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Epidemiological profiling of SARS-CoV-2 with focus on one-health approaches in mitigating COVID-19 pandemic

SHIKA TAMTA[1], O R VINODHKUMAR[1✉], A KARTHIKEYAN[1], Z B DUBAL[1], SHARUN KHAN[1], ABDUL RAHMAN A SAIED[2,3], MANISH DHAWAN[4,5], KULDEEP DHAMA[1] and Y S MALIK[6✉]

ICAR-Indian Veterinary Research Institute, Izatnagar, Uttar Pradesh 243 122 India

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ABSTRACT

Of the 1,415 human pathogens identified, 175 are responsible for causing emerging diseases, 132 are zoonotic and majority of the diseases are categorized as emerging or re-emerging. Emerging novel Coronavirus (COVID-19) is one of them, and it is responsible for causing social and economically critical disease in both humans and animals. This review presents the understanding of epidemiological characteristics of the COVID-19 pandemic related to host, agent, and the environment with transmission and spread of the disease for better prevention of the COVID-19. The inclination of the viruses to spillover between different species and determining the number of the reservoir of coronaviruses in an entirely new host to create infection is of emerging importance. The understanding of disease patterns will potentiate our expertise to alert how, when, and where the potential epidemic will occur. One health approach involves co-operation from all the sectors, including healthcare (medical and veterinary), environmental, pharmaceutical, educational, research, police, and administration, to combat the COVID-19 pandemic and reduce the public health threat.

Keywords: COVID-19, Emerging, Epidemiology, One health approach, Pandemic, Transmission, Vaccine

Emerging diseases of animal origin are increasing considerably since the last three decades. Of the 1,415 microbial diseases of humans, 61% are having animal linkage (zoonotic), whereas 13% of the diseases are categorized as emerging or re-emerging (Taylor *et al.* 2012). Before the novel coronavirus, a few emerging diseases, including severe acute respiratory syndrome (SARS) emerged during 2002 in China, the Middle East respiratory syndrome (MERS) emerged in 2012 in the Middle East region, Ebola, highly pathogenic avian influenza (HPAI), Swine influenza, Zika virus infection, Nipah virus infection and Congo Crimean hemorrhagic fever (CCHF) originated in different countries are the most cited diseases (Dhama *et al.* 2018, Singh *et al.* 2019, WHO 2020, Rabaan *et al.* 2021).

Almost a year back, at the end of 2019, a highly contagious pneumonic disease emerged and spread worldwide. The virus emerged at the seafood wholesale market in December 2019 with increase in infected cases dramatically (Phan 2020). International Committee on Taxonomy of Viruses (ICTV) named the pathogen as severe acute respiratory syndrome Coronavirus 2 (SARS-CoV-2) on February 11, 2020 (WHO 2020, Zhu *et al.* 2020), with the Coronavirus disease 2019 termed as COVID-19. The advent of zoonotic (animal-to-human) Novel-Coronavirus (2019-nCoV) transmission is supposed to be the principal path (Hui *et al.* 2020). On March 11, 2020, WHO categorized COVID-19 as a pandemic (Malik *et al.* 2020a, Miller *et al.* 2020). Until August 4, 2021, there were more than 200 million confirmed cases of COVID-19 worldwide, with more than 4.2 million deaths (WHO 2020). The total number of corona cases till July 28, 2021 reached above 195 million with over 4.2 million deaths (~2%) (WHO 2021a). To respond to COVID-19, many countries are practicing containment and mitigation activities, few vaccines have been developed and vaccination drive is in progress in most of the countries along with efforts to find out suitable drugs to treat COVID-19, however the virus is posing challenges to be controlled amid the ongoing COVID-19 pandemic with its third wave in different countries owing to emerging variants and other risk factors (Malik *et al.* 2020, Ghareeb *et al.* 2021, Pérez-Abeledo *et al.* 2021, Ashton 2021, WHO 2021a, WHO 2021b). Apart from this, there is an increased need for understanding the epidemiological aspect of COVID-19, which includes better cognizance about the host, agent, and environment at multistage levels of contact tracing. In addition to isolation

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Present address: [1]ICAR-Indian Veterinary Research Institute, Izatnagar, Uttar Pradesh. [2]National Food Safety Authority (NFSA), Aswan 81511, Egypt. [3]Touristic Activities and Interior Offices Sector (Aswan Office), Ministry of Tourism and Antiquities, Aswan 81511, Egypt. [4]Punjab Agricultural University, Ludhiana, Punjab. [5]Trafford Group of Colleges, Manchester-WA14 5PQ, United Kingdom. [6]Guru Angad Dev Veterinary and Animal Sciences University, Ludhiana, Punjab. ✉Corresponding author email: vinodhkumar.rajendran@gmail.com, malikyps@gmail.com

or quarantine history for prevention will contribute towards one health approach to mitigating the threat related to public health (Singh *et al.* 2020).

Agent: Genomic organization

In Coronaviridae*,* SARS-CoV-2 is the seventh member of lineage B (Wang *et al.* 2006) and is coming under genus *Betacoronavirus* and sub-family Coronavirinae. The size of the genome is 27-34 kb, which is the largest among RNA viruses. The other six coronaviruses which can infect humans are 229E, OC43, NL63, HKU1, SARS-CoV, and MERS-CoV (Sexton *et al.* 2016, Zhou *et al.* 2020).

Coronavirus is like a spherical particle in shape with pleomorphic characteristics having bulbous surface projections looking as club-like spikes, which projects from their surface and encoding of RNA contains 10 genes and 26 proteins (Goldsmith *et al.* 2004). The diameter of virus particle is 120 nm with single-stranded ribonucleic acid (RNA) and volume with mass has been reported of 10^6 nm^3 and 10^3 MDa, respectively. The replication time of COVID-19 in tissue cells involve entry of virion in cells (10 min), eclipse period (10 h), and the burst size is 10^3 virions (Yinon *et al.* 2020). There are four important structural proteins named as spike, envelope, membrane, and nucleocapsid that contribute to virulence. The function and the number of accessory proteins is distinctive depending on the particular coronavirus (Fehr *et al.* 2015). The SARS CoV-2 genome has a 52 cap structure and a 32 poly (A) tail. Two third of the genome (about 20 kb) is occupied by the non-structural proteins (Nsps), the remaining one-third (about 10 kb) is engaged by the accessory and structural proteins. The genome orientation of the coronavirus is 52 -leader-UTR-replicase-S (Spike)–E (Envelope)-M (Membrane)-N (Nucleocapsid)-32 UTRpoly (A) tail with accessory genes located at 3′ end of the genome and interspersed within the structural genes. In viral pathogenesis, only some accessory proteins have shown importance while other accessory proteins almost were found exclusively non-essential for replication (Zhao *et al.* 2012).

The sequence of SARS-CoV-2 has shown typical structural similarity to that of other coronaviruses and found quite similar to the coronavirus that caused SARS outbreak in 2002. Even though, reported incubation period of the virus is about 5–6 days but it goes up to 14 days (Li *et al.* 2020). The interaction of human angiotensin-converting enzyme 2 (ACE2) with SARS-CoV virus occurred due to the presence of an explicit composition comprising of 14 binding residues similar to SARS-CoV-2. It was suspected earlier that coronaviruses were responsible for only mild respiratory infections in humans until the emergence of SARS and MERS but the clinical spectrum of this disease can be very heterogeneous. Inactivation of coronavirus can be performed by heat (56°C within 30 min), peracetic acid, ultraviolet rays, 75% ethanol and chlorine-containing disinfectant (Zhou *et al.* 2020), which destroy the viral lipid envelope.

The R_0 value represent reproductive ratio, which means the number of secondary cases arising from an average primary case in the susceptible population. The value should be below 1 to get herd immunity. According to WHO, R_o value is 1.4 to 2.5 (WHO 2020), however in starting of the outbreak (December 2019), R_o value was from 0.8 to 2.4, while thereafter increased to a mean value of 2.6 (Range 2.1-5.1). Usually, the R_0 value varies geographically, on varying population structure, viral evolution, changes in the environment, and immunity.

Probable origin of the SARS-CoV2

For viral evolution in nature, Nucleotide substitution plays a critically important role. The rapid spread of SARS-CoV-2 and its evolution is probably driven by mutations. The mutations and deletions on different regions give emergence to the genetic diversity of this novel coronavirus (Phan 2020). A novel mutation in Indian isolated strains of SARS-CoV-2 at 4809C >T (S1515F) associated with NSP3 gene (Joshi and Paul 2020) has been recorded with substantial positive selection in *Betacoronaviruses* against evolutions (Wu *et al.* 2020). Coronaviruses have a subgenomic identical sequence, found to be responsible for viral replication. The three significant mutations in the spike protein (3403A>G), *NSP3* gene (3037C > T71 (synonymous)), and RNA primase (14408C>T) have been reported along with co-evolvement of important mutation. The interaction between *NSP3* genes with 86 nucleocapsid protein in SARS-CoV has occurred via N-terminal ubiquitin-like domain (Ubl) (Hurst *et al.* 2013). The cross-species transmission of coronavirus may have happened between bats and pigs due to the availability of common evolutionary precursor between PEDV and BtCoV/512/2005 (Schulz and Tonsor 2015). An analysis of six genomes of Malayan pangolins in Guangxi denoted GX/P1E, GX/P2V, GX/P3B, GX/P4L, GXP5E, and GX/P5L and two of Guangdong GD/P2S and GD/P1L find a gene homology of 85.5 to 92.4% for SARS-CoV-2 (Wu *et al.* 2020). Recently, scientists have revealed a 96.2% whole-genome sequence similarity index between bat and human. The jumping of virus from one host to another is frequent and have been seen similarly in MERS-CoV, the coronavirus caused MERS in 2012, jumped from bats to another intermediate host, the dromedary camel, before infecting humans. After research in Malayan pangolins, it has been discovered that genetic sequences of a coronavirus received from lung samples were highly similar to SARS-CoV-2. Both of these viruses have a similarity of 91% in their genetic sequences (Forstera *et al.* 2020). The spike protein present on the surface of the virus helps to enter the host cell. To note, complete genome-based identity between currently happened outbreak in China and United States of SARS-CoV-2 isolates are ranges from 99.8 to 100% on the nucleus (Malik *et al.* 2020).

Mutations in coronavirus lead to the emergence of new lineages. Three new lineages have been identified in circulation after a complete phylogenetic network analysis of 160 complete human SARS-CoV-2 genomes and differentiated based on their amino acid and named A, B and C. The causes behind mutation are three deletions in the genomes of SARS-CoV-2 from Japan (Aichi), the USA (Wisconsin), and Australia. Two deletions (three nucleotides and twenty-four nucleotides) were in the ORF1ab polyprotein, and one deletion (ten nucleotides) was in the 32 end of the genome. Nucleotide sequence alignment also revealed a total of 93 mutations associated with entire genomes of SARS-CoV-2 in the nucleotide sequence alignment. 42, 29 and eight missense mutations were identified in all the major non-structural and structural proteins, ORF1ab polyprotein and spike surface glycoprotein. The spike surface glycoprotein is responsible for host cell receptors binding and tropism, leading to conformational changes and drastic changes in its antigenicity (Phan *et al.* 2020). Comparing bat (ancestor of SARS-CoV-2) and Pangolin coronavirus, it has been found that out of 19 amino acids that were on the spike protein of bat coronaviruses, only 5 amino acids were found different suggesting that COVID-19 is the hybrid of Coronaviruses (Zhang *et al.* 2020).

Host

Role of animals: Coronaviruses can also be the major pathogens in animal populations like bat and pig, as bat acts as a reservoir. Apart from this, it causes the porcine epidemic diarrhoea virus (PEDV) in pigs, which lead to a 3.21% decrease in the US pig population from September 2012 to August 2014. In April 2013, the first case of porcine epidemic diarrhoea virus (PEDV) appeared (Schulz and Tonsor 2015). By May 2014, 29 of the contiguous states had identified this. PEDV is an enveloped coronavirus with RNA that causes pig morbidity and is fatal for pre-weaned pigs. Transmission occurred through direct and indirect interaction through the faecal-oral pathway. It affects the host pigs with no intermediate host while bat has been reported as potential reservoir associated with certain bat *Alphacorona* viruses (Tang *et al.* 2006, Chan *et al.* 2012). A researcher in China has reported that cats can catch the coronavirus infection that causes COVID-19, and also can spread it to other cats, but dogs cannot. Further, a team at Harbin Veterinary Research Institute, also conducted a study, that has concluded that chickens, pigs and ducks are not likely to catch the virus (Shi *et al.* 2020), but all infected cats were found asymptomatic.

During the SARS pandemic, it was evident that there is no indication of transmission from cats to humans (Martina *et al.* 2003) although there is a reported case about cat-to-human transmission of another respiratory virus, H7N12 in New York City animal shelters (Lee *et al.* 2017). Serological and virological studies have shown that Chinese ferret badgers *(Melogale moschata*), masked palm civets (*Paguma larvata*) and raccoon dogs (*Nyctereutes procyonoides*) may get an infection with a virus, which is very similar to SCV (Guan *et al.* 2003, Singh *et al.* 2020). Monkeys were found to be susceptible and cats, dogs, tigers, lions, gorilla, and minks have tested SARS-CoV-2 positive (Dhama *et al.* 2020a, Tiwari *et al.* 2020, do Vale *et al.* 2021, Hedman *et al.* 2021). Recent SARS-CoV-2 outbreak highlights the hidden reservoir of deadly viruses in wild animals and the potential threat of spillover zoonoses (Dhama *et al.* 2020a, Maurin *et al.* 2021). The skin scales of pangolin are used in Chinese medicine and the pangolins are being trafficked into the Chinese seafood market from several regions of the world (Guan *et al.* 2003).

Reservoirs of SARS-CoV-2: Initially, the focus was on Himalayan palm civets and raccoon dogs which act as strong reservoirs of SARS-CoV infection, but different reports suggest that palm civets are opportunistic hosts but not a reservoir and finally conclude that bat acts as a reservoir. According to reports after bioinformatics analysis, more than three possible transmission events were responsible for the completion of the transmission chain from bat to human: the bats roosted around or near open markets that sold civets in China; viruses can be transmitted to civets through faecal, oral shedding, raw and improperly cooked civet meat (Smith and Wang 2013). The current identification SARS-like Coronaviruses associated with the bat in Chinese population of horseshoe bats which have the ability to use both the bat ACE2 and human ACE2 receptor for cross the host immunity strongly supports the theory that SARS-CoV originated as human infection straight from a bat reser-voir (Ge *et al.* 2013). Seafood wholesale market, fish with other animals involving poultry, bats, snakes are suggested for possible coronavirus transmission (Lu *et al.* 2020). For different viruses associated with humans, viz. Nipah, Rabies, Hendra, Ebola, and severe acute respiratory syndrome Coronavirus (SARS-CoV) the bats act as a reservoir (Dhama *et al.* 2020b).

A study was conducted in Southern China, to identify some SARS-related coronaviruses in bats and their association with humans. The newly developed enzyme-linked immunosorbent assays (ELISA) were used to detect the four bat-borne coronaviruses. Survey data were used to characterize associations between human-animal contact and bat coronavirus spillover risk. A total of 1,596 residents were enrolled in the study from 2015 to 2017. Nine participants (0.6%) tested positive for bat coronaviruses. 265 (17%) participants reported severe acute respiratory infections (SARI) and/or influenza-like illness (ILI) symptoms in the past year, which were associated with poultry, carnivore, rodent/shrew, or bat contact, with variability by family income and district of residence. This study provides serological evidence of bat coronavirus spillover in rural communities in Southern China (Li *et al.* 2019). Canine coronavirus-human pneumonia-2018 (CCoV-HuPn-2018) is a recently identified novel canine-feline recombinant *alphacoronavirus*. It was first isolated from a human patient with pneumonia in Sarawak, Malaysia (Vlasova *et al.* 2021). The available evidence indicates that it might be the eighth coronavirus to cause disease in humans after SARS-CoV-2 (Abdelgadir *et al.* 2021, Vlasova *et al.* 2021).

Though SARS-CoV-2 infection is reported in several animal species worldwide, mustelids and felids are considered the most susceptible group of animals (Sharun *et al.* 2021a, b). The interaction between the host angiotensin-converting enzyme 2 (ACE2) and the spike protein of SARS-CoV-2 is an important part of the infection process. Therefore, the significant differences in the interacting residues contribute to the difference in susceptibility to SARS-CoV-2 infection (Soté *et al.* 2021). The higher susceptibility of certain free-living wild animals indicates the possibility of spillover and establishment of SARS-CoV-2 viral reservoirs in the wild (Delahay *et al.* 2021). In addition to the potential for human-to-animal transmission, interspecies transmission of SARS-CoV-2 is also reported, namely mink-to-cat transmission further increasing the risk for onward spread (van Aart *et al.* 2021). The feral cats and dogs living in close proximity to infected mink farms were found to be infected with SARS-CoV-2 (van Aart *et al.* 2021). Jemeršiã *et al.* (2021) conducted a large-scale investigation to detect the presence of SARS CoV-2 specific antibodies and viral RNA among the free-living and captive wild animals in Croatia. The samples (blood, muscle extract, cloacal swabs, and faecal samples) were collected from free-living red foxes (*Vulpes vulpes*), wild boars (*Sus scrofa*), and jackals (*Canis aureus*), yellow-legged gulls (*Larus michahellis*), and several zoo animals. Although jackals (4.6%), wild boars (3.9%), and red foxes (2.9%) gave positive ELISA results, the findings were not confirmed by surrogate virus neutralization test (Jemeršiæ *et al.* 2021). In addition, the study failed to detect viral RNA in the collected samples further confirming the absence of SARS-CoV-2 infection among the free-living and captive wild animals in Croatia. However, SARS-CoV-2 infection is reported in two American minks (*Neovison vison*) that are caught in the wild confirming the transmission from farm minks to the wild minks (Aguiló-Gisbert *et al.* 2021). In addition, natural SARS-CoV-2 infection is also reported in kept ferrets as a result of humans-to-ferret transmission (Gortázar *et al.* 2021). SARS-CoV-2 binds to ACE2-expressing cells of the respiratory tract of cattle and sheep *in vitro* and bovine and ovine respiratory tissues are able to sustain viral replication (Di Teodoro *et al.* 2021)

Recent trend indicates the emergence of several SARS-CoV-2 variants having superior transmission potential and infectivity. Some of these variants are categorized as a variant of concern (VOC) due to their impact on the neutralization capacity and efficacy of available vaccines and monoclonal antibodies (Sharun *et al.* 2021c). One of the VOC, SARS-CoV-2 B.1.1.7 variant was also identified in a pet dog and cat from the same household in USA (Hamer *et al.* 2021). The rapid transmission of SARS-CoV-2 among the minks in farms of Denmark and the subsequent spilled-back into humans contributed to the accumulation of mutations/deletions altering the virulence and antigenicity (Lassaunière *et al.* 2021, Sharun *et al.* 2021b). Cluster 5 is a mink-associated SARS-CoV-2 variant characterized by four amino acid deletions and 11 amino acid substitutions compared to Wuhan-Hu-1 (Lassaunière *et al.* 2021).

Environment

Viruses are found in the environment as dormant microorganisms, and their life cycle begins once they infect a living body (Saied *et al.* 2021). With the help of investigating, the relationship between environmental factors and prevalence of SARS-CoV-2 plays a vital role in the prevention and control of the disease. All the animals, humans and plants are coexisting in the same environment where one cannot stay in isolation. The factors like temperature, humidity and air velocity, air as well as food, water and sewage, insects can contribute to the increased frequency and transmission of the virus and have the ability to remain viable and infectious in aerosols for hours and surfaces up to days Fig. 1 (Wu *et al.* 2020). A raise in temperature can facilitate the SARS-CoV-2 destruction and when the minimum ambient air temperature increases by 1°C, the cumulative number of cases decreases by 0.86%. Contaminated water or sewage plays no role in the transmission of SARS-CoV-2. Most of the reports suggested that with increasing humidity and wind speed, the prevalence has decreased (Eslami and Jalili 2020). SARS-CoV-2 can be stable at 4 °C for a long time, but not at 70 °C. In general, heat, high or low *p*H, and sunlight can facilitate the destruction of the coronavirus (WHO 2020). Coronaviruses have the ability to adapt to different geographical conditions and can be transmitted to new species too (Graham *et al.* 2013). For direct transmission, close and unprotected exposure is required and fomites in the immediate environment need to contact infection. The person responsible (through sneezing or coughing) for transmission who attended the social events in circumscribed areas such as office spaces or cruise ships (Rothe and Sothmann 2020). To mitigate the negative repercussions of any possible disease outbreak, it is critical to understand environmental variables which play vital roles in the spread of the disease. Innovative technology developments alongside current technologies, as well as forecasting hazards due to environmental interaction, can be employed to reduce the delirious consequences of environmental factors (Sanchez-Galan *et al.* 2021, Benkeblia *et al.* 2021). Moreover, government policies such as strict social distancing, import and export of goods can be adjusted in response to environmental conditions, which can aid in the preparation for post-pandemic concerns (Hawryluck *et al.* 2004, Wang *et al.* 2020, Nez-Delgado A. 2020).

Transmission and spreading ability of the virus

Epidemiological data in China advise that family clusters account for up to 85% of human-to-human transmission on the basis of respiratory tract samples of the cases were collected for the nucleic acid detection of virus by RT-PCR. From 2 primary cases, 6 family members acquired infection and five secondary cases had onsets earlier than or on the same day indicating that SARS-CoV-2 is contagious in the incubation period (WHO 2020) and as evidence 2,055 healthcare workers got the infection (Singh

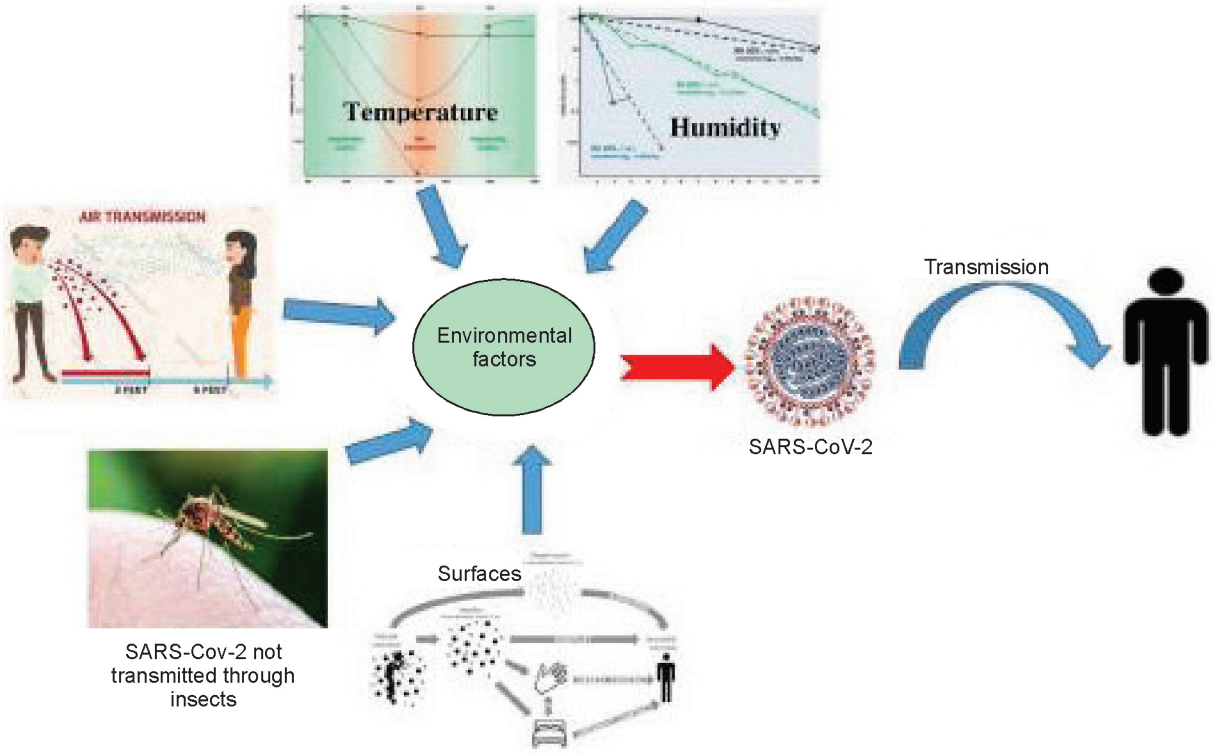

Fig. 1. Possible transmission routes of Coronaviruses through environment.

et al. 2020). Respiratory fomites play a critical role in human-to-human transmission (CDC 2020) and they can be spread from animals to humans due to their zoonotic nature. Recent research on Pangolins showed that they can act as intermediate hosts for COVID-19 pandemic and the possibility to establish the missing link for the transmission of the emerged coronavirus from bats to humans. The 2002 (SARS) pandemic, a close relative of SARS-CoV-2, was transmitted by the masked palm civet (Intermediate host) from bats to which subsequently infected humans (Zhang *et al.* 2020). Nosocomial transmission has not played a major role as an amplifier of transmission. Infectivity will depend on the interaction of Coronavirus spike proteins with complement host cell receptors (Cui *et al.* 2019). The report suggested the presence of virus in bronchoalveolar-lavage (Zhu *et al.* 2020), sputum (Lin *et al.* 2020), throat (Bastola *et al.* 2019) and nasopharyngeal swabs.

The role of asymptomatic carriers in transmitting infection is not yet completely understood. Possibilities are there that human-to-human transmission can occur because of asymptomatic incubation period i.e. 2-10 days (Li *et al.* 2019). Pre-symptomatic infectiousness is a concern (To *et al.* 2020, Zou *et al.* 2020 and Kim *et al.* 2020) and now 1–2 days of symptom onset are being used as a start day for contact identification (Lu *et al.* 2020). SARS-CoV-2 RNA is also detected in the human stool samples suggesting the potential for transmission via faecal-oral route. The same scenario occurred with SARS-CoV-1 which was detected in the patients' faeces and sewage (Chan *et al.* 2004, Wang *et al.* 2005). Therefore, the prolonged faecal shedding may contribute to the presence of SARS-CoV-2 in environmental compartments like sewage and wastewater (Dhama *et al.* 2021). The faecal-aerosol route of SARS-CoV-2 transmission was also documented (Kang *et al.* 2020).

Coughing or sneezing may help the virus to move up to 8 meters and droplets of varying size have the stability to travel 23 to 27 feet, or 7-8 meters, withholding pathogen (WHO 2020). The origin of SARS-CoV and MERS-CoV is responsible for the risk of interspecies transmission which can lead to the transmission to humans also (Menachery *et al.* 2015). SARS-CoV re-emergence from viruses currently spreading in bat populations can possess major risk for the future (He *et al.* 2014, Woo *et al.* 2012, Anthony *et al.* 2013, Ravichandran *et al.* 2020). The virus discovered up to 2 - 14 days in untreated sewage (Singh *et al.* 2020) and the transmission of COVID-19 to the population is largely due to asymptomatic individuals or those with mild symptoms (Ravichandran *et al.* 2020).

One health approach to combat pandemic COVID-19

In order to establish real integration of multidisciplinary and intersectoral organisations to control and prevent zoonoses, it is also critical to monitor the "One Health" technique while retraining students, research centres, research institutions, and international bodies. One Health (OH) is a collaborative, interdisciplinary, holistic, and multi-sectoral strategy that works at the local, regional, nationwide, and international levels to achieve optimal health outcomes by recognising the interconnection of humans, animals, plants, and their common surroundings (Aggarwal and Ramachandran 2020, Chen *et al.* 2021). Following many zoonotic disease outbreaks, including the animal spillover, cross-species jumping and zoonotic implications of SARS-CoV-2, the one health approach need to be widely adopted and strengthened for surveillance and monitoring of the virus in animals and wildlife species so as to check the possibilities of virus transmission at animal-human interface and limit zoonotic risks (Dhama *et al.* 2013, Bonilla-Aldana *et al.* 2020, Mobasheri 2021, Banerjee *et al.* 2021, Davis *et al.* 2021, Delahay *et al.* 2021, Hedman *et al.* 2021). India's policy measures are devoted to institutionalizing One Health (OH) methods and encouraging intersectoral, transdisciplinary collaboration and cooperation. The OH principle must be imagined in contexts other than zoonoses. While the conservation, ecological and veterinary professions are becoming more involved in OH, the majority of medical/clinical, and social science professionals are only vaguely aware of its complexities. Working across ministries, negotiating latent institutional structures, and distributing leadership positions are all part of the OH efforts, which are fundamentally interdisciplinary in character. The formation of One Health Committees (OHC) at the state and district levels will be the natural operational step (Dasgupta *et al.* 2021). In this context, understanding the interaction between host, agent and environment is needed to combat the COVID-19 and we need collective, efficient and strategic support from the sectors discussed below:

International aspect to combat COVID-19 and recommendations for international traffic

One health is a collaborative, multi-sectoral, and trans-disciplinary approach working at the local, regional, national, and global levels linking human, animal, and environmental health scientists and researchers. To combat the COVID-19 by implementing the one health approach certain steps are crucial. WHO continues to advice against the implementation of travel or trade restrictions to countries experiencing COVID-19 outbreaks. Only movement restrictions measures are not enough to prevent the outbreak. The basis of restrictions should be risk assessment, be proportionate to the public health risk, short duration, and based on the current situation. So it will become economically and socially helpful. Health declarations at the time of arrival, contact details and tracing will improve risk assessment. Sick travellers like an elderly traveller with chronic diseases should avoid travel to affected areas and take care of their hygiene (WHO 2020).

Public support

- The virus survives in the environment and objects. Therefore, after proper cleansing of the vegetables, fruits and other household materials need to be sanitized with 10–20 ppm sodium hypochlorite solution followed by sun-drying which may reduce the viral load.
- Frequent washing of hands, simultaneouse use of personal protective equipment (PPE) like facemask, gloves, etc. and social distancing are proven to be effective tools. The used gloves should be disposed-off after being dipped in the chlorinated water (10–20 ppm) for at least 2 h.
- Once infected, one must self-quarantine (home isolation) to stop the spread of the disease in the community. Avoid social gatherings or ceremonies. Monitoring of migratory people for their isolation, laboratory testing and quarantine for at least 14 days is very crucial and important to combat the disease.
- Several episodes of the fight between local police and the public have been reported by the newspaper/media. People should understand their safety and cooperate with the local police to maintain the social distancing/lockdown (WHO 2020).

Government support

- Prohibiting national and international travel. Monitoring (higher risk zoonotic area where professions have greater exposure), surveillance and implementation of powerful plans for preventing, detecting, and controlling outbreak (Li *et al*. 2020).

Healthcare support and veterinary laboratory support

- Clinical efficacy with safety guidelines surveys should be conducted before using this type of drugs for patients with COVID-19 pneumonia (Ge *et al*. 2013) with adequate financial support for medicos.
- No clinically proven drugs are available for the treatment of COVID-19. There is a need to fasten the procurement and supply chain management to confirm the availability of adequate stocks of personal protective equipment and essential medications and to enable equitable access to new diagnostics, therapeutics, and vaccines during health emergencies.
- Another line for combating COVID-19 is using oral and nasal health products, focussing in the predominant sites of SARS-CoV-2.
- SARS outbreak of 2003 ended before the vaccine was finished. In addition, all of the funds have been directed toward the creation of new vaccines. In case of SARS-CoV, out of all structural proteins, S protein was found capable of neutralizing antibody and that's why S protein is targeted for vaccine development. Coronavirus vaccines have been shown to be immunogenic in animal models that resemble human disease, but they have not been shown to effectively prevent disease transmission (Alexandra *et al*. 2020) and there are possibilities of adverse reactions in man and animals associated with SARS-Co-V-2, such as antibody-dependent enhancement (ADE) and lung immunopathology (Clinical Trials. gov. 2020). A measles vaccine trial to prevent COVID-19 in health care workers in Egypt (ClinicalTrials.gov. Identifier:

NCT04357028. Measles Vaccine in HCW (MV-COVID-19) 2020. Available from https//clinicaltrials.gov/ct2/show/NCT04357028 (2020)) and BCG vaccine administration are underway in healthcare workers in Australia, Netherlands and South Africa has been registered with oral polio vaccines are being considered in the United States of America (Desai *et al*. 2021).

- The vaccination campaign was launched by the Indian government on January 16, 2021, and about 49.53 crore people (as of August 4th) have been vaccinated, with priority given to healthcare and other frontline staff. Two types of vaccines have been produced in India namely "Covishield" and "Covaxin". When two doses of Covishield are given four weeks apart, the average efficacy is 70%. This information comes from a meta-study (a pooled analysis of multiple studies) of four Covishield trials involving 11,636 participants, three of which were single-blind and one double-blind, and all of which were conducted in three different countries while Covaxin phase-3 interim results show the efficacy of 81%. This information comes from a 28,500-patient double-blind sample in India. Although, there are side effects associated with both types of vaccines. Both vaccines are effective against the strain of the novel coronavirus first identified in the UK, according to preliminary research, but there is no information on their effectiveness against the mutations present in South Africa and Brazil. Both of these vaccines have yet to produce data against these two variants (Desai *et al.* 2021).

Environmental support

- Environmentalists need to identify all the contaminating sites right from the home of the infected person to the hospital premises and the burial sites and apply proper decontaminating strategies (Ge *et al*. 2013). The role of periodic environmental samples as an early warning system is well appreciated.

Educational and Research support

- Education about COVID-19 in the population and its role in preventing its spread will play a major role in the prevention and control of the virus. Everyone in country should be aware of the impact of COVID-19, its symptoms, measure for their protection, the importance of social distancing, etc. It can be achieved through the press and media. Therefore, the press and media could be launching frequent programs on such issues. One of the most interesting initiatives in developing countries is developing the medical media to be easily accessible to the public, avoiding claims and misinformation about the disease.
- There is need for development of rapid, promising and cost-effective diagnostics kit. The research field should emphasize viral genomics and proteomics with bioinformatics. Sero-epidemiological survey about the human-animal interface is required to combat COVID-19.

Police and administration support

- Tracing the infected and suspected cases through mobiles could be an effective management tool. Effective implementation of restrictions/containments needs to be monitored.

International support and cooperation

- Three key international organizations, i.e. WHO, FAO, and the OIE have started working combined and bringing long-lasting vision into practice by consolidating a formal partnership to combat the risk related to the health of the human-animal-environment.
- In this joint action and partnership, they declared and published an official guide (Taking a multi-sectoral, one health approach) that delivers principles and practices to assist countries. The international community has requested US$ 675 million to protect states with fragile health systems as part of its Strategic Preparedness and Response Plan (WHO 2020).

One Health strategy that integrates a wide variety of sectors is an effective and efficient way to decrease the danger of future disease outbreaks. The feasibility and effectiveness of the One Health idea, on the other hand, have been presented and debated in the past (Rabinowitz *et al.* 2013). Furthermore, it has been demonstrated to be a superior strategy for diseases prevention when compared to other traditional techniques. Although it is not an easy or straightforward approach that necessitates a large number of interdisciplinary activities by many experts and professionals from many disciplines, it is nevertheless a more cost-effective investment than the existing scenario. As the number of persons infected with COVID-19 grows, so does the amount of ambiguity and worry around it. As a result, psychologists are needed to help people deal with their mental health concerns (Greenberg *et al.* 2020, Magalhaes *et al.* 2021). Authorities from the One Health Commission, as well as medical experts, should insist that improved environmental and industrial regulations be implemented (Jorwal *et al.* 2020). Furthermore, several preventive steps should be considered and implemented in the future to prevent any possible recurrence.

1. Strict regulations against the domestication and consumption of wild animals should be implemented (Zhou *et al.* 2020), and considerable caution during handling these animals is required with avoiding any negative impact of inappropriate COVID-19 related actions taken on biodiversity (Dasgupta *et al.* 2021).
2. Modern design and guidelines for wet animal markets.
3. Certified training to treat, handle, and trade in animals will help the rapid alert system.

4. Vaccination of people with a high risk of exposure to SARS-CoV-2, such as healthcare workers, veterinarians, slaughterhouse workers, sellers, and market vendors is advisable (Müller *et al.* 2015).
5. Sharing experience and learning from all geographical regions and across disciplines.
6. Molecular surveillance of SARS-CoV-2 in companion animals of infected patients or even in the same area. If SARS-CoV-2 infected patients had previous contact with animals, these animals must be isolated and tested to SARS-CoV-2 on their skin, blood, and body fluids and also antibodies.
7. Human populations' behaviour, such as sexual practices, fear, confidentiality, inadequate technology, information networks, unsafe breastfeeding, burial practices, agricultural practices, intensification of domestic animal farming in bat-rich biodiversity (hot spot) areas such as Southeast Asia, international wildlife trade, and global spread of vectors such as mosquitoes, increasing human population, crowding, human travel, environmental change, and sanitary inadequacy, all contribute to the spread of pandemics (Rodrigo *et al.* 2016). Coronaviruses are not the only lethal viral emergences linked to human activity (Morens *et al.* 2004).
8. Usage of SARS-CoV-2 viral detection in sewage as early warnings of outbreaks of pathogenic viruses such as Hepatitis A and Poliovirus (Orive *et al.* 2020, Dhama *et al.* 2021).
9. Asymptomatic or undiagnosed patients act as super-spreaders and make the outbreaks incompletely preventable at the community level, even with vaccines and antiviral drugs. We urgently need the concept of using foods as medicines to enhance our immunity and aid in preventing and controlling such pandemic situations in some aspects.

Conclusion

Similar pandemics may arise in the near future due to climate change, rapid population growth, consumption of exotic meat/bush meat, the decreasing production space, changing lifestyle, and human encroachment which increases the interaction with wildlife and free-ranging animals (Korath *et al.* 2021). Although, COVID-19 has a significant similarity pattern with SARS and MERS, but having a low mortality rate (2–3%). It can be suggested that human-animals' interactions have been a primary risk factor to increase zoonotic impact of COVID-19 and animal-to-human spreading events that lead to emerging diseases are less examined. The mechanism by which asymptomatic carriers could acquire and spread the coronavirus that causes COVID-19 requires further research. As we all know the human population with social changes occurring continuously with time and human contact with pet and wild animals is also increasing, so there might be chances of increasing emerging zoonotic disease including COVID-19 in future, which will play crucial role in a worldwide pandemic. So as to know the exact origin of the outbreak; it is mandatory to involve the animal in research and trace the definitive transmission caused by animals which is arising as public health threat. Speedy diagnosis with quarantine and consolidated interventions will be of a great effect on future aspects and patterns of the outbreak. Furthermore, combining one health strategy with other control measures can be a long-term and successful approach for managing pandemics such as COVID-19. Due to the inclusion of a variety of elements and the complexity connected with them, implementing the one health strategy could be difficult, but it is evident that it can avoid future zoonotic illnesses or outbreaks in the community.

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