

## ORIGINAL ARTICLE

# Changing epidemiology of SARS-CoV in the context of COVID-19 pandemic

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## Keywords

COVID-19 • SARS-CoV • Changing epidemiology • Evolution

## Summary

SARS-CoV-2 is a new form of  $\beta$ -coronavirus that has been recently discovered and is responsible for COVID 19 pandemic. The earliest infection can be traced back to Wuhan, China. From there it has spread all over the world. Keeping in view the above perspective, an attempt is made in order to find out the epidemiological pattern of COVID 19 pandemic, if any, in different geo-climatological regions of the world in terms of case incidence and mortality. This study is also an endeavor to review and analyze the gradual changes of the genetic makeup of SARS-CoV from evolutionary and epidemiological perspectives. The raw data of COVID-19 cases and death incidences were collected from the World Health Organization (WHO) website from the time period: 1<sup>st</sup> April to 6<sup>th</sup> April, 2020. The data that are utilized here for general and Case fatality rate (CFR) based analysis. Western pacific region, European region and Americas have the greatest number

of infected cases ( $P < 0.001$ ); whereas deaths have been found to be significantly higher in Europe ( $P < 0.001$ ). Total number of confirmed cases and deaths in south-east Asia are comparatively lower ( $P < 0.001$ ). Case fatality rate (CFR) has also found significant for European region. SARS-CoV-2 is considered to be a strain of SARS-CoV that has a high rate of pathogenicity and transmissibility. Result indicated that the European region has been affected mostly for both cases and death incidences. The novel mutations in SARS-CoV-2 possibly increase the virus infectivity. Genetic heterogeneity of this virus within the human population might originate as the representatives of naturally selected virus quasispecies. In this context, the presence of the asymptomatic individuals could be a significant concern for SARS-CoV-2 epidemiology. Further studies are required to understand its genetic evolution and epidemiological significance.

## Introduction

Coronavirus (CoV) is a positive single stranded RNA virus which causes a respiratory tract infection in human [1]. Earlier in 2002 and 2012, the emergence of severe acute respiratory syndrome (SARS) coronavirus (SARS-CoV) and Middle East respiratory syndrome (MERS) coronavirus (MERS-CoV) have attracted the researchers to explore the epidemic potential [1] of these viruses. A newly discovered  $\beta$ -coronavirus led to the occurrence of a number of pneumonia cases in Wuhan, China, in December 2019. Initially (on 12 January 2020), it was given the name, the 2019-novel coronavirus (2019-nCoV) by the World Health Organisation (WHO). Later, the disease was officially renamed as coronavirus disease 2019 (COVID-19) by WHO. The new coronavirus was termed as SARS-CoV-2 by the *Coronavirus Study Group (CSG) of the International Committee*, on 11 February 2020 [2]. The SARS-CoV-2 also develops an upper respiratory tract infection much alike its earlier ancestor SARS-CoV, however, the recent pandemic due to this novel mutated SARS-CoV-2 virus infection created a critical pandemic situation throughout the globe [3]. Until now, different researches are being performed to understand the infection severity and virus transmissibility of novel SARS-CoV-2. Keeping in view the above perspective, an attempt is made in order to find

out the epidemiological pattern of COVID-19 pandemic, if any in different geo-climatological regions of the world in terms of case incidence and mortality. In addition, this study is also an endeavor to review and analyze the gradual changes of the genetic makeup of SARS-CoV from evolutionary and epidemiological perspectives.

## CORONAVIRUS (CoV) AND ITS CHARACTERISTICS

Coronaviruses are non-segmented, enveloped and positive sense single-stranded RNA virus genomes. They have a size ranging from 26 to 32 kilobases. The virion consists of a nucleocapsid composed of genomic RNA and phosphorylated nucleocapsid (N) protein, covered by two different types of spike proteins: the hemagglutinin-esterase (HE) (found in some CoVs) and the spike glycoprotein trimmer (S) (found in all CoVs). The S protein in the virus envelop consists of the membrane (M) protein and the envelope (E) protein [2]. The  $\alpha$ ,  $\beta$ ,  $\gamma$  and  $\delta$  coronaviruses are the four genera into which the coronavirus subfamily is genotypically and serologically divided [4]. Gastroenteritis in animals and respiratory illness in humans are caused by  $\alpha$ -coronaviruses and  $\beta$ -coronaviruses. The two deadly and extremely pathogenic  $\beta$ -coronaviruses and 2002 SARS-CoV and the 2012 MERS-CoV, cause severe respiratory diseases in humans. HCoV-NL63 and HCoV-229E, the  $\alpha$ -coronaviruses and HCoV-OC43 and HKU1,

# The relationship between bats and human coronavirus: An exploratory review

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## Abstract

**Introduction:** Bats are known to harbour several coronaviruses including the progenitor of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), which has caused COVID-19 pandemic. The emergence of SARS-CoV-2 has unwittingly fueled widespread apprehension and fear in the general public about bats. Aim of this paper was to review human coronaviruses in bats, the possible transmission dynamics of bat-borne viruses, and the impact of deforestation and climate change on bats.

**Methods:** A narrative review was conducted by using electronic databases- PubMed/Medline, Google scholar, Wiley Online Library, Semantic Scholar, and medXiv- for searching all types of peer-reviewed and not peer-reviewed articles in English language, published from 2002 to 2020. All the findings and observations in this review were listed in references and main findings were summarized in a table.

**Results:** Certain species of bats are being progressively acknowledged as important natural reservoirs for several groups of viruses; some of which cause epidemics. Anthropogenic activities like encroachment of wildlife habitat, deforestation, developmental activities and close encounter with wild animals, cause disturbances in ecosystem functioning. This ecological imbalance threatens the bat populations and creates selection pressure leading to random mutations in the viruses. This may eventually cause viral spillover to humans and other animal hosts due to forced proximity, leading to outbreaks of novel diseases. Although bats are considered likely reservoirs of most of the human coronaviruses causing epidemics, yet they cannot be considered as a public health threat as the transmission dynamics is influenced by human behavior/ activities.

**Conclusion:** The complex eco-epidemiological situation calls for a judicious approach in assessing the role of bats in nature. Bats, on their own, may not pose public health threat, however there is a need to adopt comprehensive environmental health management policies based on the principles of conservation medicine to address this likely public health threat from bats.

**KEY WORDS:** Human Coronaviruses, Public health threat, Deforestation, Threatened Bat population, Ecological imbalance.

# COULD NOVEL CORONA VIRUS (SARS-CoV-2) BE THE EVOLVING FACE OF A NEW GENERATION OF GENETICALLY COMPLEX EPIDEMIOLOGICAL CHALLENGE?

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## ABSTRACT

The recent outbreak of the novel Corona virus (SARS-CoV-2), that has taken the world by storm, is a disturbing case of severity posed by a highly dynamic viral strain. Suspected to have originated from bats, a reservoir host of many deadly viral diseases, the COVID-19 pandemic might be an alarming but a substantially preliminary instance of a much complexly evolving future of disease epidemiology, at the interface of rapid and robust genetic recombination, mutation and highly adaptable strains of the *Coronaviridae* family. Keeping these attributes in mind, the idea of host(s) as “mixing pot” is introduced through this review to capture the plausible future of the Corona virus dynamics through a vector-borne transmission.

**Keywords:** *Coronavirus, Zoonotic, Mixing Pot, Recombination, RNA Virus, Reservoir Host, Host Switching*

## INTRODUCTION

The recent COVID-19 pandemic owing to the viral strain SARS-CoV-2 of the *Coronaviridae* family, has wreaked havoc across the globe. Preliminary findings suggest its origin in bats, which thereafter crossed the species barrier from an intermediate host, eventually spreading within humans. However, such instances have been seen in the past, as evident in the SARS epidemic of 2002 or the MERS-CoV outbreak in 2012 (Perlman and Netland, 2009; Afelt *et al.*, 2018). A wide range of infectious diseases are in fact caused by zoonotic pathogens originating in wildlife and then spreading to humans (Klimpel and Mehlhorn, 2014; Kading and Schountz, 2016; Bhattacharya *et al.*, 2019). Bats are an important reservoir of several pathogenic agents, mainly viruses, and many of them have already caused disease outbreaks worldwide (Wang *et al.*, 2009; Anthony *et al.*, 2017; Monchatre *et al.*, 2017). This is hypothesized to be attributed to the fact that bats are the only mammals with the capability of powered flight, which enables them to have a longer range of migration compared to land mammals. They are also the second largest order of mammals, accounting for about a fifth of all mammalian species, and are distributed worldwide (Fan *et al.*, 2019). Moreover, the increase in the rate of viral infections involving bats, is attributed to an expanding overlap between bat and human habitats, a classic example of man-animal conflict.

## REVIEW OF LITERATURE

### Corona-Viruses: An Insight

Since the early 1960's, Corona-viruses (CoVs) have been defined as a novel virus causing mild to severe respiratory tract infections (Huang *et al.*, 2016). CoVs have the largest RNA viral genomes, ranging from 26 to 32 kilobases in length. Their expanded genome size may be due to increased fidelity of replication, after acquiring genes encoding RNA-processing enzymes (Fan *et al.*, 2019). Expansion of genome can increase the repertoire of genes encoding accessory proteins that are essential for CoVs to adapt to a specific host (de Haan *et al.*, 2005). Thus, among CoVs, genetic recombination events, gene interchange, and gene insertion or deletion are of common occurrence. Next generation sequencing tools have made it possible to detect new strains in the *Coronaviridae* family and as such it is expanding rapidly. As a result, CoV taxonomy is constantly changing (Subissi, *et al.*, 2014). In fact, this large family of viruses are common among many different species of animals, such as camels, cattle, cats, rodents and bats. Rarely, animal CoVs can infect humans and, as a result, may spread among humans during epidemics such as MERS, SARS, and SARS-CoV-2 (COVID-19).

### Bats as Reservoir Hosts of CoVs

Advanced virological and genetic studies have shown that bats are reservoir hosts of both SARS-CoV and MERS-CoV and before these viruses spread to humans,



Review Article

# Emergence of a Zoonotic Pathogen - Novel Coronavirus (SARS-CoV-2) in the Context of Changing Environment

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## A B S T R A C T

A newly discovered strain of coronavirus is the causal agent of COVID-19 pandemic. Preliminary findings suggest that this novel coronavirus - Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) might have originated in bats, and thereafter crossed the species barrier from an intermediate host; eventually spreading within humans. Bat coronaviruses are older than the coronaviruses identified in other animals and have shown a consistent growth rate. The diverse natures of coronaviruses in different bat species have witnessed repeated introductions and occasional establishment in other animal species. The dispersion of animal diseases and zoonotic pathogens is facilitated by rapid globalization, international trading and the ever-growing flow of goods and people. Climate change coupled with globalization and extensive deforestation can act as a significant selection pressure which can lead to onsets of future coronavirus transmission cycles. Climate change alters the availability of viable habitat for the hosts as well which results in the redistribution of host ranges and host densities relative to habitat resources. An attempt has been made in this review to assess and analyze the possible causes of the emergence of a zoonotic pathogen having pandemic potential, the novel coronavirus (SARS-CoV-2) and its subsequent spill over to humans causing COVID-19.

**Keywords:** SARS-CoV-2, Reservoir Host, Man-animal Encounter, Climate Change, Deforestation, Travel and Trade

## Introduction

Most of the human infectious diseases, especially caused by the viral pathogens that are surfacing recently, originate from animals and presents a significant global health burden.<sup>1</sup> Twenty-seven cases of pneumonia were identified

in Wuhan City, within the Hubei province in China, with unknown etiology, on 31st December 2019.<sup>2</sup> The identified pathogen was subsequently named Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) and the disease is named as COVID-19.<sup>3</sup> Coronaviruses (CoVs) belong to the family Coronaviridae, subfamily Orthocoronavirinae and the

