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Review

Bio-safety and bio-security: A major global concern for ongoing COVID-19 pandemic

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ABSTRACT

Besides its impacts on governance, economics, human culture, geostrategic partnership and environment, globalization greatly exerted control over science and security policies. Biosecurity is the critical job of efforts, policy and preparation to protect health of human, animal and environmental against any biological threats. With the transition into a global village, the possibility of biosecurity breaches has significantly increased. The COVID-19 pandemic is an example of an infringement on biosecurity that has posed a serious threat to the world. Since the first report on the recognition of COVID-19, a number of governments have taken preventive measures, like; lockdown, screening and early detection of suspected and implementing the required response to protect the loss of life and economy. Unfortunately, some of these measures have only recently been taken in some countries, which have contributed significantly to an increased morbidity and loss of life on a daily basis. In this article, the biological risks affecting human, animal and environmental conditions, biosafety violations and preventive measures have been discussed in order to reduce the outbreak and impacts of a pandemic like COVID-19.

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1. Introduction

The National Guidelines for Disaster Management define the 'scenario for large scale infections and disability and mortality among people, plants and animals as a result of poisons, virus diseases, living organisms or their products' Biological catastrophes (Alshehri et al., 2016; Biological and chemical terrorism, 2000). These biological catastrophes can be natural as pandemics or epidemics as of existing, emerging or re-emerging diseases or as a laboratory designed for deliberate use of disease-causing agents in biological warfare or bio-terrorism incidents (Adalja et al., 2015; Morens et al., 2009; Spengler et al., 2016). Natural and man-made biological disasters are broadly classified into two types: primary and secondary disasters (Alshehri et al., 2016). The term "primary disaster" refers to a major disaster that may be produced, for example, by the large-scale transmission of certain types of living organisms, such as a virus or bacteria, which can lead to epidemics/pandemics (Shaluf, 2007). As like primary, secondary catastrophes could occur due to the effects of natural or man-made hazards; for example, following various natural disasters such as earthquakes, inundations, tsunamis etc., numerous disease outbreak (like; Mucormycosis post tornado in USA, acute respiratory infection after earthquake in Iran, etc.) and man-made biological devastation due to insufficient both biosecurity and biosafety procedures in research and clinical laboratories (example; killing of many workers from Anthrax spores exposure, released by accident from a clandestine military facility in the Soviet research center in 1979) and bio-terrorist attack of different pathogens (like, Anthrax in USA and Botulinum in Japan between 1990 and 1995)..

As per earlier report, the terms pandemic and epidemic were used during the 17th and 18th centuries in both medical and social contexts. Epidemic is a Greek term which means "rapid spread of any disease to large number of people in a given population within short span of time and which kills many and is usually arbitrary in the way it does, not deciding whether the victims are old or young, fit or not" (Green et al., 2002). The WHO defines pandemic as the global spread of a disease; nevertheless, seasonal epidemics that cross international borders and affect a large number of people are not termed pandemics (Morens et al., 2009).

According European Committee for Standardization, biosafety describes the technologies, principles and practices of containment measures used to prevent or accidentally release unintended exposures to biological agents or toxins. Whereas, biosecurity describes protection, control and accountability for the preservation, theft, misuse, disposition and non-authorized access to and intentional unauthorized release of biological agents and toxins. Effective biosafety and biosecurity measures can be used to minimize risks from natural, accidental and deliberate introduction of diseases and also to reduce the risk of life science research misuse (Standard, 2011).

The world has already faced many episodes of pandemics as well as epidemics accounting for the deaths of millions in last few centuries (LePan, 2020). Numerous evidence-based studies

demonstrate how pathogens resulting in epidemics and pandemics affect animals, the environment and millions of people around the globe (Lloyd-Smith et al., 2009; El-Sayed and Kamel, 2020). The well-known outbreaks of pandemics have been seen as significant threats to human health, the environment, flora and fauna and economy and have adverse impacts on the local, regional and international level (Heymann, 2005). Several previous outbreaks have been documented; for example swine flu, developed in 2009, caused more than 200,000 deaths and HIV leading to AIDS, diagnosed in 1981 in the USA, which has killed more than 38 million people worldwide till now (Singer, 2009; Martini et al., 2019; Greene, 2007). Spanish flu is another example of a declared 1918 pandemic, considered to be one of the worst by its large-scale impact and death toll, as it is estimated to report some 50 million deaths worldwide (Greene, 2007). Furthermore, cholera, small pox, leprosy, measles, polio and yellow fever are well known pandemics, which have been widely considered for imposing economic, physical, psychological and social burden on each of the individual worldwide. The reemergence of the pathogenic strains are generally correlated with advancement of the pathogens in particular at genomic level, which results in subsequent outbreaks; for example, cholera outbreaks mostly encountered in the world. After first cholera outbreak several outbreaks of cholera were reported in Haiti, Kenya, Tanzania and India, highlighting the severity of the pathogen (Kanungo et al., 2010; Piarroux et al., 2011; Mutonga et al., 2013). In addition, in 2002, Severe Acute Respiratory Syndrome Corona Viruses (SARS CoV) appeared in China which was rapidly spreading and a new strain of the same family, SARS-CoV-2 emerged in the end of year 2019, which is relatively more contagious (Böger et al., 2020; Law et al., 2020). COVID-19 is a severe acute coronavirus syndrome2 viral illness (SARS-CoV-2). The WHO classified this outbreak a pandemic on March 11, 2020 (Law et al., 2020). Till date, SARS-CoV-2 has affected millions of people; pushed hundreds of thousands into the well of death; insisted to change their life style and most importantly, majority of the world population is incapable to tolerate the economic, social and psychological burden (Fernández-Fontelo et al., 2020).

2. COVID-19 pandemic

In 1962, Human Corona Viruses (HCoVs) were first identified as the pathogen causing acute upper respiratory infection (Kendall et al., 1962; El-Sahly et al., 2000). HCoVs were found more commonly associated with serious infection of the upper and lower respiratory system during the last few years (Monto et al., 2014). Two extremely pathogenic human coronaviruses have been recognized in the last two decades: one is the Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV), identified in china and other parts of the world and other one is Middle East Respiratory Syndrome (MERS-CoV), detected in the Middle East region (Monto et al., 2014). In December 2019 a novel pathogenic strain of virus emerged in Wuhan, China that has since spread all over the world within the short course of time (Bogoch et al., 2020). Analysis of

nasal/throat swabs or sputum of infected individual showed that in some instances the virus was etiologically different from other coronavirus and hence initially named as a novel coronavirus 2019 (2019-nCoV) later on, renamed Severe Acute Respiratory Syndrome-2 (SARS-CoV-2) by international committee of taxonomy of viruses (of the International CSG, 2020). This virus has imposed a global emergency with the highest transmissibility and exacerbating death. SARS-CoV-2 has infected over 170 million people and killed over 3.5 million people worldwide as of May 2021.

CoVs are members of the Coronaviridae family, which includes the genera Alpha, (α) Beta (β), Gamma (γ), and Delta (δ) - coronaviruses. SARS-CoV-2 is a beta genus of corona virus with largest genomes among positive stranded RNA viruses with a unique replication method and largest replicating RNA (Monchatre-Leroy et al., 2017). Coronaviruses are a big family of viruses; most of these viruses cause infection in human and animals, such as camels, bats, cats, birds, etc (Li et al., 2005). There are now seven coronavirus species known to cause human disease (Wang et al., 2008). Three of these viruses, especially the Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV), can cause severe viral disorders, resulting in the 2002–2003 SARS outbreak in China and other parts of the world (Peiris et al., 2003); the Middle East Respiratory Syndrome Coronavirus (MERS-CoV), which first appeared in the Arabian Peninsula in 2012 and has since caused repeated outbreaks with intermediate reservoir camels (Zaki et al., 2012; Chan et al., 2015); and SARS-CoV-2, which emerged recently in Wuhan, China that causes coronavirus disease 2019 (COVID-19) (Meo et al., 2020; Malik et al., 2020). The other four corona viruses 229E, OC43, NL63 and HKU1, generally cause mild respiratory conditions such as common cold symptoms (Corman et al., 2018).

Furthermore, molecular and structural analysis revealed that receptor binding domain (RBD) of SARS-CoV-2 and RaTG13 show approximately 85% similarity but share only one residue out of six critical residues, which needed for binding (Wrapp et al., 2020). According to previous data on genomic sequence and report, SARS-CoV-2 is one of the Beta coronavirus genus and subgenus Sarbecovirus, which also includes SARS-CoV (Zhou et al., 2020). It is also not surprising that the SARS-CoV-2 genome structure resemble with that of the other beta-coronaviruses with gene order 5'-replicase ORF1ab-S-envelope-E, membrane-N-3' (Beniac et al., 2006). Genomic analysis of corona virus RaTG13 from a bat species *Rhinolophus affinis* demonstrated approximately 96% similarity with SARS-CoV-2 at nucleotide order level (Zhou et al., 2020). Sequence and structural comparison suggest that RBD of SARS-CoV-2 is well compatible for affinity interaction with human ACE2 that was also used by SARS-CoV (Beniac et al., 2006). As per earlier report, it is clear that bat is the reservoir of SARS-CoV and MERS-CoV. Both SARS-CoV and MERS-CoV are closely related to SARS-CoV-2. Nonetheless, biological difference between these viruses are remarkable. Plausibly bat is the most likely reservoir host of this virus; but their ecological separation from human suggests the possibility of some other mammalian as intermediate or optimizing host (Wan et al., 2020; Sheahan et al., 2008). As it has been seen in the case of MERS-CoV, camel was the intermediate reservoir and civets for SARS-CoV. Similarly, it has also been predicted that SARS-CoV-2 has propensity of an unusual jumping species boundary i.e., bat to some intermediate host and then to human, which emerged shortly before Chinese Spring Festival, a greatest travel period in a major population and tourist.

There are two hypotheses of its possible origin, man-made and natural. The SARS-CoV-2 spike protein's high affinity binding to human ACE2 is most likely the product of natural selection on a human or human-like ACE2 that allows another optimal binding solution to emerge. This can be compelling proof that SARS-CoV-2 is not a result of deliberate modification. Furthermore, one of

the multiple reverse-genetic techniques available for beta coronaviruses would almost certainly have been employed if genetic modification had been conducted. The genomic facts, on the other hand, conclusively reveal that SARS-CoV-2 is not generated from any previously utilized virus backbone (Cui et al., 2019). In any case, whether the virus is modified or natural, there is a big question mark regarding many international health systems (including the biosafety and biosecurity measurements) that have so far failed to contain the disease and prevent its spread over the world up to now.

Many different coronaviruses that cause a wide range of human and veterinary diseases have emerged over the last few decades. Because of their ability to integrate, transform and invade various species and cell types, these viruses are likely to persist to emanate and evolve, going to cause both human and veterinary outbreaks (Sheahan et al., 2008; Cui et al., 2019). Many aspects of viral replication and pathogenesis are being studied in coronavirus research. First, trying to understand the ability of these viruses to hop between species, acquire infection in a new host, and identifying significant coronavirus reservoirs would greatly improve our ability to predict when and where possible epidemics will occur. Second, several of the non-structural and accessory proteins encoded by these viruses have yet to be characterized, and their role in viral replication and pathogenesis is unidentified (Chinese, 2004; Zhou et al., 2012). These investigations could result in a significant increase in the number of viable therapeutic targets for fighting infections. It will be critical to establish mechanisms of action for these proteins, as well as defining their role in viral replication and pathogenesis. Third, acquiring a thorough understanding of the RTC's complexities would provide a basis for comprehending the viruses' unique RNA replication mechanism. Last but not least, pinpointing the mechanism by which coronaviruses cause disease and comprehending the host immune-pathological response would vastly enhance our ability to develop vaccines and moderate disease encumbrance.

3. Biological risk assessment for working with SARS-COV-2

The regulations imposed by the Chinese government were pertinent, but came too late: the first official case of the corona virus was reported nearly two months earlier, and the length of period it took for China's state-controlled media to reveal the nature of the disease was too long. This can be directly linked to the Chinese public health ministry's failure to conduct proper risk assessment and management. The World Health Organization (WHO) declared COVID-19 a "public-health emergency of international concern" on 11th of March 2020 (Chan et al., 2020). However, by the time travel was brought to a halt, huge number of people from China had passed through the affected area, unaware of the risk. In order to carry out a biological risk evaluation for an agents, all risk factors like agent identity, transmission of agents, disease severity and other factors that may be involved in the transmission of the agent need to be identified.

3.1. Risk factors

COVID-19 can affect anybody, and the disease can cause moderate to serious symptoms. It is in the top priority of CDC to perform surveillance and field surveys to understand why some people develop more severe COVID-19 disease. As we know, COVID-19 is a new disease, more work needed to better understand the risk factors for severe illness and its transmission mainly from asymptomatic cases. The disease severity may depend upon a number of factors such as age, gender; presence of secondary infections, poor immunity and blood level of inflammatory cytokines (Huang et al.,

2020). Recent study based on structural analysis of spike protein of virus, has revealed that SARS-CoV-2 has significantly greater affinity than the SARS virus for the receptor (ACE2), which is an important molecular basis for high SARS-CoV-2 infectivity (Andersen et al., 2020).

3.1.1. Agent identity

SARS-CoV-2, like other emerging, high-threat pathogens, has become an important public health concern, and so various problems have been identified in preventing COVID-19 propagation such as, highly contagious nature and various unidentified sources of transmission. The majority of viral diseases have a zoonotic origin, as history states. Genomic analysis suggest SARS-CoV-2 is zoonotic origin however, primary and intermediate host or reservoir of this virus has not clearly identified yet.

3.1.2. Agent transmission

The exact mechanism of the SARS-CoV2 virus's dissemination remains a mystery. Since the first cases of SARS-CoV-2 were discovered in Wuhan's live animal markets, there have been suspected of being a source of the virus. There is limited or vague knowledge about the source of SARS-CoV-2, but transmission from human to human has been confirmed that it take place through close contact, respiratory droplets from cough or sneezes etc. This virus could also be transmitted by many different routes, as it isolated from the throat, fecal swab and blood (Tang et al., 2020).

3.1.3. Disease severity

According to one report, the earlier dynamics of this epidemic's outbreak in Wuhan, China, which turned into a pandemic, were estimated to have a doubling time of 2.3–3.3 days (Sanche et al., 2020). The estimated R0 of SARS-CoV-2 was much higher, ranging from 4.7 to 6.6 before the initial control measures, indicating that this virus is far more contagious and infectious than previously thought. As a result, the health-care system may have collapsed, resulting in the death of more infected people. However, after implementation of surveillance, contact tracing, social distancing and many more biosafety measures, significantly reduced transmissibility and exacerbating death.

3.1.4. Treatment & prophylaxis

Since SARS-CoV-2 is a novel corona virus, until now there is no single antiviral treatment or vaccine available that is fully effective against SARS-CoV-2 infection. The main therapy currently being adopted for patients with COVID-19 includes symptomatic treatment, support therapy, available antiviral drug (antivirals used in earlier viral diseases), certain antimalarial drug and traditional medicine (Mulangu et al., 2019; Wang et al., 2020). Symptomatic treatment and supportive therapy primarily include symptom relief, supportive treatment and organ protection and treatment of respiratory complications, including oxygen ventilator support if necessary. Multiple existing drugs (such as remdesivir, radevir, ralproveravir, ritonavir, ribavirin and others) have been studied in antiviral therapy in combination with certain cytokines or alone against SARS-CoV-2, which have shown significant inhibitory response in previous outbreaks such as MERS, SARS, Ebola, HIV, and others. Besides these antiviral drugs, clinical trials of Chinese and other traditional drugs (such as Qingwen, lianuha, chloroquine/hydroxyl chloroquine and others) against COVID-19 have also been conducted and significant responses have been observed (Zhang et al., 2020).

Currently, thirteen different vaccines have been developed based on various parameters, including viral vector/DNA based vaccines from Oxford-AstraZenca, Sputnik V, Johnson & Johnson and Covidecia, RNA based vaccines from Pfizer-BioNtech and Moderna, virus inactivated vaccines Covaxin, CoviVac, CoronaVac,

BBIBP-CorV, and WIBP-CorV, and protein subunit based vaccines RBD-dimer and EpiVacCorona. In clinical trial phase III, these candidate vaccines have shown different levels of efficacy varying from 65% to 95% (Polack et al., 2020; Knoll and Wonodi, 2021). Beside these, there are more than 300 vaccines in different stage of clinical trials also.

3.2. Biosecurity measures

Timely surveillance and identification of biosecurity threats, risk analysis of influencing factors and variation of natural versus unnatural epidemics are indeed requirements of biosecurity in risk management. Increased biosafety and biosecurity, as well as lower risks of inadvertent pathogen exposure and acquirement, are dependent on coordination and collaboration, international policies, systems integration, rapid alert and early diagnosis (Meyerson and Reaser, 2002).

3.2.1. Surveillance

Previously, the Early Alerting and Reporting (EAR) project was launched with the goal of early and rapid detection of biological threats through the use of epidemic intelligence and internet-based surveillance as part of a global health security initiative focused on improving global early warning and providing it as a working model demonstrating the high commitment of international institutions (Riccardo et al., 2014). Traditional disease surveillance does not provide the necessary timeliness for early detection of emerging and re-emerging pathogens. During strong surveillance and isolation, the times of infection in the community are decreased.

Since no specific treatment is available for coronaviruses, global monitoring of people infected with COVID-19 is urgently needed. The joint role and technology of the Internet of Things (IoT) can be crucial to prevent the spread of zoonotic infectious diseases (Adly et al., 2020). Intelligent disease control systems can enhance reporting and concurrent monitoring, connectivity from edge to edge, data selection and analysis, surveilling and alerts. Remote medical help to identify and control zoonotic outbreaks of infectious diseases should also be adopted (Ting et al., 2020). In the case of the COVID-19 pandemic, epidemiological surveillance and contact traceability in certain countries such as Singapore and South Korea were very significant. As a result, they demonstrated a strong understanding of case-detection in the COVID-19 pandemic (Covid-19 National Emergency Response Center E, 2020). In contrast, as a result of the delay in beginning surveillance, some countries' low surveillance contributed to the spread of the COVID-19 pandemic around the world.

3.2.2. Prevention

Eliminating the infection source, cutting off transmission routes and safeguarding vulnerabilities are the basic principles of infectious disease prevention and control. Preparation of professionals and forefront workers, alliance with the sponsoring organization, leadership and policy regulations can all help to reinforce biosafety and biosecurity as part of a quality management system. Knowledge, skills, and handling competencies are not only important for researchers, doctors, hospital staff, and public health laboratory professionals, but they are also important for academicians, employees, and students because they play a critical role in the success of any prevention program against any infectious disease, establishing a milestone for the improvement of biosecurity and public health (Callihan et al., 2021). It is difficult to ensure that all affected people have been identified when an emerging and re-emerging pathogen appears and causes infection in the community. There are many elements that contribute to biosecurity in

prevention programs, such as an integrated risk and impact assessment and quarantine process.

The role of live animal markets in both SARS and COVID-19 epidemics in China highlights the need for proper and strict regulations governing their sale and use. The best conservative approach to escaping zoonotic transmission would be closure or suspension of these markets, but China has long history of live markets and is improbable to sanction them permanently. In this instance, it would be ideal to use suitable hygiene and protocols to limit contact between animals and humans, and to improve epidemiological surveillance and monitoring. To avoid epidemic outbreaks, more research should be conducted on the development of effective methods for the early and timely detection of zoonotic transmission and monitoring of the emergence of any type of illness.

In order to avoid/prevent spread of any outbreak in the form of endemic/pandemic, basic epidemiological parameters such as the individual, place, time and date of diagnosis, as well as clinical signs and associated symptoms, infection consequence, intensity, exposures, and the history of travel must be determined for each case. Though, these strategies were adopted strictly by very few countries as mentioned *vide-supra*. Future study should focus on how IoT technology may be used to track the spread of illness and the ramifications of doing so. To avoid the unpredictability of ongoing outbreaks in China, as well as the likelihood of a local outbreak becoming a worldwide pandemic, necessary efficient steps must be adopted. To summarize, more effective steps are needed in the future to minimize the unanticipated hazards of ongoing outbreaks in China, which may turn into a global pandemic.

3.2.3. Early detection

Monitoring and alarming biological threats can be accomplished through the use of multimodal analysis, early or rapid detection, field research and genome sequencing to identify new and previously identified pathogens, thereby strengthening biosafety and biosecurity threats (Hulme et al., 2020). Early detection of an emerging or re-emerging pathogen requires a significant investment of time. The longer it takes to detect or announce a pathogen, the more expensive it is to manage and less likely it is to be eradicated. This is precisely what happened with the Covid-19 pandemic, as it was not detected quickly, contributed to its global spread and difficulty in controlling it.

For any infectious disease, there are primarily two conventional tests used, namely; serological test and molecular analysis of genetic material. Serological assays used for COVID-19 test detects viral antigen from a respiratory swab or antibody from a blood sample whereas (Haveri et al., 2020), in molecular analysis reverse transcription process detects genetic material, RNA of virus (Bogoch et al., 2020; Fehr and Perlman, 2015). The specificity of serological tests for COVID-19 detection using ELISA is approximately 95%. Currently, the gold standard for COVID-19 diagnosis in conventional method, is the real-time reverse transcription polymerase chain reaction (RT-PCR). However, the sensitivity and specificity of the RT-PCR test are not absolute and, importantly, are dependent on personnel skill in that techniques, operation of standard lab practice and safety procedures. Beside serological and RT-PCR test, Chest CT observations have been indicated as substantial evidence for diagnosing of SARS-CoV-2 infection disorders, and it has been found to be an important clinical outcome for early detection of the diseases (Kanne, 2020).

CRISPR-Cas based technologies recently acquainted with therapeutic and molecular diagnosis of infectious diseases besides being used as a tool of gene editing in research. On the basis of CRISPR-Cas systems, several novel diagnostics have been developed. Compare to RT-PCR technique, CRISPR-Cas technology have been found

more specific, rapid and cheaper as well (Field et al., 2021). This technology has not introduced commercially yet. However, CRISPR-Cas based diagnostic platform can easily be used to diagnose emerging infectious viral diseases as point of cares (POCs) in any area with limited resource. Plausibly, in near future this technology can be introduced commercially to screen large infected population to avoid and restrict the spread of carrier or asymptomatic individuals.

3.2.4. Rapid response

Once a novel or re-emerged pathogen is identified, all approaches must be used to warn quickly and maximize the possibilities for containment or control. To quickly implement the effective measure, there must be cooperation between state and local authorities to restrict as soon as any potentially harmful pathogen is detected (Baker, 2001). There are several effective measures which must be adopted to facilitate rapid alert, such as; institute an easily and commonly accessible funding mechanisms for emergency action, develop or amend policies and directions to support rapid response and establish or enhance techniques to either control or eliminate emerged pathogens.

After learning the etiology of an unknown pneumonia and the severity of infectivity, morbidity and mortality caused by the novel corona virus SARS-CoV-2, Chinese authorities imposed a travel ban to and from the city of Wuhan on January 23rd, by suspending airlines, trains and other means of transport. Due to the delayed response of understanding the severity of infectivity and morbidity of SARS-CoV-2 and imposing travel restriction or ban by Chinese authority, ensued spread of COVID-19 to many cities of China and other countries.

4. Bio-risk evaluation of other pandemic caused by β -corona viruses

Over the last two decades, research has revealed that there is a large pool of coronaviruses circulating among bats and other animals, implying that the introduction of highly pathogenic coronaviruses into the human population is not only likely, but unavoidable. A decade of SARS outbreaks, the resurgence of another coronavirus causing severe disease, Middle East Respiratory Syndrome (MERS) and the recent emergence of SARS-CoV-2 in humans have demonstrated that coronaviruses pose a significant threat to human health. Therefore, further researches are badly needed to delineate their replication mechanisms, to recognize the potential therapeutic targets and to develop appropriate defensive measures.

SARS: Being the first pandemic of the twenty-first century, it was the most severe coronavirus-caused disease. Coronaviruses were previously not recognized as agents for serious human diseases, so SARS-CoV emergence was a complete surprise (Tambyah, 2004). SARS-CoV, β -coronavirus of group 2b was identified as the potential cause of the 2002–2003 Severe Acute Respiratory Syndrome (SARS) outbreak in China's Guangdong Province. SARS-CoV also spread globally, because many of the disease's clinical features were unknown early in the outbreak, as well as the huge variations in clinical infection management among South East Asian countries. In contrast to the situation in China, there were insufficient supplies of protective equipment for the public, which could have slowed down the progression of the disease if they had been readily accessible. SARS clinical symptoms and signs appeared quickly, and health-care providers and hospital administrators were caught off guard. This, integrated with the Chinese government's inefficient communication with the public, sparked widespread panic. Furthermore, the inadequate infrastructure in

China, such as infectious disease health care facilities and related requirements, complicated its control (Tambyah, 2004).

MERS-CoV is group 2c of beta corona virus; has an integral connection with bat coronaviruses, HKU4 and HKU5 that have been identified previously (Annan et al., 2013). Earlier several reports of genomic comparisons show that the virus originated in bats, but most probably had an intermediate host, since humans seldom have contact with bat excrement. Drawing inferences from the discovery of MERS-CoV antibodies in Middle Eastern dromedary camels, as well as MERS-high CoV's permissiveness capacity and replication in camel cell lines, it is alluring to conjecture that dromedary camels are the natural host (Chan et al., 2014). MERS-CoV is an enzootic virus found in camels throughout the Middle East and other African countries, causing mild upper respiratory infection in the camel reservoir and occasional but seldom human infections. Since the first preliminary report, a slow investigative process for the next two to three years demonstrated a virus that had infected the vast majority of adult camels in Saudi Arabia, as well as all across Middle East and parts of Africa (Alagaili et al., 2014). Recent research in both camels and humans in close proximity in Saudi Arabia discovered nearly identical MERS-CoVs, providing more conclusive evidence. It remains unknown precisely how the virus is transmitted to people, but a close and long exposure seems to be a requirement. Till now, it is unknown how many MERS-CoV cases can be attributed to an intermediate host rather than human-to-human transmission. Although MERS-CoV infection causes the equivalent of a "common cold" in dromedary camels, the virus may be a more severe and opportunistic pathogen in humans, with up to 40% of cases resulting in death. MERS, on the other hand, has taken longer to spread across the world, owing to the lower probability of human-to-human transmission (Group WM-CR, 2013).

5. Discussion

In recent decades, bio-safety has become an increasingly important concept for gathered technologies, processes and practices to avoid involuntary exposure to biological agents, owing to the trend toward globalization and the concurrent growth of international contact, transport and trading. According to WHO report from 2007, 'global public health security' is defined as "active and responsive measures required to limit the vulnerability of populations living across geographical areas and international boundaries to acute public health events that jeopardize community health." (IHR: International Health Regulations (IHR). IHR, 2016). To achieve global health security and control any epidemic or pandemic, WHO developed International Health Regulations (IHR 2005) and numerous guidelines related to biosafety and biosecurity measurements. The recent outbreaks of highly contagious diseases including COVID-19, highlight the critical need for effective biological risk prevention, detection and response in accordance with International Health Regulations (Stuckelberger and Urbina, 2020). The IHR (2005) will assist in ensuring early warning and efficient international management of a biological catastrophe, whether naturally occurring or planned form, by implementing the guidelines, policies and procedures, and operational and technical capability required by the IHR (2005), in that way it can endorse national health security.

Recent research has also concentrated on laboratory-based infections, which have received a lot of attention, because they have the potential to be one of the causes of infectious disease transmission from laboratory to community via microbiological research, clinical and animal labs. Moreover, the improper handling, transport, storage and disposal of pathogens due to the lack of training can lead to accidental discharge of the pathogen, leading to misuse of biological agents and support for biological crime

(Bavoil, 2005). As a result, the current situation requires the global scientific community to address the risk factors associated with the improper use and disposal of biologic agents, as well as to analyze and streamline research on the most contagious biological agents only by trained researchers in a well-protected environment and advanced biological safety systems.

Timely surveillance and identification of biosecurity threats, risk analysis of impacts and differentiation of natural versus unnatural outbreaks are the key needs in risk analysis for biosecurity. Conventional surveillance and response lacks the sensitivity necessary to evaluate emerging and re-emerging pathogens. Recent public health systems rely on validated data from many sources such as hospital and laboratory data, which are important for analyzing trends over time, but do not meet rapid epidemic intelligence needs for early detection of epidemics (Yan et al., 2017). Any epidemic with a reproductive number more than one (MacIntyre and Bui, 2017) grows exponentially, so every day of delay in detection could significantly increase morbidity and mortality.

Emergence and recurrence of zoonotic pathogens illustrates the integral connection between human, animal and environmental health. To address the problem, efforts to minimize the effect of animal-borne viruses on public health must integrate research across disciplines, using a "one health" approach from the field to the laboratory (approach that is collaborative, multispectral and transdisciplinary, working at the local, regional, national and global levels to achieve optimal health outcomes) (Cui et al., 2019). The future of zoonotic virus research, particularly bat virus research, lies in a collaborative and coordinated effort to assess the molecular and meta risk factors of transmission, give insight about which viruses have the propensity to spread, and to execute massive and cross sectional surveillance studies that would support the adoption and evaluation of next-generation intervention strategies. However, new and serious challenges remain with the appearance of SARS-CoV-2. A dramatic improvement in pathogen knowledge combined with a quick all-out aggressive response to track zoonotic spillover events has been clearly demonstrated by the ongoing COVID-19 pandemic.

As demonstrated by the rapid response to the MERS outbreak in South Korea in 2015, coordination between government entities and outside entities can be critical in combating disease transmission through strategic planning and propagating community health knowledge (Cowling et al., 2015). COVID-19 has been subjected to controls, despite the fact that the timing of these steps and the relative speed at which the current virus is spreading suggest that lessons learned from both SARS and MERS epidemics have not been considered. In relation to the outbreak in question, a week after the virus was isolated, the Chinese Health Ministry shared the genetic sequence of the COVID-19 virus, allowing others to quickly diagnose the virus using rapid testing methods, though government transparency was not ideal at first. From the first case of virus, the Chinese government took about four weeks to launch an emergency response, conduct a case investigation and to investigate the wild animal and sea food market. When the Wuhan Health Commission declared the outbreak, the Chinese authorities took almost ten days to formally proclaim the new coronavirus as the cause. Improper evaluations of the situation's severity, as well as inadequate information on the virus within China, have contributed to COVID-19's rapid expansion across mainland China and into adjacent and distant countries (Bogoch et al., 2020; Sanche et al., 2020).

6. Conclusive remarks

In order to safeguard the people against public health emergencies, a national health security policy envisioned to include a wide

range endemism, natural epidemics or pandemics, mishaps involving biological agent release, bioterrorism assaults, and biological warfare are examples of threats, must be commissioned. Moreover, preparing for a natural disaster or non-natural, the unifying factor is the need for a quick and agile response, as well as a responsive public healthcare system that can provide timely indications and medical support. The current century should not have foreseen a pandemic like Covid-19, because all legislation, law, and regulations that could contain a pandemic are available. Therefore, to avoid the spread of infectious diseases (endemic/pandemic) of zoonotic origin or from laboratory working on infectious agents, following four area must be strengthened in the future: (i) biosecurity on markets for wildlife trade; (ii) identifying and monitoring high-risk pathogens associated with wildlife; (iii) continuous monitoring of the health status of individuals who work with wildlife or domestic animals to avoid disease spillover; and (iv) research on highly contagious biological agents by trained researchers in a well-protected environment and advanced biological safety systems and disposal of biohazards.

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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