**Research Article**

# A Phylogenomic and Evolutionary Perspectives of COVID-19

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## I N F O

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## A B S T R A C T

From the time immemorial, all drastic pandemics and associated pathogens have been under the spotlight of research in our attempts to identify, characterise, control and trace back their origin. Quite often such attempts have enabled mankind to find effective solutions to overcome such pathogen outbreaks and turn them to pages of history. In the wake of repeated infections in different corners of the world, its quite essential to evaluate if they are the cruel aftermaths of nature or any manmade error. In such as scenario, recent developments in the molecular evolutionary analysis offer us more information in-depth regarding the virus emergence, molecular epidemiology, virulence and evolutionary concepts, adding to the conventional strategies in viral epidemiology. The nucleotide sequences were retrieved from NCBI. The present study revealed the genetic variability of CoV, 2019-nCoV against previously reported corona viruses. Moreover, the genetic variability of COVID-19 from different affected corners of the globe are evaluated to get a better understanding of their modes and routes of spread across our planet.Such nucleotide sequence-analyzed information gathered from this investigation will definitely assist the intention and implementation of effective pandemic control measures.

**Keywords:** COVID-19, Coronavirus, Phylogenetic tree, SARS, MERS

## Introduction

The rapid spread of corona virus infections have once again been fetched world-wide attention following the emergence of COVID-19 out-break in 152 countries. The current outbreak of COVID-19 is principally considered as the third renowned spillover of an animal coronavirus to human population.[3] The confirmation of infections in 152 countries as of March 18, 2020 underpins the significance for COVID-19 to hastily emerge into an international pandemic. Concerning the viral outbreak, it is significant to analyze whether the outbreak is instigated by a new virus or a modified version of the previously reported virus; as

for the reason that studies based on the aforementioned concept will definitely help the scientific community to decide which actions and strategies are most effective and apposite to track the infectious agent, thereby can prevent the consequences of the COVID-19 outbreak.

There is no effective candidate drugs are presently available against the COVID-19. Therefore, gaining insights into the molecular perspectives of 2019-nCoV with special inference on the SARS CoV and MERS CoV would definitely be helpful to analyze and prevent the COVID-19 epidemiology over the world. The present investigation has intended to find out the evolutionary aspects of COVID-19 towards the

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previously reported corona viruses such as SARS CoV and MERS CoV to explore the evolutionary characterization in disease prevention.

## Materials and Methods

### Molecular Perspectives of COVID-19

The nucleotide sequences of SARS CoV, MERS CoV, 2019-nCoV were retrieved from NCBI data base. The evolutionary history was inferred by using the Maximum Likelihood method based on the Tamura 3-parameter model.9 The tree with the highest log likelihood (-19335.43) is shown. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. The analysis involved 28 nucleotide sequences. Codon positions included were 1st+3rd. There were a total of 5978 positions in the final dataset. Evolutionary analyses were conducted in MEGA7.[1,2,5] The red colored signals in the Figure 1, represents the COVID-19 (SARS-CoV-2) while the green colored and orange colored signals represents the SARS-CoV and MERS-CoV.
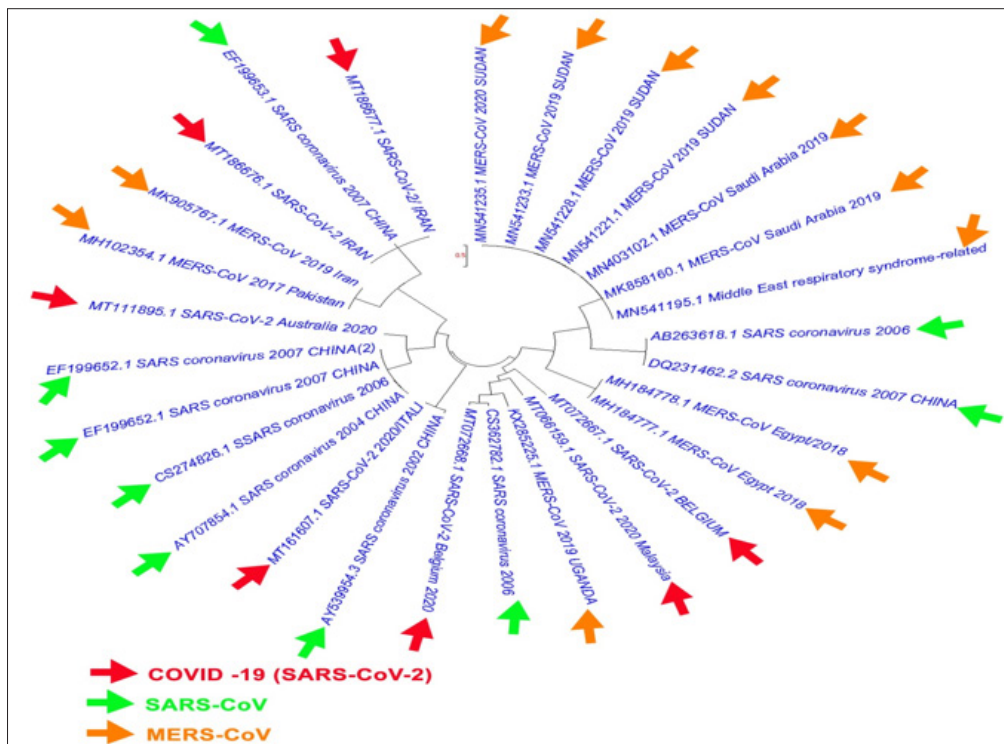


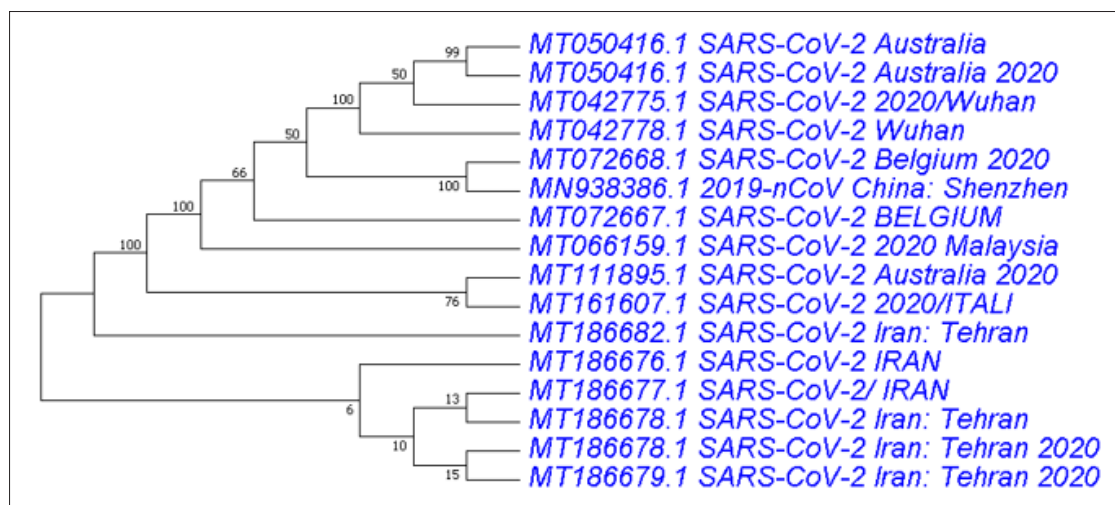**Figure 1.Molecular phylogenetic analysis by maximum likelihood method**



**Figure 2.Molecular phylogenetic analysis of COVID-19**

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## Molecular Phylogenetic Analysis of COVID-19 of Severely Affected Areas

Neighbor-Joining method was used to reveal the phylogenetic perspectives of SARS CoV, MERS CoV, 2019-nCoV.[8] The bootstrap method used 1000 replications to derive the numbers displayed on branches. The evolutionary distance has been anslysed using p-distance method. The analysis involved 16 nucleotide sequences. Codon positions included were 1st+3rd. All ambiguous positions were removed for each sequence pair. There were a total of 801 positions in the final dataset.

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## Result and Discussion

Here, we enumerate an assessment of the evolutionary aspects of SARS-CoV-2 (2019-nCoV/ COVID-19), a newly recognized human coronavirus. Based on the phylogenetic analysis of the corona sequences retrieved from the NCBI database, the present study revealed that the SARS-CoV-2 (2019-nCoV/ COVID-19) has exposing a sister clade to previously reported corona virus as illustrated in Figure 1. The identification and taxonomical classification of infectious agents need to identify based on the genetic differences that occur in their strains, which are being reported in the current scenario. Studies concerning the aforementioned concepts will definitely raise the question of how the genetic variations between the virus strains are enough to identify the contestant virus as a novel one.[3] The clustering patterns effectively approved the previous studies reports since the SARS-CoV-2 clustered with other SARS-CoVs belonging to the Betacoronaviru genus.[6,7,11] In agreement with our results, few studies3 have mentioned the differences between SARS-CoV-2 and other zoonotic coronaviruses such as MERS-CoV and SARS-CoV, emerged in the world during the twenty-first century. Molecular phylogenetic analysis of COVID-19 of severely affected areas clearly indicates the genetic diversity as illustrated in Figure 2.

The data regarding the clinical and epidemiological aspects for SARS-CoV-2 indicates that the virulence and disease spectrum of SARS-CoV-2 differ from other previously reported viruses such as MERS- CoV and SARS- CoV.[4,10] Due to the various differences exhibited by the virus, the diagnostic approaches employed to confirm COVID-19 are not same to those of other zoonotic viruses like sars-cov. Having now found out the evolutionary aspects of sars-cov-2, the authors hope that the results gathered from this study will add a better understanding of the existing knowledge on the various strains, their stability and virulence in various geographical conditions since the present study have analysed the nucleotide sequences from various provinces of the world with special inference on the evolutionary aspects.

## Conclusion

A comparative analysis of the spread of Coronaviruses viz, SARS in 2003 (26 countries), MERS in 2012 (Arabian Penisula) and COVID-19 (152 countries) clearly indicates the global infectivity of these viruses. An evaluation on the phylogenetic relationships the three corona viruses of this study indicate that they are highly mutating as times goes ahead. The genetic variability of SARS from MERS and COVID-19 and vice versa is an evidence of this fact. However, the alarming fact is that the severity and fatality of the diseases caused by corona viruses are increasing drastically after each outbreak. Thus strict quarantine measures of blocking an infected area from other parts of the globe becomes quite essential in the near future considering the influence of flight travel in the spread of such pandemics. The analysis of public genome sequence data from COVID-19 and related viruses from the affected countries found that this virus is the product of natural evolution and rule out the likelihood of a made bioweapon or otherwise engineered within the Laboratory. However, history from the lessons of SARS also warns us that negligence of even a single research facility could lead to the resurgence of such pandemics. Thus the prevention and control of every pandemic relies on the efficient and time-bound action initiated by mankind.

## Ethical Statement

This article does not contain any studies with human participants or animals performed by any of the authors.

**Conflicts of Interest:** None

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