

Review

A Review on SARS-CoV-2 Genome in the Aquatic Environment of Africa: Prevalence, Persistence and the Future Prospects

Kingsley Ehi Ebomah ^{1,*}, Luyanda Msolo ¹ and Anthony Ifeanyi Okoh ^{1,2}

¹ SAMRC Microbial Water Quality Monitoring Centre, University of Fort Hare, Alice 5700, South Africa; lmsolo@ufh.ac.za (L.M.); aokoh@ufh.ac.za (A.I.O.)

² Department of Environmental Health Sciences, College of Health Sciences, University of Sharjah, Sharjah P.O. Box 27272, United Arab Emirates

* Correspondence: kingsleyebomah.ke@gmail.com; Tel.: +27-635-857-544

Abstract: The COVID-19 pandemic (Coronavirus disease 2019) remains problematic in all its manifestations on the global stage where countless events of human-to-human exposure have led to fatal cases; thus, the aftermath being an unprecedented public health concern, with inaccessible health care and the instability of economies and financial institutions. These pose massive obstacles that can insatiably devour existing human resources causing negative impacts, especially in developing countries. Tracking the origin, dissemination and mutating strains of the novel severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) on population-wide scales is a somewhat overwhelming task, with the urgent need to map the dissemination and magnitude of SARS-CoV-2 in near real-time. This review paper focuses on the poor sanitation of some waterbodies and wastewater management policies in low-income African countries, highlighting how these contribute to the COVID-19 pandemic on the continent. Since the outbreak of the novel coronavirus pandemic, there has been an upsurge in scientific literature and studies concerning SARS-CoV-2 with different opinions and findings. The current paper highlights the challenges and also summarizes the environmental aspects related to the monitoring and fate of the SARS-CoV-2 genomes in the aquatic milieu of Sub-Saharan Africa.

Keywords: coronavirus; COVID-19; environment; public health; SARS-CoV-2



Citation: Ebomah, K.E.; Msolo, L.; Okoh, A.I. A Review on SARS-CoV-2 Genome in the Aquatic Environment of Africa: Prevalence, Persistence and the Future Prospects. *Water* **2022**, *14*, 2020. <https://doi.org/10.3390/w14132020>

Academic Editor: Constantinos V. Chrysikopoulos

Received: 31 March 2022

Accepted: 22 June 2022

Published: 24 June 2022

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1. Introduction

Emerging viruses have been described by several authors [1–3] as predominant infectious agents that have frequently been increasing in prevalence and geographical patterns. It has been established that many emerging viruses have ribonucleic acid (RNA) genomes compared to the few with deoxyribonucleic acid (DNA) genomes [4]; however, RNA viruses are typically less conservative than viruses with DNA genomes; the argument is that this dissimilarity primarily reveals their differing evolutionary rates. Several studies have revealed that many emerging viruses have respective animal reservoirs; by such means, the emerging viral infections could typically be classified as cross-species transference [5]. For instance, human immunodeficiency virus (HIV) type 1 (HIV-1) has its phylogeny linked to the HIV strain found in chimpanzees [6]. Of the other emerging viruses, the novel SARS-CoV-2 (i.e., severe acute respiratory syndrome coronavirus-2) is regarded as a virus with positive sense single stranded RNA (ssRNA) belonging to the Coronaviridae family, established as the microbial pathogen that caused the novel coronavirus disease-2019 (COVID-19) [7]. SARS-CoV-2 is also closely related to coronaviruses affecting the Himalayan palm civet (also known as *Paguma larvata*) [8].

The ongoing COVID-19 pandemic was first reported in December, 2019, in Wuhan, China and has rapidly spread throughout the world; presently, there are only eight countries without reported COVID-19 cases. COVID-19 is still a serious public health threat claiming millions of lives across the globe as the emergence of different coronavirus variants becomes worrisome as we witness a second wave of COVID [9]. The current outbreak is the third

documented spill-over of an animal coronavirus to humans in two decades that gave rise to a global epidemic [10].

Coronaviruses comprise members of the sub-family *Coronavirinae* which belongs to the family *Coronaviridae* in the order Nidovirales. *Coronavirinae* is divided into four genera, namely alphacoronavirus (ACoV), betacoronavirus (BCoV), gammacoronavirus (GCoV) and deltacoronavirus (DCoV) [11]. Genus *Betacoronavirus* is made up of SARS and Middle East respiratory syndrome (MERS) as well as the novel SARS-CoV-2 [12]. To date, six coronaviruses have been identified to be pathogenic human viruses (PHV). Four coronaviruses have been reported to be prevalent and these human coronaviruses (HCoV) consist of HKU1, NL63, OC43 and 229E [13]. ACoV consists of HCoV- NL63 and 229E, while BCoV comprises HCoV-HKU1, OC43, SARS-CoV, as well as MERS-CoV. However, GCoV contains avian infectious bronchitis (AIB) virus and many other coronaviruses, and DCoV includes the presently revealed avian coronavirus [14].

The novel COVID-19 is closely related to SARS and MERS concerning its genomic features; recently, a study reported that the recent human strain SARS-CoV-2 shared 99% sequence similarity with the pangolin [15,16]. Previously, some reports linked SARS-CoV-2 with milder infections. Likewise, both SARS and MERS were primarily associated with nosocomial spread, whereas SARS-CoV-2 is easily disseminated in the environment. Arguably, MERS, SARS and SARS-CoV-2 have become the latest and prime health threats all over the world [17]. The most common COVID-19 symptoms include cough, fever, sputum, dyspnea, myalgia, sore-throat/swollen gums, abdominal pain, conjunctivitis and loss of smell or taste (olfactory), nausea, anorexia, vomiting, among others; bats were recognized as the presumptive natural reservoir [18,19]. Preceding studies have highlighted that in South Africa alone, there has been a significant rise in the number of deaths occurring in individuals of all ages [20,21]. As of March 2020, the report from the World Health Organization (WHO) estimated the rate of COVID-19-related deaths worldwide to be about 3.4% and it is increasing [22]. Presently, the United States of America (USA) has the highest number of COVID-19 positive cases and this has led to unprecedented fatalities among immunosuppressed individuals, with an initial hospitalization rate of about 12.3 patients for every 100,000 population in the US. The current COVID-19 has become an unadorned disease in the elderly, and those with the highest risk of death have been perceived to be individuals aged over 80 years [23,24].

The ongoing COVID-19 outbreak is considered as the medical condition related to the novel SARS-CoV-2 infection; categorized by a respirational syndrome with an inconstant degree of severity, extending from a minor infection of the upper respiratory tract to acute interstitial pneumonia as well as critical respiratory distress syndrome [25]. Some scientists recently analyzed the information from a commonly used symptom-tracking application and discovered six different types of COVID-19, respectively differentiated by a group of other symptoms which include persistent headaches, fatigue, muscle pains, diarrhea and shortness of breath and also loss of appetite [26,27]. Another study by Rahman et al. reported coronavirus strains swiftly adapting to diverse environments but there have been few studies on the detection of coronavirus in the aquatic milieu [28]. In the past decade, several studies have reported inadequately treated wastewater effluents as one of the major contributors in the circulation of human enteric pathogens in our communities and subsequently resulting in illness and outbreaks, a major human health concern [29–31]. SARS-CoV-2 are envelope viruses and may have the ability to survive harsh conditions.

In such a short space of time, many lives have been impacted by the COVID-19 pandemic with continuous waves ongoing, along with spikes in cases; thus, there is a need for more surveillance studies in order to contribute to the scarcity of information. Figure 1 represents the world map showing the confirmed cases and mortality rates in the different continents. Many wastewater treatment plants (WWTPs) discharge poorly treated effluent into the various receiving watersheds and in some rural areas, influent is being emptied into the nearby waterbodies as a result of broken down plants or dilapidated facilities. There have been several studies reporting the occurrence of SARS-CoV-2 RNA in the aquatic

environs; however, due to confidentiality purposes, the names of such wastewater works (WW) are protected. An example can be seen in a study by Johnson et al. [32], who reported SARS-CoV-2 RNA in untreated wastewater in the Western Cape Province of South Africa. It has been established that some of these surface waters serve domestic functions in rural areas with the Eastern Cape Province housing numerous poor infrastructures and facing stern under-development; the locals engage in a regular practice of using rivers, dams and streams for domestic purposes. Moreover, in some communities, these water resources can serve as irrigation water for local farms [33], hence, creating a possibility of transmitting microorganisms to food stuffs including fruits and vegetables; maybe proving a point or perhaps pointing out the coronavirus journey from the toilet to the dining table [34].

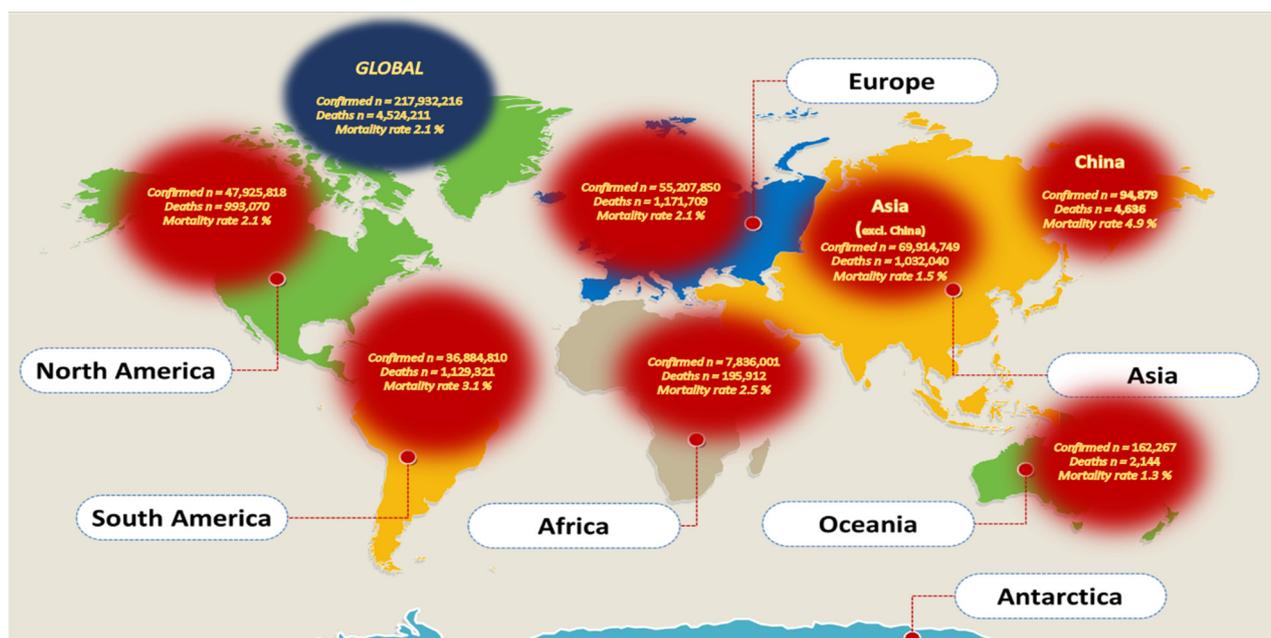


Figure 1. World map showing total cases, total deaths and mortality rates of COVID-19 (As of 31 September 2021) (Source: [shutterstock.com](https://www.shutterstock.com) (accessed on 30 March 2022)).

2. Monitoring COVID-19 Using Wastewater-Based Epidemiology (WBE)

Increased Waste Production

The production of wastewater (WW) incidentally occurs with an extensive collection of environmental components, including deforestation, air and water pollution, as well as soil erosion [35]. The guidelines involved in quarantine and self-isolation, recognized in many countries, have led people to intensify demands for online shopping and home delivery services. Subsequently, biological waste in municipal wastewater treatment plants (WWTPs) produced by households has amplified due to the global lockdown. Self-isolation periods were rampant in epic centers, hence contributing to the increased viral loads.

Several researchers have reported that the SARS-CoV-2 genome is shed through the urine and excreta of infected individuals [36]. This may imply there exists a probable complex cycle involving transmission of the viral components into the communities recurrently. The consistent unhygienic state in many Sub-Saharan African countries is distressing, accompanied by common unpleasant practices such as open-defecation and pit-latrines sometimes even close to surface waters [37,38]; this ecological condition may exacerbate the accumulation of pathogens in the environment including coronavirus [39]. Although the retention of viral RNAs in river water and WW niches remains ambiguous, nevertheless, their detection in water samples collected from low sanitation countries [40,41] points out a disquieting health risk. Many low-income countries in the African region either have obsolete WWT facilities or a complete lack of proper waste management infrastructures,

which compels them to non-hygienic practices and thereby overwhelming the limited waste management resources and subsequently impacting the aquatic environment with excessive poorly treated waste. There are various possible routes through which enteric viruses can be transmitted into the environment (Figure 2). Poor sanitation consists of indiscriminate waste disposal without proper treatment, especially in rural areas with no toilets hence, villagers excrete in bushes close to rivers and streams. Currently, there is a lack of information concerning the transmission of coronavirus by vectors; however, a study carried out in the US by Balaraman et al. [42] reported that flies could readily acquire and harbor SARS-CoV-2 RNA from virus-spiked medium or milk, but no infectious virus was recovered from any environmental samples. The study suggested that flies most likely do not play a significant role in transmitting SARS-CoV-2 to humans and susceptible animals.

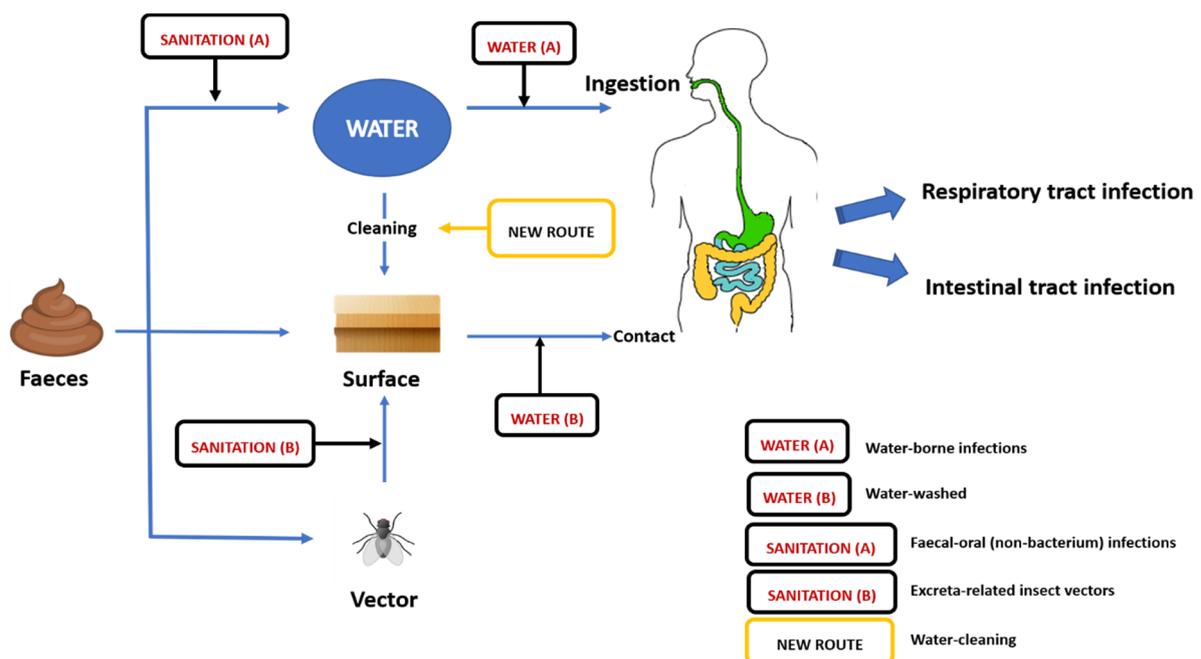


Figure 2. A flow-chart showing the possible routes of transmission of enteric viruses into the environment attributable to waste mismanagement. (Vectors such as flies which harbor bacterial strains may be involved in the spread of SARS-CoV-2; Fecal contamination of water can lead to faecal-oral infections which can result in water-borne infections including respiratory tract and intestinal tract infections) (Source: <https://ars.els-cdn.com/> (accessed on 30 March 2022)).

Moreover, inorganic waste has also increased because more food items are purchased online and are shipped [43]. In Wuhan, where the novel coronavirus was first reported, hospitals produced approximately 240 tons of medical-clinical waste (MCW) daily during the enduring pandemic as compared to the previous daily mean of 50 tons of MCW. Hence, clinical waste has also increased drastically [44]. In the USA, a rise in MCW also continues from personal protective equipment (PPE) disposal which creates another concern for sustainability [45], which justifies the upsurge of the COVID-19 crisis worldwide.

3. Reduction in Waste Management

Waste mismanagement can lead to the unknown contamination of healthcare workers (HCW) with coronavirus. The recycling of waste (specifically clinical waste) has continuously been a major environmental concern in every country worldwide [46]. Recycling is an effective technique to save energy, conserve natural resources as well as for the prevention and control of environmental pollution [47,48]. Due to the continuing COVID-19 pandemic, many countries including the USA and some affected European countries have restricted waste management and waste recycling-based programs around some major cities, as

public health authorities are worried about the danger of coronavirus dispersal in waste recycling facilities. Furthermore, these practices could contribute to certain factors that may aid the dissemination of SARS-CoV-2 genomes into the aquatic environment [49,50].

4. Ecological Impacts of COVID-19

In Africa, there are major concerns due to the inadequate resources regarding personnel, beds and medical facilities [51]. Among the challenges with which Africa is confronted, are the existing high levels of poverty coupled with a high incidence of other infectious diseases (such as HIV/AIDS, TB, malaria, cholera) and other seasonal yet very infectious diseases with proportionally high morbi-mortalities within the continent. These endemic infectious diseases include but are not limited to Ebola virus disease (EVD), dengue fever virus (DFV), Rift Valley fever (RVF). As the current pandemic (COVID-19) surges across the globe and with the prementioned infections already terrorizing the African populations, the COVID-19 pandemic exacerbates the situation even further, resulting in a disquieting health burden and subsequently a dismantled socio-economic and environmental eminence across the African region. The financial status of the countries within the African region and the indubitable lack of vital resources worsens the situation inasmuch as the COVID-19 pandemic is concerned [52,53]. Given the multitudinous number of these interconnected issues, the continued COVID-19 wave will lead to a more appalling and devastating human health burden [54]. Many studies have reported a surge in global job losses due to lockdown as several companies have gone bankrupt [55,56]. Workers have to adopt a new style of service delivery and not everyone could cope because of the rise in digital technologies. The situation led to the sitting at home and other social distancing measures for critically ill individuals, which in turn resulted in the discharge of SARS-CoV-2 genetic materials into the environment via the sewer systems.

4.1. Other Indirect Effects of SARS-CoV-2 Genome on the Ecosystem

In China, WWTPs have been fortifying the decontamination routines (mainly by improved use of antimicrobial agents) to avert the spread of SARS-CoV-2 genomes into the aquatic milieu. Nevertheless, there is an absolute scarcity of information on the persistence of the novel SARS-CoV-2 in surface water and WW effluent samples [57]. In contrast, the excessive use of disinfection (particularly chlorine) in the water and WWT facilities could have a detrimental effect on our wellbeing [58]. Notwithstanding, the disinfecting effect of free chlorine with regards to inactivating microbial activities has brought concern in the effective and efficient management of the ongoing novel COVID-19 global pandemic and if the potential secondary dissemination of SARS-CoV-2 is possibly through WW [59]. In another study by Vadiati et al. [60], the authors stated that SARS-CoV-2 is not considered robust and is less stable in the environment but the novel virus has more potential to spread in the aquatic environment. The presence of SARS-CoV-2 has not been reported in drinking water; however, in a study carried out in Ecuador, coronavirus is less persistent in water compared to other enteric viruses, thus it was suggested that SARS-CoV-2 is more susceptible to chemical inactivation, such as with solutions based on chlorine and other disinfectants [61]. The study argued that there could be a risk when sewage enters distribution systems that do not disinfect water with chlorine and that the survival and transport of SARS-CoV-2 in aquatic environs may affect drinking water supplies in places where rivers are the main sources of water.

4.2. Sewer Networks as Red Flags in the Proliferation of SARS-CoV-2

Throughout the early 1980s, since the first descriptions of AIDS, several studies have reported the causes and significances of many emergent viral infections. So far, in spite of extensive research efforts and achievements, viral diseases remain present in every living being, as established by the emerging viruses recognized ever since the upsurge of AIDS, for instance, HCV, Sin Nombre, Nipah, Hendra and currently COVID-19, and much more venerable pathogenic microbes, such as dengue virus and West Nile virus, which

in recent times have extended their global prevalence [62]. Not much progress has been made towards research in emerging viruses and advances for the future. The information mainly obtained from media releases via the National Institute for Communicable Diseases (NICD) South Africa, indicated that there is a probable effect of coronavirus infection in HIV-positive individuals living in South Africa [63]. In addition, there has been an overwhelming surge in COVID-19 cases since the start of the winter season in South Africa, and almost all provinces are considered as coronavirus red zones.

Elsewhere, the prevalence of the SARS-COV-2 genome in municipal WW sludge has been used as a principal indicator of the active disease-outbreak intricacies. Moreover; the occurrence of coronavirus in the stools of patients has been reported [64], thereby making it effortlessly easy to transmit it through feces. Additionally, since these viral particles remain viable for a few hours to several days in aerosols, contaminated objects/open surfaces (tables, door-grips, locks and other household resources) [65] and can therefore be transported to water collection and treatment facilities through drainage systems. The circulation of COVID-19 in the provinces continues to threaten the socioeconomic well-being of the country, and evidently accentuates the communal health burden brought about by this disease, justifying calls for an urgent need for a proper evaluation of this pandemic even in the low-income regions of the country. There have been several studies reporting SARS-CoV-2 RNA recovered from environmental niches in Africa including reports by Adelodun et al. [66], Amoah et al. [67], Elsamadony et al. [68], Gwenzy [69] and Street et al. [70]; however, more studies investigating SARS-CoV-2 in environmental samples are needed in the African continent.

5. Analysis of SARS-CoV-2 Genome in Environmental Niches

Effective genomic surveillance is needed. The loss of lives due to COVID-related complications is alarming. More studies are needed to establish that there is extended occurrence of SARS-CoV-2 RNA in sewer systems, with prospects for improvement as more information becomes available. A current study by Ahmed et al. reveals analysis indicating confined measures of the shedding of viral genetic materials in fecal samples collected from infected individuals in the course of hospital admission, self-isolation or lockdown [71]. The viral RNA components are estimated in the purified RNA samples through real-time quantitative PCR (RT-qPCR) and used for the quantification of viral genomes in the definite volume of WW sample. Viral levels in WW are added to the WW flow rates and then the evaluations of fecal viral load for every toilet flush, in order to carry out modelling of the estimated incidence of infection as well as the probability of illness in the sampled community [72]. This occurrence replicates the viral load defecated from ill and asymptomatic people with a few reports establishing that genomes of SARS-CoVs are existent in WW effluent for several days [73]. Studies such as that by Alygizakis et al. highlight the methodologies for detecting the SARS-CoV-2 genome in WW effluent samples [74].

Nucleocapsid (N) Gene, Standard Curve and Ct Value as an Indicator of the Viral Load

There are four structural proteins encoded in the novel SARS-CoV-2 which are the envelope (E), matrix (M), spike (S) glycoprotein and nucleocapsid (N) including N1, N2 and N3 and these targets distinct regions of the N gene [75]. Research scientists are working tirelessly to avert the spread of SARS-CoV-2 and flatten the curve, with many surveillance studies and coronavirus wastewater analyses becoming common. There are certain parameters that are relevant when analyzing the standard curve plot generated from the qRT-PCR run. The number of RNA copies in wastewater samples can be calculated via the standard curve (SC) [76]. For the SC, the parameters obtained include error (≤ 0.0), efficiency ($\geq 100\%$) and R^2 as the coefficient of correlation obtained for the standard curve (which should be >0.99). Figure 3 highlights the molecular detection of the SARS-COV-2 genome by qRT-PCR, showing the amplification plot and standard curve plot.

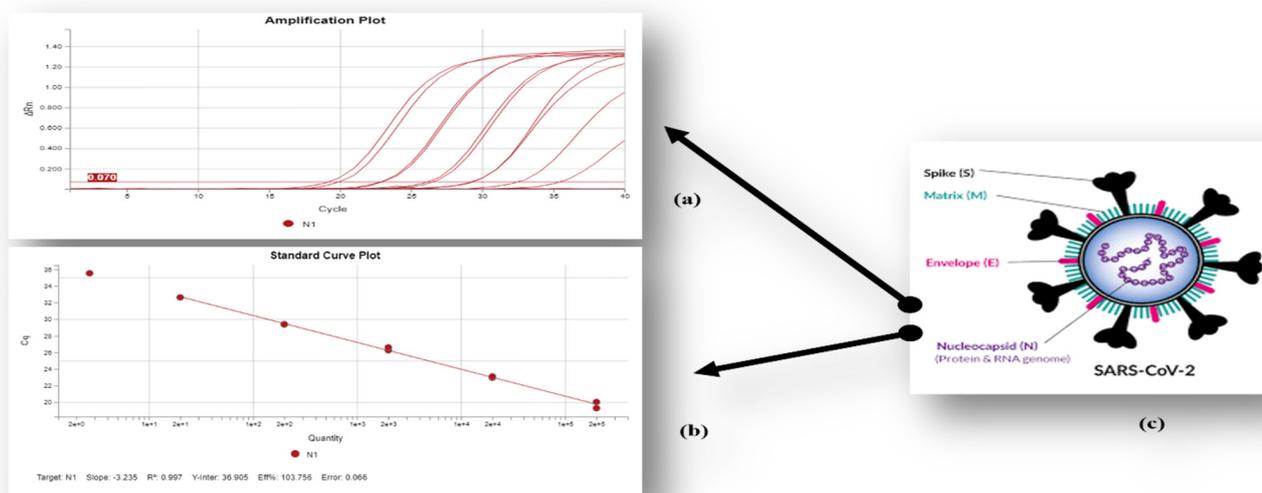


Figure 3. Molecular detection of SARS-CoV-2 genome by qRT-PCR. (a) Amplification plot; curves indicate successful amplification of N1 gene. (b) Standard curve plot; relevant parameters including slope, R^2 , efficiency (%) and error. (c) SARS-CoV-2 showing the nucleocapsid.

The cycle threshold (Ct) is the number of cycles during the accumulation of fluorescent signal; a high Ct value indicates a low concentration of viral genome which is typically associated with a lower infectivity risk [77]. With ongoing investigations, it is still unclear if the Ct value as an indicator of the estimated viral load could give the severity of COVID-19. There is a scarcity of information on the prevalence of SARS-CoV-2 in the aquatic environment in many African countries.

6. Emerging Variants and the Impending COVID Waves

According to the Centers for Disease Control and Prevention (CDC), SARS-CoV-2 variants can be classified as variants of interest (VOI), variants of concern (VOC), and variants of high consequence. There are three new variants that have swiftly become dominant within their countries and these variants include B.1.1.7 (also known as VOC-202012/01), 501Y.V2 (B.1.351), and P.1 (B.1.1.28.1). The B.1.1.7 variant (which has 23 mutations with 17 amino acid changes) was first described in the United Kingdom (UK) on 14 December 2020; while the 501Y.V2 variant (with 23 mutations with 17 amino acid changes) was first reported in South Africa on 18 December 2020; and the P.1 variant (about 35 mutations with 17 amino acid changes) was reported in Brazil on 12 January 2021. The elderly with underlying conditions and individuals with core morbidities are exposed to more health risks under the second wave of the coronavirus pandemic. The emergence of mutations in viruses is not uncommon [78], thus, new variants of SARS-CoV-2 are predominant globally, with 501.V2 recently reported in South Africa. Scientific analysis of the new variants has found that they are about 70% more transmissible than the original virus. There is a lack of information on the emergence of new variants. Concomitantly, as vaccines are being developed, additional studies are required to explore the emergence of various variants.

Most recently, there has been the emergence of the Delta variant from India which shares mutations with other VOC. Coronavirus mutations are occurring so fast, causing widespread dispersal, swift infection and also an increase in the severity of positive cases. In Belgium, there was a report on the detection of SARS-CoV-2 variants in wastewater systems and this is of great concern to public health [79]. Another study by Shao et al. [80] pointed out that SARS-CoV-2 has a strong vitality in low temperature water environs and new SARS-CoV-2 mutations are constantly emerging, further raising concerns of

increased transmissibility into the existing waterbodies [81]; hence, there is a need to develop approaches to better understand the diversity of the variants of concern, geographic dissemination and their impact globally.

More variants are still anticipated, especially those that would evade the immune response to the available vaccines. More research work is required to study how antibodies behave with the new variants. As researchers are looking out for treatments and ways to manage COVID, so also the virus is looking for a way to circumvent this mechanism; hence, the emergence of mutants. Figure 4 shows some variants along with the country of origin. Most recently, the omicron variant has evolved and this resulted in a spike in cases providing further concern as to the effectiveness of the existing vaccines.

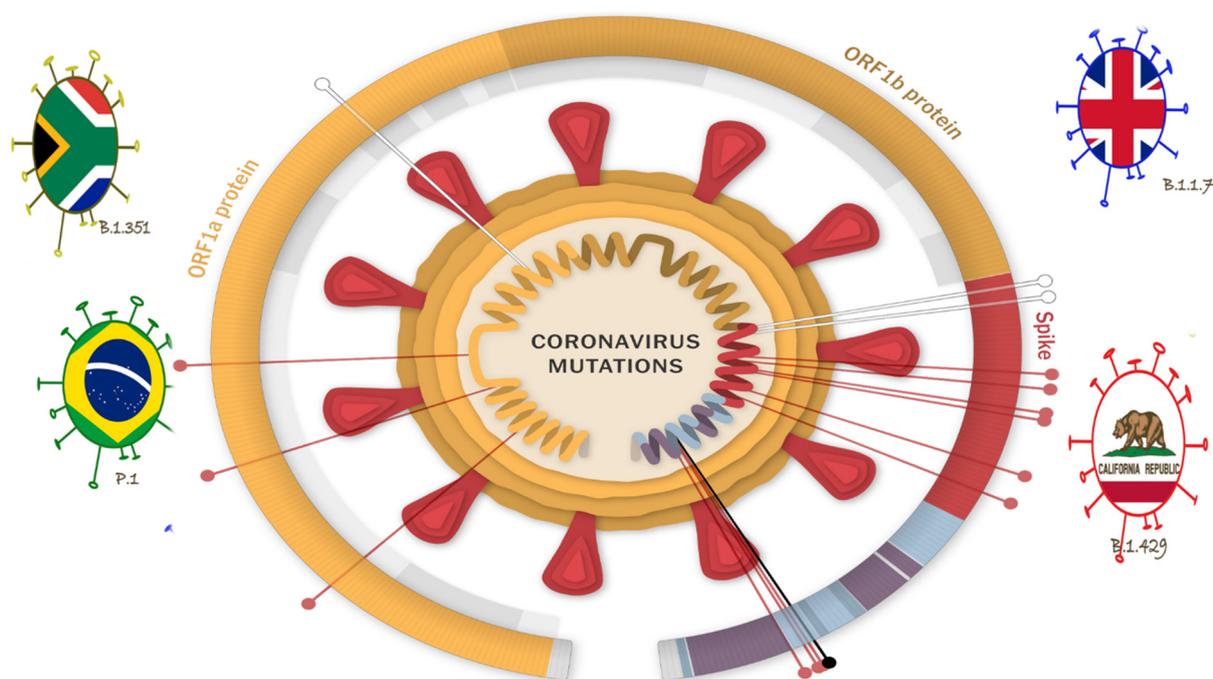


Figure 4. Emerging SARS-CoV-2 variants and the countries of origin (Source: <https://www.nytimes.com/interactive>; <https://www.tourmag.com/photo/art/> (accessed on 30 March 2022)).

7. Progress on the Development of Therapeutics for COVID-19

There are presently two approved vaccines for COVID-19 and a few other vaccines are in Phase 3 clinical trials; however, there have been reports of side effects as the vaccines are being administered across the world besides Africa. In a time of the most worrying uncertainty, researchers are still turning the screws to bring a permanent solution to the global scourge. The ability of SARS-CoV-2 to emerge swiftly as a result of an increase in the rates of genomic switch recombination (GSR) and the capability of the cross-species suggest that even vaccines may be ineffective to combat future PHV outbreaks as there is the probability for an emerging strain, as was the instance of the outbreak of SARS-CoV between the years 2003 and 2004 via a different reservoir. Some of the reports might be threatening to humanity; meanwhile it is interesting to see the developments of ways to combat the pandemic and the vaccine trials that have been included. As aforementioned, there have several limitations with the available treatments. The Centre for Disease Control and Prevention (CDC) authorized and recommended three vaccines to be used to prevent COVID-19. Table 1 summarizes a list of the few developed therapeutics for COVID-19 as well as the recently developed vaccines.

The Pfizer-BioNTech vaccine obtained full approval from the US Food and Drug Administration (FDA); however, Emergency Use Authorization (EUA) authorized a third dose for immunocompromised individuals. Over 51% of the US population have not

been double-vaccinated. Presently, vaccines are being administered across different countries, with the Johnson & Johnson vaccine being the most distributed in many countries. COVID-19 related cases have dropped worldwide but developing countries including SA are still at a risk of a fourth wave, one of the major factors being the persistence of the viral genome in the environment. There is a high tendency of transmission and likelihood of the emergence of another enteric virus or more dangerous variants in the near future; hence, more surveillance studies should be carried out in the different regions of the world. Commonly, WWTPs turn out to be a major source of antiviral drugs in existing surface water bodies, and freshwater sources, with decay rates similar to the non-enveloped viruses that are usually targeted during water treatment using antimicrobial agents including chlorine; moreover, more research is needed to further validate the therapeutic benefits of ozone therapy [82].

Table 1. List of previously used drugs and vaccines for COVID-19 with country of origin.

| Treatment Administered/ Vaccines Used | Country of Origin | Benefits/Limitations | Shelf Life | Storage | References |
|--|--|---|------------|---------|------------------------------------|
| Hydroxychloroquine | USA | Little or no effect on overall mortality. | NA | NA | Recovery Collaborative Group, [83] |
| Remdesivir | Currently not approved for marketing in any country | It is an inhibitor of the viral RNA-dependent, RNA polymerase with in vitro inhibitory action against SARS-CoV. It has little to no effect on COVID patients. | NA | NA | Hsu, [84]; Sisay, [85] |
| Lopinavir/Ritonavir | USA | Harsh side-effects may consist of pancreatitis, liver problems and high blood sugar | NA | NA | Ailabouni et al. [86] |
| Interferon | Currently available for sale in countries besides USA | Possible hepatotoxicity | NA | NA | Davoudi-Monfared et al. [87] |
| Pfizer-BioNTech COVID-19 vaccine | Authorized and recommended by CDC to prevent COVID-19. Originally developed in the USA | 95% effective; mRNA-based vaccine that produces T-cell responses specific to SARS-CoV-2 proteins. Being administered. | NA | NA | Pacheco et al. [88] |
| Moderna COVID-19 vaccine | USA is the first country to greenlight its use | Produces T-cell responses specific to SARS-CoV-2 proteins | NA | NA | Haque and Pant, [89] |
| Oxford-AstraZeneca vaccine | University of Oxford, UK | Being administered | NA | NA | Knoll and Wonodi, [90] |
| Janssen COVID-19 vaccine | Belgium | Clinical trials in progress | NA | NA | Bell, [91] |
| Novavax COVID-19 vaccine | Gaithersburg, Maryland, USA | Clinical trials in progress | NA | NA | Mehrotra et al. [92] |
| Johnson and Johnson vaccine | USA | Being administered | 2 years | −20 °C | [93] |

Among the numerous existing viruses, many of them cause zoonotic diseases and they include the following: rabies virus, hantavirus, Zika virus, Ebola virus, West Nile virus and Yellow fever virus [94]. In 2013, Porcine epidemic diarrhea virus (PEDV) is an ACoV re-emergent in the US as a new, worrying diarrheal infection in swine. PEDV circulated swiftly all over the US, instigating economic losses to the swine industry [95]. Some other factors that influence the emergence of pathogens include drastic climate change, human movements, as well as economic development and land use.

8. Conclusions

As a result of poor municipal wastewater treatment, there has been a negative impact from COVID-19 in the aquatic milieu of many African countries. The impact comes with clinical significance, pointing out hospital WW as the major source of the novel SARS-CoV-2, considering the admission of patients through the spike in coronavirus infection-related cases. Most African countries are already battling numerous challenges including poverty, inadequate sanitary resources, limited health services and the current burden of other endemic infectious diseases (e.g., HIV/AIDS, TB, malaria); with the present COVID-19 pandemic, it is certain that the African region is headed for nerve-racking public and environmental health mayhem. In spite of the lack of advanced infrastructure and wastewater treatment facilities, wastewater effluent should be properly treated before being discharged into receiving watersheds. Furthermore, surface water including rivers and streams should be treated before use for domestic functions. In addition, there is a need for the use of advanced technology techniques and more effective antimicrobial agents in hospital wastewater before its discharge into the aquatic system. Controlling the distribution and reduction in the morbidity of the ongoing pandemic is a major challenge as several vaccines are currently available. In addition, essential individual testing should be mandatory. People should be educated about and sensitized to the necessity of implementing the routine of good personal hygiene, the practice of social distancing and wearing face masks while in public places in order to manage disease progression. There is a probability of future outbreaks caused by SARS-like coronaviruses that originate from different reservoir hosts and environmental niches. Thus, rigorous studies should be carried out as well as the rapid deployment of the relevant resources and the provision of funds by health organizations to carry out source-tracking and the identification of pathogenic microorganisms, vital to extenuating the impact of global outbreaks.

Author Contributions: This paper was written with the contribution of all authors as follows: conceptualization, K.E.E., L.M. and A.I.O.; software, K.E.E.; validation, K.E.E., L.M. and A.I.O.; resources, A.I.O.; writing—original draft preparation, K.E.E.; writing—review and editing, K.E.E. and L.M.; supervision, K.E.E. and A.I.O.; project administration, A.I.O. All authors have read and agreed to the published version of the manuscript.

Funding: This research was funded by the University of Fort Hare, South Africa and South African Medical Research Council (SAMRC).

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Informed consent is not applicable.

Data Availability Statement: Not applicable.

Conflicts of Interest: The authors state no conflict of interest.

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