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RESEARCH ARTICLE

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A REVIEW OF THE IMPACT OF HOSPITAL EFFLUENTS ON HUMAN AND ANIMAL HEALTH DURING THE PANDEMIC COVID 19

Ilham Nassri*¹, Monsif Khazraji², latifa Mouhir² and Mohammed Fekhaoui¹

¹Géo-biodiversity and Natural Patrimony Laboratory, Scientific Institute, Mohammed V University, Rabat, Morocco; ²Water and Environmental Engineering Laboratory, Faculty of Science and Technology, Mohammedia, Morocco

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*Corresponding author:

Ilham Nassri

ABSTRACT

The permanent increase of the contagion focus during the COVID 19 pandemic has contributed to a continuous discharge of SARS-CoV-2 virus and a large portion of unchanged or metabolized drugs through patients' stool and urine into hospital effluents. At present, untreated hospital sewage disposal practices result in a very high and continuous overload of these micropollutants into the environment. Their discharge into rivers and coastal waters is likely to have adverse effects in all exposed environmental compartments. Furthermore, the study of the dynamics of the SARS COV2 virus associated with COVID19 focuses primarily on the diagnosis and treatment of humans. However, such an approach does not allow the prevention of transmission to humans and animals, nor does it allow the assessment of the persistence of the infectivity of this virus in the environment. Therefore, there is a need to improve knowledge of the survival and infectivity of SARS-CoV-2 in the receiving environment to prevent environmental spread and transmission to humans and animals. Nevertheless, a better understanding of the risks associated with the environmental spread of SARS-CoV-2 is necessary to control the spread of the current COVID-19 pandemic and to prepare for the emergence of future virus pandemics. The objective of this literature review is to investigate the risks of persistence of viable and infectious SARS-CoV-2 virus and its dissemination in hospital effluents due to their relatively high concentrations and damage to public health, wildlife and ecology.

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INTRODUCTION

The pandemic originated in the Chinese city of Wuhan in an illegal wildlife market. It is important to note that these wild animals are held in captivity in pitiful cages placed on or against each other. After exposure, these animals may also be immunocompromised compared to their free-ranging counterparts due to the new habitat conditions, which could reduce their resistance to the pathogen (Fagreand al., 2021). This human activity favors optimal conditions for direct interaction between living wild animals. Such interaction facilitates the exchange of genetic material of viruses by recombination, allowing them to cross the barrier between susceptible animal species and finally adapt to humans as was the case for SARS 2003. In addition, coronaviruses (SARS viruses) are well known to undergo genetic recombination (Cheng andand., 2007), due to the great plasticity of their genome, which can lead to new pathogenic genotypes. Thus, a cycle of infections is set up starting with sporadic cases of transmission of the pathogenic virus from animals to humans, as this transmission continues in the environment, the number of

infected cases increases to finally trigger a pandemic. Transmission of SARS-CoV-2 from humans to other vulnerable species in close proximity to humans has already been observed in different locations including a public zoo in New York City, in farmed areas and affecting feline species ((L. Wang and al., 2020) and farmed mink from different countries (Fenollarand al., 2021) respectively. Admittedly, these examples of transmission represent only a small fraction of the species currently in direct contact with this pandemic virus in their environment. Furthermore, the SARS-CoV-2 virus responsible for Severe Acute Respiratory Syndrome (SARS-CoV-2), belongs to the Coronaviridae family, genus Betacoronavirus, subgenus Sarbecovirus within the coronavirus species (Gorbalenyaand al., 2020). It is an enveloped single-stranded RNA positive virus (Mohan et and., 2021). Its main route of transmission, is by droplets and close contact ((Carducci and al., 2020);(Paul et al., 2021)). However, SARS-CoV-2 or coronavirus 2 can infect the gastrointestinal tract via the angiotensin-converting enzyme (ACE 2) receptor that are expressed by epithelial cells of the gastrointestinal tract ((Bivins and al., 2020); (H. Zhang and al., 2020)). Thus, the

virus (SARS-CoV-2) has the ability to replicate and persist in the gastrointestinal tract and to be shed in the stool ((Mohan and al., 2021); (Kitajima and al., 2020)). Of note, the presence of SARS-CoV-2 has also been demonstrated in the urine of patients infected with SARS-CoV-2 ((A and R, 2020);(Sun *et al.*, 2020)). Thus, excretion of the virus (SARS-CoV-2) in stool and urine, indicates a potential transmission route in wastewater ((A and R, 2020);(Kitajima *et al.*, 2020)) especially after the detection of live virus in human stool (Wölfel *et al.*, 2020). Recently, several studies could reveal viral RNA in wastewater (La Rosa *et al.*, 2020), (Rimoldi *et al.*, 2020), (Martin *et al.*, 2020)). Some studies, were able to find SARS-CoV-2 RNA in all environmental samples ((Peccia *et al.*, 2020); (Nemudryi *et al.*, 2020); (Muthuraman and Lakshminarayanan, 2021)) including septic tanks (D. Zhang *et al.*, 2020a), sludge (A and R, 2020), wastewater treatment plants (Trottier *et al.*, 2020), and even in natural waters (Bernardo-Cravo *et al.*, 2020). Other studies have shown its persistence on different substrates (steel, cardboard, plastic) ((van Doremalen *et al.*, 2020a) ((Kampf *et al.*, 2020)). A large number of published studies have been able to isolate it from different intermediate hosts. The adaptation of the SARS-CoV-2 virus in the external environment, its airborne spread, its extracellular viability and its transmission via animals as reservoir probably played an important role in the rapid transmission of this pathogen across the four corners of the world to finally evolve into this COVID 19 (CoronaVirus Disease) pandemic. Thus, the presence of SARS-CoV-2 viral RNA in the stool of infected individuals and in wastewater now shows that the environment and especially hospital effluents contain a considerable load of the virus (SARS-CoV-2) posing a risk not only to human health but also to wildlife and will require reflection on the fate of SARS-CoV-2 in the receiving environment. Based on the literature published to date, this review examines the risks associated with factors promoting viral viability and infectivity in hospital wastewater based on its occurrence, persistence and mode of transmission.

The coronavirus 2 (SARS-CoV-2): Coronavirus 2 (SARS-CoV-2) has been detected in wastewater from different countries around the world including the Netherlands (Medema *et al.*, 2020); the United States ((Peccia *et al.*, 2020); (Nemudryi *et al.*, 2020)); Brazil (Prado *et al.*, 2020); Australia (Ahmed *et al.*, 2020); France (Wurtzer *et al.*, 2020); Italy (La Rosa *et al.*, 2020); India (Kumar *et al.*, 2020); Turkiye (Kocamehi *et al.*, 2020); Japan (Haramoto *et al.*, 2020); Qatar (Saththasivam *et al.*, 2021) with concentrations that follow the epidemiological curve of COVID-19 (Peccia *et al.*, 2020); (Nemudryi *et al.*, 2020). Thus, community-wide surveillance based on the detection and quantification of SARS-CoV-2 in wastewater becomes a valuable epidemiological tool for COVID-19 to assess the prevalence and spread of the disease. ((Medema *et al.*, 2020);(Polo *et al.*, 2020); ((Nghiem *et al.*, 2020); ((Michael-Kordatou *et al.*, 2020); ((Prado *et al.*, 2020);(Wu *et al.*, 2020); (Kitajima *et al.*, 2020); (Venugopal *et al.*, 2020); (Tetteh *et al.*, 2020);(Martin *et al.*, 2020). In addition, genome sequencing can be used for phylogenetic analysis to infer viral ancestry (Nemudryi *et al.*, 2020) and to infer genotyping of circulating viral strains in the community (Nemudryi *et al.*, 2020);(Martin *et al.*, 2020). It is important to note that, wastewater monitoring based on molecular techniques does not allow for the assessment of the viability and infectivity of SARS-CoV-2 (Maal-Bared *et al.*, 2020) because the detection of its RNA does not indicate that the virus is viable and infectious ((Maal-Bared *et al.*, 2020); (Lahrich *et al.*, 2021)). At the beginning of the pandemic, data on the viability of COVID 19 virus in sewage was previously described via observations of surrogates, which are closely related to SARS-CoV-2 such as other human coronaviruses (HCoV, SARS-CoV).

At the laboratory scale, HCoV can survive for several days at 4° C, but their persistence is strongly influenced by temperature and organic or microbial pollution (Carducci *et al.*, 2020). Information on the survival of SARS-CoV-2 in wastewater is first reported by Bivins *et al.* They estimate that survival in wastewater at room temperature was 1.5 days (Bivins *et al.*, 2020) and for a much longer period at low temperatures (Mittal *et al.*, 2020). Thus, other studies have shown that there are different environmental factors that affect the survival of

SARS-CoV-2 in wastewater including temperature, UV exposure, organic matter, disinfectants, antagonistic microorganisms. ((Paul *et al.*, 2021); (Wartecki and Rzymiski, 2020) on the other hand pH may not necessarily be a major factor contributing to the persistence of coronavirus in water (unless it reaches very extreme values) especially since SARS-CoV-2 is stable in water with a wide pH range (3-10) (Mathavarajah *et al.*, 2021). In fact, increasing temperature decreases the survival capacity of SARS-CoV-2 ((Paul *et al.*, 2021), (Carducci *et al.*, 2020). An increase in temperature results in rapid inactivation of enveloped viruses and causes increased denaturation of the protein present in the virion structure. The effect of sewage temperature was clearly indicated in studies investigating the survival of SARS-CoV at 20°C, the virus could persist in sewage only for 2-3 days, while at 4°C they remained detectable for at least 14 days (Wartecki and Rzymiski, 2020). The results of in vitro experiments with decreasing temperatures suggest that coronavirus excreted in feces could reach the wastewater treatment in an infectious state, especially in cool climates (Carducci *et al.*, 2020). In the sewage system, there is still a significant probability that coronavirus discharged via feces and urine can reach treatment plants in an infectious state, especially in winter when temperatures drop substantially (Paul *et al.*, 2021).

The SARS-CoV-2 virus is an enveloped virus considered among the most sensitive microorganisms to disinfection. The presence of solvents and detergents in wastewater can either weaken its viral envelope by inactivating it or attack its genome by preventing its replication. Today, disinfection strategies for COVID-19-contaminated wastewater can target one or more viral structures involved in one of these three functions: the genomic material (COVID-19 RNA), the protein capsid, or the lipid envelope (Maal-Bared *et al.*, 2020). However, there are some factors that may affect the effectiveness of the disinfectant on the survivability of SARS-CoV-2, including aggregation of the virus in the medium (Paul *et al.*, 2021) or its adsorption to suspended matter (D. Zhang *et al.*, 2020a). Furthermore, disinfectant efficacy requires the combination of a residual concentration with a contact time to better saturate all suspended matter. This combination generates a free residual concentration sufficient to kill the virus. Therefore, SARS-CoV-2 embedded in stool and protected from disinfection by organics is slowly released as free chlorine decreases (D. Zhang *et al.*, 2020a) and thus poses a potential risk of its spread through effluent. Ultraviolet irradiation is another effective option for virus inactivation (Maal-Bared *et al.*, 2020). Exposure to ultraviolet (UV) light damages the viral genome, so that it can no longer replicate in the host, and breaks down its capsid, inhibiting the injection of genomic material into the host cell. Furthermore, exposure of infected water to UV-B decreases the SARS-CoV titer and may result in the destruction of their nucleic acids (Wartecki and Rzymiski, 2020).

It's important to note that the survival of SARS-CoV-2 is generally reduced in waters with microbial pollution (Carducci *et al.*, 2020); (Wartecki and Rzymiski, 2020). In fact, some protozoa graze on viruses and that antiviral factors can be released from algae and actinomycetes, while extracellular bacterial enzymes can inactivate viruses (Wartecki and Rzymiski, 2020). The presence of antagonistic microorganisms in wastewater is yet another factor that can affect the extent of viral inactivation. On the contrary, the presence of organic matter in suspension in wastewater plays a protective role for SARS-CoV-2 against the aggression of certain physicochemical conditions of the environment. In fact, the hydrophobic nature of its envelope facilitates its adsorption on organic particles while maintaining less solubility in water (Paul *et al.*, 2021). In addition, suspended particles as small as 7 mm can protect the virus from UV exposure and reduce their vulnerability to direct sunlight inactivation, and 0.3 mm particles can protect the virus from disinfection for their prolonged survival (D. Zhang *et al.*, 2020a). Thus, a high concentration of organic matter or solid fraction in the water corresponds to increased survival of the virus population since the organic matter particles physically protect the virus from disinfectants and other antiviral agents (Paul *et al.*, 2021). However, the transmission of SARS-CoV-2 from sewage-derived feces and its

persistence for an extended period of time in the sewage system, generate a secondary source of spread (D. Zhang *et al.*, 2020a). The adsorption capacity of the virus suggests that sediments pose a threat of being virus reservoirs in aqueous systems (D. Zhang *et al.*, 2020a) leading to additional contagion that is not generally considered (Paul *et al.*, 2021).

Viability and infectivity risks affecting human health: Results of studies on the viability of SARS-CoV-2 isolated from wastewater have shown that it depends on the environmental conditions of the receiving environment. While the infectivity of SARS-CoV-2 is difficult to show and has conflicting results. In fact, several scientific studies have failed to detect SARS-CoV-2 in an infectious state in wastewater, some believe that the lack of infectivity is due to the natural decay of viral pathogenicity over time from emission (Rimoldi *et al.*, 2020) others suggest that it is due to the inability to reproduce in vitro the perfect chemical, biological, and environmental conditions that result in host cell infection (Maal-Bared *et al.*, 2020). In contrast, other studies have been able to detect SARS-CoV-2 in the infectious state and thus show that it can remain viable, up to 4.3 and 6 days in sewage and water, respectively (Giacobbo *et al.*, 2021). Other studies reveal that this environmental detection is highly dependent on virus concentrations in feces (W. Wang *et al.*, 2020) and that SARS-CoV-2 RNA is more persistent than infectious SARS-CoV-2 further confirming that RNA detection alone does not justify the infectious risk (Bivins *et al.*, 2020). It is important to note that the ability of a virus to maintain infectivity after release from an infected individual to cause infection in a susceptible individual is highly dependent on the properties of the virus, host, environmental conditions, and mode of transmission (Prussin *et al.*, 2020)

However, the detection of SARS-CoV-2 has been well documented from human feces, sewage systems, and wastewater treatment plants until it reaches the natural environment, highlighting the risk of its presence and infectivity in wastewater and natural water. Thus, this detection placed the viability and infectivity of SARS-CoV-2 at the center of a potential risk to natural water, water industry workers, and the public who come in contact with wastewater (A and R, 2020). At the beginning of the pandemic, possible transmission routes of infectious SARS-CoV-2 from wastewater were considered unlikely. In fact, some studies show that there is no evidence of transmission of infectious SARS-CoV-2 through contact with the wastewater system ((Maal-Bared *et al.*, 2020); (Giacobbo *et al.*, 2021); (Westhaus *et al.*, 2021)) or through biosolids (Brisolara *et al.*, 2021) nor through consumption of contaminated drinking water (Naddeo and Liu, 2020); (Godoy *et al.*, 2021). These studies suggest that the risk of exposure to SARS-CoV-2 decreases with increasing treatment measures (Brisolara *et al.*, 2021); (Muthuraman and Lakshminarayanan, 2021); (Westhaus *et al.*, 2021)), while others suggest that SARS-CoV-2 is not an enteric virus and should not be managed as a waterborne pathogen (Godoy *et al.*, 2021). Recently, studies have provided epidemiological and experimental evidence of aerosol transmission of SARS-CoV-2 from sewage causing epidemics. Recently, a study provided the first evidence of transmission of SARS-CoV-2 through contaminated sewage in the Guangzhou area of China leading to a multi-person epidemic in the community (Yuan *et al.*, 2020). This mode of transmission was well proven during the 2003 SARS-CoV outbreak. In fact, aerosolization of water droplets containing SARS-CoV from a leaking sewer pipe in a residential apartment led to the spread of a cluster of cases in a community in Hong Kong (Hung, 2003). These outbreaks show that infectious aerosols pose infection risks to people in direct contact with sewage. In addition, toilets can also be a source of fecal aerosol transmission if they are misused, especially in hospitals (Ding *et al.*, 2020). It is now clear that transmission of infectious SARS-CoV-2 from sewage via aerosols is quite possible ((Mohan *et al.*, 2021); (Nghiem *et al.*, 2020); (Naddeo and Liu, 2020); (Yuan *et al.*, 2020); (Tang *et al.*, 2020)) due to its ability to remain aerosol viable and infectious for hours ((Godoy *et al.*, 2021); (Wiktorczyk-Kapischke *et al.*, 2021); (van Doremalen *et al.*, 2020)). Furthermore, the water content of virus-containing aerosols decreases when they become airborne, due to evaporation, thus becoming lighter and remaining

airborne for a long time. In addition, one study suggests that SARS-CoV-2 in aerosols of respirable size could persist and maintain infectivity for up to 16 h (Tang *et al.*, 2020). In fact, the airborne route extending from the nasal and oral openings to the distal bronchial airways with sufficient length shows the extent of transfer and deposition of inhaled SARS-CoV-2 aerosol to the mucosal surface where it can directly access ACE-2 receptors. ACE-2 receptors are widely expressed in certain types of human airway epithelial cells, promoting viral penetration and replication and thus initiating pulmonary infection. The receptor (ACE) 2 is also expressed by epithelial cells of the gastrointestinal tract (epithelial and upper glandular cells of the esophagus, ileum and colon) showing another pathway of replication. Nevertheless, infectious virus was easily isolated from throat or lung samples, but not from stool samples, despite high concentrations of viral RNA (Wölfel *et al.*, 2020). The loss of infectivity may be due to the presence of gut microbiota in the stool that interacts with SARS-CoV-2. It is quite possible that SARS-CoV-2 is influenced by the microbial community of the human gut.

To date, there is no evidence of fecal-oral transmission of SARS-CoV-2 (Wiktorczyk-Kapischke *et al.*, 2021) or evidence of epidemic outbreak through consumption of contaminated drinking water. In fact, a study in a Hong Kong population sample shows that 15.3% of patients with no gastrointestinal symptoms still shed viral RNA in their stool and that patients with diarrhea had a higher viral load than patients without diarrhea (Mukhra *et al.*, 2020). This suggests that the gut microbiome in patients with diarrhea contains bacteria that are less diverse or too low in number to confer sufficient protection against SARS-CoV-2. There is increasing evidence that the gut microbiome community of low diversity and altered metabolic state, exposing the gut to invasion and proliferation of pathogens (Bass *et al.*, 2019). In fact, the gut microbiome not only acts as a barrier to infection by defending the host from pathogen colonization but also interacts with the host immune system, providing signals to promote immune cell maturation (Bass *et al.*, 2019). In other words, a stable gut microflora is an essential prerequisite for human health ((Li *et al.*, 2021); (Schmeller *et al.*, 2020)) that can either promote or inhibit pathogenic microorganisms (Bernardo-Cravo *et al.*, 2020). The replication of SARS-CoV-2 in epithelial cells of the gastrointestinal tract has been well documented. However, further studies are needed to investigate whether or not SARS-CoV-2 can pass through the intestinal barrier into the bloodstream and develop SARS disease.

Risk of harm to wildlife: The emergence of SARS-CoV-2 in the city of Wuhan, China has sparked the interest of researchers on the origin of this pandemic in order to identify potential contagion events of this zoonotic disease. Various intermediate hosts have been suspected including bats (Paraskevis *et al.*, 2020), Mammals ((Zhao *et al.*, 2020), pangolins (Manisjavanica); (Lam *et al.*, 2020)). So, some studies suggest that pangolin is the intermediate host between the jump and the entry of SARS-CoV-2 from bat to human (Lopes *et al.*, 2020). Until then, the origin of SARS-CoV-2 transmission to the first COVID 19 patient in Wuhan as well as the intermediate sources of animal origin favoring this virus to cross the animal species barrier to infect humans remains an enigma. In addition, SARS-CoV-2 enters host cells via the binding of its Spike protein (or S protein) to the cellular ACE2 receptor (Hoffmann *et al.*, 2020). The Spike protein has a receptor-binding domain (RBD) that recognizes the ACE2 receptor of the host cell. The interaction of the ACE2 receptor with the S protein is the major constraint to the interspecific transmission of SARS-CoV-2 (Damas *et al.*, 2020). All ACE2 receptor-bearing cells in the respiratory or intestinal tract can potentially be hijacked by COVID-19 virus to replicate (Maal-Bared *et al.*, 2020). Thus, the presence of viral receptors on host cells and in target tissues and organs determine tissue tropism, pathogenesis of viral infection, and host range, (Godoy *et al.*, 2021) this therefore explains why some species are susceptible and not others to SARS-CoV-2 (Mathavarajah *et al.*, 2021). Now we see the emergence of SARS-CoV-2 infection in farm animals including farmed mink from different countries (Fenollar *et al.*, 2021). Genomic data of SARS-CoV-2 isolated from infected mink provide a natural case study of a secondary host jump

of the virus from humans to animals (van Dorp *et al.*, 2020). More recently, a wild mink considered the first free-ranging native wild animal confirmed positive for SARS-CoV-2 in Utah (USA) during screening of wildlife around farms with outbreaks, thus showing another natural case of a secondary host jump of the virus from farm animals to wild animals. Therefore, infected wild mink may become a permanent reservoir of infection for other animal species. Transmission of SARS-CoV-2 in wildlife will put susceptible species at risk and likely contribute to a significant loss of biodiversity.

However, the mechanisms of transfer of SARS-CoV-2 within animals in their natural environment are still poorly studied. Certainly, these are the same transmission routes as in humans, notably by aerosolization. It is quite possible today that the infectious SARS-CoV-2 found in the sewage system and in wastewater treatment plants directly contaminates the environment (river water, coastal water, soil, septic tanks, etc.) due to deterioration of urban infrastructures (deficiencies and degradation of sewage pipes) or inadequate treatment. Therefore, animal species near contaminated natural water systems will be exposed to this pandemic virus and will have a dramatic impact on their populations. It is currently difficult to estimate the risk of transmission of SARS-CoV-2 to other groups of aquatic animals, including fish, because there has been little research on the mechanisms of infection associated with these animals. Some studies consider that SARS-CoV-2 does not replicate in fish and amphibians because this virus is not likely to bind to the ACE2 receptor on host cells (Godoy *et al.*, 2021). In contrast, many different marine mammal species have an ACE2 receptor that is expected to bind to SARS-CoV-2 at a similar binding affinity to the human receptor, indicating that these species can contract the virus if it exists in their environment (Mathavarajah *et al.*, 2021). Many species of whales, dolphins, seals, and otters are expected to be highly susceptible to SARS-CoV-2 infection showing a potential for reverse zoonotic transmission of COVID-19 and its impact on marine wildlife (Mathavarajah *et al.*, 2021). In addition, coronavirus infections in marine mammals have already been observed. In fact, coronaviruses have been detected in marine mammals found dead including dolphins (*Tursiops aduncus* and *Delphinapterus leucas*) and seals (*Phocavitulina L*) that are in captivity in a water park and sea lions (*Zalophus californianus*) that are free-ranging on the California coast (Wartecki and Rzymiski, 2020). Based on these examples, there is concern about the devastating effects of coronaviruses on these already endangered species. Another example of risk is manifested by the interspecific transmission of these viruses. In fact, studies have shown that new coronaviruses (SARS-CoV-2) identified in both social bottlenose dolphins and beluga whales indicate a potential interspecific transmission event from belugas to dolphins (Mathavarajah *et al.*, 2021). Based on these studies, the impacts of COVID-19 on aquatic mammals can be better understood, including the loss of life of susceptible species and the likelihood of interspecific transmission of SARS-CoV-2 once it infects a population of susceptible marine species. While classes of aquatic vertebrates other than marine mammals are not likely to be a host or intermediate reservoir for SARS-CoV-2, transmission of this virus in aquatic invertebrates remains poorly studied and therefore has no specific features to report.

Risks of ecological impact: During the persistence of the COVID-19 pandemic, the destruction of SARS-CoV-2 in wastewater during disinfection or removal by other treatment processes will help eliminate the risk of transmission in the environment. According to the World Health Organization (WHO, 2020), filtration and disinfection of municipal wastewater in wastewater treatment plant systems are sufficient to inactivate the viruses. However, several factors allow the virus in hospital wastewater to escape this treatment. In fact, a defective network with collapsed pipes or pipes with fractures or cracks allows infiltration of wastewater and thus favors the spread of SARS-CoV-2 in different environments (watercourse, water body, septic tank, soil...). In addition, treatment in wastewater treatment plants is not widespread in some developing countries or even in rural areas of developed countries (Bandala *et al.*, 2021). In fact, a study in a Fangcang Hospital reported the presence of SARS-

CoV-2 viral RNA (557 to 18744 copies/L) in septic tanks after disinfection with 800 g/m³ of sodium hypochlorite, but its absence was reported when 6700 g/m³ of sodium hypochlorite was applied (D. Zhang *et al.*, 2020a). This same study estimates that the currently recommended disinfection dose (800 g/m³) could effectively remove aqueous SARS-CoV-2 viruses in wastewaters containing limited suspended solids, such as wastewater treatment plants, but this is insufficient for viruses embedded in suspended solids and require a higher level of supplemental chlorine-based disinfectant (D. Zhang *et al.*, 2020a). This study shows that a treatment system with two units: preliminary disinfection tank followed by a septic tank could be a source of environmental contamination showing that disinfection alone may not be effective. Nevertheless, the overuse of chlorine-based disinfectants raises concerns about disinfection by-products (DBPs) that are harmful to ecosystems and human health (D. Zhang *et al.*, 2020a); (Bandala *et al.*, 2021). Furthermore, some wastewater treatment plants serve as water resources for drinking water production, reuse for industry, public bathing, irrigation, recreation, and natural habitats (Westhaus *et al.*, 2021), and for the production of sludge as a fertilizer applied to soil. It is therefore not surprising that, communities without safe sanitation infrastructure in place will put many people and sensitive species at risk ((Mathavarajah *et al.*, 2021); (Nwobodo and Ejike, 2020)) and contribute to the release of these viruses into rivers, groundwater and coastal waters. In addition, land application of sludge from wastewater treatment plants contaminates the soil. Soil is an organic-rich matrix that can protect various viruses including SARS-CoV-2 (Wiktorczyk-Kapischke *et al.*, 2021) and behaves as a viral repository by deposition. Thus, once contaminated, soil can serve as a secondary source of SARS-CoV-2 spread for an extended period of time (D. Zhang *et al.*, 2020b) and poses a risk to people who may come in contact including public park lawns, golf courses, and crops (Lahrich *et al.*, 2021). It is therefore important to remember that the risk of contracting the virus is possible during recreational water use, particularly where poorly treated wastewater is discharged (Cahill and Morris, 2020). It is increasingly likely that humans and wildlife exposed to waterways contaminated by sewage effluent will be exposed to this virus. In addition, septic systems may also act as a long-term source of SARS-CoV-2 viral RNA release into waters and thus pose high ecological risks and threats to human health (D. Zhang *et al.*, 2020a).

Today, even countries with access to effective wastewater treatment have recently detected SARS-CoV-2 in their environments. In fact, one study showed contamination in outdoor environmental samples from three Wuhan hospitals with SARS-CoV-2 including soils, aerosols, sewage and wastewater treatment areas. This study suggests that this contamination is likely caused by aerosol particles from wastewater containing SARS-CoV-2. Thus, the process of spread of SARS-CoV-2 in the environment is governed by physical flow phenomena such as aerosolization of virus-laden droplets, its dispersion in the air and its deposition on surfaces. Generally speaking, relatively large droplets (>100 µm) would evaporate slowly and are likely to deposit on surfaces and smaller droplets (<100 µm) would undergo rapid evaporation and form droplet nuclei (<10 µm) that would remain in flight and disperse over a wide spatial extent (Erick R. 2021). Therefore, there are high-risk areas for the spread of SARS-CoV-2 in the outdoor environment of hospitals, calling for the sealing of the wastewater treatment unit and comprehensive sanitation to prevent the risk of COVID-19 transmission (D. Zhang *et al.*, 2020b). Furthermore, an experimental study conducted with a nebulizer device, shows that SARS-CoV-2 remains viable in aerosols for up to 3 hours (van Doremalen *et al.*, 2020). However, the maintenance of SARS-CoV-2 infectivity on different environmental surfaces (water, soil, plants, ..) is unknown and requires further study to better assess the risk of infection associated with exposure of humans and animals that would come in contact with these contaminated surfaces.

Conclusions and future research directions: Wastewater, including hospital wastewater, represents a pathway for transport of viable SARS-CoV-2 viral material to aquatic and terrestrial environments when environmental conditions (temperature, organic matter,

inadequate disinfection, humidity, exposure to sunlight ...) are favorable. Thus, the human and animal health and ecological risks associated with this exposure require evaluation of the effectiveness of wastewater treatment practices to remove or deactivate these viruses and monitoring of high-risk areas of the hospital environment. Thus, based on the knowledge of viability, infectivity of SARSCoV-2 and its mode of spread, research directions should be explored to establish a standardized monitoring protocol with thresholds of acceptability. This tool provides an early warning when SARSCoV-2 exceeds this threshold in order to provide early action and continuous improvement of wastewater treatment processes. The whole system allows to control the spread of the current COVID-19 pandemic in the environment and to prepare for the emergence of future viral pandemics.

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