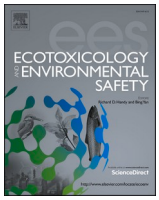
Ecotoxicology and Environmental Safety 202 (2020) 111015

Contents lists available at ScienceDirect

Ecotoxicology and Environmental Safety

journal homepage: www.elsevier.com/locate/ecoenv



Review

An updated min-review on environmental route of the SARS-CoV-2 transmission

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ARTICLE INFO

Keywords:
SARS-CoV-2
Environment
Water
Wastewater
Solid waste
Air
Transmission
Virus

ABSTRACT

The risk of newly emerging diseases is constantly present in a world where changes occur significantly in climatic, commercial, and ecological conditions, in addition to the development of biomedical investigations in new situations. An epidemic respiratory disease instigated by a new *coronavirus* was initially identified in and has resulted in the current global dissemination. This viral strain and its related disease has been termed "*SARS-CoV-2*" and "coronavirus disease 2019" (abbreviated "COVID-19" or "2019-nCoV"), respectively, which is transmitted simply between individuals. The World Health Organization (WHO) announced the COVID-19 outburst as a pandemic on March 11, which necessitates a cooperative endeavour globally for mitigating the spread of COVID-19.

The absence of previous, and minimum present-day information, particularly concerning the path of contagion have precluded the control of this disease. The present article, therefore, describes the *SARS-CoV-2* paths of contagion such as drinking water, solid waste, sewer water, ambient air, and the rest of emerging likely paths.

1. Introduction

As classified by the International Committee for Taxonomy of Viruses (ICTV), *coronaviruses* (*CoV*) are a member of the genus Coronavirus in the *Coronaviridae* family (Gorbalenya et al., 2020). Pleomorphism is seen in the RNA of all *CoVs* viral strains, characterized by having crown-shaped peplomers 80–160 nm in size (Fehr et al., 2017; Fehr and Perlman, 2015; Sahin et al., 2020). The viruses have a positive-sense, single-stranded ribonucleic acid (RNA) genome with a length in the range of 26–32 kilobases (kb) hence containing the biggest RNA of viral genome (Ahmad and Rodriguez-Morales, 2020; Fehr et al., 2017; Roosa et al., 2020). Recombination of *CoVs* occur at intensely high rates since there are constant development of transcription errors and RNA-related RNA polymerase (RdRP) vaults (Sahin et al., 2020). Such a high mutation rate renders *coronaviruses* zoonotic pathogens found in humans and a variety of animals with a wide-ranging clinical properties, from an symptomless period to the need for hospital care in the intensive care unit, which causes infections in the respiratory, gastrointestinal, hepatic, and neurologic systems (Desforges et al., 2019; Fehr et al., 2017; Roosa et al., 2020; Rothan and Byrareddy, 2020). The viruses are sometimes capable of causing more severe disease in young, elderly, or immunocompromised people (Rothan and Byrareddy, 2020; Tang et al., 2020). These viral strains are subdivided into four major subclasses of alpha, beta, gamma, and delta. Alpha and beta coronaviruses have their mammalian (bats) origins, whereas gamma and delta coronaviruses are of swine and avian origins (Burrell et al., 2017; Tao et al., 2017; Wang

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https://doi.org/10.1016/j.ecoenv.2020.111015
Received 2 May 2020; Received in revised form 5 July 2020; Accepted 6 July 2020
Available online 9 July 2020

et al., 2019). In humans, infection is caused by seven coronaviruses, namely *HCoV-229E* (*alpha coronavirus*), *HCoV-NL63* (*alpha coronavirus*), *HCoV-OC43* (*beta coronavirus*), *HCoV-HKU1* (*beta coronavirus*), Middle East Respiratory Syndrome, or *MERS-CoV* (*beta coronavirus*), Severe Acute Respiratory Syndrome, or *SARS-CoV* (*beta coronavirus*) (Burrell et al., 2017), and the Novel Coronavirus (*2019-nCoV*) detected recently in 2019 (Ahmad et al., 2020; Lippi et al., 2020), known as *SARS-CoV-2*, which causes the Coronavirus Virus Disease of 2019 (COVID-19). Four of seven common human *CoVs (HCoVs)* result in common self-limited upper respiratory diseases: *HCoV-229E*, *HCoV-OC43*, *HCoV-NL63*, and *HCoV-HKU1* (Chang et al., 2020). Of more than 60 *coronaviruses (CoVs)* isolates obtained from bats (*BtCoV*), the majority belong to the genus *betacoronavirus*. Bats function as huge (and very movable) *CoV* sources; most of bat species possess their specific exclusive *BtCoV*, which suggests that they have coevolved over a highly prolonged history (Payne, 2017). In humans, *coronaviruses* fall into the range of viruses causing the common cold and also more serious respiratory diseases, specially, severe acute respiratory syndrome (SARS, 2002) and the Middle East respiratory syndrome (MERS, 2014), both of which are zoonotic diseases initially detected by the culture of viruses from patients with common colds in the mid-1960s (Li et al., 2019; Lu et al., 2020).

1.1. The host of SARS-CoV-2

As suggested by evolutionary assays by the use of ORF1a/1b, S, and N genes, *SARS-CoV-2* is probably a new coronavirus with independent transfer from animals to humans (Chen et al., 2020a; Lai et al., 2020). A close identity was established between *SARS-CoV-2* and two bat--*SARS-like CoV* (*bat-SL-CoV ZC45* and *bat-SL-CoV ZXC21*), particularly the sequence identities of the E gene in *bat-SL-CoV ZC45* (GenBank accession no. MG772933.1), *bat-SL-CoVZXC21* (GenBank accession no. MG772934.1) existed 98.7% among 13 gene sites, but it was more apart from *SARS-CoV* (~79% similarity) and Middle East respiratory syndrome coronavirus (MERS-CoV) (~50% resemblance)(Jiang et al., 2020; Lu et al., 2020; Ren et al., 2020). An analysis of data obtained from the initial outburst using a full-length genome study revealed that the *SARS-CoV-2* sequence had a 79.5% sequence identity in common with *SARS-CoV* (Zhou et al., 2020). Sequence and phylogenetic analyses illustrated that *SARS-CoV*-2 had a longer spike protein, a dissimilar relative phylogeny of the complete RNA-reliant RNA polymerase gene, and a differing apparent genetic distance (Ahmed et al., 2020; Zhou et al., 2020), indicating that *SARS-CoV-2* is a novel *betacoronavirus*, not the *SARS-CoV* (Ahmed et al., 2020). Nevertheless, *SARS-CoV-2* and *SARS* have a common ancestor to the bat *HKU9-1 coronavirus* (Xu et al., 2020c). In Wuhan, *SARS-CoV-2* is a member of the genera *beta coronavirus* and genome analysis indicates that *SARS-CoV*-2 has closer relations to *bat-SARS-like (SL)-ZC45* and *bat- SL-ZXC21* (Zhou et al., 2020). Even so, the dissimilarities are also possibly suggestive of additional intermediate hosts present between bats and humans. An investigational group observed that 70% of pangolins possessed *β-CoV*. A coronavirus isolate obtained from the pangolins contained a genome with a high similarity to that from *SARS-CoV-2,* and a genome sequence resemblance of 99% indicates that pangolin is likely the intermediate host of *SARS-CoV-2* (Peng et al., 2020b).

1.2. Diseases caused by coronaviruses

Among the seven subtypes of *coronaviruses* capable of infecting humans, *beta-coronaviruses* can possibly induce serious disease and mortalities. The initial isolates of *coronaviruses* were obtained from fowls with respiratory disease (infective bronchitis) in the 1930s (Burrell et al., 2017). Until 2002, *human coronaviruses* (*HCoVs*) were linked only to mild respiratory tract disease, which were estimated to cause 15 %–25% of the entire common colds (Geller et al., 2012). This underwent a change in 2002 upon identification of a *human coronavirus* as the causative agent of an emerging disease named SARS. The SARS spread was taken under control, but a different new CoV isolate was collected from patients admitted to hospitals with severe respiratory disease in Saudi Arabia during 2014 (Fehr et al., 2017; Roosa et al., 2020; Zumla and Hui, 2014). Since the majority of affected patients were the inhabitants or travellers to Middle East countries, the newly detected disease was termed MERS and the causative *coronavirus* was named *HCoV-MERS* (Zumla and Hui, 2014). The transmission of most animal and human *CoVs* occurs via the faecal-oral path, and their primary proliferation place is in epithelial cells, in which virus reproduction induces local respiratory symptoms or diarrhoea (Burrell et al., 2017). Yet, *CoVs* is capable of causing acute to lethal disease. Besides seasonal flu, the recounted pathogens of pneumonia consist of *adenovirus*, *coronavirus 229E/NL63/OC43*, *human bocavirus*, *human metapneumovirus*, *parainfluenza virus 1/2/3*, *rhinovirus*, and *respiratory syncytial virus A/B* (Chou et al., 2019; Lee et al., 2019a, 2019b; Su et al., 2019). Additionally, these viruses are able to induce co-infection in the situation of public-derived bacterial pneumonia (Lai et al., 2020).

1.3. The transmission routes

Due to the relationship of the *SARS-CoV-2* to the genus *betacoronavirus*, the diseases and transmission paths for the genus are depicted in Fig. 1.

The usual spread paths of the novel coronavirus are spreading directly (cough, sneeze, and droplet inhalation transmission) and contact transmission (contact with oral, nasal, and eye mucous membranes) (Otter et al., 2016; Peng et al., 2020b; Tellier et al., 2019). Eye contact can likely pave the ground effectively for the viral entry into the body (Peng et al., 2020a, 2020b; To et al., 2020). Despite an insignificant risk of contract with *SARS-CoV-2* from the faeces of a patient, there are proofs indicating that *SARS-CoV-2* is likely to result in enteric contagion and be found in faeces (Gu et al., 2020). About 2–10% of patients with established COVID-19 manifested with diarrhoea two reports indicated that SARS-*CoV-2* viral RNA segments were detected in the stool of COVID-19 patients (Chen et al., 2020b; Huang et al., 2020; Wang et al., 2019, 2020a). Up to now, there is only one report on the culture of *SARS-CoV-2* from a single stool sample (Holshue et al., 2020). Investigations observing viral nucleic acids in these patients, additional studies are required to discover the existence of viral elements and nucleic acid levels for demonstrating faecal-oral contagion (Xiao et al., 2020). Moreover, research has demonstrated that respiratory viruses are transmittable among individuals via contacting directly or indirectly, or coarse or small droplets, and *SARS-CoV-2* is transmittable through direct or indirect salivary route (To et al., 2020). To be precise, aerosols denote particles suspending in a gas (Tellier et al., 2019). As shown by a study in 2010, the likelihood of transmitting influenza by aerosols could be reduced by improving ventilation design and prevention of generating aerosols (Wong et al., 2010). It is usually believed that transmitting by aerosols is plausible due to the high risk of cross-infection among physicians, nurses, and personnel (Hoseinzadeh et al., 2013, 2014, 2017). Research suggests that *SARS-CoV-2* is probably air-transmitted via aerosols produce during therapeutic actions (Huang et al., 2020; van Doremalen et al., 2020; Wax and Christian, 2020). Remarkably, a case of 2019-nCoV infection reported in Germany reveals that *SARS-CoV-2* may also transmitted via contacting with symptomless patients (Rothe et al., 2020). Even so, transmissions through aerosol and faecal-oral routes are those making people concerned, necessitating to be confirmed with additional studies. Fomite transmission, i.e. viral dissemination via a material, including a door handgrip, door-bell, or inhalator, also has a critical contribution to the virus spread (Kraay et al., 2018; WHO, 2020). Additionally, postnatal infection with *SARS-CoV-2*-borne pneumonia in neonates could be boosted by the contact levels of faecal infection, aerosol transmission, and contacting closely with the mother (Meng et al., 2020). Up to now, no investigations are available reporting COVID-19 transmission via exposure to blood (Zhou et al., 2020).

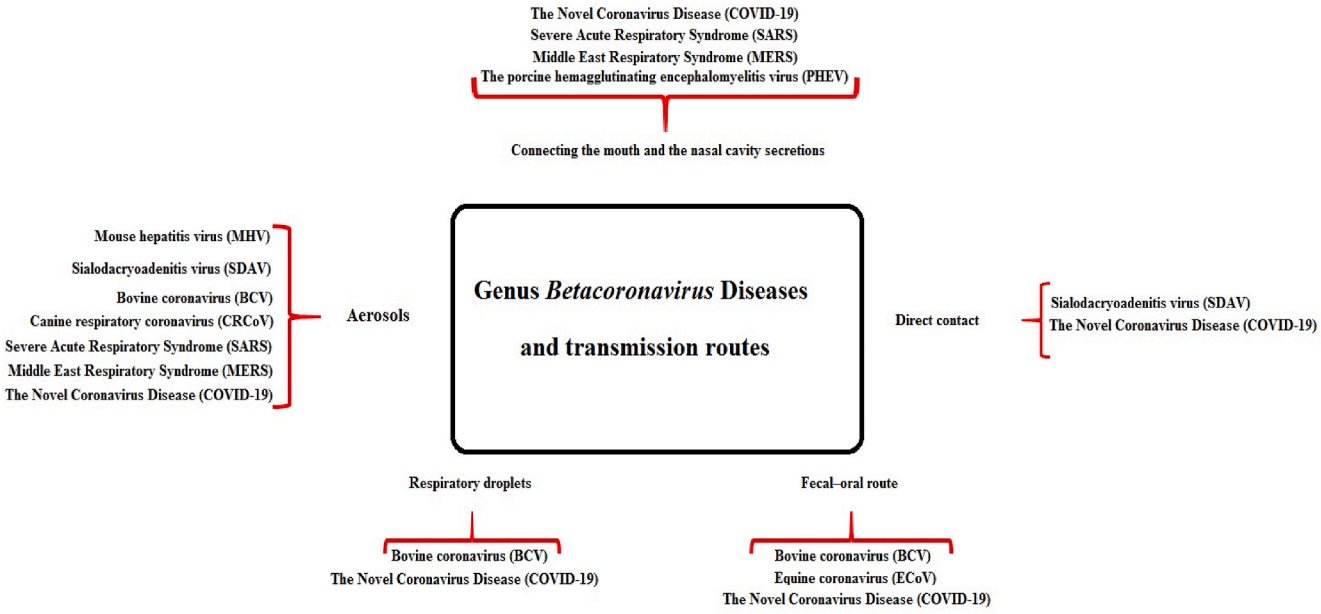

Fig. 1. Betacoronavirus diseases and transmission paths (the routes for COVID-19 under study and not yet confirmed) (Burrell et al., 2017; MacLachlan and Dubovi, 2017) for betacronovirus except *SARS-CoV-2*.

2. Environmental transmission possibility

Besides public movement and person-to-person connections, viral contagion and survivability can be impacted by environmental players (e.g., influenza), but no research has yet studied the topic about this new pathogen. Absolute humidity, described as the water content in ambient air, is a robust determining factor in the environment for other viral spreads (Hoseinzadeh et al., 2017; Wolkoff, 2018; Yang and Marr, 2012). For instance, influenza viruses live lengthier on surfaces or in droplets in cold and dry air, which increases the possibility of succeeding contagion. It is, therefore, imperative to apprehend the impacts of environmental elements on the progressive outburst to endorse making decisions on controlling the disease, particularly in places in which there is a likely underestimation of the transmission risk, including in moist and warmer areas. This paper focuses on drinking water, sewage systems, solid waste, and ambient air as potential paths of contagion in the environment.

2.1. Transmission by drinking water

As a tiny infective agent, a virus proliferates only within the organismal living cells but not within contaminated cells, or in the event of contaminating cells. Viruses are found independently in the form of particles. Waterborne viruses are different with regard to their genome contents and capsid proteins, but such viruses have some common attributes making them of specific interest concerning the risk of disease endemics related to drinking water infections (Gall et al., 2015). Water-spread viral pathogens, categorized in terms of moderate to high health importance by the WHO, consist of *adenovirus, astrovirus, hepatitis A* and *E viruses, rotavirus, norovirus*, and other *caliciviruses*, as well as *enteroviruses* including *coxsackieviruses* and *polioviruses* (Gall et al., 2015). Also, viruses of urine urinary excretion (e.g. *polyomaviruses* and *cytomegalovirus*) have the potential to be disseminated via water (Gall et al., 2015; Goetsch et al., 2018; WHO, 2011). Other viruses (e.g. *influenza* and *coronaviruses*) have been considered as organisms being transmittable via drinking water, but there is indecisive evidence (Gall et al., 2015; WHO, 2011). Besides, the COVID-19 virus has not been shown to be present in drinking water sources, and existing documentation indicate a low risk to water sources (WHO, 2020). Extreme numbers of viruses are excreted in fecal matter even in a symptomless manner. For instance, up to 10^{11} *norovirus* particles are detectable per gram of faeces (Gall et al., 2015). Additionally, non-enfold viruses can survive in water for prolonged time-periods (Firquet et al., 2015; Pinon and Vialette, 2018). With taking account of these features, insufficient sanitization of faecal-infected drinking water facilitates endemics of viral gastroenteritis from consumption. Remarkably, drinking water is also capable of transmitting viruses through inhalation or aspiration (e.g., water-bathing) or contacting with skin and eyes (e.g., swimming), which cause respiratory and ophthalmic contaminations (Pinon and Vialette, 2018). COVID-19 virus is an encased virus with a brittle exterior membrane. Encased viruses have in general less environmental stability with more susceptibility to such oxidants as chlorine (Pinon and Vialette, 2018). Although no documentation is available hitherto on the COVID-19 virus survivability in water or sewerage (WHO, 2020), the virus can probably be deactivated considerably quicker than non-encased human intestinal viruses (e.g., *adenovirus, norovirus, rotavirus*, and *hepatitis A*) with confirmed transmission ability through water. Heller et al. by considering the detection of *SARS-CoV-2* in stools and sewage, proposed the faecal-oral transmission of COVID-19 from environment to human(Heller et al., 2020). According to other concordant investigations, the *human coronavirus* illustrated a 99.9% die-out from 2 days to 2 weeks at 23 °C and 25 °C, respectively, (WHO, 2020). The die-out is facilitated by heat, high or low pH, sunshine, and commonly used sanitizers (e.g., chlorine) (Pinon and Vialette, 2018).

2.1.1. Water treatment process against viruses

Commonly used water purification methods globally are physical removal of pathogenic agents by treating conventionally and inactivation of pathogenic agents via application of ultraviolet light or chemical oxidizing agents including chlorine, chloramines, ozone, and chlorine dioxide. Due to the tiny size of viruses (mostly with a diameter ranging between 5 and 400 nm), though some *paramyxoviruses* may be up to 14,000 nm long, traditional purification, including filtration (Fig. 2), is not effective in physical removal of viruses.

Fujioka et al. reported bacterial removal rates of 95·2 %-99·3% during full-scale water filtering (Fujioka et al., 2019). Thus, viral removals are not expectedly lower than bacterial ones (>0.2 μm in size) due to the size. The use of sanitizers is greatly dependent upon water

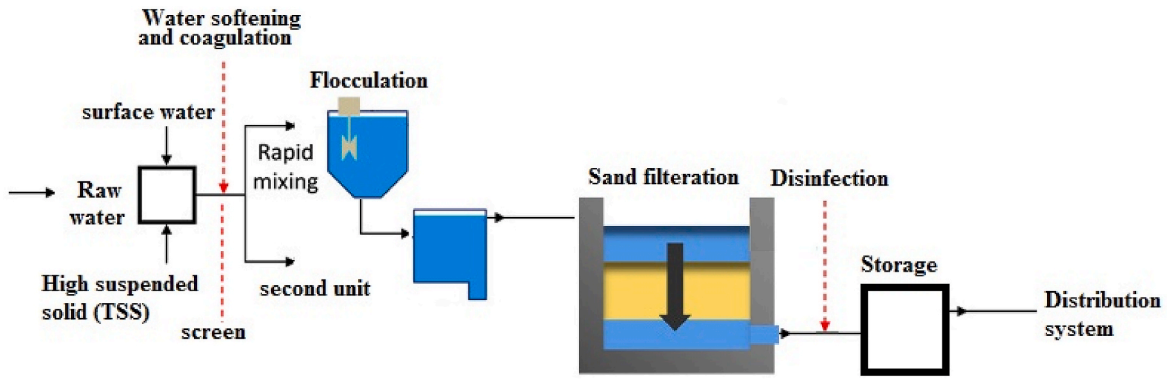

Fig. 2. Schematic flow diagram of a drinking water treatment plant.

chemistry and regional rules. Free chlorine (i.e., the sum of hypochlorous acid and hypochlorite ions produced by dissolving and hydrolysing chlorine gas in water) is the disinfection agent with the uppermost usage around the world (Hoseinzadeh, 2019). This powerful oxidizing agent inactivates the majority of viruses (Pinon and Vialette, 2018). Nonetheless, treat with free chlorine may form regularized toxic disinfection by-products (DBPs). *Adenovirus* has susceptibility to deactivation with free chlorine with high resistance to deactivation using both monochloramine and UV light (Pinon and Vialette, 2018). Chlorine dioxide and ozone are also robust oxidizing agents, both of which can effectively control viruses (Gall et al., 2015). Irrespective of the sanitization utilized at a drinking water facility, the travel of purified water from the treatment plant to the tap can lead to cross-contamination all over the extent of water dissemination substructure because of cavitation and random depressurisation; thus, it is necessary to utilize alternative sanitizers in distribution systems. Free chlorine and monochloramine are the only two sanitizers that can maintain remains in the distribution system. In spite of more powerful disinfecting effect of free chlorine in terms of inactivating pathogens, monochloramine leaves residues with a higher stability in distribution systems hence both are useable. *Human coronavirus* can persist for only two days in dechlorinated tap water and hospital effluent at 20 °C (WHO, 2020). A main barricade to extensive use of water quality settings is that not a single sanitization technique is effectual towards the whole viruses. To have efficient concentrated sanitization, free chlorine remaining concentration must be $\geq$ 0·5 mg/L following a minimum of 30 min after contact time at pH $<$ 8·0 (WHO, 2011). A chlorine residue should remain all over the distribution system.

2.1.2. Detection of viruses in drinking water

Water purification facilities routinely examine the existence of faecal coliforms in water sources, but they do not examine the existence of infective viruses due to either impossibility or unfeasibility of detecting or propagating infective viral particles cost-effectively and in a well-timed fashion. Whereas, viral proteins or genomes can be detected swiftly utilizing enzyme-linked immunosorbent assay (ELISA) or quantitative polymerase chain reaction (qPCR)-based technologies, respectively, the techniques cannot discriminate between infective and non-infective viral particles. Integrated cell culture-PCR (ICC-PCR) lowers the time demands of conventional plaque tests allowing infective viruses to proliferate in host cells, but a cell culture used in the technique is not even practical at water treatment facilities (Gall et al., 2015). Despite advancements obtained in collecting viruses from huge volumes of water, it remains as a fast way of detecting survivable viruses. Multiple existing barricades preclude detection of viruses in drinking water. To consider technologically, viral replication needs using tissue culture, a system requiring elevated time, workforce, skill, and costly apparatus. Additionally, some of these viruses are not culturable simply (*adenovirus* serotypes 40 and 41) or at all (*human norovirus, hepatitis A virus*) in culture media. Accordingly, conventional viral development tests (plaque assays) are either inaccessible or highly time-taking rendering them impractical for water treatment facilities. Generally, the potential of *SARS-CoV-2* transmission via water sources is low(Cahill and Morris, 2020) but more research need to study the viability of the virus and contamination of water source that can transmit the *SARS-CoV-2* to humans.

2.2. Transmission by sewerage systems

The majority of faecal-oral-spread viruses have high resistance in the water milieu, in which they are likely to present improved survival in spite of the sanitization procedures usually utilized to treat drinking water and sewerage (Hoseinzadeh, 2019). The bulk of such viruses are non-encased viruses, such as *norovirus, enterovirus, Aichi virus, parechovirus, hepatitis A* and *E viruses* (*HAV* and *HEV*, respectively), *astrovirus, rotavirus,* and *adenovirus* (*Ad*) (Gall et al., 2015). These viruses are detectable in effluents as people excrete about 100g of stool daily, and 10^5- 10^9 intestinal viral particles per gram of stool are released every day from a diseased person (Wigginton et al., 2012). Since 10^7-10^{13} viral particles are excreted daily from an diseased person (Wigginton et al., 2012), a possibly helpful tool is to analyse entering effluent to disclose the existence and quantification of defecated human pathogenic agents, thereby providing an estimate of the numbers of diseased individuals(La Rosa et al., 2020). If the virus is present, it will not indicate a relation between the viral sequences in effluent and those from patients of the same sampling time and area (Hellmér et al., 2014). Multiple virus recognition methods were designed for detecting *poliovirus* in effluent in accordance to the WHO polio removal program (Matrajt et al., 2018). Seven weekly combined untreated effluent samples from Ryaverket (a large wastewater treatment plant in Gothenburg) were analysed to determine the existence of seven differing intestinal viruses: *norovirus, astrovirus, rotavirus, adenovirus, Aichi virus, hepatitis A virus,* and *hepatitis E virus* (Hellmér et al., 2014). The virus is detectable prior to occurring an endemic, as reported by a research on *norovirus*, because the virus may be defecated in stool prior to the incidence of indications (Carter, 2005), which is 1–2 days for *norovirus* GII and 4–5 days for *astrovirus*(Lee et al., 2013) whereas, the defecation duration is lengthier for *hepatitis A* and *E viruses*, occurring for about 7 weeks (Richardson et al., 2001). No documentation is available hitherto about the COVID-19 virus transmission through sewer systems, with or without wastewater treatment. Besides, no proof can be found regarding the counteraction with SARS by effluent and wastewater treatment staffs. Genetically compared effluent viruses with those from clinical periodic cases and endemics can put forward a model to understand the epidemiology of intestinal viral pathogens in the population. Thus, surveillance of effluent regularly for such viruses can offer an ahead-of-time alarm of a potential forthcoming outbreaks. The encumbrance of contagion in a special population can also be estimated by the use of typing as an instrument. Based on a research work in Helsinki, Finland, *poliovirus* was detectable in effluent

if only 1 in 10,000 residents defecated the virus (Hovi et al., 2001). Even so, it may identify genomes from non-infective viral particles as well (Hellmér et al., 2014). A study conducted in Spain on six wastewater treatment plants in an area with lowest COVID-19 prevalence revealed that two secondary water sample were polluted. Comparison of the data with data of confirmed COVID-19 cases at municipally level revealed that people were shedding *SARS-CoV-2* RNA in their faeces even before the first cases were reported by local or national authorities (Randazzo et al., 2020). In case of identifying only viral segments, it will continue providing an acceptable denotation about the types of viruses circulating in the community and those infecting individuals not seeking therapeutic care. It is recommendable to utilize this procedure for forecasting COVID-19 in the public(Randazzo et al., 2020). As a fraction of a merged population health strategy, effluent passed through sewer systems should undergo ideal treatment in decently established and properly controlled consolidated wastewater treatment utilities. Finally, it is possible to consider a decontamination phase if available sewer water purification plants are not subjected to optimisation to for viral removal. It is essential to follow the best applications to protect the professional health of labours at sanitization treatment installations. Labours need to put on suitable personal protective equipment (PPE), including protecting outer wear, gloves, boots, goggles, or face shields, masks, regularly hand hygiene, and avoiding the touch of the eyes, nose, and mouth with dirty hands.

2.3. Transmission by healthcare waste

Leftovers created during health care activities possess great potentiality for contamination, and its insufficient managing practices exposes health care personnel (e.g., physicians, nurses, and laboratory staffs), waste carriers, and patients in hospitals to health risks both directly and indirectly (Amsalu et al., 2016). Health-care waste (HCW) carries a vast array of pathogenic agents. Professional risk associated with COVID-19 contact is a main concerning issue, particularly in developing countries in which people do not rigorously follow a protocol for waste treatment. Documentations are absent about human exposure directly and insecurely throughout treatment of HCW resulting in the COVID-19 endemic. A report by the WHO (2004) indicate that urban and solid HCW have identical contents of microorganisms, and that 2% of blood-stained waste tested positively for *hepatitis viruses*, *poliovirus*, and *echovirus* identified in the defiled diapers of household waste(WHO, 2004). Pathogenic viruses, such as *NoVs* and *hepatitis B virus*, have been identified in human tissue waste (WHO, 2004)(WHO, 2004). There is little information suggesting that viral RNA was detectable in the plasmas or sera of COVID-19 infected people (Chang et al., 2020). Even so, observations of researches conducted experimentally demonstrated that some viruses (e.g. respiratory syncytial virus) have partial survivability under settings possibly found in a variety of wastes (Park et al., 2009), and that viral loads are usually low. Thus, an essential issue is that labours follow group and personal protecting procedures including gloves, respiratory masks, glasses, and overalls that are previously supplied in all working environment security plans (Carducci et al., 2013). Since minor amounts of information are available from individual plants, it is necessary to perform more inclusive surveillance examinations. All HCW created throughout the care of COVID-19 patients need to be gathered securely in engineered vessels and bags, handled, and then carefully discarded and/or treated, preferably in situ (WHO, 2020). In case of moving wastes ex situ, its treatment and destruction place and mechanism must be understood critically. Prior to treatment of HCW, it is necessary to wear suitable PPE (boots, apron, long-sleeved gown, thick gloves, mask, and goggles), and perform appropriate hand sanitation after elimination. To gain more data, the reader is referred to the WHO Safe Management of Wastes from Health-Care Activities guidance(WHO, 2014). An emphasis is placed on necessary trainings in preventing contagion, in particular concerning waste treatment and removal. It is imperative to follow the most acceptable operations to safely manage HCW, such as assignment of accountability and providing adequate human and material resources for safe removal of waste.

2.4. Transmission by inanimate surfaces

Non-encased viruses (e.g. *coxsackieviruses, rotavirus,* or *poliovirus*) can be viable for prolonged times on surfaces whereas, encased viruses, such as *H1N1* and *human coronaviruses*, are still infective on surfaces after few days. A variety of environmental situations and parameters including heat, moisture, pH, and surface type influence the viability of desiccated viruses (Firquet et al., 2015). The ingredients of the media can affect the viability of viruses as well. Environmental surfaces probably contribute to the spread of hospital-derived viral contaminations (Ryu et al., 2020; Wang et al., 2020b; Ye et al., 2020). At times of endemics in health care services, samples taken from surfaces discovered *SARS-CoV* nucleic acids on surfaces and non-living substances (Casanova et al., 2010), suggesting that surfaces could be sources of virus spread for *SARS-CoV-2*. Environmental viral tests identify them in protein-laden media (such as serum) and protein-poor media, including water. Hydrophobic substances prevent the spread of droplets, and their non-porous feature improves viral survivability (Firquet et al., 2015). Survival duration of the COVID-19 causing virus on surfaces is not certainly known, but it apparently behaves the same as other *coronaviruses*. Recently, reviewing the viability of *human coronaviruses* on surfaces revealed high survivability, in the range of 2 h–9 days(WHO, 2020). Casanova et al. (2010) demonstrated that infective *SARS-CoV* survived for a period of 28 days at 4 °C, and the deactivation was lowermost at 20% relative humidity (RH). Faster deactivation occurred at 20 °C than at 4 °C at all moisture levels; the viruses were viable for 5–28 days, and a low RH led to the slowest deactivation. Deactivation of viruses was more rapid at 40 °C than at 20 °C (Casanova et al., 2010). The association between deactivation and RH was not monotone, and low RH (20%) and high RH (80%) resulted in better persistence or a higher protecting impact than at mild RH (50%) (Casanova et al., 2010). Deactivation is dividable into two steps of initial represented by water loss because of evaporating free water from the surface (Zhao et al., 2012), exposing viruses to a liquid-air interface, which leads to viral deactivation. The discrepancy can be attributed to rehydration, noticeably inactivating non-lipid viruses, including *poliovirus* (Zhao et al., 2012). Even so, iterative drying cannot influence non-encased viruses. Encased viruses showed more sensitivity than non-encased ones in the second stage of viral survival, which began once the liquid could not be seen on the lids anymore. Probably, the viruses survived for days or even weeks on dry hydrophobic surfaces (Firquet et al., 2015; WHO, 2011). Media constituents and component contents had a clear contribution upon exposure of virus suspensions to desiccation (Firquet et al., 2015; WHO, 2011). *Coronaviruses* are encased, positive-sense, and single-stranded RNA viruses. They typically show vulnerability to acid-pH, basic-pH, and heat, but apparently have more stability at 4 °C. The lipid bilayer casing of these viruses has rather sensitivity to dryness, heat, and detersives; thus, their sterilisation is simpler than non-encased viruses (Firquet et al., 2015; WHO, 2011). Several studies report that a succeeding elevation in solute concentrations in droplets could modulate the survivability of viruses against desiccation. Because the contents of media has a contribution the survivability of viruses subjected to desiccation, further investigations are necessary on the viral viability in natural media (clinical or environmental), rather than determined media. Contamination of surfaces in hospital was investigated by et al. (Razzini et al., 2020)which reported that 35% of COVID-19 patient's ward, 50% undressing room and no clean areas were contaminated with COVID-19. The most contaminated surfaces were hand sanitizer dispensers, medical equipment, medical equipment touch screens, and shelves for medical equipment, bedrails and door handles, respectively. Kampf et al. presented evidence that efficient inactivation of *coronaviruses* would be possible by surface sanitizers containing 62%-71% ethanol, 0·5% hydrogen peroxide, or 0·1% sodium hypochlorite for

approx. 1 min, but other biocides, e.g. 0·05%-0·2% benzalkonium chloride or 0·02% chlorhexidine digluconate, presented lower effectiveness (Kampf et al., 2020).

2.5. Transmission by ambient air

Various pathogens c are present in the air and have the potential to be spread over extended spaces (Hoseinzadeh et al., 2017), which comprise *influenza virus, SARS virus*, *Mycobacterium tuberculosis*, foot and mouth disease, and several other ones. The majority of patients with COVID-19 were affected severely by acute respiratory infection, including fever, cough, and shortness of breath, leading to death of most of such people. Given that respiratory spread and the spread of survivable virus placed on the surfaces is possible, the viability of air-transmitted viral aerosolised should be importantly investigated in ambient air(Morawska and Cao, 2020). Felipe FalcãoSobral et al. found the negative association between air temperature and COVID-19 cases. In addition, they found rainfall as an important climate factor in *SARS-CoV-2* transmission(Sobral et al., 2020). Furthermore, the impact of weather on COVID-19 pandemic in Turkey assessed by Mehmet Şahin. He found inverse correlation between wind speed, air humidity and temperature as the weather parameters with COVID-19 cases(Şahin, 2020). The similar results obtained by Wu et al. (2020); Yao et al. (2020) as well. A study(Xu et al., 2020a) showed a significant relation (Poisson regression model) between air quality index (AQI) that determine the ambient air quality with COVID-19 cases for Chinese cities. A recent extensive research has studied the persistence of diverse strains of air-conveyed *influenza virus* and (Pyankov et al., 2012) observed that infectious virus were present following 90 min of aerosolisation. Air temperature and humidity, microbial resistance to external physical and biological stresses, and solar intensity have been introduced to be some significant factors of air that affect the persistence and distribution of microorganisms (Pyankov et al., 2012). Cases may be transmitted continually and grow (exponentially) and rapidly within an spectrum of humidity varying from cold and dry provinces in China, including Jilin and Heilongjiang, to hot regions, such as Guangxi, and Singapore (Luo et al., 2020). A conclusion can be drawn that climatic changes lonely (i.e., rises of temperature and humidity upon reaching spring and summer months in the Northern Hemisphere) will not essentially result in reductions in case frequencies with no execution of widespread public health interventions. Carducci et al. (2013) reported that totally 30% (12/40) of air samples and 13·5% (5/37) of surface samples obtained from the solid waste removal location were positive for the virus. Pyankov et al. (2018) investigated the persistence of aerosolised *MERS-CoV* in ambient air. They detected a rather high count of viral particles at 25 °C, as opposed to influenza strains, with over 63% of living particles staying in the air following 60 min of aerosolisation. The inactivation was much more effectual at 38 °C, with merely 4·7% live viruses observed after completing the 60 min run. The reported findings illustrate that the strain is capable of surviving during prolonged times and has the potential of spreading because of respiratory contagion even under tropical and arid weather situations relating to the Middle Eastern area, the place of origin for this virus. Doremalen et al. found identical persistence of *HCoV-19* and *SARS-CoV* under the settings examined experimentally (van Doremalen et al., 2020). According to their findings, *HCoV-19* retained its viability in aerosols in the course of their experimental period (3 h) with a reduced in infective titre between $10^{3.5}$ and $10^{2.7}$ $TCID_{50}$/L, to the same as that noticed for *SARS-CoV*, from $10^{4.3}$ to $10^{3.5}$ $TCID_{50}$/mL. The above surveys suggest that aerosol and fomite spread of *HCoV-19* is probable because the virus is able to retain its viability in aerosols for several hours and on surfaces for a number of days. Ogen studied the nitrogen dioxide (NO_2) levels of ambient air as a causal factor to coronavirus (COVID-19) fatality in Turkey. The results showed as the NO_2 can lead to lung inflammatory and may be increasing susceptibility to air pollution, so chronic airway disease due to long-term exposure to air pollutants can increase the COVID-19 fatality(Ogen, 2020). In regard with impact of particulate matter, Mehmood et al. stated that although the short- and long-term exposure with $PM_{2.5}$ resulted in higher incidence of lethality of COVID-19, however, estimation of $PM_{2.5}$ incidence is required to experimental and epidemiological studies(Mehmood et al., 2020). Correia et al. addressed indoor and environmental transmission of the *SARS-CoV-2* through Heating, Ventilation and Air Conditioning Systems (HVAC)(Correia et al., 2020). By controlling this transmission routs the pandemic control of COVID-19 can be more effective. However, Faridi et al. (2020)did not found viral RNA in air samples taken from patient room with confirmed COVID-19 at distance of 2–5 m from the beds.

3. New ways of *SARS-CoV-2* transmission that maybe facilitated by angiotensin-converting enzyme 2 (ACE2)

The commonly observed indications of COVID-19 at disease incidence are fever, fatigue, dry cough, myalgia, and dyspnoea (Wang et al., 2020a). Few patients could also present headache, dizziness, abdominal pain, diarrhoea, nausea, and vomiting (Wang et al., 2020a). Illness incidence may result in continuous respiratory inability because of alveolar harm and even demise. The expression and dissemination of angiotensin-converting enzyme 2 (ACE2) in the human body can be indicative of the possible entrance of *SARS-CoV*-2 that play as a receptor (*Bosso* et al., *2020*). High ACE2 expression was detected in type II alveolar cells (AT2) of the lung, oesophagus, upper and stratified epithelial cells, absorptive enterocytes from the ileum and colon, cholangiocytes, myocardial cells, kidney proximal tubule cells, and bladder urothelial cells (Xu et al., 2020b; Zhang et al., 2020). These observations revealed that the organs with high ACE2-expressing cells would be regarded as those with high potential risk for *SARS-CoV-2* contamination (Xu et al., 2020b). Xu et al. modelled the spike protein of the receptor for *SARS-CoV-2* and found that ACE2 might be the receptor for this viral strain (Xu et al., 2020b). Likewise, ACE2 is a receptor for *SARS-nCoV* and *NL63* (Cao et al., 2020). Based on their model, the coupling strength is greater between *SARS-CoV-2* and ACE2 than the limit needed for viral contamination, though it is poorer than that between *SARS-nCoV* and ACE2. Zhou et al. carried out viral contamination assays and detected that ACE2 would be necessary for entering *SARS-CoV-2* into HeLa cells (Zhao et al., 2020). Such information demonstrate that ACE2 may be the receptor for *SARS-CoV-2*. Zhao et al. examined normal lung tissue cells of eight healthy persons and noticed that the only Asian donor presented over five times the ACE2 expressing cell ratio as white and African American donors. These findings suggest that the Asian population is likely to be increasingly susceptible, though such a conclusion requires further documentation. Hao Xu et al. (2020b) presented evidence of ACE2 expression on the mucosa of the oral cavity. It is interesting that this receptor contained a high bulk of epithelial cells of the tongue, which have justified the basic mode of action by which the oral cavity has the potential of a high risk for *SARS-CoV-2* contamination sensitivity; such discoveries also present proof of forthcoming preventing policies in dental clinical practice (Peng et al., 2020b) and everyday life. The observations also imply that ACE2 has a significant contribution to cellular entrance(Choi et al., 2020); hence, ACE2-expressing cells can serve as target cells, and have susceptibility to *SARS-CoV-2* contamination. It may be the *SARS-COV-2* virus uses the ACE2 receptor to improvement access the cell interior that the virus can do replication there easily(Li et al., 2020).

4. Conclusion

The accessible data about environmental spread paths for *SARS-CoV*-2 that have not been earlier investigated to date were reviewed here, indicating the availability of scarce or unavailable documentation concerning thereof. Despite the unconfirmed contagion of *SARS-CoV-2* via drinking water, sewer systems, and ambient air revealed by accessible guidelines, reviewed data strengthen the suspicion by highlighting the

robust potential of environmental spread via these paths hence necessitating extra studies. Moreover, the ACE2 that was recognised as a cellular doorway for *SARS-CoV-2 entrance the cells by some studies*, which may be useable for identifying novel paths of *SARS-CoV-2* contagion.

Data availability statement

All datasets generated for this study are included in the article/supplementary material.

Author contributions

EH did conception and design, acquisition of data, or analysis and interpretation of data, and writing. MT did conception and design, interpretation of data, and drafting the article or revising it critically for important intellectual content. MF, SJ, FM and HH did revising it critically for important intellectual content and final approval of the version to be published.

Funding

The authors thank Gonabad University of Medical Sciences (Grant number: 99.01.01) for financial and technical support.

Declaration of competing interest

We declare there is no competing interest.

Acknowledgement

We would like to express my special thanks of gratitude to Dr. Chiang Wei from The Experimental Forest, College of Bio-Resources and Agriculture, National Taiwan University, Taipei, Taiwan for his valuable comments.

References

Ahmad, T., Rodriguez-Morales, A.J., 2020. Emergence of COVID-19 (formerly 2019-novel Coronavirus): a new threat from China. Revista Panamericana de Enfermedades Infecciosas, pp. 37–38.
Ahmad, T., et al., 2020. COVID-19: Zoonotic Aspects. Travel Medicine and Infectious Disease, p. 101607.
Ahmed, S.F., et al., 2020. Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARS-CoV immunological studies. Viruses 12, 254.
Amsalu, A., et al., 2016. The exposure rate to hepatitis B and C viruses among medical waste handlers in three government hospitals, southern Ethiopia. Epidemiology and health 38 e2016001-e2016001.
Bosso, M., et al., 2020. The two faces of ACE2: the role of ACE2 receptor and its polymorphisms in hypertension and COVID-19. Molecular Therapy - Methods & Clinical Development 18, 321–327.
Burrell, C.J., et al., 2017. Chapter 31 - coronaviruses. In: Burrell, C.J., et al. (Eds.), Fenner and White's Medical Virology, fifth ed. Academic Press, London, pp. 437–446.
Cahill, N., Morris, D., 2020. Recreational waters – a potential transmission route for SARS-CoV-2 to humans? Sci. Total Environ. 740, 140122.
Cao, Y., et al., 2020. Comparative genetic analysis of the novel coronavirus (2019-nCoV/SARS-CoV-2) receptor ACE2 in different populations. Cell Discovery 6, 11.
Carducci, A., et al., 2013. Virus occupational exposure in solid waste processing facilities. Ann. Occup. Hyg. 57, 1115–1127.
Carter, M., 2005. Enterically infecting viruses: pathogenicity, transmission and significance for food and waterborne infection. J. Appl. Microbiol. 98, 1354–1380.
Casanova, L.M., et al., 2010. Effects of air temperature and relative humidity on coronavirus survival on surfaces. Appl. Environ. Microbiol. 76, 2712–2717.
Chang, L., et al., 2020. Coronavirus disease 2019: coronaviruses and blood safety. Transfus. Med. Rev.
Chen, L., et al., 2020a. RNA based mNGS approach identifies a novel human coronavirus from two individual pneumonia cases in 2019 Wuhan outbreak. Emerg. Microb. Infect. 9, 313–319.
Chen, N., et al., 2020b. Epidemiological and clinical characteristics of 99 cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study. Lancet 395, 507–513.
Choi, J.-Y., et al., 2020. Altered COVID-19 receptor ACE2 expression in a higher risk group for cerebrovascular disease and ischemic stroke. Biochem. Biophys. Res. Commun. 528, 413–419.
Chou, C.-C., et al., 2019. Recommendations and guidelines for the treatment of pneumonia in Taiwan. J. Microbiol. Immunol. Infect. 52, 172–199.
Correia, G., et al., 2020. Airborne route and bad use of ventilation systems as non-negligible factors in SARS-CoV-2 transmission. Med. Hypotheses 141, 109781.
Desforges, M., et al., 2019. Human coronaviruses and other respiratory viruses: underestimated opportunistic pathogens of the central nervous system? Viruses 12, 14.
Faridi, S., et al., 2020. A field indoor air measurement of SARS-CoV-2 in the patient rooms of the largest hospital in Iran. Sci. Total Environ. 725, 138401.
Fehr, A.R., Perlman, S., 2015. Coronaviruses: an overview of their replication and pathogenesis. Methods Mol. Biol. 1282, 1–23.
Fehr, A.R., et al., 2017. Middle East respiratory syndrome: emergence of a pathogenic human coronavirus. Annu. Rev. Med. 68, 387–399.
Firquet, S., et al., 2015. Survival of enveloped and non-enveloped viruses on inanimate surfaces. Microb. Environ. 30, 140–144.
Fujioka, T., et al., 2019. Online assessment of sand filter performance for bacterial removal in a full-scale drinking water treatment plant. Chemosphere 229, 509–514.
Gall, A.M., et al., 2015. Waterborne viruses: a barrier to safe drinking water. PLoS Pathog. 11.
Geller, C., et al., 2012. Human coronaviruses: insights into environmental resistance and its influence on the development of new antiseptic strategies. Viruses 4, 3044–3068.
Goetsch, H.E., et al., 2018. Fate of the urinary tract virus BK human polyomavirus in source-separated urine. Appl. Environ. Microbiol. 84 e02374-17.
Gorbalenya, A.E., et al., 2020. The species Severe acute respiratory syndrome-related coronavirus: classifying 2019-nCoV and naming it SARS-CoV-2. Nat. Microbiol.
Gu, J., et al., 2020. COVID-19: Gastrointestinal Manifestations and Potential Fecal-Oral Transmission. Gastroenterology.
Heller, L., et al., 2020. COVID-19 faecal-oral transmission: are we asking the right questions? Sci. Total Environ. 729, 138919.
Hellmér, M., et al., 2014. Detection of pathogenic viruses in sewage provided early warnings of hepatitis A virus and norovirus outbreaks. Appl. Environ. Microbiol. 80, 6771–6781.
Holshue, M.L., et al., 2020. First case of 2019 novel coronavirus in the United States. N. Engl. J. Med.
Hoseinzadeh, E., 2019. Nitrogen Removal Processes for Wastewater Treatment. Bentham Science Publishers.
Hoseinzadeh, E., et al., 2013. Evaluation of bioaerosols in five educational hospitals wards air in Hamedan, during 2011-2012. Jundishapur J. Microbiol. 6.
Hoseinzadeh, E., et al., 2014. Evaluation of fungal and bacterial aerosols in the different wards of Malayer city's hospitals in 2011-2012. J. Hospital 13, 99–108.
Hoseinzadeh, E., et al., 2017. Indoor air fungus bioaerosols and comfort index in day care child centers. Toxin Rev. 36, 125–131.
Hovi, T., et al., 2001. Poliovirus surveillance by examining sewage specimens. Quantitative recovery of virus after introduction into sewerage at remote upstream location. Epidemiol. Infect. 127, 101–106.
Huang, C., et al., 2020. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. Lancet 395, 497–506.
Jiang, S., et al., 2020. An emerging coronavirus causing pneumonia outbreak in Wuhan, China: calling for developing therapeutic and prophylactic strategies. Emerg. Microb. Infect. 9, 275–277.
Kampf, G., et al., 2020. Persistence of coronaviruses on inanimate surfaces and its inactivation with biocidal agents. J. Hosp. Infect.
Kraay, A.N., et al., 2018. Fomite-mediated transmission as a sufficient pathway: a comparative analysis across three viral pathogens. BMC Infect. Dis. 18, 540.
La Rosa, G., et al., 2020. First detection of SARS-CoV-2 in untreated wastewaters in Italy. Sci. Total Environ. 736, 139652.
Lai, C.-C., et al., 2020. Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and coronavirus disease-2019 (COVID-19): the epidemic and the challenges. Int. J. Antimicrob. Agents 55, 105924.
Lee, R.M., et al., 2013. Incubation periods of viral gastroenteritis: a systematic review. BMC Infect. Dis. 13, 446.
Lee, J.-Y., et al., 2019a. Community-acquired adenoviral and pneumococcal pneumonia complicated by pulmonary aspergillosis in an immunocompetent adult. J. Microbiol. Immunol. Infect. 52, 838–839.
Lee, K.H., et al., 2019b. Characteristics of community-acquired respiratory viruses infections except seasonal influenza in transplant recipients and non-transplant critically ill patients. J. Microbiol. Immunol. Infect.
Li, X., et al., 2019. Human coronaviruses: general features. Reference Module in Biomedical Sciences. Elsevier.
Li, G., et al., 2020. Assessing ACE2 expression patterns in lung tissues in the pathogenesis of COVID-19. J. Autoimmun. 102463.
Lippi, G., et al., 2020. Thrombocytopenia is associated with severe coronavirus disease 2019 (COVID-19) infections: a meta-analysis. Clin. Chim. Acta.
Lu, R., et al., 2020. Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. Lancet 395, 565–574.
Luo, W., et al., 2020. The Role of Absolute Humidity on Transmission Rates of the COVID-19 Outbreak. medRxiv.
MacLachlan, N.J., Dubovi, E.J. (Eds.), 2017. Academic Press, Boston. Chapter 24 - Coronaviridae.
Matrajt, G., et al., 2018. A review of the most commonly used methods for sample collection in environmental surveillance of poliovirus. In: Clinical Infectious Diseases, vol. 67. an official publication of the Infectious Diseases Society of America, pp. S90–S97.
Mehmood, K., et al., 2020. Can exposure to PM2.5 particles increase the incidence of coronavirus disease 2019 (COVID-19)? Sci. Total Environ. 741, 140441.

Meng, L., et al., 2020. Coronavirus disease 2019 (COVID-19): emerging and future challenges for dental and oral medicine. J. Dent. Res., 0022034520914246
Morawska, L., Cao, J., 2020. Airborne transmission of SARS-CoV-2: the world should face the reality. Environ. Int. 139, 105730.
Ogen, Y., 2020. Assessing nitrogen dioxide (NO2) levels as a contributing factor to coronavirus (COVID-19) fatality. Sci. Total Environ. 726, 138605.
Otter, J.A., et al., 2016. Transmission of SARS and MERS coronaviruses and influenza virus in healthcare settings: the possible role of dry surface contamination. J. Hosp. Infect. 92, 235–250.
Park, H., et al., 2009. Detection and hazard assessment of pathogenic microorganisms in medical wastes. J. Environ. Sci. Health Part A 44, 995–1003.
Payne, S., 2017. Chapter 17 - family Coronaviridae. In: Payne, S. (Ed.), Viruses. Academic Press, pp. 149–158.
Peng, X., et al., 2020a. Transmission routes of 2019-nCoV and controls in dental practice. Int. J. Oral Sci. 12, 1–6.
Peng, X., et al., 2020b. Transmission routes of 2019-nCoV and controls in dental practice. Int. J. Oral Sci. 12, 9.
Pinon, A., Vialette, M., 2018. Survival of viruses in water. Intervirology 61, 214–222.
Pyankov, O.V., et al., 2012. Inactivation of airborne influenza virus in the ambient air. J. Aerosol Sci. 53, 21–28.
Pyankov, O.V., et al., 2018. Survival of aerosolized coronavirus in the ambient air. J. Aerosol Sci. 115, 158–163.
Randazzo, W., et al., 2020. SARS-CoV-2 RNA in wastewater anticipated COVID-19 occurrence in a low prevalence area. Water Res. 181, 115942.
Razzini, K., et al., 2020. SARS-CoV-2 RNA detection in the air and on surfaces in the COVID-19 ward of a hospital in Milan, Italy, 742. Science of The Total Environment, p. 140540.
Ren, L.-L., et al., 2020. Identification of a novel coronavirus causing severe pneumonia in human: a descriptive study. Chinese Med J.
Richardson, M., et al., 2001. Evidence base of incubation periods, periods of infectiousness and exclusion policies for the control of communicable diseases in schools and preschools. Pediatr. Infect. Dis. J. 20, 380–391.
Roosa, K., et al., 2020. Real-time forecasts of the COVID-19 epidemic in China from february 5th to february 24th, 2020. Infectious Disease Modelling 5, 256–263.
Rothan, H.A., Byrareddy, S.N., 2020. The epidemiology and pathogenesis of coronavirus disease (COVID-19) outbreak. J. Autoimmun. 102433.
Rothe, C., et al., 2020. Transmission of 2019-nCoV infection from an asymptomatic contact in Germany. N. Engl. J. Med.
Ryu, B.-H., et al., 2020. Environmental contamination of SARS-CoV-2 during the COVID-19 outbreak in South Korea. Am. J. Infect. Contr.
Şahin, M., 2020. Impact of weather on COVID-19 pandemic in Turkey. Sci. Total Environ. 728, 138810.
Sahin, A.R., et al., 2020. 2019 novel coronavirus (COVID-19) outbreak: a review of the current literature. EJMO 4, 1–7.
Sobral, M.F.F., et al., 2020. Association between climate variables and global transmission oF SARS-CoV-2. Sci. Total Environ. 729, 138997.
Su, I.C., et al., 2019. Severe community-acquired pneumonia due to Pseudomonas aeruginosa coinfection in an influenza A(H1N1)pdm09 patient. J. Microbiol. Immunol. Infect. 52, 365–366.
Tang, B., et al., 2020. Coronavirus disease 2019 (COVID-19) pneumonia in a hemodialysis patient. Kidney Medicine.
Tao, Y., et al., 2017. Surveillance of bat coronaviruses in Kenya identifies relatives of human coronaviruses NL63 and 229E and their recombination history. J. Virol. 91 e01953-16.
Tellier, R., et al., 2019. Recognition of aerosol transmission of infectious agents: a commentary. BMC Infect. Dis. 19, 101.
To, K.K.-W., et al., 2020. Consistent detection of 2019 novel coronavirus in saliva. Clinical Infectious Diseases.
van Doremalen, N., et al., 2020. Aerosol and Surface Stability of HCoV-19 (SARS-CoV-2) Compared to SARS-CoV-1. medRxiv.
Wang, N., et al., 2019. Characterization of a new member of alphacoronavirus with unique genomic features in Rhinolophus bats. Viruses 11, 379.
Wang, D., et al., 2020a. Clinical characteristics of 138 hospitalized patients with 2019 novel coronavirus–infected pneumonia in wuhan, China. J. Am. Med. Assoc.
Wang, J., et al., 2020b. SARS-CoV-2 RNA detection of hospital isolation wards hygiene monitoring during the Coronavirus Disease 2019 outbreak in a Chinese hospital. Int. J. Infect. Dis. 94, 103–106.
Wax, R.S., Christian, M.D., 2020. Practical recommendations for critical care and anesthesiology teams caring for novel coronavirus (2019-nCoV) patients. Can. J. Anesth./Journal canadien d'anesthésie. 1–9.
WHO, 2004. Review of Health Impacts from Microbiological Hazards in Health-Care Wastes. World Health Organization. Department of Blood Safety and Clinical Technology and Department of Protection of the Human Environment, Geneva, Switzerland.
WHO, 2011. Guidelines for drinking-water quality 38, 104–108.
WHO, 2014. In: Chartier, Y., et al. (Eds.), Safe Management of Wastes from Health-Care Activities, second ed., p. 329.
WHO, 2020. Water, Sanitation, Hygiene and Waste Management for COVID-19: Technical Brief, 03 March 2020. World Health Organization.
Wigginton, K.R., et al., 2012. Virus inactivation mechanisms: impact of disinfectants on virus function and structural integrity. Environ. Sci. Technol. 46, 12069–12078.
Wolkoff, P., 2018. Indoor air humidity, air quality, and health – an overview. Int. J. Hyg Environ. Health 221, 376–390.
Wong, B.C., et al., 2010. Possible role of aerosol transmission in a hospital outbreak of influenza. Clin. Infect. Dis. 51, 1176–1183.
Wu, Y., et al., 2020. Effects of temperature and humidity on the daily new cases and new deaths of COVID-19 in 166 countries. Sci. Total Environ. 729, 139051.
Xiao, F., et al., 2020. Evidence for Gastrointestinal Infection of SARS-CoV-2 medRxiv. 2020.02.17.20023721.
Xu, H., et al., 2020a. Possible environmental effects on the spread of COVID-19 in China. Sci. Total Environ. 731, 139211.
Xu, H., et al., 2020b. High expression of ACE2 receptor of 2019-nCoV on the epithelial cells of oral mucosa. Int. J. Oral Sci. 12, 8.
Xu, X., et al., 2020c. Evolution of the novel coronavirus from the ongoing Wuhan outbreak and modeling of its spike protein for risk of human transmission. Sci. China Life Sci. 63, 457–460.
Yang, W., Marr, L.C., 2012. Mechanisms by which ambient humidity may affect viruses in aerosols. Appl. Environ. Microbiol. 78, 6781–6788.
Yao, M., et al., 2020. On airborne transmission and control of SARS-Cov-2, 731. Science of The Total Environment, p. 139178.
Ye, G., et al., 2020. Environmental contamination of SARS-CoV-2 in healthcare premises. J. Infect.
Zhang, H., et al., 2020. Angiotensin-converting enzyme 2 (ACE2) as a SARS-CoV-2 receptor: molecular mechanisms and potential therapeutic target. Intensive Care Med. 1–5.
Zhao, Y., et al., 2012. Effects of temperature, relative humidity, absolute humidity, and evaporation potential on survival of airborne Gumboro vaccine virus. Appl. Environ. Microbiol. 78, 1048–1054.
Zhao, Y., et al., 2020. Single-cell RNA expression profiling of ACE2, the putative receptor of Wuhan 2019-nCov. BioRxiv.
Zhou, D., et al., 2020. Emerging Understanding of Etiology and Epidemiology of the Novel Coronavirus (COVID-19) Infection in Wuhan. China.
Zumla, A., Hui, D.S., 2014. Infection control and MERS-CoV in health-care workers. Lancet 383, 1869–1871.