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Review Article

Risk of activation of human viruses lurking in ambient following COVID-19 prevention supplies excessive use

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Abstract

Due to extensive COVID-19 prevention measures, millions of tons of chemicals penetrated the natural environment. Alterations of viruses in the environment, the neglected perceiver of environmental fluctuations, remain obscure. Chemicals especially trihalomethane restrained the virus community diversity. Segments of SARS-CoV-2 RNA have been detected near hospitals that suggesting the environment as a missing link in the transmission route. Human viruses lurking in the environment were potentially activated by pandemic prevention chemicals, warning an overlooked burden to human health. This letter warns of the risk of activation of human viruses in the environment following the overuse of COVID-19 prevention devices and emphasizes the long-term monitoring of environmental viruses in the post-pandemic period.

More Information

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Introduction

Potential health threats originating from viruses in the environment have been a neglected subject. Equipped with the small genome (< 200 kb), high mutation rates, and frequent gene recombination, viruses evolve to be the most abundant biological entities on earth [1]. Non-culture methods (e.g., metagenomics, virome) [2] and specialized taxonomy approaches [3] make it possible to progressively unfold environmental virology from behind the veil. Viruses that host prokaryotes, animals, plants, and even humans have been confirmed to be extensively present in environmental media such as air [4], ocean (105-107 virus-like particles mL-1), and soil (103-109 virus-like particles g-1). Compared with other microorganisms, the current understanding of environmental viruses is still at a preliminary level. One of the urgent tasks is to illuminate the sensitive relationship between environmental viruses and human health [5].

During a pandemic, the environment fluctuated greatly with anthropogenic activities aimed at preventing and treating COVID-19. Viruses lurking in the environment are one of the first to realize this vacillation [6]. The average use of disinfectants in wastewater treatment plants increased during the pandemic. Chlorine and surfactants containing excessive biocidal agents were used to disinfect hospitals, residential areas, and wastewater treatment plant systems [6,7].

The played role of the natural environment in the outbreak of COVID-19 is becoming clearer with clues of the SARS-CoV-2 in vitro [8]. The distribution of SARS-CoV-2 during COVID-19 can be the last and most essential piece that completes the puzzle. So that SARS-CoV-2 RNA was found in water in sewage [9] and also, SARS-CoV-2 aerosol particles were detected in air at PM2.5 [10, 11]. To determine the origin of environmental SARS-CoV-2 RNA the areas of hospitals should be considered. As the pivot between artificial and natural habitats, the wastewater treatment plant is a potential reservoir of SARS CoV-2 [12]. Therefore, the areas around the wastewater treatment plant effluent receivers were crucial in assessing the transmission path through the environment. To substantiate the hypothesis that chemicals resulting from pandemic prevention measures alter the virus community and thus pose a fundamental risk, soil and ambient water samples near hospital areas and wastewater treatment plants should be collected and evaluated.

Detection of SARS-CoV-2 RNA in the environment

SARS-CoV-2 RNA has been found in the environment during treatment processes when the pandemic broke out [13]. Some studies quantified SARS-CoV-2 in raw sewage [14], wastewater [15], or receiving water of wastewater treatment plant effluent [16] through RT-qPCR, also, gene segments of SARS-CoV-2 may exist in natural water irrelevant with wastewater discharges. SARS-CoV-2, which is thought to be a fecal transmitted virus [17], can persist in the water environment [18]. Given that SARS-CoV-2 cannot survive disinfection in wastewater treatment plants [19]. the genetic material of the new coronavirus in the natural water nearby the hospitals may originate through direct contact or bioaerosol from COVID-19 patients [11]. In fact, RNA fragments of SARS-CoV-2 in natural water indicate a transmission pathway in which the aquatic environment served as an intermediate host. The virus may also be lurking in an environment that has not yet been identified. Several forms of SARS-CoV-2 including integrated enveloped particles were found to be stable in water for 12 days [20]. Despite this, whether or not SARS-CoV-2 was viable in actual aquatic conditions is vital to completing the through of spreading in the environment. Attempts have been made to evaluate the infectiousness of SARS-CoV-2 in water in terms of cytopathic effect [21]. Further efforts are imperative to assess the threat of the SARS-CoV-2 in the natural environment.

The virus community succession following the use of COVID-19 prevention supplies

Chemicals generated from COVID-19 pandemic prevention supplies lead to ecological impacts through the re-constructing of the virus community. Although the level of environmental pollution was thought to be drastically reduced due to widespread and severe lockdown [22,23], secondary pollution from disinfectants and medical treatment threatens the ecological balance [24]. The environment is considered to be a huge reservoir of viruses [25] and many viruses within were be detected to potentially infect humans. Members of human-related *Picornaviridae* such as *Enteroviruses*, *Coxsackieviruses*, *Echoviruses*, *Polioviruses*, *Hepatitis A virus* along *Rotaviruses* belong to *Reoviridae* have been observed in aquatic environments including rivers, lakes, sewage and even drinking water [26]. H5N1 virus [27] and H7N9 [28] virus as well as *Norovirus* [29] in soil posed threat to human health. The viruses that lurk in the environment are undoubtedly a threat to human health when they stimulate from dormant to a viable state. Therefore, monitoring for environmental viruses must be done immediately, especially when a public health crisis such as broke out of the COVID-19 pandemic. As adjunctive therapy, glucocorticoids are recommended for the treatment of moderate to severe patients [30] and are used clinically at a proportion of 44.5% [31]. Residue and by-products of excessively used corticosteroids drugs and disinfectants eventually flew into the environment through sewage, medical waste, and surface runoff. This would add the extra stress from chemicals such as trihalomethane, total chlorine, quaternary ammonium surfactants, and glucocorticoids to the virus in the environment. However, the effect of chemicals related to pandemic prevention sources on the viruses is unknown. Examining the environment-virus interaction with the concept of One Health helps to claim the growing concern about the excessive usage of pandemic devices [32,33].

In particular, the glucocorticoids from treatment and trihalomethane, total chlorine, quaternary ammonium surfactants from the disinfectants enter the ecology through household and medical waste. Undoubtedly the microbes in the environment were confronted with the interference of the above chemicals, which has been so far been ignored. This mini-review shed light on the short-term collapse of viruses and emphasized the ecological damage caused by pandemic prevention supplies from a dimension of the environmental microbial community, especially the viral one. In general, the microbial community succession followed the cycle of collapse, reorganization, exploitation, and conservation [34]. Pathogens, such as human viruses have a tendency to be predominant during succession [35]. Therefore, subsequent monitoring should be greatly important to comprehensively depict the succession process and avoid ecological threats in this procedure.

Human virus thriving following excessive disinfection

Viruses, especially some human viruses whose abundance increased with trihalomethane, evolve to gain resistance under excessive disinfection. Based on a study, *human gammaherpesvirus 4* and *Orf virus* responded to trihalomethane in positive correlation. Trihalomethane, a typical chlorination by-product, measured the chlorine-containing disinfectants consumption. The high concentration of trihalomethane in the effluent receptor of the wastewater treatment plant is consistent with the excessive usage of disinfectants during the COVID-19 pandemic. It is found that excessive use of disinfectants is the cause of the evil of microbial resistance [8].

Transforms of physiological state, for example, increased membrane permeability, stress response, and SOS response offered easier access to the resistance of microorganisms after disinfection [36]. It has been widely acknowledged that the virus frequently integrates and acquires host genes [37]. Equipped with the horizontal transfer, viruses served as a gene pool [38] and accumulated resistance through transduction [39]. The long-term exposure of disinfection byproduct is led to gene mutation [40]. Under the induction of disinfectants during the COVID-19 pandemic, human *gammaherpesvirus 4* and *Orf virus*, which are highly correlated with trihalo methane, may gain resistance through gene mutation or horizontal transfer.

In addition, the trihalomethane-virus coexistence implied intrinsic features that made it difficult to remove *Human gammaherpesvirus 4* and *Orf virus* through disinfection. In general, viruses are more resistant to disinfection than other pathogens [41]. Therefore, the endure simultaneously of viruses with trihalomethane in excessive disinfection circumstances is normal [42]. In addition, the herpes virus [43], as well as the *Orf virus* [44], were discovered to unite as vesicles. Depending on this morphology, viruses can effectively combat adversities such as disinfection [45]. Despite the prevalence of *Orf virus* [44] and *human gammaherpesvirus 4* [46], few types of research have focused on distribution in the natural environment that should be considered in a wider geographical range. Also, the mechanism of the amplifying link between trihalomethane and human viruses still needs to be explained through a small microcosm simulation experiment.

The proliferation of human viruses caused by gluco corticoids

Glucocorticoids are positively corresponded with potential virus viability, indicating a positive co-occurrence relationship between each other. In recognition of SARS-CoV-2 RNA genomes as well as glucocorticoid concentrations in a lake adjacent to a hospital during the COVID-19 pandemic, by considering the distance and amount of medical waste accumulation, the possibility of SARS-CoV-2 RNA and glucocorticoids through the hospital leakage to the adjacent lake was found [47]. The glucocorticoid, for example, methylprednisolone was used in the clinical treatment of 18.6% of COVID-19 patients [31]. Therefore, glucocorticoids may some extent represent hospital-related contaminants and embodied a novel coronavirus infection status. Glucocorticoids, as a double-edged sword, caused to stimulate dormant virus [48] and accelerate virus replication [49,50]. Presumably, glucocorticoids interacted directly with these viruses via idiosyncratic responsive elements. The herpesvirus replication gene expression is activated by glucocorticoids through ES-1 fragment-mediated interaction [51]. SARS-CoV-2 is bounded to glucocorticoids via the main protease Mpro based on computational calculations [52]. However, retaining this type of communication may be advantageous for SARS-CoV-2 [53]. Rare research to date has referred to the glucocorticoid-virus association in the aqueous medium. In situations where hormone residues in the environment have become a widespread problem [54], it is important to conduct research on the environmental interaction between glucocorticoids and viruses.

Conclusion

This mini-review focused on the characteristics of environmental viruses using high-intensity use of pandemic prevention resources during the COVID-19 epidemic. The abundance and viability of specific human viruses are potentially enhanced by trihalomethane and glucocorticoids, leading to a neglected threat to human health. From the vision of environmental virology, this study revealed environmental damage under unconventional human activities, that is, the excessive usage of pandemic prevention resources. It is important to study the mechanisms between viruses and epidemic prevention chemicals systematically at the community, species, and gene level. Studies should also be launched to assess the subsequent dynamics of the virus community and to track community succession trends. This review serves as a proposal for the development of environmental management policy in the post-epidemic period and emphasizes the need for regular monitoring of the human virus in the environment.

Declaration of interest

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