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Review article

Surveillance strategies for SARS-CoV-2 infections through one health approach

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A R T I C L E   I N F O

A B S T R A C T

Coronavirus disease-2019 (COVID-19), caused by the severe acute respiratory syndrome-coronavirus-2 (SARS-CoV-2), is an emergent disease that threatens global health. Public health structures and economic activities have been disrupted globally by the COVID-19 pandemic. Over 556.3 million confirmed cases and 6.3 million deaths have been reported. However, the exact mechanism of its emergence in humans remains unclear. SARS-CoV-2 is believed to have a zoonotic origin, suggesting a spillover route from animals to humans, which is potentially facilitated by wildlife farming and trade. The COVID-19 pandemic highlighted the importance of the One Health approach in managing threats of zoonosis in the human-animal-environment interaction. Implementing vigilant surveillance programs by adopting the One Health concept at the interfaces between wildlife, livestock, and humans is the most pertinent, practical, and actionable strategy for preventing and preparing for future pandemics of zoonosis, such as COVID-19 infection. This review summarizes the updated evidence of CoV infections in humans and animals and provides an appropriate strategy for preventive measures focused on surveillance systems through an On Health approach.

1. Introduction

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is the coronavirus disease 2019 (COVID-19) causative agent [1]. Coronaviruses (CoVs) are classified into *Nidovirales*, comprising the *Coronaviridae, Aeteiciridae, Roniviridae,* and *Mesoniviridae* families [2]. Three large CoV epidemics have been reported to date. From 2002 to 2003, a novel CoV infection outbreak occurred, and 8437 cases of severe acute respiratory syndrome (SARS) were reported in 32 countries [3–6]. Following the SARS-CoV outbreak, an epidemic of Middle East respiratory syndrome coronavirus (MERS-CoV) was reported in Saudi Arabia in 2012 [7,8], and pandemic coronavirus disease 2019 (COVID-19) emerged in 2019 [9]. CoVs also cause respiratory infections in animals, such as bats, camels,

palm civets, and avian species [1]. The exact mechanism of CoV infection in humans remains unclear. SARS-CoV-2 is believed to have a zoonotic origin, suggesting a spillover route from animals to humans, potentially facilitated by wildlife farming and trade [10–12].

Zoonoses are infectious diseases transmitted from vertebrate animals to humans through direct contact, food, water, or vectors [12,13]. Zoonotic pathogens may be bacteria, viruses, or parasites. Humans, animals, and the environment are conventional reservoirs of pathogens. Changes in this interface may drive the emergence of new pathogens, host ranges, and modes of infection. Approximately 60–70 % of emerging/re-emerging infectious diseases originate from animal kingdoms, with 75 % originating from wild animals [14]. Increased contact between humans and animals or occasional spills among human and animal species increases the probability of interspecies transmitting pathogens [15]. It indicates that zoonosis outbreaks pose more health risks and threaten non-humans' health [16]. Epidemiological data on CoV outbreaks suggest that identifying the reservoirs of SARS-CoV-2 is crucial for controlling its spread among humans and wildlife [15]. Control measures primarily focus on a human-centered approach that prioritizes identifying new cases to inform surveillance and swift response efforts. Critical strategies such as hygiene, isolation, self-testing, and vaccination are vital. However, it is essential to acknowledge the influence of various factors, particularly the indirect effects of environmental factors such as climate change and animal transmission. These factors can modify ecological niche determinants and may result in unforeseen transmission patterns of infection. Therefore, it is crucial to adopt a holistic understanding of the interactions among human, animal, and environmental factors to develop comprehensive strategies that address transmission routes across species, ultimately enhancing both human and animal health [17]. In the future, prevention strategies focusing on human-animal interfaces and adopting a One Health approach are of practical importance [18]. This review aims to summarize current evidence of CoV infections in humans and animals and propose preventive measures focused on surveillance systems using the One Health approach.

This review adhered to international standards for conducting and reporting systematic reviews, including the Preferred Reporting Items for Systematic Review and Meta-Analyses (PRISMA) guidelines [19]. The databases were systematically searched using tailored strategies. Several online databases, including MEDLINE (National Library of Medicine, Bethesda, Maryland, USA), PubMed, EMBASE, Web of Science, and Google Scholar, were searched to identify relevant published literature. The search utilized keywords such as "SARS-CoV," "COVID-19," "One Health," "zoonosis," "epidemiology," "outbreak," "pathogenesis," and "surveillance." Papers on SARS-CoV published from 2000 onward were included in the study. Only articles published in English were reviewed, whereas those in other languages were excluded. Additional data were collected from the reference lists of pertinent papers. Articles without abstracts, letters to the editor, and opinion pieces were excluded. Review articles were referenced to identify additional relevant studies. A literature search was conducted in February and April 2024. A total of 1398 papers were identified from the databases. After screening for non-relevant articles and duplicates, 251 full-text were further assessed, excluding 142 papers due to language, quality issues, or outcomes unrelated to CoVs. Ultimately, 109 studies were included in the review.

2. Zoonosis and one health concept

In recent decades, new pathogens causing emerging diseases and the resurgence of infectious diseases have become increasingly common [20]. Research indicates that the cost of early prevention of contagious diseases is significantly lower than that of managing them once they escalate into a global pandemic [21,22]. To effectively control outbreaks of emerging zoonotic infectious diseases, it is essential to consider the environmental, social, economic, ethical, and political factors that influence the societal ecosystem [20]. Consequently, a new healthcare framework focused on pandemic prevention is needed, one that requires a global understanding of disease emergence and incorporates the One Health approach.

One Health often connects human and animal health to outbreaks of human diseases. The concept of 'One Health' acknowledges the mutual interdependence of human, animal, and environmental Health and serves as a strategy for studies of human disease, non-human disease, and ecological problems [18,23]. Implementing intelligent surveillance with epidemiological risk assessment at the interfaces between wildlife, livestock, and humans (One Health) is one of the most pertinent, practical, and actionable strategies to prevent and prepare for future pandemics such as COVID-19 [23,24]. The initial transmission of the virus from animals and wildlife to humans and the environment underscores the efficacy of the One Health approach in combating disease spread [25–27]. This approach is particularly significant, given the limited success of other early methods for controlling disease transmission. Animals act as reservoirs for the virus, while humans can serve as transmission vectors, which is a significant concern with SARS-CoV-2 [28]. The global scientific community strongly agrees that the One Health concept provides a robust strategy for addressing the spread of infectious diseases, including zoonotic viruses. More countries must adopt and support the One Health approach to effectively manage the surge in contagious diseases. Following the onset of the pandemic, initial investigations in China indicated that bats and exotic animals were the primary sources of the virus [29,30]. Human interaction with these animals was hypothesized to have triggered the pandemic [31]. CoVs are a large family of viruses commonly found among animals and wildlife [29]. The initial strains of the virus were genomically linked to bats, suggesting that the virus may have originated from them, although the exact transmission route to other animals remains unclear [31]. The zoonotic origin of these viruses highlights the risk of their transfer from wildlife to humans [32]. A previous study indicated that identifying the reservoir of SARS-CoV-2 is crucial for controlling its spread among humans and wildlife [15]. Therefore, prevention strategies focusing on human-animal interfaces and adopting a One Health approach are of practical importance [18].

3. Occurrence of SARS-CoV-2 infections

3.1. SARS-CoV-2 infection in human

To date, three significant epidemics caused by CoV have been reported, with the recent outbreak being the occurrence of CoV named SARS-CoV-2 in 2019, which is known to cause COVID-19 [1,33]. SARS-CoV-2 is proposed to have originated in China in 2019 from a CoV-infected bat of the genus Rhinolophus [34]. On December 12, 2019, the SARS-CoV-2 infection epidemic was first reported in Wuhan City, Hubei Province, China [35]. Frequently, human-animal interactions have suggested a possible transmission route for cross-species infection and spillover zoonosis [23]. However, the primary source of pathogens and transmission routes of this outbreak are unproven [34]. Following the onset of diseases, possibly facilitated by a mammalian intermediate host, the WHO announced that SARS-CoV-2 has the potential to spread globally and cause a pandemic infectious disease with efficient human-to-human transmission [9]. Owing to the SARS-CoV-2 epidemic and its international threat, the World Health Organization (WHO) declared a global emergency caused by a novel CoV infection on January 30, 2020 [36]. COVID-19 has rapidly infected people worldwide and become a global pandemic, affecting over 556.3 million confirmed cases and over 6.3 million deaths as of December 31, 2022 [37].

A previous study indicates that SARS-CoV-2 has two strains, bat-SL-CoVZC45 and bat-CoVZxC21, which share 88 % of the genetic identity [38]. Approximately 79 % similarity to SARS-CoV-1 and 50 % sequence similarity to MERS-CoV were found in the genetic sequence of SARS-CoV-2 [34,39,40]. Cross-species jumps from animals to humans, leading to genetic alterations, are less likely. Other risk factors, including environmental factors, frequency of human-animal contact, and globalization, may influence the opportunity for cross-species infection [41]. The prevalence of SARS-CoV-2 infections varies among different countries [37]. COVID-19 mainly causes respiratory illnesses but can also cause gastrointestinal (GI) illnesses [9].

3.2. SARS-CoV-2 infection in animal

Although several animal species harbor these pathogens of SARS-CoV-2, only a few suffer from severe infection [42,43]. CoVs have been found to cross the species barrier and cause SARS and MERS outbreaks [44]. Similar to SARS-CoV-1, SARS-CoV-2 invades the host cells through the angiotensin-converting enzyme 2 (ACE2) receptor. Based on the similarities between ACE2 receptors, several animals were used as subjects for the experimental study. For example, dogs, cats, ferrets, hamsters, cynomolgus macaques, African green monkeys, rabbits, cats, ferrets, and fruit bats have been proven to be susceptible to SARS-CoV-2 infection, and those animals with experimental SARS-CoV-2 infection can also transmit the virus to other animals [45–54].

In contrast, animals for experimental infection (e.g., pigs and several poultry species) were not susceptible to SARS-CoV-2 and MERS CoV infection [55]. Owing to their well-studied immune system, fast breeding cycle, simplicity, and abundant available research tools, mice (*Mus musculus*) are widely considered one of the most prevalent animal models for studying the pathological properties of
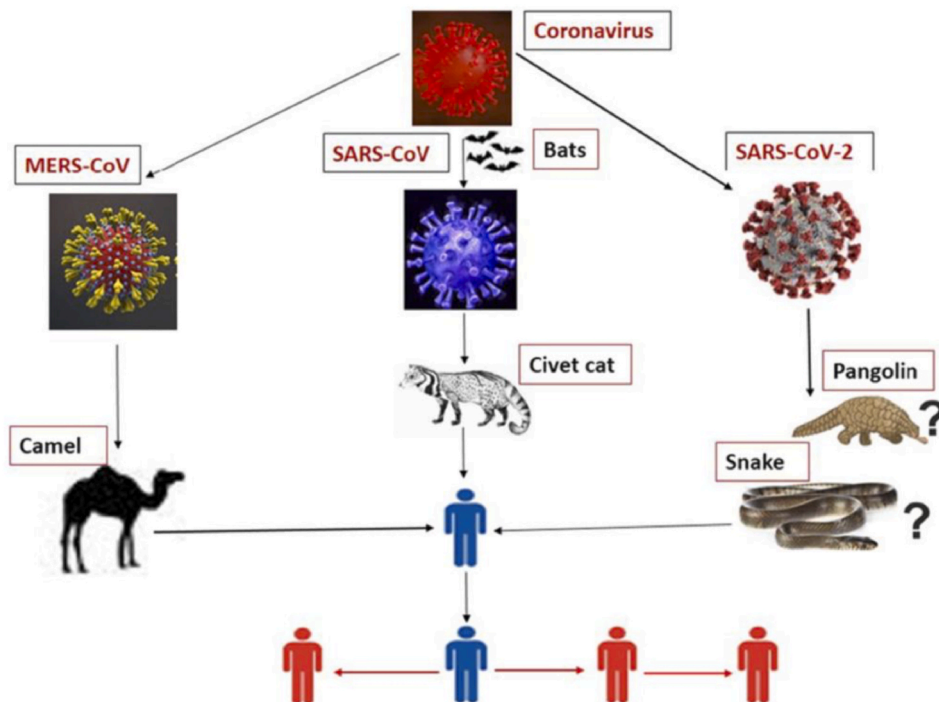

Fig. 1. Proposed zoonotic transmission modes of coronavirus infection among humans and animals. (photograph courtesy of M.N.F. Shaheen).

viruses and their effects on the host respiratory system [56]. In addition, it has been suggested that spreading SARS-CoV-2 from human to dog is a potential route of transmission. However, it does not confirm whether infected dogs can transmit the virus to other animals or back to humans [57]. In France, it has been found that cats may be infected due to having been infected with SARS-CoV-2, examined by reverse transcription polymerase chain reaction (RT-PCR) test [58]. The fruit fly *Drosophila melanogaster* [56] and the zebrafish [59] have been proposed as valuable model organisms to explore specific questions related to COVID-19. Furthermore, SARSCoV-2 tested positive in farmed mink (Neovison vison) that had signs of respiratory disease or death [60–62].

4. Transmission

4.1. Animal-to-animal transmission

Fig. 1 shows the proposed zoonotic transmission modes of CoV infection in humans and animals [15,63,64]. However, previous experimental studies suggest that several animals (such as cats and ferrets) are susceptible to SARS-CoV-2 infection and that cat-to-cat and ferret-to-ferret transmission can be found via direct contact, food, or water [33,65]. However, natural infections with SARS-CoV-2 have been found only in some animals, such as dogs, cats, tigers, lions, farmed mink, and ferrets [23]. The SARS-CoV-2 infection in animals requires further study to determine the relationship between SARS-CoV-2 and animals [65,66].

Several animals infected with SARS-CoV-2 on mink farms have been reported worldwide. A study conducted in the Netherlands showed that 54 % (69 out of 127) of mink farms had animals infected with SARS-CoV-2 between April and November 2020, indicating their possible role in transmitting the virus in the Netherlands [67]. To investigate the prevalence of SARS-CoV-2-positive cats and dogs in infected mink farms and their potential role in the transmission of the virus, throat and rectal samples were collected from 101 cats (12 domestic and 89 feral cats) and 13 dogs for examination of SARS-CoV-2 using PCR in 10 mink farms; serological assays were performed on serum samples from 62 adult cats and all 13 dogs, whole Genome Sequencing was performed on one cat sample [67]. This study found no cat-to-cat transmission, but the risk of mink-to-cat transmission among cats was 12 % (95%CI 10%–18 %). This study indicates non-human primates, cats, dogs, and minks can be infected by SARS-CoV-2 via mink-to-cat transmission.

4.2. Animal-to-Human transmission

Previous studies have indicated non-human primates, mink, dogs, cats, ferrets, and rabbits are susceptible to SARS-CoV-2 infection [67,68]. However, 68 % of residents, employees of infected mink farms, and individuals with whom they had been in contact tested positive for SARS-CoV-2 [68]. It also suggests that animal-to-human transmission of SARS-CoV-2 occurred within mink farms, according to the analysis of subjects with whole genome. This genome shows that subjects have been infected with strains with animal sequence signatures [67,68]. In China, SARS-CoV-2 has been proposed to originate from bats but may be transmitted to humans through other intermediate animals, potentially sourced from the consumption of local seafood [34].

In contrast, another study [69] indicated that the transmission route of SARS-CoV-2 to humans may be through an intermediate host because CoVs rarely infect humans directly through bats. This study also found that most (68 %) wild pangolins in China and Malaysia were infected with SARS-CoV-2-like CoVs. It demonstrated that the highest similarity (90–100 %) between the spike protein and the single receptor-binding domain (RBD) of the Pangolin-CoV and that of SARS-CoV-2, with one minor difference in one nonessential amino acid [69]. This new CoV, identified by pangolins, could predict a future threat to public health if the wildlife trade is not effectively controlled.

Previous studies have shown that, following the SARS-CoV-2 epidemic in the mink population, a new variant of mink-associated SARS-CoV-2 was found in humans and minks [70,71]. In addition, SARS-CoV-2 transmission from minks to humans has also been reported in mink farms [66,70,71]. These findings suggest that SARS-CoV-2 may have originated from viral recombination between Pangolin-CoV and Bat-nCoV before transmission to humans [69,70].

4.3. Human-to-Human transmission

In China, SARS-CoV-2 was proposed to originate from a CoV-infected bat, Rhinolophus, in 2019. Following animal emergence, possibly enhanced by a mammalian intermediate host, SARS-CoV-2 evolved and spread across the globe via efficient human-to-human transmission. A previous study [34] showed that of a family of six patients who tested positive for SARS-CoV-2. Detailed information was collected, including their contact-tracing history and epidemiological, clinical, radiological, and microbiological data. Of the six family members, one member, who had not traveled to an endemic place and yet had tested positive for SARS-CoV-2 after close contact with the family members, was classified as the first case of human-to-human transmission of SARS-CoV-2 [34]. Although researchers have proposed that an intermediate mammalian host may be present for SARSCoV-2 to facilitate SARS-CoV-2 transmission, the modes of viral transmission in this pandemic in 2019 are still unclear [72,73].

In the case of SARS-CoV-2 infection, viral contamination in hospital rooms where patients with SARS-CoV-2 infection are of concern is another mode of infection. Previous studies have indicated surface samples collected from the wards, toilet facilities, and air samples of COVID-19 patients tested positive [74,75]. These results showed evidence of viral RNA in the hospital room with COVID-19 patients. Furthermore, the highest airborne viral concentrations (19.2 and 48.2 copies/L of the virus of air) were found in the samples obtained from patients who had therapy with oxygen through a nasal cannula [74,75]. SARS-CoV-2 is found in respiratory droplets, nasopharyngeal and salivary secretions [76]. Thus, it suggests a thorough process to sterilize waiting areas and equipment, self-protection, and precautionary infection controls in hospitals to avoid potential infected sources when performing medical

procedures such as endoscopies and dental care [76].

Some studies have highlighted that fecal samples of infected patients test positive for SARS-CoV-2, suggesting the potential risk of SARS-CoV-2 proliferating within the GI tract and providing a possible route of fecal-oral transmission [77,78]. Pathogenic reactions occur when Vero E6 cells are inoculated with fecal samples obtained from infected patients [79]. Whole spherical viral particles with distinct surface spike projections were observed in the culture using electron microscopy, indicating the presence of virus progenies [79]. A study in Hong Kong found that 17.6 % of COVID-19 patients had GI symptoms; 48 % of stool samples of patients tested positive for SARS-CoV-2 RNA, even when the respiratory samples tested negative [80]. This result implies that healthcare workers should carefully operate the patients' specimens while collecting or managing patient fecal samples and performing medical examinations, such as colonoscopies, which may contaminate patients' stool samples [80,81].

Healthcare workers in intensive care units (ICU) in hospitals have a higher risk of SARS-CoV-2 infection during the COVID-19 pandemic. It is challenging for hospital practitioners to reduce the virus from patients with SARS-CoV-2 infection to other patients. For the prevention of SARS-CoV-2 spread in hospitals, strict nosocomial infection control measures have been recommended and applied to ICU regulations, including planning ICU capacity, arranging staffing workload, clinical care of severely ill COVID-19 patients, and infrastructure for infection control to reduce the risk of human-to-human transmission [82].

SARS-CoV-2 vertical transmission from pregnant mothers to children is of great concern to public health agencies, obstetrics, and neonatologists. Although some studies have reported that few newborn children have been infected with SARS-CoV-2 in amniotic fluid, cord blood, and neonatal throat swab samples, none of the patients developed severe COVID-19 pneumonia or died [83], indicating that the risk of vertical transmission is low. However, the possibility of transmission [83] must be considered.

It is now recognized that the primary mode of SARS-CoV-2 transmission is through respiratory droplets expelled by an infected individual; hence, coughing and sneezing with SARS-CoV-2 airborne particles puts non-infected individuals at risk of contracting the disease [76,84]. Additionally, indirect infection with SARS-CoV-2 can occur due to contact with contaminated objects, virus aerosolization in a confined space, or close contact with asymptomatic infected persons, which is known as fomite transmission [75]. Thus, alerting the healthcare sector to pay attention to potential transmission within hospitals is essential.

4.4. Human-to-animal transmission

Serological studies have assessed the infection rates of dogs with SARS-CoV-2 during different pandemic stages [64,85]. They indicated that companion dogs and dogs living with COVID-19 patient families had a higher risk of infection with SARS-CoV-2 during the outbreak. This evidence suggests that humans can potentially infect other species.

SARS-CoV-2 was first diagnosed in the Netherlands on two mink farms on 23 April and April 25, 2020 [68]. Despite several enhanced biosecurity procedures, including an early warning system and immediate removal of the animals in affected farms, the infection spread continued to occur between mink farms, with unknown modes of transmission [68], and humans living or working on these farms were presented to have been infected with strains with an animal sequence signature, providing evidence of the spread of SARS-CoV-2 between humans and animals within mink farms [68]. A thorough study proposed that humans might first introduce the CoV, infect minks, and then return to humans [61,68].

Taken together, subjects infected with different strains of SARS-CoV-2 have unique clinical characteristics owing to human-to-animal and animal-to-human transmissions. Adaptation and evolution of SARS-CoV-2 have increased its genetic diversity [86]. Thus, several challenges have been initiated, including the early diagnostic techniques, therapeutics, and development of vaccines that involve the current COVID-19 pandemic and events of the crossing of the species barrier.

5. Surveillance program by one health approach

Public health surveillance is a systematic, continuous collection, analysis, interpretation, and timely dissemination of animal and human health information to health authorities and stakeholders as a tool for taking sensible actions [87]. The functions of a health surveillance system are to understand the magnitude and epidemiology of specific health problems in animals or humans, generate hypotheses, evaluate control measures, monitor the effectiveness of prevention strategies, and facilitate planning [88].

It has been proposed that the pandemic's transmission of SARS-CoV-2 from humans to mink and back to humans is a zoonotic origin [61,68]. SARS-CoV-2 viral RNA was identified using PCR from the samples collected from the mink farms, indicating the possible spread routes by animal-to-animal and animal-to-human transmission [70,89]. It has been reported that SARS-CoV-2 infection in mink farms in several countries, including the Netherlands, Sweden, Italy, Denmark, France, Canada, Greece, Lithuania, and Spain [68,70]. Thus, owing to the possibility of virus mutation in mink infection, measures of the highest biosafety level are applied to control the humans infected with mink-associated SARS-CoV-2 variants [62]. This measure will raise awareness among people living and working in the mink industry, who are highly susceptible to SARS-CoV-2 infection and can present further zoonotic spread of SARS-CoV-2 interspecies [90].

In recent years, many factors, including inter-species transmission of infectious diseases [90,91], international trade [92], Public Health, and economics, have contributed to an increasing appreciation of the inter-dependency of human, animal, and ecosystem health worldwide [93,94]. With a rising number of emerging diseases, most have an animal source [94]. These findings highlight the importance of developing effective and efficient animal health surveillance systems. Additionally, wild and exotic animals used in economic trade are potential transmission routes of novel organisms into the human population via closer human-wild animal contact [95]. This trade action may cause inter-species transmission and emergent infectious diseases [96]. Zoonosis, which has occurred in recent decades, has provided evidence that it is an interaction between humans, animals, and their environment [97]. Although few

new pathogens have been detected in such interactions and later cause a pandemic, new pathogens can be prevented through an effective surveillance strategy using the One Health approach [97].

A "One Health" approach is essential for solving the significant public health problems associated with COVID-19 [1,98,99]. The initial transfer pattern of the virus from animals and wildlife to the environment and humans confirms that the One Health approach can be applied to tackle the spread of the disease because of outright failure or limited success achieved with other preliminary methods deployed to control the transmission of the disease [25,26]. One health approach involves several professionals, including human, animal, and environmental health professionals, collaborating nationally and internationally to improve the ecosystem between humans and animals [22,100,101]. The measures of coordination and collaboration include establishing human and animal surveillance, sharing information, enforcing communication between veterinary and public health departments, strengthening laboratory facilities for animal and human examinations, and developing preventive measures for animals and humans against COVID-19 [102,103]. Such multi-sectoral partnerships may begin with surveillance and data sharing for COVID-19 and enhancements of laboratory testing and outbreak response capacities, and then create and strengthen the effective detection and response to emerging COVID-19 threats in the human and animal health sectors [18,104]. Therefore, strategic surveillance by the One Health approach is only feasible with a comprehensive and multi-sectoral approach; however, despite some successful examples in Rwanda and Senegal, the vision for the One Health approach is still not shared by other countries, often poorly structured, and not operational [18,105].

Fig. 2 shows the proposed One Health perspective on CoV transmission and susceptibility dynamics [63,87,105]. Effective control measures for zoonosis depend on a massive effort to apply inter-sectoral intervention strategies that synergistically promote social and economic improvement and a better quality of life [106]. Considering the human-animal interface of zoonotic diseases, zoonosis is difficult to control using traditional measures before identifying a novel agent. Moreover, developing therapeutic drugs and vaccines to manage COVID-19 is time-consuming, high-technology, and expensive. Therefore, the prevention of the next outbreak of CoV infection is important. The SARS-CoV-2 surveillance system monitors the spread of SARS-CoV-2 infection among humans, livestock, companions, pets, zoo animals, handlers, and other wildlife species. A broader One Health approach, mitigation strategies, and preventive and control strategies to contain pathogens and zoonosis should be considered.

Animal CoVs pose a significant risk to farmed animals, wildlife, and humans because of their ability to mutate, recombine, and increase transmissibility and virulence [22]. They also facilitate cross-species and zoonotic transmissions. This phenomenon implies the importance of a One Health perspective, which helps us better understand the evolutionary trajectories of CoVs and the potential risks of spillover events to humans. Furthermore, with limited time to produce and test the SARS-CoV-2 immunotherapy, we need to explore the duration of protection and risk of reinfection after natural infection, the effectiveness of vaccination for at-risk groups, and availability of medicine/drugs for infected patients, particularly with the emergence of more transmissible variants of COVID-19 [107]. A previous study indicated that the One Health approach could yield higher statistical power to elucidate meaningful public health relationships than one-dimensional investigations or post-hoc analyses [98]. Across a project or multi-sector health study, a One Health approach can improve resource efficiency, resulting in cost savings (35 % in the presented case) [98,107].

6. Conclusions

According to the available data, the zoonotic origin of the SARS-CoV-2 pandemic has affected human health and economic growth globally. Several communicable tools influence the control and prevention of SARS-CoV-2 infection, including progress in surveillance, epidemiology, diagnosis, treatment, drugs, vaccine development, and environmental change [107,108]. The COVID-19 pandemic highlights the new strategy of the One Health approach for managing zoonotic epidemics. The surveillance program using the One Health approach is an important measure to detect the epidemiology of the disease in animals and humans, and it should be possible to determine the role of the various animal species and humans during the pandemic. Based on this information, holistic strategies can be planned to control and prevent this pandemic [108,109].
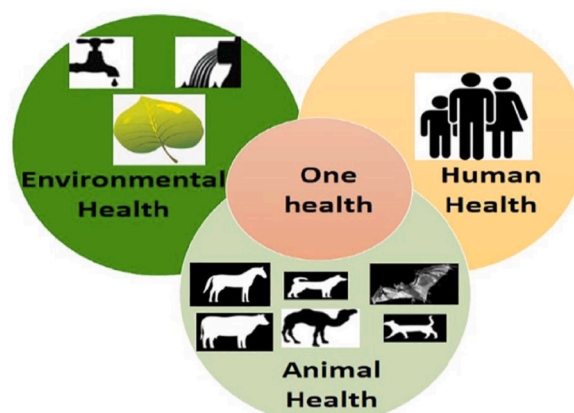

Fig. 2. Proposed One Health perspective on coronavirus transmission and susceptibility dynamics. (photograph courtesy of M.N.F. Shaheen).

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CRediT authorship contribution statement

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Declaration of competing interest

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

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