

General Opinion about Natural Resources of Coronavirus

Shirley Carroll*

Department of Immunology, University of Manchester, Manchester, United Kingdom

DESCRIPTION

Coronaviruses are single-stranded positive-sense enveloped RNA viruses that caused the ongoing coronavirus disease outbreak in 2019. This outbreak is relatively competitive and has become a global threat due to its rapid spread. Even though coronaviruses have been identified as veterinary pathogens for a long time because of their widespread distribution in various animals, they have also been identified as a causative agent of disease in humans, with coronavirus stress being identified as the causative agent of the not unusual place bloodless in humans. Since then, various traces of coronavirus have been observed to cause disease in humans. Coronavirus's high mutation and recombination rates, as well as its diverse herbal reservoir, provide the virus with an excellent opportunity to conform and evolve. As a result, the virus has been implicated in a number of outbreaks, including Severe Acute Respiratory Syndrome Coronavirus (SARS), Middle East Respiratory Syndrome (MERS) and COVID-19. According to investigations, all of the viruses causing those outbreaks have zoonotic origins. However, we know very little about the SARS-CoV-2 virus, which is the causative agent of COVID-19, in contrast to other types of outbreaks, is a virulent disease that kills hundreds of thousands of people worldwide. Different pieces of evidence showed that bats are the original host of MERS-CoV. Like SARS, severe cases of MERS can result from a weakened immune system, older age, diabetes, cancer, renal disease, and chronic lung disease MERS-CoV patients have acquired the infection through infected humans, camels, bats and other domesticated animals. However, dromedary camels appear to be the most likely source of animal-to-human transmission as an intermediate host. This is supported

by the study conducted by Alshukairi et al., on camel workers which reveals approximately 50% of camel workers in the Kingdom of Saudi Arabia were infected. Considering its impact, various research establishments are working to expand its vaccines through the use of unique strategies. Among the strategies, the nucleic acid-primarily based completely is the most promising. Several DNA and RNA-primarily based totally COVID-19 vaccines, including Moderna, Pfizer, and Johnson-Johnson vaccines, have been developed and are being used. On the other hand, other vaccines, such as CureVac and CVnCoV vaccines, are awaiting approval, proving that the nucleic acid-based COVID-19 development method is superior.

Even though CoVs are host-specific, they can infect humans and a variety of unique animals. They have long been recognized as veterinary pathogens due to their widespread distribution in unique animals such as dogs, palm civets, camels, pets, poultry, livestock, humans, and bats. Thirty years after CoV was first identified as a disease-causing agent in animals, Tyrrell and Bynoe discovered the first Human CoV (HCoV) in 1965. Since then, numerous CoVs have been identified, including SARS-CoV in 2002, Human CoV-NL63 in 2004, HCoV-HKU1 in 2005 and MERS-CoV in 2012. According to the report, all HCoVs are zoonotic. CoVs have been found in a wide variety of hen and bat species as herbal hosts. Bats are known as a natural reservoir of various human pathogenic viruses, including rabies virus, Nipah virus, Hendra virus, Ebola virus, Marburg virus, and influenza virus. Bats are also thought to be a reservoir for a variety of emerging viruses, including coronaviruses that can cause SARS, MERS, Porcine Epidemic Diarrhea (PED), and Extreme Acute Diarrhea Syndrome (SADS).

Correspondence to: Shirley Carroll, Department of Immunology, University of Manchester, Manchester, United Kingdom, E-mail: ShirleyCarroll@bristol.ac.uk

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