

Comparative Evolution of Animal and Human Coronaviruses, their Varieties and Virulence

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ABSTRACT

Coronaviruses are a group of enveloped viruses with single-stranded and RNA genomes that cause a wide-ranging spectrum of animal and human diseases. Initially, the pneumonia sort of disease was found in the Wuhan city of China, which later was identified as the novel coronavirus in November 2019. Recent studies have shown that HCoV, 229E, and OC43 develop flu-like symptoms which cause mild illness. This virus has then been declared a pandemic for its spread to several countries. Several types of research suggest that these were the birds and animals i-e bats and pangolins, which caused this virus to spread to humans. Human coronavirus has been attacking humans since 1962 by making changes in itself. However, Novel coronavirus has been proven to be a wide-spreading one. The SARS-COV is the most recent MERS-COV confirming that the coronavirus causes severe respiratory diseases, including fever and the common cold. As COVID-19 is pandemic worldwide, it primarily affects upper respiratory tracts (nose and throat), later on, infects lower respiratory tracts (lungs), and leads to pneumonia. SARS-COV-2 and MERS-COV2 are animal species that infect humans, causing severe illness. The reason behind this is that animal species can replicate at 37°C. The objective of the study is to collect reports from various databases for analysis. Globally, researchers have warned against the further spreading of the virus. If not controlled, this can result in more deaths and leave long-lasting consequences on global health and the economy. As compared with earlier episodes of SARS and MERS, the novel corona is more dangerous. Vaccination is required for future prevention against COV-19.

KEYWORDS: Coronavirus, pandemic, Chiroptera, Respiratory infection, SARS.

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INTRODUCTION

Coronavirus is a single-stranded RNA genome ~ 30,000 nucleotides 80x160 nm in diameter having a crown appearance^{1,2}. SARS-Cov-2 belongs to orthocoronavirinae, which's parent virus is coronaviridae. Coronaviridae can be grouped into four types; a) 229E, b) NL63, c) OC43, and HKU1, A and B coronaviruses can infect humans. However, Delta coronaviruses can be found in animal's only³.

FIGURE a: 229 E

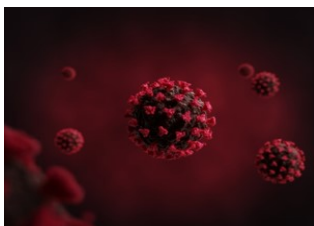


FIGURE c: OC43

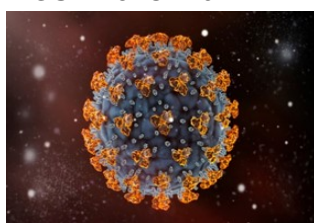


FIGURE b: NL63 E

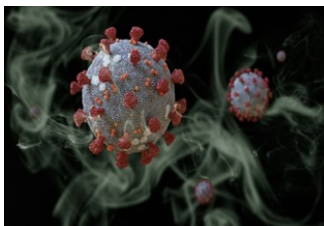
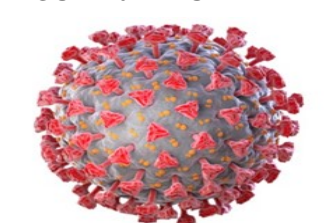


FIGURE d: HKU1



Initial findings revealed that Covid-19 infection spread from Wuhan's seafood market because of early conditions, and even some deaths were reported from there⁴. The infected ones were either residents of the area or were there in the market to earn a livelihood. They had direct contact with living animals and birds to be sold in the market. Bat involvement was reported in many places as a transmitter into a human as a potential carrier of this virus, which caused the initial spread of this virus to human beings⁵.

There is a resemblance of SARS-COV-2 to bat SARS-COV like Coronaviruses. Bats serve as reservoir RATGI3 bat (Chiroptera) virus closest too⁶. There are also possibilities of the spread of this virus from pangolins. They could also be potential carriers of this virus. SARS Coronavirus uses an angiotensin-converting enzyme (ACE2) which can infect human cells at large^{7,8}.

Novel Coronavirus SARS-COV-2 disease COVID-19 is animal species having severe respiratory disease, including fever and common cold^{9,10}. COVID-19 is a pandemic worldwide, primarily affecting the upper respiratory tract, nose, and throat. Later on, the virus infects the lower respiratory tract (lungs) and leads to pneumonia. While sources of some other species are unexplained^{11,3}, 229E, NL63, and HKU1 circulate in the human population and cause respiratory infections

but have no importance in adults and children¹².

DISCUSSION

Till 2019, there were six varieties of coronaviruses that could infect humans by causing respiratory illness. Early varieties can be named HCOV-229E, HCOV-OC43, HCOV, NL63, and HKU1. The types mentioned above of viruses can cause upper respiratory disorder, and in a few cases, these could cause severe illness to infants, middle-aged children, and older adults. However, SARS-COV and MERS COV infect humans. At the end of 2019, Novel coronavirus (Covid-19) included itself in the family of coronaviruses. Researchers have found that the novel coronavirus could have been clustered from bat SARS which was isolated back in 2015 because several genetic similarities were identified between the novel coronavirus and bat SARS. HKU2 is associated with bat SARS. HKU2 is associated with bat SARS. Some coronaviruses have the characteristics of infected birds and animals, were found potential carriers of such viruses. Bat coronavirus (HKU2) and Swine syndrome coronavirus, fatal viruses, triggered massive infections in pigs in Southern China; a large number of pigs infected with the viruses were found dead.

The 2019 n-COV has a similar phylogenetic lineage to SARS and MERS. There is no specific diagnostic. However, only PCR Real-time is an option for the diagnosis. WHO and local health organizations need to provide essential equipment in regions to prevent and control novel Coronavirus so that any misshapen at a global level can be prevented.

Global public health is under the dark cloud of the threat of the virus. A new variant of the corona has been identified in the United Kingdom and South Africa. South Africa named variant 501Y.V2 because of the N501Y mutations found in the spike protein. This mutation, among others, is also found in the new U.K strain, and it is thought to be similarly more transmissible. The new variant is more contagious and life-threatening. After the United Kingdom and South Africa, more cases of a new Coronavirus variant are being witnessed in various countries. Recently Japan nation institute of infection diseases had detected a new variant of Coronavirus in four travelers arriving from Brazil. Pakistan is not an exemption to it. On 29th December 2020, six cases of the new variant were confirmed in Pakistan. The cases are growing worldwide. The world is striving to get rid of this pandemic. Many countries have started vaccinating masses. Researches are underway to ascertain whether the current vaccinating will develop immunization against the new variant or not.

CONCLUSION

The result of high-frequency events in COVID is the generation of novel Coronavirus with unpredictable

changes in virulence during human infections with multiple animal species that may interact with one another. Coronaviruses attack the respiratory system. These viruses infect, affecting respiratory tracts. Humans are also at high risk of these viruses. Take the example of Covid-19, which infected people of all age groups. The world health institutions should be focused on the proper diagnosis of viruses, which is the only way to find a cure for viruses. The recent resurgence of the Novel coronavirus has proved that we, humans, are at a high risk of meeting fatal viruses. Recent mutations in the virus's genome paved the way for further studies on different aspects of viruses. This study will promote epidemiological and pathological studies for identifying new viruses carrying the potential risk of infecting the respiratory system. It is a need of the hour too.

It is time to modify our public health organizations for proper detection, diagnosis, and prevention against viruses having zoonotic origin.

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AUTHOR CONTRIBUTIONS

Rustamani S: The author declares that this work was done by her and all liabilities about claim relating to the content of this article.

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