepatitis A virus; NoV GI, norovirus GI.)

shellfish are harvested from coastal areas impacted by sewage discharges. For example, as high as a 10% detection frequency of EV genomes was observed in the wild shellfish in Morocco growing near the outlet of a sewage drainage system [267]. According to Campos et al. the total concentration of NoV in shellfish, predicted by the model at 300:1, 1000:1 and 5000:1 ratios of estuarine water to sewage effluent, was 1200, 600, and 200 genome copies·g^{-1}, respectively [268]. Epidemiological evidence indicates that most cases of shellfish-related illness are gastroenteritis caused by viruses, especially for NoV GI and NoV GII [269].

To guarantee the safe implementation of the WWTP effluent reuse, countries and organizations have implemented different regulations and guidelines on pathogens spread control [270], where the fecal coliforms and *Escherichia coli*, rather than virus, were the main pathogens indicators for the reuse of treated wastewater; thus, the inclusion of the virus dissemination index in the discharging guidelines and regulation of WWTPs should be seriously considered.

8. Challenges and future perspectives

The ongoing COVID-19 pandemic has clearly revealed the challenges and knowledge gaps in the viability and the reduction/inactivation mechanisms of viruses during wastewater collection, transmission, treatment and reuse/desalination processes. Future works in this regard could focus on the following:

- Public health departments should promote wastewater surveillance programs for monitoring the typical virus concentrations over their entire journey from source (especially for hospital wastewater) through collection (especially for septic tanks and combined sewer systems) and treatment, especially for SARS-CoV-2 and its variants, to avoid virus dissemination.

- The outbreak of viral diseases is mostly clustered; thus, these residential areas should have an effective septic tank system, properly sealed floor drains and bathroom vent pipes, and operable drain traps in flush toilets to reduce the atomization of wastewater infected with viruses and prevent secondary dissemination.

- Since enveloped viruses (e.g., SARS-CoV-2) are more susceptible to temperature, the removal of enveloped viruses at low water temperatures is a challenge for WWTPs. In addition, studies on the persistence of enveloped viruses in wastewater, removal efficiency and inactivation mechanisms during wastewater treatment, especially in disinfection (UV, chlorine, chlorine dioxide, ozone, etc.), are still scarce and require additional exploration.

- Construction and operation of primary treatment units of WWTPs are extremely essential for the bulk removal of viruses, especially for SARS-CoV-2. Meanwhile, MBR is more effective in viruses reduction than conventional secondary treatment. However, UV is not as effective as expected in the inactivation of AdV, and the same is true of chlorine dioxide for SARS-CoV-2. Thus, "primary treatment+ MBR+chlorine" was recommend for a better removal of viruses in practical operation of WWTPs.

- Diffused aeration is more reliable than surface aeration due to lower gaseous emissions of viral RNAs [271]; thus, we strongly recommend that diffused aeration be extensively used in the secondary treatment of WWTPs. In addition, the impact of SARS-CoV-2 spreading by

airborne bioaerosols is ambiguous; thus, studies of fecal bioaerosols as a possible SARS-CoV-2 transmission route should be conducted to aid the prevention and spread of current and future pandemics.

9. Conclusion

This review highlighted the occurrence, removal and dissemination of typical viruses in wastewater during their collection, transmission, and treatment in WWTPs. The occurrence of typical viruses (including SARS-CoV-2) among the different sources (patient feces, slaughterhouse wastewater, and hospital wastewater) underlines a significant role of wastewater in the transmission of viruses. The wide range of concentration distributions of viruses in collection systems and the effects of combined sewer systems provide critical information for quantitative risk assessment and the upgrading of sewers. By comparing the efficiency, mechanisms and influencing factors of typical virus removal in WWTP units, we provided useful data for the parameter optimization of virus inactivation. The membrane-based desalination technologies used prior to effluent reuse are highly efficient for virus removal. However, wastewater is discharged into receiving waters without being inadequately treated, and the reuse of WWTP effluent still pose a risk of dissemination of virus-related diseases to humans. The majority of viruses in wastewater are eventually transferred into sewage sludge; the combination of thermal hydrolysis and anaerobic digestion was the most effective method for the reduction of viruses. Fecal-oral aerosol transmission and direct contact are key mechanisms of the fecal droplet respiration transmission of viruses, and aerosolization in sewer systems and WWTPs may be a concern during the ongoing global COVID-19 pandemic.

CRediT authorship contribution statement

Jian-ju Li: Conceptualization, Writing-Original Draft, Writing–review & editing. Jing Liu: Investigation, Visualization, Writing-original draft. Hang Yu: Investigation, Writing-original draft, Writing-review & editing. Wei-xin Zhao: Visualization, Writing–review & editing. Xin-hui Xia: Investigation, Writing-review & editing. Shi-jie You: Conceptualization, Project administration. Jun Zhang: Conceptualization, Supervision. Hai-long Tong: Conceptualization, Writing-Original Draft, Writing–review & editing. Liang-liang Wei: Conceptualization, Writing-Original Draft, Writing–review & editing, Project administration, Funding acquisition.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.desal.2022.115798.

References

[1] A.E. Hagstrom, et al., Sensitive detection of norovirus using phage nanoparticle reporters in lateral-flow assay, PLoS One 10 (5) (2015), e0126571, https://doi.org/10.1371/journal.pone.0126571.

[2] I.A. Hamza, et al., Detection of human viruses in rivers of a densly-populated area in Germany using a virus adsorption elution method optimized for PCR analyses, Water Res. 43 (10) (2009) 2657–2668, https://doi.org/10.1016/j.watres.2009.03.020.

[3] Crites, Small and decentralized wastewater management systems, in: McGraw-Hill Series in Water Resources and Environmental Engineering, 1998.

[4] R. Lozano, et al., Global and regional mortality from 235 causes of death for 20 age groups in 1990 and 2010: a systematic analysis for the global burden of disease study 2010, Lancet 380 (9859) (2012) 2095–2128, https://doi.org/10.1017/S0022172400068947.

[5] WHO. Number of deaths: WORLD by cause. http://apps.who.int/gho/data/node.main.CODWORLD?lang=en.

[6] E.D. Sunkari, et al., Sources and routes of SARS-CoV-2 transmission in water systems in Africa: are there any sustainable remedies? Sci. Total Environ. 753 (2021), 142298 https://doi.org/10.1016/j.scitotenv.2020.142298.

[7] T. Prado, et al., Quantification and molecular characterization of enteric viruses detected in effluents from two hospital wastewater treatment plants, Water Res. 45 (3) (2011) 1287–1297, https://doi.org/10.1016/j.watres.2010.10.012.

[8] K. Qin, et al., A review of ARGs in WWTPs: sources, stressors and elimination, Chin. Chem. Lett. 31 (10) (2020) 2603–2613, https://doi.org/10.1016/j.cclet.2020.04.057.

[9] P. Foladori, et al., SARS-CoV-2 from faeces to wastewater treatment: What do we know? A review, Sci. Total Environ. 743 (2020) 140444, https://doi.org/10.1016/j.scitotenv.2020.140444, 223p.

[10] G. La Rosa, et al., Coronavirus in water environments: occurrence, persistence and concentration methods - a scoping review, Water Res. 179 (2020), 115899, https://doi.org/10.1016/j.watres.2020.115899.

[11] D.A. Larsen, et al., Tracking COVID-19 with wastewater, Nat. Biotechnol. 38 (10) (2020) 1151, https://doi.org/10.1038/s41587-020-0690-1.

[12] H. Katayama, et al., One-year monthly quantitative survey of noroviruses, enteroviruses, and adenoviruses in wastewater collected from six plants in Japan, Water Res. 42 (6–7) (2008) 1448, https://doi.org/10.1016/j.watres.2007.10.029.

[13] A. Bhatt, et al., Occurrence, fates and potential treatment approaches for removal of viruses from wastewater: a review with emphasis on SARS-CoV-2, J. Environ. Chem. Eng. 8 (5) (2020), 104429, https://doi.org/10.1016/j.jece.2020.104429.

[14] S. Arora, et al., Sewage surveillance for the presence of SARS-CoV-2 genome as a useful wastewater based epidemiology (WBE) tracking tool in India, Water Sci. Technol. 82 (12) (2020) 2823–2836, https://doi.org/10.2166/wst.2020.540.

[15] M. Harakeh, et al., Inactivation of human rotavirus, SA11 and other enteric viruses in effluent by disinfectants, J. Hyg. 93 (1) (1984) 157–163, https://doi.org/10.1017/S0022172400061040.

[16] S. Mohapatra, et al., The novel SARS-CoV-2 pandemic: possible environmental transmission, detection, persistence and fate during wastewater and water treatment, Sci. Total Environ. 765 (2021), 142746, https://doi.org/10.1016/j.scitotenv.2020.142746.

[17] S.M. Parsa, Reliability of thermal desalination (solar stills) for water/wastewater treatment in light of COVID-19 (novel coronavirus "SARS-CoV-2") pandemic: what should consider? Desalination 512 (2021), 115106 https://doi.org/10.1016/j.desal.2021.115106.

[18] C.J. Hurst, et al., Fate of viruses during wastewater sludge treatment processes, Crit. Rev. Environ. Sci. Technol. 18 (4) (1989) 317–343, https://doi.org/10.1080/10643388909388352.

[19] E.J. Lefkowitz, et al., Virus taxonomy: the database of the international committee on taxonomy of viruses (ICTV), Nucleic Acids Res. 46 (D1) (2018) D708–D717, https://doi.org/10.1093/nar/gkx932.

[20] M.V.A. Corpuz, et al., Viruses in wastewater: occurrence, abundance and detection methods, Sci. Total Environ. 745 (2020), 140910, https://doi.org/10.1016/j.scitotenv.2020.140910.

[21] M. Pilevar, et al., Recent advances in biosensors for detecting viruses in water and wastewater, J. Hazard. Mater. 410 (2021) 124656, https://doi.org/10.1016/j.jhazmat.2020.124656.

[22] C. Yeo, et al., Enteric involvement of coronaviruses: is faecal-oral transmission of SARS-CoV-2 possible? Lancet Gastroenterol 5 (4) (2020) 335, https://doi.org/10.1016/S2468-1253(20)30048-0.

[23] S. Iizuka, et al., Detection of sapoviruses and noroviruses in an outbreak of gastroenteritis linked genetically to shellfish, J. Med. Virol. 82 (7) (2010) 1247–1254, https://doi.org/10.1002/jmv.21791.

[24] M.E. Barrios, et al., Viral tools for detection of fecal contamination and microbial source tracking in wastewater from food industries and domestic sewage, J. Virol. Methods 262 (2018) 79–88, https://doi.org/10.1016/j.jviromet.2018.10.002.

[25] P. Machnowska, et al., Detection and characterization of potentially zoonotic viruses in faeces of pigs at slaughter in Germany, Vet. Microbiol. 168 (1) (2014) 60–68, https://doi.org/10.1016/j.vetmic.2013.10.018.

[26] F.M. Ruggeri, et al., Rotavirus genotypes in sewage treatment plants and in children hospitalized with acute diarrhea in Italy in 2010 and 2011, Appl. Environ. Microbiol. 81 (1) (2015) 241–249, https://doi.org/10.1128/AEM.02695-14.

[27] H. Fenaux, et al., Molecular features of hepatitis E virus circulation in environmental and human samples, J. Clin. Virol. 103 (2018) 63–70, https://doi.org/10.1016/j.jcv.2018.04.003.

[28] R. Vivek, et al., Characterization of hepatitis E virus from sporadic hepatitis cases and sewage samples from Vellore, South India, Trans. R. Soc. Trop. Med. Hyg. 107 (6) (2013) 363–367, https://doi.org/10.1093/trstmh/trt030.

[29] A. Hundesa, et al., Development of a qPCR assay for the quantification of porcine adenoviruses as an MST tool for swine fecal contamination in the environment, J. Virol. Methods 158 (1) (2009) 130–135, https://doi.org/10.1016/j.jviromet.2009.02.006.

[30] F.X. Lescure, et al., Clinical and virological data of the first cases of COVID-19 in Europe: a case series, Lancet Infect. Dis. 20 (6) (2020), https://doi.org/10.1016/S1473-3099(20)30429-1.

[31] N. Zhang, et al., Comparative study on virus shedding patterns in nasopharyngeal and fecal specimens of COVID-19 patients. Science China, Life Sci. (2020) 1–3, https://doi.org/10.1007/s11427-020-1783-9.

[32] M. Achak, et al., SARS-CoV-2 in hospital wastewater during outbreak of COVID-19: a review on detection, survival and disinfection technologies, Sci. Total Environ. 761 (2021), 143192, https://doi.org/10.1016/j.scitotenv.2020.143192.

[33] J.A. Vanchiere, et al., Frequent detection of polyomaviruses in stool samples from hospitalized children, J. Infect. Dis. 192 (4) (2005) 658–664, https://doi.org/10.1086/432076.

[34] M. Rusinol, et al., Description of a novel viral tool to identify and quantify ovine faecal pollution in the environment, Sci. Total Environ. 458–460 (2013) 355–360, https://doi.org/10.1016/j.scitotenv.2013.04.028.

[35] F. Yılmaz, et al., Investigation of children with acute gastroenteritis by multiplex PCR method in central part of Turkey, J. Pediat. Inf. Dis.Ger. 17 (01) (2022) 048–052, https://doi.org/10.1055/s-0041-1740372.

[36] X. Shen, et al., A novel and highly sensitive real-time nested RT-PCR assay in a single closed tube for detection of enterovirus, Diagn Micr Infec Dis 90 (3) (2018) 181–185, https://doi.org/10.1016/j.diagmicrobio.2017.11.015.

[37] S.Y. Zhao, et al., Observation on intestinal viral shedding time of hand, foot and mouth disease induced by coxsackievirus A6, Zhonghua Er Ke Za Zhi 55 (5) (2017) 369–372, https://doi.org/10.3760/cma.j.issn.0578-1310.2017.05.012.

[38] W.J. Lodder, et al., Feasibility of quantitative environmental surveillance in poliovirus eradication strategies, Appl. Environ. Microbiol. 78 (11) (2012) 3800–3805, https://doi.org/10.1128/AEM.07972-11.

[39] K. Kumthip, et al., Detection of poliovirus infection in children with acute gastroenteritis in Chiang Mai, Thailand, J. Med. Virol. 89 (5) (2017) 775–781, https://doi.org/10.1002/jmv.24694.

[40] Q.H. Wang, et al., Prevalence of noroviruses and sapoviruses in swine of various ages determined by reverse transcription-PCR and microwell hybridization assays, J. Clin. Microbiol. 44 (6) (2006) 2057–2062, https://doi.org/10.1128/JCM.02634-05.

[41] C. Ibrahim, et al., Detection of sapoviruses in two biological lines of tunisian hospital wastewater treatment, Int. J. Environ. Health Res. 29 (4) (2019) 400–413, https://doi.org/10.1080/09603123.2018.1546835.

[42] K.S. Cheung, et al., Gastrointestinal manifestations of SARS-CoV-2 infection and virus load in fecal samples from a Hong Kong cohort: systematic review and meta-analysis, Gastroenterology 159 (1) (2020) 81–95, https://doi.org/10.1053/j.gastro.2020.03.065.

[43] R.M. Atlas, Sanitation and disease - health aspects of excreta and waste-water management, J. Am. Water Resour. Assoc. 20 (5) (1984) 803, https://doi.org/10.1111/j.1752-1688.1984.tb04765.x.

[44] R. Sinclair, et al., Persistence of category a select agents in the environment, Appl. Environ. Microbiol. 74 (3) (2008) 555–563, https://doi.org/10.1128/AEM.02167-07.

[45] W. Zhang, et al., Faecal virome of cats in an animal shelter, J. Gen. Virol. 95 (Pt 11) (2014) 2553–2564, https://doi.org/10.1099/vir.0.069674-0.

[46] A. Carratala, et al., A novel tool for specific detection and quantification of chicken/turkey parvoviruses to trace poultry fecal contamination in the environment, Appl. Environ. Microbiol. 78 (20) (2012) 7496–7499, https://doi.org/10.1128/AEM.01283-12.

[47] GBD, Estimates of the global, regional, and national morbidity, mortality, and aetiologies of diarrhoea in 195 countries: a systematic analysis for the Global Burden of Disease Study 2016, Lancet Infect Dis 18 (11) (2018) 1211–1228, https://doi.org/10.1016/S1473-3099(18)30362-1.

[48] M. Kargar, et al., First molecular detection of group A rotavirus in urban and hospital sewage systems by nested-RT PCR in Shiraz, Iran, J. Environ. Health Sci. 11 (1) (2013) 4, https://doi.org/10.1186/2052-336X-11-4.

[49] O.R.C. Pic, et al., The route of antimicrobial resistance from the hospital effluent to the environment: focus on the occurrence of KPC-producing Aeromonas spp. and Enterobacteriaceae in sewage, Diagn. Microbiol. Infect. Dis. 76 (1) (2013), https://doi.org/10.1016/j.diagmicrobio.2013.02.001.

[50] A. Korajkic, et al., Persistence and decay of fecal microbiota in aquatic habitats, Microbiol. Mol. Biol. Rev. 83 (4) (2019), https://doi.org/10.1128/MMBR.00005-19.

[51] A. Muirhead, et al., Zika virus rna persistence in sewage, Environ. Sci. Technol. Lett. 7 (9) (2020) 659–664, https://doi.org/10.1021/acs.estlett.0c00535.

[52] S. Jia, et al., Biological HRPs in wastewater, in: High-Risk Pollutants in Wastewater, 2020, pp. 41–78, https://doi.org/10.1016/B978-0-12-816448-8.00003-4.

[53] Y. Ye, et al., Reactivity of enveloped virus genome, proteins, and lipids with free chlorine and UV254, Environ. Sci. Technol. 52 (14) (2018) 7698–7708, https://doi.org/10.1021/acs.est.8b00824.

[54] M. Kumar, et al., A chronicle of SARS-CoV-2: seasonality, environmental fate, transport, inactivation, and antiviral drug resistance, J. Hazard. Mater. 405 (2021), 124043, https://doi.org/10.1016/j.jhazmat.2020.124043.

[55] L. Casanova, et al., Survival of surrogate coronaviruses in water, Water Res. 43 (7) (2009) 1893–1898, https://doi.org/10.1016/j.watres.2009.02.002.

[56] B. Haji Ali, et al., Wastewater aerosols produced during flushing toilets, WWTPs, and irrigation with reclaimed municipal wastewater as indirect exposure to SARS-CoV-2, J. Environ. Chem. Eng. 9 (5) (2021) 106201, https://doi.org/10.1016/j.jece.2021.106201.

[57] W. Ahemd, et al., Decay of SARS-CoV-2 and surrogate murine hepatitis virus RNA in untreated wastewater to inform application in wastewater-based epidemiology, Environ. Res. 191 (2020), 110092, https://doi.org/10.1016/j.envres.2020.110092.

[58] X. Wang, et al., Study on the resistance of severe acute respiratory syndrome-associated coronavirus, J. Virol. Methods 126 (1) (2005) 171–177, https://doi.org/10.1016/j.jviromet.2005.02.005.

[59] K. Seo, et al., Effect of temperature, pH, and NaCl on the inactivation kinetics of murine norovirus, J. Food Prot. 75 (3) (2012) 533–540, https://doi.org/10.4315/0362-028X.JFP-11-199.

[60] V. Moresco, et al., Thermal and temporal stability on the enteric viruses infectivity in surface freshwater, Water Sci. Technol. Water Suppl. 16 (3) (2016) 620–627, https://doi.org/10.2166/ws.2015.171.

[61] C. Gantzer, et al., Influence of environmental factors on the survival of enteric viruses in seawater, Oceanol. Acta 21 (6) (1998) 983–992, https://doi.org/10.1016/s0399-1784(99)80020-6.

[62] S. Carroll, et al., Integrated risk framework for onsite wastewater treatment systems, Environ. Manag. 38 (2) (2006) 286–303, https://doi.org/10.1007/s00267-005-0280-5.

[63] S.P. Carroll, et al., Assessment of environmental and public health risk of on-site wastewater treatment systems, in: Site Wastewater Systems, 2004, https://doi.org/10.13031/2013.15796.

[64] K. Tollestrup, et al., Cryptosporidium infection, onsite wastewater systems and private wells in the arid southwest, J. Water Health 12 (1) (2014) 161–172, https://doi.org/10.2166/wh.2013.049.

[65] P. Diplina, et al., A review of the impact of environmental factors on the fate and transport of coronaviruses in aqueous environments, Npj Clean Water 4 (1) (2021) 1–13, https://doi.org/10.1038/s41545-020-00096-w.

[66] M.G. Lusk, et al., A review of the fate and transport of nitrogen, phosphorus, pathogens, and trace organic chemicals in septic systems, Crit. Rev. Environ. Sci. Technol. 47 (7) (2017) 455–541, https://doi.org/10.1080/10643389.2017.1327787.

[67] O. Schmoll, et al., Protecting Groundwater for Health: Managing the Quality of Drinking-water Sources, World Health Organization, 2006, https://doi.org/10.2166/9781780405810.

[68] W.J. Kim, et al., Diurnal fluctuation of indicator microorganisms and intestinal viruses in combined sewer system, Water Sci. Technol. 60 (11) (2009) 2791–2801, https://doi.org/10.2166/wst.2009.732.

[69] F.J. Simmons, et al., Release of infectious human enteric viruses by full-scale wastewater utilities, Water Res. 45 (12) (2011) 3590–3598, https://doi.org/10.1016/j.watres.2011.04.001.

[70] G.J. Medema, et al., Catchment characterisation and source water quality, in: Assessing Microbial Safety of Drinking Water, World Health Organisation, Geneva, Switzerland, 2003, pp. 111–158.

[71] J. Zhou, et al., Source identification of bacterial and viral pathogens and their survival/fading in the process of wastewater treatment, reclamation, and environmental reuse, World J. Microb. Biot. 31 (1) (2015) 109–120, https://doi.org/10.1007/s11274-014-1770-5.

[72] W.J. Lodder, et al., Presence of noroviruses and other enteric viruses in sewage and surface waters in the Netherlands, Appl. Environ. Microbiol. 71 (3) (2005) 1453–1461, https://doi.org/10.1128/AEM.71.3.1453-1461.2005.

[73] D.S. Francy, et al., Comparative effectiveness of membrane bioreactors, conventional secondary treatment, and chlorine and UV disinfection to remove microorganisms from municipal wastewaters, Water Res. 46 (13) (2012) 4164–4178, https://doi.org/10.1016/j.watres.2012.04.044.

[74] J. Nordgren, et al., Prevalence of norovirus and factors influencing virus concentrations during one year in a full-scale wastewater treatment plant, Water Res. 43 (4) (2009) 1117–1125, https://doi.org/10.1016/j.watres.2008.11.053.

[75] K. Charles, et al., in: Buffer Distances for On-site Sewage Systems in Sydney's Drinking Water Catchments 47, 2003, pp. 183–189, https://doi.org/10.2166/wst.2003.0688 (7-8).

[76] C. Press, Septic tank system effects on ground water quality, J. Environ. Qual. 34 (3) (1985) 313, https://doi.org/10.9774/GLEAF.978-1-909493-38-4_2.

[77] D.H. Kuo, et al., Assessment of human adenovirus removal in a full-scale membrane bioreactor treating municipal wastewater, Water Res. 44 (5) (2010) 1520–1530, https://doi.org/10.1016/j.watres.2009.10.039.

[78] P. Le Cann, et al., Quantification of human astroviruses in sewage using real-time RT-PCR, Res. Microbiol. 155 (1) (2004) 11–15, https://doi.org/10.1016/j.resmic.2003.09.013.

[79] M.B. Gotkowitz, et al., Effects of climate and sewer condition on virus transport to groundwater, Environ Sci Technol 50 (16) (2016) 8497–8504, https://doi.org/10.1021/acs.est.6b01422.

[80] N. Amin, et al., Pathogen flows from on-site sanitation systems in low-income urban neighborhoods, Dhaka: a quantitative environmental assessment, Int. J.

Hyg. Environ. Health 230 (2020), 113619, https://doi.org/10.1016/j.ijheh.2020.113619.

[81] K.M. Barrella, et al., Longitudinal study on occurrence of adenoviruses and hepatitis A virus in raw domestic sewage in the city of Limeira, SAo Paulo, Braz. J. Microbiol. 40 (1) (2009) 102–107, https://doi.org/10.1590/S1517-83822009000100017.

[82] K. Inoue, et al., Spatial and temporal profiles of enteric viruses in the coastal waters of Tokyo Bay during and after a series of rainfall events, Sci. Total Environ. 727 (2020), 138502, https://doi.org/10.1016/j.scitotenv.2020.138502.

[83] R.A. Rodríguez, et al., The impact of combined sewage overflows on the viral contamination of receiving waters, Food Environ. Virol. 4 (1) (2012) 34–40, https://doi.org/10.1007/s12560-011-9076-3.

[84] H. Katayama, et al., One-year monthly quantitative survey of noroviruses, enteroviruses, and adenoviruses in wastewater collected from six plants in Japan, Water Res. 42 (6–7) (2008) 1441–1448, https://doi.org/10.1016/j.watres.2007.10.029.

[85] E.C. Pollard, et al., in: The Physics of Viruses 1, Academic Press, 1954, p. 1, https://doi.org/10.1001/jama.1955.02950330094034.

[86] R.C. Valentine, et al., Virus particle adsorption I. Theory of adsorption and experiments on the attachment of particles to non-biological surfaces, Biochim. Biophys. Acta 34 (1) (1959) 10–23, https://doi.org/10.1016/0006-3002(59)90228-8.

[87] P. Payment, S. Fortin, et al., Elimination of human enteric viruses during conventional waste water treatment by activated sludge, Can. J. Microbiol. 32 (12) (1986) 922–925, https://doi.org/10.1139/m86-170.

[88] P. Payment, et al., Removal of indicator bacteria, human enteric viruses, giardia cysts, and cryptosporidium oocysts at a large wastewater primary treatment facility, Can. J. Microbiol. 47 (3) (2001) 188–193, https://doi.org/10.1139/cjm-47-3-188.

[89] L.Y.C. Leong, Removal and inactivation of viruses by treatment processes for potable water and wastewater–a review, Water Sci. Technol. 15 (5) (1983) 91–114, https://doi.org/10.2166/wst.1983.0043.

[90] S. Balboa, et al., The fate of SARS-CoV-2 in wastewater treatment plants points out the sludge line as a suitable spot for incidence monitoring, Sci. Total Environ. 772 (2021), 145268, https://doi.org/10.1016/j.scitotenv.2021.145268.

[91] A.P. Loboda, et al., Lysine-specific post-translational modifications of proteins in the life cycle of viruses, Cell Cycl. 18 (17) (2019) 1995–2005, https://doi.org/10.1080/15384101.2019.1639305.

[92] J.T. Cookson, et al., Adsorption of viruses on activated carbon. Equilibriums and kinetics of the attachment of Escherichia coli bacteriophage T4 on activated carbon, Environ. Sci. Technol. 1 (1) (1967) 46–52, https://doi.org/10.1021/es60001a002.

[93] J.M. Mazurkow, et al., Nano-sized copper (oxide) on alumina granules for water filtration: effect of copper oxidation state on virus removal performance, Environ. Sci. Technol. 54 (2) (2020) 1214–1222, https://doi.org/10.1021/acs.est.9b05211.

[94] M. Pham, E.A. Mintz, et al., Deposition kinetics of bacteriophage MS2 to natural organic matter: role of divalent cations, J. Colloid Interface Sci. 338 (1) (2009) 1–9, https://doi.org/10.1016/j.jcis.2009.06.025.

[95] T.A. Ternes, et al., A rapid method to measure the solid-water distribution coefficient (Kd) for pharmaceuticals and musk fragrances in sewage sludge, Water Res. 38 (19) (2004) 4075–4084, https://doi.org/10.1016/j.watres.2004.07.015.

[96] M.D. Sobsey, et al., Enteric virus survival in algal-bacterial wastewater treatment systems—I: laboratory studies, Water Res. 7 (5) (1973) 669–685, https://doi.org/10.1016/0043-1354(73)90085-7.

[97] M.R. Templeton, et al., Particle-associated viruses in water: impacts on disinfection processes, Crit. Rev. Environ. Sci. Technol. 38 (3) (2008) 137–164, https://doi.org/10.1080/10643380601174764.

[98] T. Kohn, et al., Association with natural organic matter enhances the sunlight-mediated inactivation of MS2 coliphage by singlet oxygen, Environ. Sci. Technol. 41 (13) (2007) 4626–4632, https://doi.org/10.1021/es070295h.

[99] J.F. Schijven, et al., Removal of viruses by soil passage: overview of modeling, processes, and parameters, Crit. Rev. Environ. Sci. Technol. 30 (1) (2000) 49–127, https://doi.org/10.1080/10643380091184174.

[100] R.G. Webster, Principles of virology: molecular biology, pathogenesis, and control, J. Am. Med. Assoc. 285 (7) (2001) 942–943, https://doi.org/10.1001/jama.285.7.942-JBK0221-2-1.

[101] W. Randazzo, et al., SARS-CoV-2 RNA in wastewater anticipated COVID-19 occurrence in a low prevalence area, Water Res. 181 (2020), 115942, https://doi.org/10.1016/j.watres.2020.115942.

[102] N.A. Clarke, et al., Removal of enteric viruses from sewage by activated sludge treatment, Am. J. Public Health Nations Health 51 (8) (1961) 1118–1129, https://doi.org/10.2105/AJPH.51.8.1118.

[103] N. Montazeri, et al., Pathogenic enteric viruses and microbial indicators during secondary treatment of municipal wastewater, Appl. Environ. Microbiol. 81 (18) (2015) 6436–6445, https://doi.org/10.1128/AEM.01218-15.

[104] C.J.A. Campos, et al., Human norovirus in untreated sewage and effluents from primary, secondary and tertiary treatment processes, Water Res. 103 (2016) 224–232, https://doi.org/10.1016/j.watres.2016.07.045.

[105] I. Ouardani, et al., Efficiency of hepatitis a virus removal in six sewage treatment plants from Central Tunisia, Appl Microbiol Biot 99 (24) (2015) 10759–10769, https://doi.org/10.1007/s00253-015-6902-9.

[106] M.E. Verbyla, et al., A review of virus removal in wastewater treatment pond systems, Water Res. 71 (mar.15) (2015) 107–124, https://doi.org/10.1016/j.watres.2014.12.031.

[107] J. Wu, et al., Indigenous somatic coliphage removal from a real municipal wastewater by a submerged membrane bioreactor, Water Res. 44 (6) (2010) 1853–1862, https://doi.org/10.1016/j.watres.2009.12.013.

[108] J.P.S. Sidhu, et al., Comparative enteric viruses and coliphage removal during wastewater treatment processes in a sub-tropical environment, Sci. Total Environ. 616–617 (2018) 669–677, https://doi.org/10.1016/j.scitotenv.2017.10.265.

[109] X. Kang, et al., Current state and challenges of full-scale membrane bioreactor applications: a critical review, Bioresour. Technol. 271 (2018) 473–481, https://doi.org/10.1016/j.biortech.2018.09.061.

[110] Y. Zhu, et al., Virus removal by membrane bioreactors: a review of mechanism investigation and modeling efforts, Water Res. 188 (2021), 116522, https://doi.org/10.1016/j.watres.2020.116522.

[111] T. Ueda, et al., Fate of indigenous bacteriophage in a membrane bioreactor, Water Res. 34 (7) (2000) 2151–2159, https://doi.org/10.1016/S0043-1354(99)00382-6.

[112] Nguyen, Biofouling of water treatment membranes: a review of the underlying causes, monitoring techniques and control measures, Membranes 2 (4) (2012) 804–840, https://doi.org/10.3390/membranes2040804.

[113] A. Mb, et al., Advanced control of membrane fouling in filtration systems using artificial intelligence and machine learning techniques: a critical review, Process Saf. Environ. Prot. 123 (2019) 229–252, https://doi.org/10.1016/j.psep.2019.01.013.

[114] Q.L. Liu, et al., Application of MBR for hospital wastewater treatment in China, Desalination 250 (2) (2010) 605–608, https://doi.org/10.1016/j.desal.2009.09.033.

[115] H. Huang, et al., Mechanisms of virus removal from secondary wastewater effluent by low pressure membrane filtration, J. Membr. Sci. 409 (2012) 1–8, https://doi.org/10.1016/j.memsci.2011.12.050.

[116] R.M. Chaudhry, et al., Impact of virus surface characteristics on removal mechanisms within membrane bioreactors, Water Res. 84 (2015) 144–152, https://doi.org/10.1016/j.watres.2015.07.020.

[117] T. Miura, et al., Removal properties of human enteric viruses in a pilot-scale membrane bioreactor (MBR) process, Water Res. 75 (2015) 282–291, https://doi.org/10.1016/j.watres.2015.02.046.

[118] Y. Ye, et al., Survivability, partitioning, and recovery of enveloped viruses in untreated municipal wastewater, Environ. Sci. Technol. 50 (10) (2016) 5077–5085, https://doi.org/10.1021/acs.est.6b00876.

[119] P.M. Gundy, et al., Pepper, survival of coronaviruses in water and wastewater, Food Environ. Virol. 1 (1) (2008) 10–14, https://doi.org/10.1007/s12560-008-9001-6.

[120] R.M. Chaudhry, et al., Mechanisms of pathogenic virus removal in a full-scale membrane bioreactor, Environ. Sci. Technol. 49 (5) (2015) 2815–2822, https://doi.org/10.1021/es505332n.

[121] H. Wang, et al., Differential removal of human pathogenic viruses from sewage by conventional and ozone treatments, Int. J. Hyg. Environ. Health 221 (3) (2018) 479–488, https://doi.org/10.1016/j.ijheh.2018.01.012.

[122] F.J. Simmons, et al., Removal of human enteric viruses by a full-scale membrane bioreactor during municipal wastewater processing, Water Res. 45 (9) (2011) 2739–2750, https://doi.org/10.1016/j.watres.2011.02.001.

[123] W. Morsy El-Senousy, et al., Removal of astrovirus from water and sewage treatment plants, evaluated by a competitive reverse transcription-PCR, Appl. Environ. Microb. 73 (1) (2007) 164–167, https://doi.org/10.1128/AEM.01748-06.

[124] Z. Wu, et al., Comparative fate of CrAssphage with culturable and molecular fecal pollution indicators during activated sludge wastewater treatment, Environ. Int. 136 (2020), 105452, https://doi.org/10.1016/j.envint.2019.105452.

[125] F. El-Gohary, et al., Membrane bioreactor technology for wastewater reclamation, Egypt J. Chem. 61 (5) (2018) 883–896, https://doi.org/10.21608/ejchem.2018.4128.1361.

[126] T. Miura, et al., Virus type-specific removal in a full-scale membrane bioreactor treatment process, Food Environ. Virol. 10 (2) (2018) 176–186, https://doi.org/10.1007/s12560-017-9330-4.

[127] W.M. El-Senousy, et al., Prevalence of rotaviruses groups a and C in egyptian children and aquatic environment, Food Environ. Virol. 7 (2) (2015) 132–141, https://doi.org/10.1007/s12560-015-9184-6.

[128] H. Abu Ali, et al., Tracking SARS-CoV-2 RNA through the wastewater treatment process, ACS ES&T Water 1 (5) (2021) 1161–1167, https://doi.org/10.1021/acsestwater.0c00216.

[129] T. Prado, et al., Performance of wastewater reclamation systems in enteric virus removal, Sci. Total Environ. 678 (2019) 33–42, https://doi.org/10.1016/j.scitotenv.2019.04.435.

[130] C.M. Zhang, et al., Elimination of viruses from domestic wastewater: requirements and technologies, World J. Microb. Biot. 32 (4) (2016) 69, https://doi.org/10.1007/s11274-016-2018-3.

[131] A.K. Thakur, et al., Secondary transmission of SARS-CoV-2 through wastewater: concerns and tactics for treatment to effectively control the pandemic, J. Environ. Manag. 290 (2021), 112668, https://doi.org/10.1016/j.jenvman.2021.112668.

[132] N. Shirasaki, et al., Effects of reversible and irreversible membrane fouling on virus removal by a coagulation-microfiltration system, J. Water Supply Res. Technol. 57 (7) (2008) 501–506, https://doi.org/10.2166/aqua.2008.048.

[133] E. Arkhangelsky, et al., Impact of chemical cleaning on properties and functioning of polyethersulfone membranes, J. Membr. Sci. 305 (1) (2007) 176–184, https://doi.org/10.1016/j.memsci.2007.08.007.

[134] A. Antony, et al., Removal efficiency and integrity monitoring techniques for virus removal by membrane processes, Crit. Rev. Environ. Sci. Technol. 42 (9) (2012) 891–933, https://doi.org/10.1080/10643389.2011.556539.

[135] N. Yasui, et al., Removal characteristics and fluctuation of norovirus in a pilot-plant by an ultrafiltration membrane for the reclamation of treated sewage, Environ. Technol. 37 (21–24) (2016) 1, https://doi.org/10.1080/09593330.2016.1164760.

[136] Y. Qiu, et al., Assessment of human virus removal during municipal wastewater treatment in Edmonton, Canada, J. Appl. Microbiol. 119 (6) (2016) 1729–1739, https://doi.org/10.1111/jam.12971.

[137] N. Boudaud, et al., Removal of MS2, Qβ and GA bacteriophages during drinking water treatment at pilot scale, Water Res. 46 (8) (2012) 2651–2664, https://doi.org/10.1016/j.watres.2012.02.020.

[138] O. Ferrer, et al., Direct ultrafiltration performance and membrane integrity monitoring by microbiological analysis, Water Res. 83 (2015) 121–131, https://doi.org/10.1016/j.watres.2015.06.039.

[139] S. Lee, et al., Improvement of virus removal by pilot-scale coagulation-ultrafiltration process for wastewater reclamation: effect of optimization of pH in secondary effluent, Water Res. 114 (2017) 23–30, https://doi.org/10.1016/j.watres.2017.02.017.

[140] L.C. Campos, et al., Biomass development in slow sand filters, Water Res. 36 (18) (2002) 4543–4551, https://doi.org/10.1016/S0043-1354(02)00167-7.

[141] M.A. Elliott, et al., Virus attenuation by microbial mechanisms during the idle time of a household slow sand filter, Water Res. 45 (14) (2011) 4092–4102, https://doi.org/10.1016/j.watres.2011.05.008.

[142] T.T. Eighmy, et al., Microbial populations, activities and carbon metabolism in slow sand filters, Water Res. 26 (10) (1992) 1319–1328, https://doi.org/10.1016/0043-1354(92)90126-O.

[143] M.T. Yahya, et al., Virus removal by slow sand filtration and nanofiltration, Water Sci. Technol. 27 (3–4) (1993) 445–448, https://doi.org/10.2166/wst.1993.0389.

[144] J.F. Schijven, et al., A mathematical model for removal of human pathogenic viruses and bacteria by slow sand filtration under variable operational conditions, Water Res. 47 (7) (2013) 2592–2602, https://doi.org/10.1016/j.watres.2014.07.033.

[145] A. Torrens, et al., Removal of bacterial and viral indicators in vertical flow constructed wetlands and intermittent sand filters, Desalination 246 (1–3) (2009) 169–178, https://doi.org/10.1016/j.desal.2008.03.050.

[146] W.B. Anderson, et al., Influence of design and operating conditions on the removal of MS2 bacteriophage by pilot-scale multistage slow sand filtration, J. Water Suppl. Res. Technol. 58 (7) (2009) 450, https://doi.org/10.2166/aqua.2009.140.

[147] K.R. Pfannes, et al., Selective elimination of bacterial faecal indicators in the Schmutzdecke of slow sand filtration columns, Appl. Microbiol. Biot. 99 (23) (2015) 10323–10332, https://doi.org/10.1007/s00253-015-6882-9.

[148] K.R. Wigginton, et al., Virus inactivation mechanisms: impact of disinfectants on virus function and structural integrity, Environ. Sci. Technol. 46 (21) (2012) 12069–12078, https://doi.org/10.1021/es3029473.

[149] L. Chen, et al., Comparison study on hospital wastewater disinfection technology, Adv. Mater. Res. 884–885 (2014) 41–45, https://doi.org/10.4028/www.scientific.net/AMR.884-885.41.

[150] A.R. Petrinca, et al., Presence and environmental circulation of enteric viruses in three different wastewater treatment plants, J. Appl. Microbiol. 106 (5) (2009) 1608–1617, https://doi.org/10.1111/j.1365-2672.2008.04128.x.

[151] W.A.M. Hijnen, et al., Inactivation credit of UV radiation for viruses, bacteria and protozoan (oo)cysts in water: a review, Water Res. 40 (1) (2006) 3–22, https://doi.org/10.1016/j.watres.2005.10.030.

[152] C.S. Heilingloh, et al., Susceptibility of SARS-CoV-2 to UV irradiation, Am. J. Infect. Control 48 (10) (2020) 1273–1275, https://doi.org/10.1016/j.ajic.2020.07.031.

[153] M.R. Templeton, et al., Inactivation of particle-associated viral surrogates by ultraviolet light, Water Res. 39 (15) (2005) 3487–3500, https://doi.org/10.1016/j.watres.2005.06.010.

[154] M. Jekel, Chemistry of ozone in water and wastewater treatment - from basic principles to applications, Gwf 154 (5) (2013) 589, https://doi.org/10.2166/9781780400839.

[155] S.C. Von, Free-radical-induced DNA Damage and Its Repair, Springer, Berlin Heidelberg, 2006, https://doi.org/10.1007/3-540-30592-0.

[156] S.A. Tyrrell, et al., Inactivation of bacterial and viral indicators in secondary sewage effluents, using chlorine and ozone, Water Res. 29 (11) (1995) 2483–2490, https://doi.org/10.1016/0043-1354(95)00103-R.

[157] C. Wolf, et al., Kinetics of inactivation of waterborne enteric viruses by ozone, Environ Sci Technol 52 (4) (2018) 2170–2177, https://doi.org/10.1021/acs.est.7b05111.

[158] X. Xia, et al., A review study on sulfate-radical-based advanced oxidation processes for domestic/industrial wastewater treatment: degradation, efficiency, and mechanism, Front Chem 8 (2020), https://doi.org/10.3389/fchem.2020.592056.

[159] M. Jin, et al., Chlorine dioxide inactivation of enterovirus 71 in water and its impact on genomic targets, Environ Sci Technol 47 (9) (2013) 4590–4597, https://doi.org/10.1021/es305282g.

[160] M. Jin, et al., The 40–80 nt region in the 5'-NCR of genome is a critical target for inactivating poliovirus by chlorine dioxide, J. Med. Virol. 84 (3) (2012) 526–535, https://doi.org/10.1002/jmv.23221.

[161] B. Xue, et al., Effects of chlorine and chlorine dioxide on human rotavirus infectivity and genome stability, Water Res. 47 (10) (2013) 3329–3338, https://doi.org/10.1016/j.watres.2013.03.025.

[162] T.L. Cromeans, et al., Inactivation of adenoviruses, enteroviruses, and murine norovirus in water by free chlorine and monochloramine, Appl. Environ. Microbiol. 76 (4) (2010) 1028–1033, https://doi.org/10.1128/AEM.01342-09.

[163] Y.S. Chen, et al., Inactivation of human and simian rotaviruses by chlorine dioxide, Appl. Environ. Microbiol. 56 (5) (1990) 1363–1366, https://doi.org/10.1128/AEM.56.5.1363-1366.1990.

[164] J. Simonet, et al., Degradation of the poliovirus 1 genome by chlorine dioxide, J. Appl. Microbiol. 100 (4) (2006) 862–870, https://doi.org/10.1111/j.1365-2672.2005.02850.x.

[165] J.A. Thurston-Enriquez, et al., Inactivation of enteric adenovirus and feline calicivirus by ozone, Water Res. 39 (15) (2005) 3650–3656, https://doi.org/10.1016/j.watres.2005.06.006.

[166] H. Abu Ali, et al., Tracking SARS-CoV-2 RNA through the wastewater treatment process, ACS ES&T Water 1 (5) (2021) 1161–1167, https://doi.org/10.1021/acsestwater.0c00216.

[167] S. Nuanualsuwan, et al., Ultraviolet inactivation of feline calicivirus, human enteric viruses and coliphages, Photochem. Photobiol. 76 (4) (2002) 406, https://doi.org/10.1562/0031-8655(2002)0760406UIOFCH2.0.CO2.

[168] D. Schoenen, Role of disinfection in suppressing the spread of pathogens with drinking water: possibilities and limitations, Water Res. 36 (15) (2002) 3874–3888, https://doi.org/10.1016/S0043-1354(02)00076-3.

[169] A. Carducci, et al., Viral removal by wastewater treatment: monitoring of indicators and pathogens, Food Environ Virol 1 (2) (2009) 85–91, https://doi.org/10.1007/s12560-009-9013-x.

[170] M. Moazeni, et al., Estimation of health risks caused by exposure to enteroviruses from agricultural application of wastewater effluents, Water Res. 125 (2017) 104–113, https://doi.org/10.1016/j.watres.2017.08.028.

[171] S.W. Hasan, et al., Detection and quantification of SARS-CoV-2 RNA in wastewater and treated effluents: surveillance of COVID-19 epidemic in the United Arab Emirates, Sci. Total Environ. 764 (2021), 142929, https://doi.org/10.1016/j.scitotenv.2020.142929.

[172] M. Kitajima, et al., Relative abundance and treatment reduction of viruses during wastewater treatment processes–identification of potential viral indicators, Sci. Total Environ. 488–489 (2014) 290–296, https://doi.org/10.1016/j.scitotenv.2014.04.087.

[173] T.M. Fumian, et al., Detection of norovirus epidemic genotypes in raw sewage using next generation sequencing, Environ. Int. 123 (2019) 282–291, https://doi.org/10.1016/j.envint.2018.11.054.

[174] S.P. Sherchan, et al., First detection of SARS-CoV-2 RNA in wastewater in North America: a study in Louisiana, USA, Sci. Total Environ. 743 (2020), 140621, https://doi.org/10.1016/j.scitotenv.2020.140621.

[175] M. Kitajima, et al., Temporal variations in genotype distribution of human sapoviruses and Aichi virus 1 in wastewater in Southern Arizona United States, J. Appl. Microbiol. 124 (5) (2018) 1324–1332, https://doi.org/10.1111/jam.13712.

[176] Y. Qiu, et al., UV inactivation of human infectious viruses at two full-scale wastewater treatment plants in Canada, Water Res. 147 (2018) 73–81, https://doi.org/10.1016/j.watres.2018.09.057.

[177] B. Prevost, et al., Deciphering the diversities of astroviruses and noroviruses in wastewater treatment plant effluents by a high-throughput sequencing method, Appl. Environ. Microb. 81 (20) (2015) 7215–7222, https://doi.org/10.1128/AEM.02076-15.

[178] S. Beyer, et al., Detection and characterization of hepatitis E virus genotype 3 in wastewater and urban surface waters in Germany, Food Environ Virol 12 (2) (2020) 137–147, https://doi.org/10.1007/s12560-020-09424-2.

[179] O. Dienus, et al., Norovirus dynamics in wastewater discharges and in the recipient drinking water source: long-term monitoring and hydrodynamic modeling, Environ Sci Technol 50 (20) (2016) 10851–10858, https://doi.org/10.1021/acs.est.6b02110.

[180] E. Gonzales-Gustavson, et al., Quantitative risk assessment of norovirus and adenovirus for the use of reclaimed water to irrigate lettuce in Catalonia, Water Res. 153 (2019) 91–99, https://doi.org/10.1016/j.watres.2018.12.070.

[181] H. Wang, et al., Variations among viruses in influent water and effluent water at a wastewater plant over one year as assessed by quantitative PCR and metagenomics, Appl. Environ. Microb. 86 (24) (2020), https://doi.org/10.1128/AEM.02073-20.

[182] E. Haramoto, et al., First environmental surveillance for the presence of SARS-CoV-2 RNA in wastewater and river water in Japan, Sci. Total Environ. 737 (2020), 140405, https://doi.org/10.1016/j.scitotenv.2020.140405.

[183] T.G. Aw, et al., Environmental surveillance and molecular characterization of human enteric viruses in tropical urban wastewaters, J. Appl. Microbiol. 109 (2) (2010) 716–730, https://doi.org/10.1111/j.1365-2672.2010.04701.x.

[184] E. Haramoto, et al., Seasonal profiles of human noroviruses and indicator bacteria in a wastewater treatment plant in Tokyo, Japan, Water Sci Technol 54 (11-12) (2006) 301–308, https://doi.org/10.2166/wst.2006.888.

[185] E. Haramoto, et al., Quantification and genotyping of torque Teno virus at a wastewater treatment plant in Japan, Appl. Environ. Microbiol. 74 (23) (2008) 7434–7436, https://doi.org/10.1128/AEM.01605-08.

[186] A. Hata, et al., Wastewater analysis indicates that genetically diverse astroviruses, including strains belonging to novel clades MLB and VA, are circulating within japanese populations, Appl. Environ. Microbiol. 81 (15) (2015) 4932–4939, https://doi.org/10.1128/AEM.00563-15.

[187] X.Q. He, et al., One-year monthly survey of rotavirus, astrovirus and norovirus in three sewage treatment plants (STPs) in Beijing, China and associated health risk assessment, Water Sci. Technol. 64 (6) (2011) 1202–1210, https://doi.org/10.2166/wst.2011.080.

[188] M. Kitajima, et al., Detection of genogroup IV norovirus in wastewater and river water in Japan, Lett. Appl. Microbiol. 49 (5) (2009) 655–658, https://doi.org/10.1111/j.1472-765X.2009.02718.x.

[189] M. Kitajima, et al., Development of a reverse transcription-quantitative PCR system for detection and genotyping of Aichi viruses in clinical and environmental samples, Appl. Environ. Microbiol. 79 (13) (2013) 3952–3958, https://doi.org/10.1128/AEM.00820-13.

[190] S.R. Vaidya, et al., Polymerase chain reaction-based prevalence of hepatitis a, hepatitis E and TT viruses in sewage from an endemic area, J. Hepatol. 37 (1) (2002) 131–136, https://doi.org/10.1016/s0168-8278(02)00106-x.

[191] M.A. Adefisoye, et al., Quantitative PCR detection and characterisation of human adenovirus, rotavirus and hepatitis A virus in discharged effluents of two wastewater treatment facilities in the Eastern Cape, South Africa, Food Environ Virol 8 (4) (2016) 262–274, https://doi.org/10.1007/s12560-016-9246-4.

[192] E.M. Elmandy, et al., Molecular detection of human adenovirus in urban wastewater in Egypt and among children suffering from acute gastroenteritis, J. Water Health 17 (1–2) (2019) 287–294, https://doi.org/10.2166/wh.2019.303.

[193] W.M. El-Senousy, et al., Coxsackievirus B4 as a causative agent of diabetes mellitus type 1: is there a role of inefficiently treated drinking water and sewage in virus spreading? Food Environ. Virol. 10 (1) (2017) 89–98, https://doi.org/10.1007/s12560-017-9322-4.

[194] I. Ouardani, et al., Detection and molecular characterization of hepatitis a virus from tunisian wastewater treatment plants with different secondary treatments, Appl. Environ. Microbiol. 82 (13) (2016) 3834–3845, https://doi.org/10.1128/AEM.00619-16.

[195] M.N.F. Shaheen, et al., Environmental monitoring of astrovirus and norovirus in the Rosetta branch of the River Nile and the El-Rahawy drain, Egypt, Water Supply 19 (5) (2019) 1381–1387, https://doi.org/10.2166/ws.2019.004.

[196] J.C. Chang, et al., UV inactivation of pathogenic and indicator microorganisms, Appl. Environ. Microbiol. 49 (6) (1985) 1361–1365, https://doi.org/10.1128/AEM.49.6.1361-1365.1985.

[197] G.A. Shin, et al., Reduction of Norwalk virus, poliovirus 1, and bacteriophage MS2 by ozone disinfection of water, Appl. Environ. Microbiol. 69 (7) (2003) 3975–3978, https://doi.org/10.1128/AEM.69.7.3975-3978.2003.

[198] G.R. Taylor, et al., A comparison of the virucidal properties of chlorine, chlorine dioxide, bromine chloride and iodine, J. Hyg. 89 (2) (1982) 321–328, https://doi.org/10.1017/S0022172400070856.

[199] Q.S. Meng, et al., Comparative inactivation of enteric adenoviruses, poliovirus and coliphages by ultraviolet irradiation, Water Res. 30 (11) (1996) 2665–2668, https://doi.org/10.1016/S0043-1354(96)00179-0.

[200] J.A. Thurston-Enriquez, et al., Inactivation of enteric adenovirus and feline calicivirus by chlorine dioxide, Appl. Environ. Microbiol. 71 (6) (2005) 3100–3105, https://doi.org/10.1128/AEM.71.6.3100-3105.2005.

[201] G.A. Shin, et al., Enhanced effectiveness of medium-pressure ultraviolet lamps on human adenovirus 2 and its possible mechanism, Water Sci. Technol. 60 (4) (2009) 851–857, https://doi.org/10.2166/wst.2009.414.

[202] C. Sigmon, et al., Establishing surrogate–virus relationships for ozone disinfection of wastewater, Environ. Eng. Sci. 32 (6) (2015) 451–460, https://doi.org/10.1089/ees.2014.0496.

[203] T. Sanekata, et al., Evaluation of the antiviral activity of chlorine dioxide and sodium hypochlorite against feline calicivirus, human influenza virus, measles virus, canine distemper virus, human herpesvirus, human adenovirus, canine adenovirus and canine parvovirus, Biocontrol Sci 15 (2) (2010) 45–49, https://doi.org/10.4265/bio.15.45.

[204] D.A. Battigelli, et al., The inactivation of hepatitis a virus and other model viruses by UV irradiation, Water Sci. Technol. 27 (3–4) (1993) 339–342, https://doi.org/10.2166/wst.1993.0371.

[205] J.M. Vaughn, et al., Inactivation of human and simian rotaviruses by ozone, Appl. Environ. Microbiol. 53 (9) (1987) 2218–2221, https://doi.org/10.1128/AEM.53.9.2218-2221.1987.

[206] D. Berman, et al., Inactivation of simian rotavirus SA11 by chlorine, chlorine dioxide, and monochloramine, Appl. Environ. Microbiol. 48 (2) (1984) 317–323, https://doi.org/10.1128/AEM.48.2.317-323.1984.

[207] J.A. Thurston-Enriquez, et al., Inactivation of feline calicivirus and adenovirus type 40 by UV radiation, Appl. Environ. Microbiol. 69 (1) (2003) 577–582, https://doi.org/10.1128/AEM.69.1.577-582.2003.

[208] R. Zoni, et al., Investigation on virucidal activity of chlorine dioxide. experimental data on feline calicivirus, HAV and Coxsackie B5, J. Prev. Med. Hyg. 48 (3) (2007) 91, https://doi.org/10.15167/2421-4248/jpmh2007.48.3.99.

[209] J.M. Vaughn, et al., Effects of ozone treatment on the infectivity of hepatitis a virus, Can. J. Microbiol. 36 (8) (1990) 557–560, https://doi.org/10.1139/m90-097.

[210] H. Inagaki, et al., Rapid inactivation of SARS-CoV-2 with deep-UV LED irradiation, Emerg Microbes Infect 9 (1) (2020) 1744–1747, https://doi.org/10.1080/22221751.2020.1796529.

[211] C.S. Heilingloh, et al., Susceptibility of SARS-CoV-2 to UV irradiation, Am. J. Infect. Control 48 (10) (2020) 1273–1275, https://doi.org/10.1016/j.ajic.2020.07.031.

[212] L. Rizzo, et al., Best available technologies and treatment trains to address current challenges in urban wastewater reuse for irrigation of crops in EU countries, Sci. Total Environ. 710 (2020), 136312, https://doi.org/10.1016/j.scitotenv.2019.136312.

[213] S.Y. Jasim, et al., Reuse of treated sewage effluent (TSE) in Qatar, J. Water Process Eng. 11 (2016) 174–182, https://doi.org/10.1016/j.jwpe.2016.05.003.

[214] M. Xu, et al., A research on application of water treatment technology for reclaimed water irrigation, Int. J. Hydrog. Energy 41 (35) (2016) 15930–15937, https://doi.org/10.1016/j.ijhydene.2016.05.020.

[215] W. Suwaileh, et al., Membrane desalination and water re-use for agriculture: state of the art and future outlook, Desalination 491 (2020), 114559, https://doi.org/10.1016/j.desal.2020.114559.

[216] Y. Zhang, et al., Treatment of reused comprehensive wastewater in iron and steel industry with electrosorption technology, J. Iron Steel Res. Int. 18 (6) (2011) 37–42, https://doi.org/10.1016/S1006-706X(11)60075-7.

[217] J. Shi, et al., Review on treatment technology of salt wastewater in coal chemical industry of China, Desalination 493 (2020), 114640, https://doi.org/10.1016/j.desal.2020.114640.

[218] V. Moresco, et al., Microbiological and physicochemical analysis of the coastal waters of southern Brazil, Mar. Pollut. Bull. 64 (1) (2012) 40–48, https://doi.org/10.1016/j.marpolbul.2011.10.026.

[219] L. Kaas, et al., A 1-year study on the detection of human enteric viruses in New Caledonia, Food Environ. Virol. 8 (1) (2015) 46–56, https://doi.org/10.1007/s12560-015-9224-2.

[220] J. Dias, et al., Detection and quantification of human adenovirus (HAdV), JC polyomavirus (JCPyV) and hepatitis A virus (HAV) in recreational waters of Niteroi, Rio de Janeiro, Brazil, Mar. Pollut. Bull. 133 (2018) 240–245, https://doi.org/10.1016/j.marpolbul.2018.05.031.

[221] J.Y. Hu, et al., in: Removal of MS2 Bacteriophage Using Membrane Technologies 47, 2003, pp. 163–168, https://doi.org/10.1016/S0043-1354(02)00272-5 (12).

[222] F.T.D. Nascimento, et al., Efficacy of a solar still in destroying virus and indicator bacteria in water for human consumption, Rev. Ambiente Água 13 (4) (2018) 1–12, https://doi.org/10.4136/ambi-agua.2084, 223p.

[223] O. Bait, Direct and indirect solar–powered desalination processes loaded with nanoparticles: a review, Sustain. Energy Technol. Assess. 37 (2020), 100597, https://doi.org/10.1016/j.seta.2019.100597.

[224] S. Balboa, et al., The fate of SARS-COV-2 in WWTPS points out the sludge line as a suitable spot for detection of COVID-19, Sci. Total Environ. 772 (2021), 145268, https://doi.org/10.1016/j.scitotenv.2021.145268.

[225] Z. Paluszak, et al., Survival rate of suid herpesvirus (SuHV-1, Aujeszky's disease virus, ADV) in composted sewage sludge, Pol. J. Vet. Sci. 15 (1) (2012), https://doi.org/10.2478/v10181-011-0113-9.

[226] M.R. Goddard, et al., Recovery of indigenous enteroviruses from raw and digested sewage sludges, Appl. Environ. Microbiol. 42 (6) (1981) 1023–1028, https://doi.org/10.1128/AEM.42.6.1023-1028.1981.

[227] A. Serra-Compte, et al., Elimination of SARS-CoV-2 along wastewater and sludge treatment processes, Water Res. 202 (2021), 117435, https://doi.org/10.1016/j.watres.2021.117435.

[228] D.A. Brashear, et al., Inactivation of indigenous viruses in raw sludge by air drying, Appl. Environ. Microbiol. 45 (6) (1983) 1943–1945, https://doi.org/10.1128/AEM.45.6.1943-1945.1983.

[229] T. Mondal, et al., Factors affecting decay of salmonella Birkenhead and coliphage MS2 during mesophilic anaerobic digestion and air drying of sewage sludge, J. Water Health 13 (2) (2015) 459, https://doi.org/10.2166/wh.2014.313.

[230] T.M. Straub, I.L. Pepper, et al., Hazards from pathogenic microorganisms in land-disposed sewage sludge, Rev. Environ. Contam. Toxicol. 132 (1993) 55–91.

[231] K. Wong, B.M. Onan, et al., Quantification of enteric viruses, pathogen indicators, and salmonella bacteria in class B anaerobically digested biosolids by culture and molecular methods, Appl. Environ. Microbiol. 76 (19) (2010) 6441–6448, https://doi.org/10.1128/AEM.02685-09.

[232] T. Prado, A. Gaspar, et al., Detection of enteric viruses in activated sludge by feasible concentration methods, Braz. J. Microbiol. 45 (1) (2014) 343–349, https://doi.org/10.1590/S1517-83822014000100049.

[233] A.D. Schlindwein, et al., Detection of enteric viruses in sewage sludge and treated wastewater effluent, Water Sci. Technol. 61 (2) (2010) 537–544, https://doi.org/10.2166/wst.2010.845.

[234] S. Monpoeho, et al., Quantification of enterovirus RNA in sludge samples using single tube real-time RT-PCR, Biotechniques 29 (1) (2000) 88–93, https://doi.org/10.2144/00291st03.

[235] K. Bibby, et al., Identification of viral pathogen diversity in sewage sludge by metagenome analysis, Environ. Sci. Technol. 47 (4) (2013) 1945–1951, https://doi.org/10.1021/es305181x.

[236] A. Serra-Compte, et al., Elimination of SARS-CoV-2 along wastewater and sludge treatment processes, Water Res. 202 (2021), 117435, https://doi.org/10.1016/j.watres.2021.117435.

[237] B.A. Kocamemi, et al., SARS-CoV-2 Detection in Istanbul Wastewater Treatment Plant Sludges, 2020, https://doi.org/10.1101/2020.05.12.20099358.

[238] M. Elsamadony, et al., Possible transmission of viruses from contaminated human feces and sewage: implications for SARS-CoV-2, Sci. Total Environ. 755 (2021), 142575, https://doi.org/10.1016/j.scitotenv.2020.142575.

[239] I.T. Yu, et al., Evidence of airborne transmission of the severe acute respiratory syndrome virus, N. Engl. J. Med. 350 (17) (2004) 1731–1739, https://doi.org/10.1056/NEJMoa032867.

[240] Y. Chen, et al., The presence of SARS-CoV-2 RNA in the feces of COVID-19 patients, J. Med. Virol. 92 (7) (2020) 833–840, https://doi.org/10.1002/jmv.25825.

[241] W. Lodder, et al., SARS-CoV-2 in wastewater: potential health risk, but also data source, Lancet Gastroenterol. Hepatol. 5 (6) (2020) 533, https://doi.org/10.1016/S2468-1253(20)30087-X.

[242] D.M. Berendes, et al., Safely managed sanitation for all means fecal sludge management for at least 1.8 billion people in low and middle income countries, Environ. Sci. Technol. 51 (5) (2017) 3074–3083, https://doi.org/10.1021/acs.est.6b06019.

[243] S. Fathi, et al., Assessment of microbial aerosol emissions in an urban wastewater treatment plant operated with activated sludge process, Aerobiologia 33 (4) (2017) 1–9, https://doi.org/10.1007/s10453-017-9486-2.

[244] E.S. Amirian, Potential fecal transmission of SARS-CoV-2: current evidence and implications for public health, Int. J. Infect. Dis. 95 (2020) 363–370, https://doi.org/10.1016/j.ijid.2020.04.057.

[245] K.R. Wigginton, Y. Ye, et al., Emerging investigators series: the source and fate of pandemic viruses in the urban water cycle, Environ. Sci. Water Res. Technol. 1 (6) (2015) 735–746, https://doi.org/10.1039/c5ew00125k.

[246] H. Heinonen-Tanski, et al., Airborne enteric coliphages and bacteria in sewage treatment plants, Water Res. 43 (9) (2009) 2558–2566, https://doi.org/10.1016/j.watres.2009.03.006.

[247] P. Piqueras, et al., Real-time ultrafine aerosol measurements from wastewater treatment facilities, Environ. Sci. Technol. 50 (20) (2016) 11137–11144, https://doi.org/10.1021/acs.est.6b05469.

[248] M. Titcombe Lee, et al., Partitioning of viruses in wastewater systems and potential for aerosolization, Environ. Sci. Technol. 3 (5) (2016) 210–215, https://doi.org/10.1021/acs.estlett.6b00105.

[249] L.M. Li, et al., Distribution characterization of microbial aerosols emitted from a wastewater treatment plant using the Orbal oxidation ditch process, Process Biochem. 46 (4) (2011) 910–915, https://doi.org/10.1016/j.procbio.2010.12.016.

[250] M.A. Sanchez-Monedero, et al., Effect of the aeration system on the levels of airborne microorganisms generated at wastewater treatment plants, Water Res. 42 (14) (2008) 3739–3744, https://doi.org/10.1016/j.watres.2008.06.028.

[251] S. Gholipour, et al., COVID-19 infection risk from exposure to aerosols of wastewater treatment plants, Chemosphere 273 (2021), 129701, https://doi.org/10.1016/j.chemosphere.2021.129701.

[252] E. Brisebois, et al., Human viral pathogens are pervasive in wastewater treatment center aerosols, J. Environ. Sci. 67 (2018) 45–53.

[253] K. Lin, et al., Aerosolization of ebola virus surrogates in wastewater systems, Environ Sci Technol 51 (5) (2017) 2669–2675, https://doi.org/10.1021/acs.est.6b04846.

[254] F.G. Masclaux, et al., Assessment of airborne virus contamination in wastewater treatment plants, Environ. Res. 133 (2014) 260–265, https://doi.org/10.1016/j.envres.2014.06.002.

[255] K. Uhrbrand, et al., Exposure to airborne noroviruses and other bioaerosol components at a wastewater treatment plant in Denmark, Food Environ. Virol. 3 (3) (2011) 130–137, https://doi.org/10.1007/s12560-011-9068-3.

[256] S. Zhu, et al., Survival of human norovirus surrogates in water upon exposure to thermal and non-thermal antiviral treatments, Viruses 12 (4) (2020), https://doi.org/10.3390/v12040461.

[257] R.M. Callejón, et al., Reported foodborne outbreaks due to fresh produce in the United States and European Union: trends and causes, Foodborne Pathog. Dis. 12 (1) (2015) 32–38, https://doi.org/10.1089/fpd.2014.1821.

[258] P.K. Singh, P.B. Deshbhratar, D.S. Ramteke, Effects of sewage wastewater irrigation on soil properties, crop yield and environment, Agric. Water Manag. 103 (2012) 100–104, https://doi.org/10.1016/j.agwat.2011.10.022.

[259] L.G. Brown, et al., Outbreak characteristics associated with identification of contributing factors to foodborne illness outbreaks, Epidemiol. Infect. 145 (11) (2017) 2254–2262, https://doi.org/10.1017/S0950268817001406.

[260] J. Pearce-Walker, et al., Managing leafy green safety from adenoviruses and enteroviruses in irrigation water, Agric. Water Manag. 240 (2020), 106272, https://doi.org/10.1016/j.agwat.2020.106272.

[261] T. Ito, et al., Target virus log10 reduction values determined for two reclaimed wastewater irrigation scenarios in Japan based on tolerable annual disease burden, Water Res. 125 (2017) 438–448, https://doi.org/10.1016/j.watres.2017.08.057.

[262] T. Okubo, et al., Health impact of agricultural drainage water for farmers in the West Nile Delta, Int J Environ Res 13 (2) (2019) 319–325, https://doi.org/10.1007/s41742-019-00176-x.

[263] G.G.R.V. Vergara, et al., Risk assessment of noroviruses and human adenoviruses in recreational surface waters, Water Res. 103 (2016) 276–282, https://doi.org/10.1016/j.watres.2016.07.048.

[264] J.M. Venter, et al., Hepatitis a virus in surface water in South Africa: what are the risks? J. Water Health 5 (2) (2007) 229–240, https://doi.org/10.2166/wh.2007.006.

[265] W. Ahmed, et al., Quantitative microbial risk assessment of microbial source tracking markers in recreational water contaminated with fresh untreated and secondary treated sewage, Environ. Int. 117 (2018) 243–249, https://doi.org/10.1016/j.envint.2018.05.012.

[266] M. Islam, et al., Quantifying public health risks from exposure to waterborne pathogens during river bathing as a basis for reduction of disease burden, J. Water Health 18 (3) (2020) 292–305, https://doi.org/10.2166/wh.2020.045.

[267] Y. Karamoko, et al., Assessment of enterovirus contamination in mussel samples from Morocco, J. Microbiol. Biotechnol. 22 (2) (2006) 105–108, https://doi.org/10.1007/s11274-005-9003-6.

[268] C. Campos, et al., Determining the zone of impact of norovirus contamination in shellfish production areas through microbiological monitoring and hydrographic analysis, Water Res. 124 (2017) 556–565, https://doi.org/10.1016/j.watres.2017.08.021.

[269] M. Iwamoto, et al., Epidemiology of seafood-associated infections in the United States, Clin. Microbiol. Rev. 23 (2) (2010) 399–411, https://doi.org/10.1128/cmr.00059-09.

[270] F. Shoushtarian, et al., Worldwide regulations and guidelines for agricultural water reuse: a critical review, Water-Sui 12 (4) (2020) 971, https://doi.org/10.3390/w12040971.

[271] M. Pourakbar, et al., Comprehensive investigation of SARS-CoV-2 fate in wastewater and finding the virus transfer and destruction route through conventional activated sludge and sequencing batch reactor, Sci. Total Environ. 806 (4) (2022) 151391, https://doi.org/10.1016/j.scitotenv.2021.151391.