

Mini Review Article



Origin and Spillover of Coronaviruses: Prospects of One Health Action

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Abstract | Coronaviruses are a large group of viruses causing diseases in mammals, including humans and birds. Bat and rodents act as a reservoir of alphacoronavirus and betacoronavirus whereas, gamacoronavirus and deltacoronavirus originate in avian species. Domestic animals also play a critical role in disease transmission as they are found seropositive against different coronaviruses. At least seven coronaviruses are known to have been spilled over from animal to human. SARS-CoV-2 is the recent one that showed pneumonia-like syndrome named COVID-19. It was assumed that SARS-CoV-2 was initially a spillover from bats due to its genomic similarity with Bat-CoV-RaTG13, where pangolins may have acted as an intermediate host. Wild trade, ecotourism, destruction of wild habitat, and other anthropogenic activities disrupt the human-wildlife barrier which leads to the spillover process. In these circumstances, a One Health approach is crucial to implement multisectoral collaborative action among physicians, veterinarians, wildlife experts, epidemiologists, environmental scientists, and microbiologists to curb the COVID-19. One health encourages joint disease surveillance by establishing laboratory networks and regulating proper biosafety, biosecurity, and risk communication to facilitate strong disease prevention and control strategy by which we could prevent the next coronavirus outbreak in humans.

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Introduction

Coronaviruses (CoVs) are single-stranded RNA viruses that were identified in the year 1960. The family of this virus is comprised of four genera: Alpha coronavirus, beta coronavirus, gamma coronavirus and delta coronavirus that infect humans and animals, including birds and mammals. It was believed that almost all of our well-reared animal species like dogs, cats, cattle, and pigs might show seropositivity for at least one coronavirus in their early life. It is estimated that bats may harbor more than 3,200 CoVs and most of them remain as unidentified (Anthony *et al.*, 2017). Mostly, Asiatic horseshoe bats or other chiropteran species possess coronavirus. A recent

study in Myanmar reported the finding of previously unknown coronaviruses, which included three beta coronaviruses and three alpha coronaviruses (Valitutto *et al.*, 2020). Alpha coronavirus group contains a virulent Feline Coronavirus biotype (FeCV) and highly lethal Feline infectious peritonitis (FIP) (Addie *et al.*, 2020) and Human coronavirus HCoV 229-E, as well as different canine coronaviruses which cause self-limiting enteritis in pups. Currently, four alphacoronaviruses are also found circulating in swine. Beta coronavirus genus is important as it consists of the three dangerous viruses infecting human beings Middle East respiratory syndrome coronavirus (MERS-CoV), severe acute respiratory syndrome coronavirus (SARS-CoV), and the recent

SARS-CoV-2, as well as another common human coronavirus HCoV-OC43 which causes simple cold (EAZWV, 2020). This family also represents many coronaviruses found in a wide range of mammalian species like bovine, bats, hedgehogs, etc. Western European hedgehog bats and rodents act as a reservoir for most of these viruses. Gamma coronaviruses and delta coronaviruses are mainly found in birds and cetaceans hosts, but few gamma coronavirus are rarely found in other species like Beluga whale coronavirus SW1 (BWCov-SW1) in Whale, and in a leopard, which was found positive in a recent study (Wacharapluesadee *et al.*, 2015).

Spillover of coronaviruses

As known, most coronaviruses are species-specific but SARS, MERS, and bovine coronavirus (Bov-CoV) possess a broad host range, including humans, bats, camels, swine, and dogs (Erken, 2008). Besides mutations and recombination's contributing to receptor binding ability, temperature adaptation enzymes, and genetic variation were attributed in the spillover of coronavirus to a new hosts (Erken, 2008). SARS-CoV infected human beings through masked palm civets, whereas, MERS-CoV was transmitted from dromedary camels (Rodriguez-Morales *et al.*, 2020). Moreover, low pathogenic human coronaviruses also depend on domestic animals in their transmission cycles, like how the transmission of HCoV-OC43 and HCoV-229E that require cattle and alpacas respectively (Lorusso *et al.*, 2020). A recently emerged swine acute diarrhea syndrome (SADS) in China was also caused by coronavirus spillover from bats to pigs (Zhou *et al.*, 2018).

Coronaviruses in human

Including the recent SARS-CoV-2, seven coronaviruses have been reported to have infected humans. However, coronaviruses were not considered as highly pathogenic to humans until the first coronavirus outbreak SARS-CoV in China in 2002. Then, the second virulent coronavirus outbreak was MERS-CoV in Saudi Arabia and other Middle East countries in 2012 (Zaki *et al.*, 2012). Besides SARS-CoV and MERS-CoV, the other four less significant human coronaviruses, included two beta coronavirus (HCoV-OC43 and HCoV-HKU1) and two alphacoronavirus (HCoV-229E and HCoV-NL63). HCoV-NL63 causes bronchiolitis in children and remaining three are responsible for common cold (Biscayart *et al.*, 2020)

SARS-CoV-2 outbreak

The SARS-CoV-2 outbreak is the third coronavirus spillover to humans, which causes a pneumonia-like illness named COVID-19. This new virus has a 96% generic similarity with another known SARS-like coronavirus named RaTG13 (Rodriguez-Morales *et al.*, 2020) which was found in the *Rhinolophus affinis* bats (horseshoe bat) in China. Therefore, it was assumed that SARS-CoV-2 may also have an animal origin. However, this virus could use multiple animal species to complete the spillover process and scientists highly predict the role of Malayan Pangolin as an intermediate host because these Pangolins species possess a coronavirus which expresses five key amino acids like SARS-CoV-2 used to invade human cells (Lam *et al.*, 2020). Although the novel coronavirus could bind to human-like ACE2 receptor in the alveolar cell of pigs, ferret, cats, and some non-human primates with similar efficiency, to date no studies recognized that livestock could be infected or could transmit this novel coronavirus (Deng *et al.*, 2020).

Prospects of one health approach

Wildlife trade, live animal market, and different anthropogenic activities like hunting, ecotourism facilitate close contact among wildlife, livestock, and human population, increasing the risk for virus spillover to humans. Extension of urbanization, large-scale livestock production, and wild habitat reduction influence the invasion of wild animals to the human locality as well as the transmission of novel viruses to the urban areas using livestock as intermediate hosts. So one of the most effective ways to control the spillover is to regulate the natural barrier between wildlife and human (Johnson *et al.*, 2020), which needs cross-sectorial collaboration at the human animal environment interface among different stakeholders. This multi disciplinary engagement at local, regional, and global levels is called 'One Health'. Optimization of One Health action is the key to early detect the infection, determination of disease transmission and prevention model, and lessen the future spillovers (Ahmad *et al.*, 2020). Different livestock and pet animals might act as intermediate hosts for transmitting different emerging diseases to humans due to their proximity and social interactions with humans. A study stated that domestic animals could transmit the maximum number of viruses to human beings (Johnson *et al.*, 2020). These species could also contribute to the emergence of new viral strains. The implementation and development of One

Health action on a global scale are critical to reduce the threats of emerging viruses (Kelly *et al.*, 2017). The existing five-year One Health framework (2017–2021) of Bhutan is now considered as their main strength in controlling COVID-19 successfully (Impakter, 2020a).

The involvement of the veterinarians and wildlife professionals for large scale surveillance among wild, domestic, and pet animal species for identification and characterization of existing coronaviruses to explore the risk of zoonotic spillover are necessary. An interdisciplinary team from wildlife, veterinary, and agriculture, named Eco Health, have surveyed for detecting Coronaviruses in Vietnam and found high proportions of positive samples among different wild and domestic animals used for human consumption (The Star, 2020).

The introduction of a screening program for influenza-like illness (ILI) in the human population, especially animal owners and handlers, veterinarians, and wildlife researchers have paramount importance for tracing the possible spillover of viruses and early detection of potential outbreaks. Veterinary schools and even private animal disease diagnostic laboratories are contributing to COVID-19 testing in different developed and developing countries around the world. In India, COVID-19 samples of both animals and humans have been tested at the Indian Veterinary Research Institute (IVRI) (Hindustan Times, 2020) and in Bangladesh, the Chattogram Veterinary and Animal Sciences University (CVASU) and Bangladesh Livestock Research Institute (BLRI) are testing human samples (BLRI, 2020).

Capacity development of microbiologists and laboratory researchers to follow laboratory biosafety and biosecurity practices along with bio risk management systems could prevent laboratory-acquired infections and outbreaks. African center for disease control and prevention implementing One health approach to correlate human and animal health at the laboratory level in different African countries. For instance, Biological Safety Level 3 laboratory facilities have been planned to established in Zambia to analyze both human and animal viruses (Impakter, 2020b).

Strong veterinary services to maintain the biosecurity in all stages of livestock production from farm to marketing as well as active monitoring in animal markets are crucial to regulate food safety and security.

The agricultural research network “CGIAR” and the London School of Hygiene and Tropical Medicine (LSHTM) have jointly worked for post COVID food security and policies in low- and middle-income countries (Mirage, 2020).

The establishment of the proper acts and strong marketing channels for controlling the human-wildlife interaction, including the wet markets, and eating bushmeat with respect to ethics and culture, is important to break the disease transmission cycle. Recently, the government of India introduced a special program to reveal the existing complex inter-relationship between biodiversity and human health (Clear, 2020). Awareness campaigns on zoonotic diseases, hygiene, and sanitation to adopt a healthy lifestyle might have a positive impact on zoonotic disease prevention. Inclusion of One Health education and training for common workforce development is essential to fulfill the future needs of improving global health security. However, One Health advocates could confirm the support of governments and other regulatory and funding bodies towards the development and implementation of relevant policies aiming a healthy future.

Sustainable development goals (SDGs) also could be a leading measure to enhance countries’ capacity in outbreak management and improve the health care systems (Impakter, 2020c). Although there are 17 SDGs, none are directly related to emerging infectious diseases. The third goal, “health and wellbeing”, is the main goal for health, where target 3.3 deals with major infectious diseases, but neglected tropical diseases, and water-borne diseases did not mention the human-animal-environmental interface. United Nations should take the leadership steps to modify the SDGs and extend its activities aiming to prevent the next pandemic.

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Ethical approval

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Conflict of interest

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