

# An Overview On The Zoonotic Aspects of Covid-19

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## Abstract

Disruption of pristine natural habitat has a strong positive correlation with this increase in pandemics and thus, the zoonotic aspects are the most important part to uncover scientifically. On the other hand, containment and mitigation are the two basic strategies to stop a pandemic. The route of infection is of utmost importance for any pandemic and often left behind in combating the fatalities in real time. The increase in recent pandemics, from ebola outbreak to ongoing COVID-19 havoc, exerts implicit significance in the search of zoonotic transmissions of the diseases. Thus, a conceptual summary has been made through this article in understanding the basic zoonotic mechanism of the disease COVID-19

based on available published data and schematic presentation has been drawn on the route of transmission, so far discovered.

**Keywords** Coronavirus, Covid-19, Zoonotic aspects, andemic

## 1. Introduction

The pandemic caused by the novel corona virus is undoubtedly the worst in a century wide time frame owing to its magnitude of impact on public health and socio-economic conditions and thus need to be analyzed by its all possible aspects. Severe infectious disease like SARS-CoV-2 or CoVID-19 must be analyzed zoonotically as 61% of the human infecting pathogens out of 1415 reported pathogens including viruses, bacteria and others are reportedly Zoonotic [1]. Previous outbreaks of several zoonotic diseases were linked to human interaction pertaining to companionistic or economic practices or incidental exposures like at fairs or live animal markets [2]. Encroachment of anthropogenic activities in wilderness, leading to enhanced human-animal interaction, is a key factor in the increased frequency of emergence of novel zoonotic diseases [3]. On the other hand, reservoirs of infectious pathogens are to be recognized accurately as segregation and destroying the pathogen reservoir is the principle focus in combating zoonotic diseases where vaccine is lacking [4]. Detection of the human-wildlife interface of any zoonotic disease is crucial and is to be analyzed holistically to envisage and avoid future outbreaks [5]. In the late December 2019, a global stirring happened into a reality of a pandemic of the corona virus disease (Covid-19) caused by a highly

transmissible *Severe Acute Respiratory Syndrome Coronavirus 2* (SARS-CoV-2) originated from the Wuhan City of Hubei Province, People's Republic of China with an unknown etiology [6]. This virus belongs to the ortho-coronaviridae subfamily, coronaviridae family and nidovirales order. Within the subfamily ortho-coronaviridae four genera are present namely Alpha- coronavirus ( $\alpha$ -CoV), Betacoronavirus ( $\beta$ -CoV), Gammacoronavirus ( $\gamma$ -CoV) and Deltacoronavirus ( $\delta$ -CoV). Of the four genera, both  $\alpha$ - and  $\beta$ -CoV were previously known to transmit a disease to mammals, whilst  $\delta$ - and  $\gamma$ -CoVs were documented to infect birds [7]. Previously reported health casualties by viruses from this subfamily like SARS-CoV-1 and MERS-CoV belonged to  $\beta$ -CoV genus only. Presently corona virus is affecting 212 countries and territories throughout the globe and two international conveyances and WHO has declared that Covid-19 is a Public Health Emergency of International Concern (PHEIC). The significance of zoonotic aspects analysis of this disease is of utmost importance as all these diseases were thought to occur in animals only until the outbreak of SARS-CoV-1 in 2002. The future progression, variation, adaptation and multiplication of this novel virus warrant urgent zoonotic investigation.

Here, through the present study, we methodically review the pandemic of Covid-19 with all possible zoonotic aspects including its origin, epidemiology, natural or primary reservoir hosts, secondary or intermediate hosts, potential reservoirs, transmission routes in a conceptual way based on

the available information till date.

## 2. Origin

The emergence of corona viruses relies on the accumulation of new point mutations and genome recombination between different strains or species. Till date six corona viruses have infected humans to a greater extent. Amongst those, four (HCoV-229E, HCoV-OC43, HCoV-NL63, HCoV-HKU1) are endemic and cause mild respiratory illness. However another two SARS-CoV (Severe Acute Respiratory Syndrome Corona virus) and MERS-CoV (Middle East Respiratory Syndrome Corona virus) have caused severe respiratory syndromes and resulted in epidemics.

The viral replication of corona viruses rely on RNA-dependent RNA polymerase (RdRp) which accounts for a vital mutation source with a measured value of  $1 \times 10^{-6}$  mutation per replication per site [8], [9]. Recent insight in the structure of COVID-19 through homologous recombination analyses of cellular receptor seeking spike glycoprotein suggests that it was developed from a SARS-CoV (CoVZXC21 or CoVZC45) and a beta-CoV of unknown nature [10]. However, the role of another intermediate host was obvious in the cross species transmission of novel human corona virus [11].

## 3. Epidemiology

Rate of transmission of disease from one person to another is an imperative aspect of an epidemic. A sudden rise of the frequency of infected persons, with no contact history with wildlife, has a high transmissibility from person to person.

High transmissibility is positively correlated with high value of effective disease reproductive number (R). A value of R around 2.9 has made COVID-19 highly transmissible pandemic in comparison to other SARS where average R is around 1.77 [12]. The mean incubation of COVID-19 is  $4.8 \pm 2.6$  days [13]. Report suggests that the median age of most of the patients ranges in between 35-57 [14], where the majority of the patients are male (50-75%) exhibiting very fewer cases amongst the children and infants [15], [16].

Already, 38.05 million people have been affected by this COVID-19 virus till date with a mortality of 1.08 million worldwide.

#### **4. The natural reservoirs of COVID 19**

The sources of initiation and transmission of any pandemic are significant to be resolved in order to build up protective strategy to contain the infection. As, COVID-19 genome is over 80% identical to the previous human coronavirus i.e., SARS-like bat CoV [17], the initial focus pertaining to the possible natural reservoir of SARS-CoV was partially on the omnivorous, indigenous canid of East Asia, *Nyctereutes procyonoides* [18], colloquially known as racoon dogs. They belong to the family canidae under the mammalian order carnivora. Seasonal dietary variance like carnivory on mainly rodents in autumn and winter, omnivory on fruits and amphibians during spring and mainly targeting birds during summer [19] made this animal highly apprehensive for the natural reservoir of corona virus. Along with racoon dogs, palm civets, *Paradoxurus hermaphrodites*,

were also presumed to be a key reservoir host of corona viruses [11]. They are placed in the mammalian family viverridae under sub-order feliformia and order carnivora. However, these animals were found to be transient or accidental host not persisting reservoirs. Possessions of anti-SARS-CoV antibodies in *Rhinolophus affinis* bats confirmed the role of bats as persistent source or reservoir of natural infections [20]. The Middle East respiratory syndrome corona virus (MERS-CoV) infecting humans was isolated from camels as primary source and thus resulted in the hypothesis of multiple zoonotic introductions of human corona virus [21]. On the other hand, *Nycteris* and *Pipistrellus* bats were found as natural reservoirs of novel human betacoronavirus EMC/2012. Even genetic relatedness indicated EMC/2012 originated from bats [22]. The initial suggestions of snake being the key host and transmitting agent was discarded through genomic sequence analyses. Genomic similarity index of COVID-19 with SARS-like bat viruses suggested that bats could be the key reservoirs [17]. Further, pathogenic corona viruses were isolated from *Pteropus* and *Rousettus* species of bats from different Indian territories [23].

### **5. The intermediate host of COVID-19**

Bat was the most probable natural reservoir or the primary host owing to the origin of the SARS-CoV-2. But the genomic analyses suggest the involvement of different intermediate hosts in shaping the new Covid-19 virus. A metagenomic similarity index of 99% of pangolin with Covid-19 (SARS-CoV-2) suggested that pangolin might have

played a role of secondary or intermediate host [24]. A restructuring experiment of Covid-19 through the association of pangolin corona virus with Bat-CoVRaTG13 further supported this hypothesis. However, detailed phylogeny and molecular analyses revealed that Covid-19 was not directly derived from pangolin and hypothesized the involvement of other animals supporting multiple zoonotic introductions [25]. More work is needed to provide more precise information about the original reservoir and intermediate hosts of SARS-CoV-2.

## **6. The prospective hosts of COVID-19**

Previous experiments with animal models have shown that SARS-CoV-1 might infect monkeys [26], ferrets and cats [27], mice [28], pigs, chickens [29] and guinea pigs [30]. These animals were deliberately infected with SAR-CoV-1 for vaccine development and infection among them suggested their potential role as prospective hosts. However, these studies lacked the evidence of human transmissions and didn't warrant the role of these animals as amplifying hosts. Most of these animal models are under the same trial for vaccine development and may act as prospective reservoirs of COVID-19 (SARS-CoV-2) also in its future propagation and thus need more zoonotic analyses in future.

## **7. Mode of transmissions**

The novel coronavirus, isolated from the affected patients in China, was thought to have originated from the seafood market of Wuhan. It posed the threat of zoonotic

transmission. Due to enormous similarity with the SARS-CoV-2 with bat CoV-RaTG13 it was supposed that bat was the primary host and pangolin was the intermediate host (figure 1). However, It easily moved across species [24] and before infecting humans it got further modifications in other intermediate hosts which are still unknown. Humans acted as the amplifier host and human to human secondary transmission was the most fatal way of transmission. However, there was no doubt that the secondary transmissions of Covid-19 occurred through community spreading [10], [15].

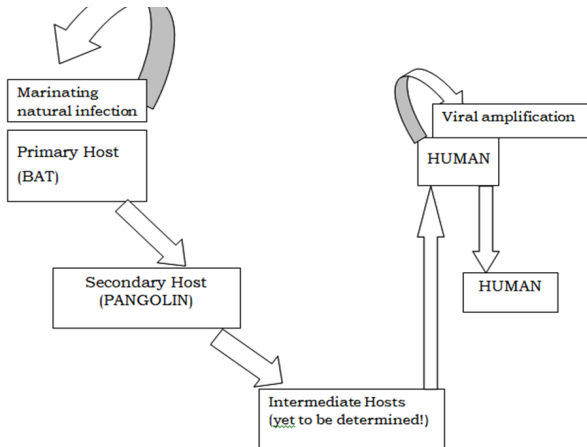


Fig 1: A conceptual diagram on the probable zoonotic transmission path of COVID-19. Where, the bat acted as the natural reservoir. Involvement of pangolin as secondary host



was quite obvious. However another zoonotic involvement occurs which is yet to be determined and then the infection goes to humans.

## **8. Conclusions**

Zoonoses of viruses encompass various modes in transmission. In direct zoonosis, transmission occurs from animals to man through bites or saliva or through the involvement of infected media. Such mode of transmission is quite common. However, the involvement of intermediate hosts as amplifier is also common in direct zoonosis. No significant sign or symptoms are generally seen by these intermediate hosts that further make the path of transmission tough to unwind. Reverse zoonosis or anthroponosis is another way of transmission when human viruses infect other animals. However at any point of contact between human and animals there is a possible zoonotic transmission way. A significant amount of recent pandemic diseases including ebola, nipah are zoonotic. Even, AIDS is also regarded as zoonotic disease which transmitted to humans in early 20<sup>th</sup> century and now mutated to human only form. Many species of swine and bird flu are the result of zoonoses. As the host pathogen interaction is dynamic equilibrium by evolutionary perspectives, more time is necessary to understand the pathogenicity of COVID-19. It is undoubtedly a zoonotic disease as per the published data is concerned. The future of this disease depends on a detail study on the zoonotic aspects to check its fatality and resist the other pandemics to immerge.

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