

Emergence and Re-Emergence of Human Coronaviruses: What Next?

Sayed Sartaj Sohrab^{1,2*} and Esam Ibraheem Azhar^{1,2}

¹Special Infectious Agents Unit, King Fahd Medical Research Center, King Abdulaziz University, Jeddah, Saudi Arabia

²Department of Medical Laboratory Technology Sciences, Faculty of Applied Medical Sciences, King Abdulaziz University, Jeddah, Saudi Arabia

***Corresponding Author:** Sayed Sartaj Sohrab, Special Infectious Agents Unit, King Fahd Medical Research Center, King Abdulaziz University, Jeddah, Saudi Arabia.

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Abstract

The unusual pneumonia was caused by a newly identified coronavirus designated as SARS-CoV-2 from the Wuhan city, China, which resulted into a global pandemic in 2019. Since then, this virus has been spread to more than 219 countries with 109413506 confirmed cases and 2412141 deaths (15th February 2021, 9:14 GMT). This virus belongs to the same family of coronaviruses as Severe Acute Respiratory Syndrome and Middle East respiratory syndrome coronavirus. Currently, a total of seven human coronaviruses have been emerged and known to cause disease in humans globally. The bats, palm civet and camels are well known to serve as a primary and natural host for coronavirus transmission to human. The emergence of coronaviruses happens due to many factors such as favorable climatic conditions, genetic mutation, recombination, amplification, frequent transmission, non-proper sanitations, non-proper disposal off the solid waste materials, preferences of new host receptors and many other factors. The emergence and re-emergence of human coronaviruses poses a serious threat to global human and animal population.

Keywords: Coronaviruses; Emergence; Genetic Mutations; Human Population; Global Health

Introduction

The first unusual case of pneumonia (COVID-19) caused by SARS-CoV-2 was reported in mid-December 2019 from the Wuhan sea food market, Hubei province, China. Coronavirus Disease 2019 (COVID-19) is an emerging viral infectious disease caused by the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) [1]. Human coronaviruses (HCoVs), such as: Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) and SARS-CoV-2, lead the global epidemics resulted into high morbidity and mortality. The first major pandemic of the new millennium was caused by a novel severe acute respiratory syndrome (SARS) coronavirus (SARS-CoV) in early 2003 and again small re-emergence in late 2003 [2]. The first human coronavirus identified in 1960 and after that many human coronaviruses have been identified. Coronaviruses belong to the family *Coronaviridae* are enveloped with a linear, non-segmented, positive sense, ssRNA genome of around 27 - 32 kb [3]. In 2003, the first major pandemic caused by SAR-CoV was reported [3] followed by the second pandemic with the emergence of SARS-CoV-2. As of 14th February 2021, SARS-CoV-2 has spread to more than 219 countries and territories with 111,693,989 confirmed cases and 2,473,339 deaths (21th February 2021, 9:34 GMT), (<https://www.worldometers.info/coronavirus/>) After the emergence of SARS-2, a considerable discussion and many publications have been made and provided a detailed information about this virus. There are four main groups of coronaviruses known as alpha, beta, gamma, and delta. Among these types, only alpha and beta CoV are known to cause disease in humans. But there is still missing information about what next? Which coronavirus will emerge in the future? The main objective of this to provide an insight information about the possible emergence of new coronavirus in the near future.

Human coronaviruses: Currently, seven human coronaviruses are known to cause disease human and non-human globally and they have been discussed below.

SARS-CoV

This virus was first reported from Guangdong province of southern China in the year 2002 and 2003, an epidemic occurred by SARS and spread to over 30 countries among five continents with 8,096 cases and 774 deaths and the crude fatality rate of about 10% was reported. After 2004, no human cases are reported [4].

HKU-1

The human coronavirus HKU1 (HCoV-HKU1) was isolated and reported from an old pneumonia patient who returned to Hong Kong from Shenzhen, China in 2005. The causative virus was originated from infected mice [5]. But the HCoV-HKU1 RNA was identified in 2003 from a 35 year-old woman suffering from pneumonia.

NL63

The human coronavirus NL63 (HCoV-NL63) was identified in late 2004 from a seven month old child in the Netherlands with a bronchitis symptom [6].

229E

The human coronavirus 229E (HCoV-229E) was first identified in 1966 and isolated in 1967 and known to infect both humans and bats [7]. HCoV-229E transmits via droplet-respiration and fomites. Recently the 229E related CoVs have been identified from camels in Arabian Peninsula and Africa [8].

HCoV-OC43

The Human coronavirus OC43 (HCoV-OC43) was isolated in 1960. The 'OC' name was given based on the isolation of virus from organ culture. This virus causes common cold symptoms in 10-15% cases and infection in the lower respiratory tract resulting in pneumonia. This virus is known to infect humans and cattle [7].

MERS-CoV

The MERS-CoV is a novel human coronavirus that was emerged and identified from Saudi Arabia in mid-2012 [8]. Currently, this has spread to 27 countries with a total of 2468 laboratory-confirmed infections and 851 deaths. The transmission of camel to human has been identified based on full-genome sequencing of samples from both human and camel [9].

SARS-CoV-2

The SARS-COV-2 was first identified in late December 2019 from the sea food market of Hubei province, China [4] and declared as pandemic and tentatively designated as COVID-19 but finally known as SARS-CoV-2. SARS-CoV-2 is the seventh known coronavirus to infect human [5]. This virus has closed genomic similarity to SARS-CoV. The bats are known as the primary source of the virus along with an unknown intermediate host.

The emergence of coronaviruses: Should we be ready for new coronavirus? What next?

Due to recent emergence of the new SARS-CoV-2 from China poses as serious threat and the emergence of a new coronavirus in the near future, if the suitable conditions for genetic mutations, frequent recombination, mixed infection, amplification, climatic conditions, and transmission are available in a specific area and location. Currently, we does not know which virus will emerge as next coronavirus with more deadly characteristics and extended hosts? The emergence of human coronaviruses has been presented in figure 1. In the most cases of coronavirus emergence, bats, palm civets, raccoon dogs, and camels are identified as a major sources of human infections. The continuous exposure of animal handlers to the infected animals and sources causes the transmission and introduction of virulent SARS-CoV-2. The frequency of mutation results in easy adaptation and more efficient transmission and infection to humans and finally resulted in a massive global pandemic. In 2002 - 2003 epidemics, SARS-CoV virus with variations in seven nucleotides and six amino acid changes in the spike protein gene resulted in low pathogenicity properties that were identified from palm civets and raccoon dogs. Most of the coronaviruses use different receptors like ACE-2, DPP4 and APN during their binding to host cells and viral entry. Spike protein gene is well known for host cell attachment and in emergence and re-emergence of coronaviruses. In the Hong Kong outbreak, 99.8% sequences identity was observed with SARS-CoV isolated from animals but interestingly a 29-bp insertion between Orf8a and Orf8b was identified in the animal isolates and further this segment with 29-nucleotide was deleted either before or soon after crossing the host species barrier to human. This suggests that due to molecular adaptation, the interspecies transmission occurred from animal to human. Any mutation, deletion, insertion, and recombination in the spike protein gene play a significant role in the host switching by enabling an altered organ tropism in the recipient host. This suggests that due to molecular adaptation, the interspecies transmission occurred from animal to human to cause the disease in human population [10].

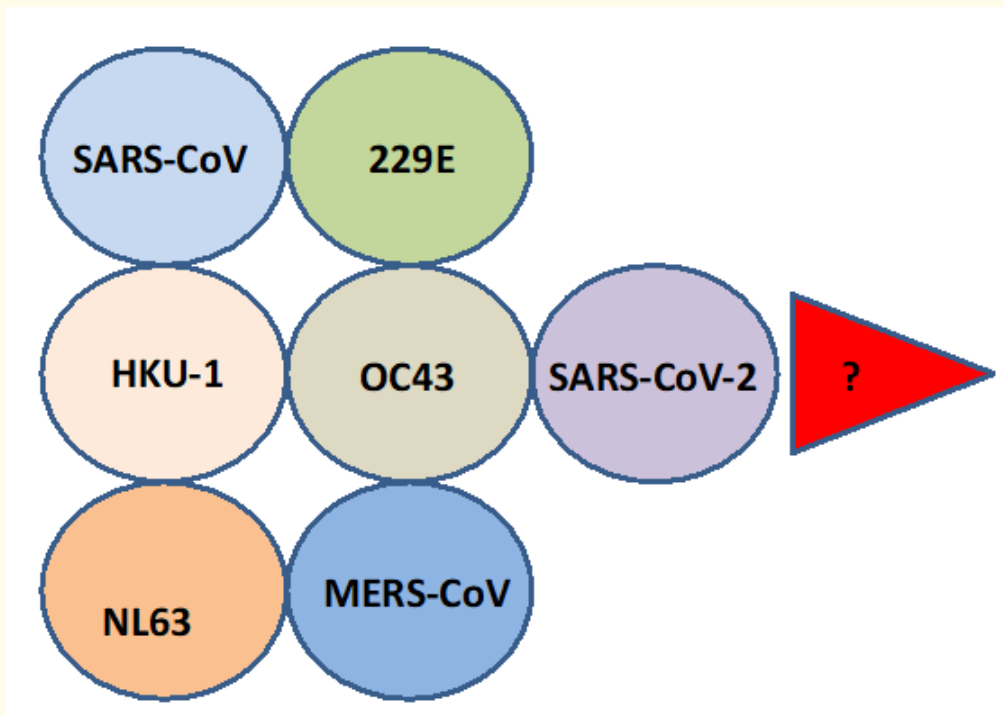


Figure 1: Emergence of human coronaviruses.

Discussion and Conclusion

Despite these achievements, there are long gaps exist like; it is still unclear about the intermediate hosts, source of the reservoir, virus maintenance and prevalence in various species of animals (reservoirs(s), the basis of virus stability in the physical surface, transmissibility, the molecular and immunological basis of disease pathogenesis in humans, early diagnosis of the virus in symptomatic and asymptomatic carriers, antivirals, effective vaccinations and effect on immune enhancement. In the future, there is a possibility of the emergence of new coronavirus due to many factors favors the virus emergence. These factors include favorable conditions, exposure to infected animals, environmental changes, non-proper sanitations, non-disposal off the solid waste materials, resumption of animal and seafood market, genetic mutations, preferences of new host receptors, clinical and environmental factors, presence of asymptomatic carriers, lack of vaccines, antivirals, proper disease management, and public awareness [11]. Taken together, we should be prepared for the possibility of the emergence and re-emergence of a novel coronavirus in the future [12]. Based on the current information about the coronaviruses, it is concluded that the suitable factors as like Wuhan sea food market may favor the emergence of any new coronavirus in the near future and pose a global threat to human population and cause another epidemic or pandemic and we should explore many options to avoid the emergence of a new coronavirus.

Conflict of Interest

The author declared that there is no conflict of interest.

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