ORIGINAL ARTICLE

COVID 19-A Novel Zoonotic Disease: Origin, Prevention and Control

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ABSTRACT

Breaking out contagious diseases is of many threats to human-beings, and coronavirus disease-2019 (COVID-19) is an example. Because of its initial cases happened in a market specialized for sea food stuff that eat living creatures, it was verified as an infectious zoonotic disease. The first case was infected with SARS-CoV-2 was an old and infirm person suffering from symptoms on 1st December 2019. Neither of his family associates got infected, and his virus origin still unidentified. The persistence of Covid-19 pandemic may be another evidence of diseases coming out of the human-animal overlapping and disseminating through globe. Some reports proposed that bat birds and pangolins were the source of infection since coronavirus-development of such two animals undertook analogous genomic sequence for Covid-19. When Covid19 happens, many aspects shall be noticed and grasped like origin, innate hosts and intermediary hosts. Dipping down the vulnerability of disseminating from natural host to human-beings may be thoroughly requiring understanding of the natural environment of the pathogen. Identifying SARS-CoV-2 origins and intermediate hosts help understanding the outbreak dynamics, with a probability of reverse zoonosis .Whereas, failing to recognize and uncover the origins and intermediate hosts in the disease cycle can create forthcoming diseases.

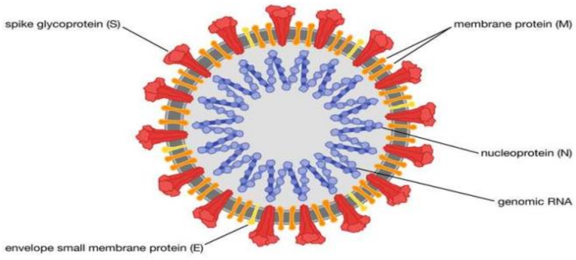
KeyWords :Covid-19,virus,infection.

A NOVEL CORONAVIRUS - SARS-COV-2

SARS-COV-2 is a kind of coronavirus category, the 7th coronavirus which infects humans. SARS-CoV and MERS CoV are the two categories of coronavirus that can result in severe pulmonary diseases, whilst 229E, HKU1, NL63 and OC43 cause mild symptoms. It is considered the 3rd zoonotic Beta coronavirus of them. SARS-CoV first appeared in 2002, which formerly disseminated from China in 2003, and MERS-COV which was identified in the Middle East in 2012 for the first time (1).

Coronavirus is the sub-family orthocoronavirnae within the Coronavirdae family. According to phylogenic bunching, the Orthocoronavirnae sub-family was categorized into 4 genera, the α, β, γ and δ coronaviruses. Only mammals get infected with Alpha and Beta coronaviruses. The γ and δ viruses infect bird and sometimes even infect mammalians including rodents & bats. Gamma-coronaviruses and Beta-coronaviruses are known to cause respiratory diseases in humans and gastroenteritis in animals (2,3). Coronaviruses are large shrouded viruses having about 30 kilo bases positive-senses single-stranded RNA genome (figure 1). The replicas non-structural proteins gene coding has nearly 2/3 out of such genome at the (5′) end, while the structural and accessory proteins occupy nearly 1/3 of the viral genome code. Coronaviruses are efficiently preset to change the range of host and tropism of tissue (4,5). According to the analytic, phylogenic and evolutionary research, bats have been noticed to be the most zoonotic novel coronavirus disseminator and have been reported that humans be infected by aerosols through intermediate hosts infected with the viruses (6).

Figure . 1: The coronavirus SARS-CoV-2, the cause of the COVID-19 pandemic(7).



ORIGIN OF SARS-CoV-2: The World Health Organization declared a worldwide alerts concerning atypical pneumonia cases in the province of Guangdong and the special administrative region of Hong Kong, China and in Vietnam (8) on March 12, 2003. More than 8,000 persons in 32 countries were affected by SARS, which broke out and spread worldwide (9,10). The British Columbia Center for Disease Control in Canada was the first to sequence the whole SARS coronavirus genome on April, 23 2003(11), and as a result, 16 SARS coronavirus strains obtained from China, Hanoi, Hong Kong, Taiwan & Singapore have been sequenced in a short time. RNA viruses usually possess high rates of genetic mutations, which enables the virus to escape from host defences and develop into a novel viral strain (12,13). The 2019-no CoV virus was renamed as SARS-COV-2 by the International Committee On Taxonomy Of Virus (ICTV) (14), because of the likeness of their symptoms with those induced by the Severe Acute Respiratory Syndrome (SARS) and the similarity of the genome organizations (15,16). Also, it is obvious now that SARS-COV-2 can utilize the angiotensin converting enzymes 2 (ACE2), the same receptor as in SARS-COV for human-being infection (17). There is a strong evidence that all human-associated coronaviruses emerged from other animals including rodents and bats. SARS-CoV-2 genomics' sequence differs substantially from SARS-CoV approximately 76% identity. Also, molecular analyses demonstrated that the viruses have 96% similarity with horse shoe bats coronaviruses isolated from the province of Yunnan, China. Thus, SARS-CoV-2 most probably coming out of bats (18, 19). This proves that human linked coronaviruses were originated from other animals including rodents and bats (20).

Bats, according to new studies, proved that they have unique defense mechanisms allowing them to be importunately or latently infected with viruses (21). Less new findings have shown that several bat Coronaviruses are capable of infecting human cells without a need to an intermediate adaptation (22,23). In other words, human can rarely be infected directly. Therefore, there should be another host required in transmitting the virus. More evidence builds indicated that humans could be infected by pangolins (24). The pangolins are trafficked out of many global regions to the seafood market in China. Genomic sequence of pangolins from Guangdong were much less associated with SARS-CoV-2 (25). The SARS COV-2 originated from Chinese Wuhan markets backs the existence of the virus within live animal sources; anyhow, the SARS-COV-2 intermediate hosts might be the *Rhizomyideae* family Bamboo civets & rats, but not absolutely proven. The profiling of meta genomic of CoVs specifies pangolins to have beta coronaviruses(26). Pangolins were proposed to be the intermediate hosts; despite studies of viral genomic series secluded from pangolin only take a part nearly 90% of entire homology, pangolin COV is excessively similar to SARS- COV-2 in all hexagonal key residue within the domain of the receptors bindings (27). This would indicate that pangolins could be contributing to the SARSCoV-2 origin, possibly through recombination with the bat viruses (28).

Control and prevention: No effective medication or vaccination at present available to cure or prevent COVID-19 infections. Though, several preventive health measures may aid resolving patients' primary complications (29). Once the COVID-19 outbreak originated, China carried out striking measures for containing infections such as closure of entire cities, airport, train, ship and car traffic blocking, with quarantine of millions of the population (30). Also they banned contacting with patients having acute respiratory symptoms and insecure contacts with farm or wild animals. Touching mouths and faces following contact with suspicious environment was not allowed too. The control depends upon the immediate isolation and detection of symptomatic patients. It is also essential to offer better communication with the common people and informing them on the significance of social distancing and personal hygiene regarding infection outbreak, and undertaking self-isolation until examination for probable viral infection has been completely performed. The common people need to be provided with transparent information and advices, and understand that they are also responsible for helping and preventing the viral spread, as a part of community health response (31,32). It is preferred that human-beings must avoid animal contacts and care unless there is a kind of necessity, such as fundamental hygiene procedures, that must always be there during caring for and handling the animal and/or animal product. Generally, countries should adopt specific universal health measures in controlling and prevention strategies to restrict infections from breaking out among both animals & humans, which can pose a positive effect on control and prevention and respectively on the economy.

CONCLUSIONS

Zoonotic infections threaten the agencies of global health. The cooperative worldwide efforts, like "One-Human-Environmental-Animal Health" is necessary to decrease the international vulnerability of zoonotic disease. Further evidence are required for the identification of the intermediate host responsible for SARS-COV-2 transmissions. Furthermore, further studies are required regarding various animal species because the exact origin and mechanism of attack are still not completely explored.

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