

**A REVIEW OF THE HISTORY OF THE CORONAVIRUS DISEASE 2019**

**AMAL A AL MOUSA\***

Department of Botany and Microbiology, College of Science, King Saud University, Riyadh, Saudi Arabia. Email: aalmosa@ksu.edu.sa

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**ABSTRACT**

The coronavirus (CoV) family has many more pathological causes for humans and animals. CoV disease 2019 (COVID-19) has spread very rapidly worldwide is endemic, was first identified, isolated from pneumonia, and sourced to Wuhan is located in central China in 2019. The last reports have proposed that severe acute respiratory syndrome-associated CoV (SARS-CoV) deems altered CoV from bat source that came to many people as a due of zoonosis relocation. CoV was treated as a simple non-fatal virus until 2002, then started showing deaths SARS-CoV-1 from 2003 at a rate of 9.6%, in 2004, the Centers for Disease Control and the World Health Organization (WHO) declared of emergency. Middle East respiratory syndrome CoV has been discovered in dromedaries and has continued to kill humans since 2012, and the WHO was confirmed by the Chinese government of several cases of pneumonia by the end of 2019 and these cases were related to the Seafood Market in Huanan, 2020, was the COVID-19 pandemic, this virus was able to spread rapidly among people in most countries of the world, which made the proportion of mortality is rising very alarmingly. Therefore, all states must be careful and take precautionary measures to avoid infection. In this article, we review the origin of CoVs, their global transmission map, and their path of entry into humans.

**Keywords:** Coronavirus, Pandemic, Coronavirus disease 2019, Severe acute respiratory syndrome-associated coronavirus, Syndrome.

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**OUTLINES THE PATHS OF TRANSMISSION OF THE VIRUS FROM ANIMALS TO HUMANS**

Over the past 1000 years, coronaviruses (CoVs) have developed frequently [1]. The first discovery of CoVs involved the detection in animals of certain diseases. This began with the isolation of the chickens' 1937 infectious bronchitis virus [2] and then the mice 1949 murine hepatitis viruses. Pigs were found to carry a U.S. transmissible gastroenteritis virus in 1946 [3]. Human CoVs were first raised in the 1960s of respiratory infections [4]. In a Canadian research, 500 sick persons were pinpointed as having flu-like syndromes and 17-18 of these situations were shown to be a polymerase chain reaction (PCR) CoV strain [5]. Since then, disparate other CoV strains have been isolated from humans using tissue culture (e.g. OC16 and OC43) [6,7]. The number of CoVs reported has risen significantly to include viruses from many other types of animals, such as rabbits, turkeys, sparrows, bats, calves, cats, and dogs [8]. Until 2002-2003, the severe acute respiratory syndrome (SARS) virus caused a pandemic of disease that resulted in deaths in 29 countries, and most cases were in China and Hong Kong. The CoV was regarded as a simple non-fatal virus. The total number of reported cases reached 8,096; 774 people died which equates to a death rate of 9.6% [9], before the disease partially died out due to strict quarantine protocols. The SARS-CoV appears to be very closely related, according to the genome sequence, to another Himalayan palm civet virus from which it may have originated [10]. The civets were subsequently considered to be an intermediate host for the SARS-CoV, with the bats as the natural host [11] undertook a 5-year survey study of harsh sharp.

Respiratory sickness (SARS)-related CoVs isolated of horseshoe bats from Yunnan county in China, in which 11 SARS-like CoVs were pinpointed [12]. In several genes, including S, ORF3, and ORF8, genome comparisons revealed high genetic diversity among these viruses. Both 11 SARS-like CoVs were still able to use the same human angiotensin-converting enzyme-2 (hACE2) receptor, despite variations in S protein sequences, suggesting a close relationship with SARS-CoV. SARS-CoV is, therefore, likely to have originated by recombining bat-like SARS-like CoVs before infecting civets from which the recombinant virus has spread to humans, causing the SARS epidemic [11,12]. Another

CoV, SARS-CoV-1, the reason of the SARS pandemic in 2003, was also closely linked to other CoVs isolated of bats. Several animal species may be affected by many of these CoVs. SARS-CoV-1 has, for example, affected civet cats and then humans, while the Middle East respiratory syndrome (MERS-CoV) virus is found in dromedaries and has continued to infect humans since 2012 [13]. Through 2003, different reports were published on the proliferation of a CoV to lot of cities, such as the United States, Singapore, Thailand, and Taiwan. Several cases of CoV-induced SARS were identified and more than 1000 patients died in 2003 [5]. Consequently, the World Health Organization (WHO) and the Centers for Disease Control and Protection reported a "case of emergencies." In 2004, another study in Hong Kong confirmed that 50 patients had SARS and 30 of them were CoV infected [5]. In 2012, Saudi Arabian reports presented several infected patients and deaths [14,15]. In 2019, COVID-19 was first recognized, isolated from pneumonia, and sourced from Wuhan, China [16,17]. The WHO was informed by the Chinese government of multiple cases of pneumonia with an unfamiliar etiology toward the end of 2019. The pandemic was initiated at the Hunan seafood market in Wuhan and rapidly infected more than 50 people [18]. Patients were originally suggested to have been infected with CoV-induced pneumonia, and only those who had attended the seafood market, where live animals were sold, or were able to treat or ingest infected animals or birds. However, further investigations revealed that some individuals contracted the infection even with no involvement with the seafood market or the food that originated there [18]. In December 2019, environmental samples from this marketplace tested positive for SARS-CoV-2, implying that the marketplace was the source of a pandemic or played a part in the initial amplification of a pandemic [13]. These observations indicated that the virus possessed a human-to-human spreading capability. Bats have been reported as being a rich source of CoVs [12,19], even though only a few of these CoVs can affect humans [20,21]. The SARS and MERS viruses have a zoonosis type of relocation depending on the studies, sources are from a bats and passing to palm civets and camels, in the order in as the intermediate hosts [22,23]. In early January 2020, SARS-CoV-2 was identified and its genetic sequence was publicly shared between January 11 and January 12. Since then, the

complete genetic sequence of SARS-CoV-2, from early human cases, and the genomes of many other human-isolated viruses in China and around the world, has shown that SARS-CoV-2 is of ecological origin in bat populations [13]. The latest studies have indicated that SARS-CoV-2 is a modified bat origins CoV [24,25] as a result of the relocation of zoonosis to humans [26,27]. It has been shown that a CoV detected from the Malayan pangolin has 99% similarity with SARS-CoV-2. The pangolin-CoV receptor-binding domain (RBD) has just one amino acid other than SARS-CoV-2; infected pangolins show similar symptoms of COVID-19 disease in humans and antibodies circulating in the blood associate with the SARS-CoV-2 spike protein [28,29]. Even though the RaTG13 CoV isolated from bats has approximately 96% SARS-CoV-2 recognition, its RBD is different from the previous, showing a low capacity to bind to the hACE2 [30]. In addition, the RBD of the pangolin-CoV S-protein is essentially identical to that of SARS-CoV-2; six receptor-binding remains are congruent in both [25]. A comparison and study of the genetic data provided to date have indicated that SARS-CoV-2 emerged from the reassociation of pangolin-CoV with bat-CoVRaTG13-like viruses [28,31,32]. Therefore, the pangolin is one of the possible intermediate hosts between bats and humans, drawing on available knowledge. Turtles, minks, and snakes are also confirmed as potential intermediate hosts [33,34]. Finally, the history of the emergence of the CoV is not new, so all countries of the world must take strict measures to prevent the spread of the disease.

#### RECOMMENDATION

- Construction of a broad global archive of technologies containing and restoring patient numbers
- Construction of a broad global database of technology with interdisciplinary cooperation (One Health approach) by cooperation between governments, epidemiologists, virologists, health authorities, veterinarians, and doctors
- Strengthen the system of geographical knowledge that works to track the disease around (spatial tracking of the epidemic, predict the transmission of the epidemic)
- Creation of options for early intervention and improved care
- Promoting volunteering in emergencies also increases communities' ability to confront the pandemic.

#### CONCLUSION

Coronaviruses originated from animal sources and genetically mutated over the years, transmitted to humans through a host like bats, civets and camels and spread all over the world and became more virulent and lethal to humanity with genetic variants becoming alarming, so a strategy must be developed A joint global support scientific research in following up the genetic infiltration of the virus to reach a rapid diagnosis of this virus, and to develop vaccines or produce drugs to prevent future outbreaks. This achieves the goals of sustainable development in development and innovation for human health and well-being in the present and the future.

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#### CONFLICTS OF INTEREST

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