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Review Article

A review on: Neocov is not new COVID it's old and similar to SARS

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ABSTRACT

Recently, Coronavirus has given great attention from the biomedical community based on the appearance and isolation coronavirus that infects humans. To understand the new MERS-COV behaviour appears to require different knowledge levels (epidemiologists, antigenic, and pathogens), and this knowledge can be produced from the most related viruses. In this study, we direct to compare between 3 species of Coronavirus, namely Middle Eastern respiratory syndrome (MERS-COV), severe acute respiratory syndrome (SARS-COV), and Neocov regarding all genomes and 6 similar proteins (E, M, N, S, ORF1A, and ORF1AB) use different bioinformatics tools to provide a better understanding of the relationship between 3 viruses at nucleotide and amino acids. All sequences have obtained from the National Center Biotechnology Center (NCBI). Greetings to target genomes phylogenetic analysis shows that MERS and SARS-COV is closer to each other compared to Neocov, and the latter has a relatively longest time. We found that all phylogenetic methods in addition to all parameters (physical and chemical properties of amino acids such as amino acid, molecular weight, atoms the composition, theoretical pi, and structural formula) show that Neocov protein is the most related to MERS-COV. All phylogenetics trees (with the maximum-possibility method and joining neighbours) show that Protein Neocov has less evolution changes except ORF1A only with the maximum possible method. Our results show a high similarity between the structural protein of the virus responsible for the virus infectivity; Therefore, we hope Neocov will appear faster in human-related infections.

1. Introduction

Neocov is a Coronavirus strain such as SARS-COV-2 and can kill one of the three affected people, researchers from Wuhan University and the biophysics institute of the Chinese biophysics academy have found.[1]

Even as the world continues to tackle SARS-COV-2 and its variants, scientists in Wuhan — the place where the virus is known to be coming from, warn about this new cov strain that can be even more deserving than covidant. Nicknamed as "neo-VOCs", the strain is linked to the respiratory syndrome of the Middle East or the Mers-Coronavirus. Combined with the high mortality rate of Mers-Coronavirus, NEO-VOC is afraid of causing deaths in one at home.[1]

The WHO manager said the virus has recently been found in bats in South Africa. While China has announced the detection of the new coronavirus to bat, both the world continues to regroup under the dangers of the SARS-COV-2 virus that causes Covid-19, scientists from China's Wuhan. Declared that this could be more contagious and possibly a lifting the coronavirus strain compared to previous detected

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persons.[2]

"That the virus detected in the study will pose a risk of man will need an additional study," said the WHO manager. In addition, the official informed that WHO is currently working closely with the World Organization for Animal Health (OIE), Food and Agriculture Organization (FAO).[3]

2. Activity and Relationship with SARS

In a new research document that has not yet been reviewed by peers, Chinese researchers have warned from Neo-VOC, a new type of coronavirus, from South Africa, which apparently has a high rate of death and transmission. It is associated with the Mers-Coronavirus, a similar type of SARS-COV-2 similar to a virus, and was first identified in Saudi Arabia in 2012. According to the research, NEO-COV can carry the high rate of MERS mortality -Coronavirus (one in three deaths) with the high rate of transmission of SAS-COV-2, which makes it a potentially deadly outbreak. According to the World Health Organization (WHO), Mers-VOC belongs to the great family of Coronavirus that can cause a multitude of disease, including common cold and SARS (severe acute respiratory syndrome). The new research carried out by scientists from the University of Wuhan and the Chinese Academy of the Biophysical Institute studied Neocov, which emerged together with Mers-VOC and found themselves in Bats in South Africa.[3]

2.1. Activity and why it's more harmful than omicron

"In this study, we have seen unexpectedly that Neocov and its close relatives, PDF-2180-VOCs, can effectively use certain types of enzyme 2 (ACE2) of Bat Angiotensin conversion and, less favourably, the human ACE2 At the entrance, "said the study.

They also stated that Neocov infection could not be neutralized by antibodies targeting SARS-COV-2 or MERS-VOCs.

ACE2 is a receiver protein on cells that provides the entry point of the coronavirus to hook and infect a wide range of cells. "Our study demonstrates the first case of ACE2 use in seas-related viruses, violates light on a potential bio-safety threat of the human emergence of an ACE2 using" MERS-COV-2 "with a rate. High mortality and transmission ", study adds.

"Our study demonstrates the first case of ACE2 use in seas-related viruses, violates light on a potential bio-safety threat of the human emergence of an ACE2 using" MERS-COV-2 "with a rate. High mortality and transmission ", the authors of the research study said.[4]

2.2. Structure of Neocov variant and why it's important to study in current scenario

Coronavirus recently received considerable attention from the biomedical community based on the emergence and isolation of a human fatal man. Understand the behaviour of the new emergence of MERS-COV requires different knowledge levels (epidemiological, antigenic and pathogens), and this knowledge can be generated from the most connected viruses. In this study, we aimed compare between 3 coronavirus species, namely, respiratory syndrome of the Middle East (MERS-VOCs), severe acute respiratory syndrome (SARS-VOCs) and NEOCOV concerning whole genomes and 6 similar proteins (E, M, N, S, ORF1A and ORF1AB) using different bioinformatic tools. Provide a better understanding of the relationship between the 3 viruses at the levels of nucleotide and amino acids. All sequences have been extracting from the National Center Information on Biotechnology (NCBI). Considers that the phylogenetic analysis of targeted genomes has shown that the first and foremost SARS-COVS closer to each other compared to Neocov, and the last relative time the longest.[5]

Wuhan Scientists warn from New Covid 'Neocov' with High Death that is die 1 out of 3, Infection rate. Wuhan scientists from China, where the Virus Covid-19 was discovered for the first time in 2019, has warned of a new type of Coronavirus 'Neocov' in South Africa, declared that it has a high rate of death and transmission, according to a report of The Russian news. Sputnik agency[6]

Scientists from Wuhan, China, have issued a warning about this new strain of coronavirus known as Neo Cov. Furthermore, this has a new form of coronavirus, so it will undoubtedly affect people if precautions or major decisions are not taken. Learn more about NeoCov New Covid Variant Symptoms to learn more about this new virus. Despite this, Wuhan scientists are warning that the new strain has the potential to infect more people than before. Soon, all of the details for the respective version will be available.[7] Many people are interested in NeoCov New Covid Variant Symptoms because they want to understand the impact of this virus. Regarding the composition, the theoretical IP and the structural formula indicated that the Neocov proteins were the most related to MERS-VOCs one. Phylogenetic trees (by maximum junction methods) indicated that NEOCOV proteins have less evolving changes, with the exception of Orf1a by a maximum method of maximum likelihood. Our results have indicated a great similarity between viral structural proteins' infectivity; Therefore, we expect that Neocov can appear to the human infection.

There is 3D image comparison of N, M, S, proteins of covid viruses- MERS-Cov, SARS and NeoCov-.[5]

3. NeoCoV in India

3.1. Peer reviewed on NeoCov

"NeoCov could penetrate human cells in the same way that the Covid-19 virus did, and is only one mutation away from

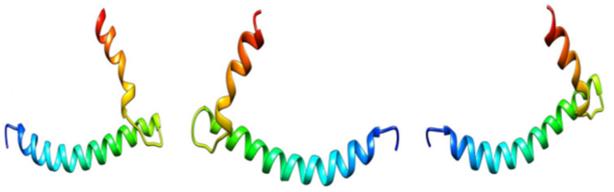
MERS-Cov SARS-Cov Neo-Cov

Fig. 1: Structure of N protien

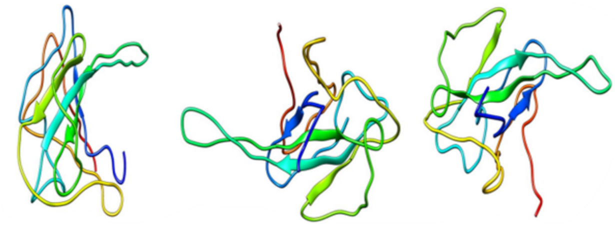
MERS-Cov SARS-Cov NeoCov

Fig. 2: Structure of M protien

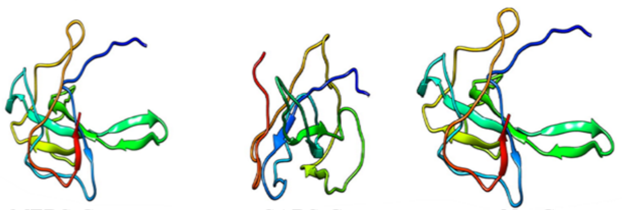
MERS-Cov SARS-Cov NeoCov

Fig. 3: Structure of S protien

becoming dangerous for humans," the Chinese said in a preprint repository BioRxiv study that has yet to be peer-reviewed.

The World Health Organization (WHO) said it is aware of the development, but the virus needs to be studied further to determine whether it poses a risk to humans, according to Russian news agency TASS.

According to the WHO, wild animals are the source of 75% of infectious diseases in humans. Coronaviruses are frequently found in animals, including bats, which serve as a natural reservoir. Medical experts in India, on the other hand, downplay the perceived threat posed by NeoCov.[8]

3.2. *MERS-CoV is a precedent*

MERS-CoV (Middle East Respiratory Syndrome) was one of three major coronaviruses that caused large-scale human fatalities, according to Rajeev Jayadevan, Vice-Chairman of the Indian Medical Association's Kerala Research Cell. It struck the world ten years ago, with an estimated mortality rate of 35%.

Researchers investigating the virus's origins searched for similar viruses in bats, which are common reservoirs for such viruses. Despite the fact that the MERS-CoV virus is thought to have jumped from camels to humans, it is thought that bats may have given the virus to camels many years ago.

The NeoCoV virus, which is genetically similar to the MERS-CoV virus, was discovered in 2014, but no human infections or deaths have been reported.[9]

3.3. *Why should you be unconcerned about neocov?*

The research paper basically says that NeoCoV, which has only been found in bats so far, may be able to infect humans if it undergoes a specific type of mutation. That's a lot of speculating. A lot of hypothesising based on a laboratory study that has yet to be peer-reviewed, which is a rigorous process that involves experts unrelated to the study in question analysing the original researchers' findings and methods.[10]

4. Conclusion

According to researchers from Wuhan University and the biophysics biophysics academy, only one mutation needed for the virus to infiltrate human cells. The research findings stated that the Coronavirus novel pose a risk because of binding to Ace2 receptors different from the Coronavirus pathogen. As a result, both antibodies and protein molecules produced by people with respiratory diseases or immunized can protect against Neocov.

According to Chinese researchers, Neocov brought a potential combination of high levels of COV MERS (one in every three infected people died) and the current SARS-COV-2 transmission rate of Coronavirus.

After briefing in Neocov, experts from the Virology of the Russian state and the biotechnology research center issued a statement on Thursday, the report stated.

"The Vector Research Center is aware of the data obtained by Chinese researchers in Neocov Coronavirus. At present, this problem is not the emergence of a new Coronavirus who can actively spread so, the potential risks described need to be studied and need more investigation on Neocov.

5. Source of Funding

None.

6. Conflict of Interest

None.

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